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Stability and backward bifurcation in a malaria-transmission model with sterile mosquitoes

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Abstract

In this paper, we establish and study a malaria-transmission dynamic model of releasing sterile mosquitoes, which focuses on the mosquito populations affected by the impact of limited resources. First, we formulate a dynamic model with mosquitoes where the releasing rate of sterile mosquitoes is constant, and analyze the existence and stability of the equilibrium. Using the stability theory and method of differential equations, the threshold value of releasing sterile mosquitoes is obtained. Furthermore, we establish a malaria-transmission dynamic model with sterile release, and derive a formula for the reproductive number of infection and investigate the existence of endemic equilibria. With the symmetry of mathematical expression, it is also shown that this model may undergo backward bifurcation, where the locally stable disease-free equilibrium coexists with an endemic equilibrium. Finally, numerical simulations to illustrate our findings and brief discussions are provided.

Keywords: Stability; Backward bifurcation; Basic reproductive number; Malaria transmission; Limited resource

1 Introduction

Malaria is an acute infectious disease caused by plasmodium through the bite of an infected female Anopheles mosquito. It is the fifth leading cause of death from infectious diseases worldwide and the second leading cause of death from infectious diseases after HIV/AIDS [1, 2]. According to the World Health Organization, there were 241 million cases of malaria in 2020, while 627 000 people died from it [3]. With the characteristics of rapid transmission, high morbidity, and high mortality, it has been widely publicized, but no vaccines are yet available.

In order to understand the dynamics of malaria transmissions, many scholars have done much research in this field. As a simple research tool, mathematical modeling can help us to perceive the population or disease invasion and provide reliable theoretical support for relevant researchers. In [4], Ross first used the differential equation to explain the mechanism of malaria transmission between humans and mosquitoes. It was suggested that the spread of the disease can be controlled only by reducing the number of local Anopheles

mosquitoes to a certain number, rather than eliminating them. Then, MacDonald further improved the model, defined the basic reproductive number, and analyzed the influence of parameters on malaria transmission [5]. However, their model is only a brief description of the transmission of malaria, and some biological factors affecting the transmission of malaria were not considered.

An effective way to prevent malaria is to control wild mosquitoes. Biological controls of mosquitoes have been proven to be biologically and economically more effective. Among those control measures, the sterile-insect technique (SIT) has been investigated in detail to reduce or eradicate wild mosquitoes. SIT is used to control the birth rate of wild mosquitoes, it is a biological control method that disrupts the production of offspring by mosquitoes [6–11]. Using rational chemical or physical methods, male mosquitoes become sterile by genetic modification. They can mate successfully with females but the females cannot produce offspring. Therefore, releasing sterile mosquitoes into the wild can successfully invade the wild populations under certain conditions, reducing the number of mosquitoes and controlling malaria spread, which has also been demonstrated in experiments [12–17]. After the precursor work, a number of scholars [18–23] made remarkable contributions to the study of malaria modeling with sterile mosquitoes. Of course, we also point out that many other models have been made to describe the dynamic behaviors of the transmission of mosquito-borne disease so that one can understand them and analyze control strategies [24–28].

Recently, we proposed a malaria-transmission model that emphasizes the impact of limited resources [29], which is as follows:

$$\begin{cases} \frac{dS_h}{dt} = \Lambda_h - r\beta_v \frac{I_v}{N_h} S_h + \theta_h R_h - \mu_h S_h, \\ \frac{dI_h}{dt} = r\beta_v \frac{I_v}{N_h} S_h - (\mu_h + \delta_h + \eta_h) I_h, \\ \frac{dR_h}{dt} = \eta_h I_h - (\theta_h + \mu_h) R_h, \\ \frac{dI_v}{dt} = r\beta_h \frac{I_h}{N_h} (N_v - I_v) - \mu_v I_v, \\ \frac{dN_v}{dt} = \frac{a_v N_v}{1+N_v} - \mu_v N_v, \end{cases}$$

where $S_h(t)$ represents the number of susceptible humans, $I_h(t)$ is the number of infective humans who are infected, $R_h(t)$ is the number of humans who have recovered from infection but have partly lost their immunity, respectively, $N_h(t) = S_h(t) + I_h(t) + R_h(t)$ is the total number of humans at time t. To account for the transmission dynamics between humans and mosquitoes, we divide the mosquito population into groups of susceptible, and infective individuals, denoted by $S_v(t)$, and $I_v(t)$, similarly, $N_v(t) = S_v(t) + I_v(t)$ is the total number of mosquitoes at time t. Λ_h is the input flow of the susceptible humans including birth, μ_h and μ_v are the natural death rates of humans and mosquitoes, respectively, δ_h is the disease-induced death rate for humans, θ_h is the rate of immunity loss for humans, η_h is the recovery rate of humans, and λ_h and λ_v are the infection rates for humans and mosquitoes, respectively, r is the average number of bites that a single mosquito makes on all human hosts, β_h is the transmission probability per bite to a susceptible mosquito, and β_v is the transmission probability per bite to a susceptible human.

In the above work, we derived a formula for the reproductive number of infections and investigated the existence of endemic equilibria. It was shown that the model may undergo backward bifurcation. In other words, even small fluctuations of parameters can

bring about a completely different result, especially as the basic reproduction number is near the subthreshold value. In addition, Bakare et al. [30] analyzed the potential impact of multiple current interventions in communities with limited resources in order to obtain optimal control strategies and provided a basis for future predictions of the most effective control measures against the spread of malaria. In this paper, we developed a deterministic mathematical model with sterile mosquitoes that captures the dynamics of malaria epidemics in human–mosquito populations using a system of ordinary differential equations. It should be noted that only the adult female mosquitoes bite humans and animals in order to take blood meals, and the male mosquitoes feed only on plant juices [31, 32]. Female mosquitoes, which are involved in the transmission of vector-borne diseases will not lay viable eggs without blood meals. Therefore, this model ignores male mosquitoes.

The remainder of this paper is organized as follows. In Sect. 2, we consider a two-dimensional dynamic model that contains only sterile mosquitoes and wild mosquitoes with limited resources, and the existence and stability of the equilibrium are analyzed. We first give general modeling descriptions, then we verify that the model is well-defined mathematically as well as biologically. Through qualitative analysis, the threshold of releasing sterile mosquitoes is obtained. Furthermore, we formulate a malaria model in the human–mosquito populations affected by limited resource, and analyze the dynamical properties of the model, including the basic reproductive number, the existence of the disease-free equilibrium and endemic equilibrium, local stability of the disease-free equilibrium, as well as backward bifurcation in Sect. 3. In Sect. 4, some numerical simulations are presented to interpret the behavior of the model. A short conclusion is given in Sect. 5.

2 The model formulation

We follow the line in [31, 32] to formulate our model. With the impact of limited resources on mosquito populations, we let $\omega(t)$ and $g(t)$ be the number of wild mosquito and sterile mosquito populations at time t, and consider the following system:

$$\begin{cases} \dfrac{d\omega}{dt} = \dfrac{a_v\omega}{1+\omega}\cdot\dfrac{\omega}{\omega+g} - \mu_v\omega, \\ \dfrac{dg}{dt} = B(\cdot) - \mu_g g. \end{cases} \tag{2.1}$$

For wild-mosquito populations, we adopt a saturated birth-rate function $a_v\omega/(1+\omega)$, where a_v is the maximum value of the recruitment rate of viable mosquito eggs (we always assume that $a_v > \mu_v$), μ_v and μ_g are the natural death rates of wild and sterile mosquitoes. We assume that the number of releasing sterile mosquitoes per unit time is constant. That is to say, $B(\cdot) = b$. Then, the differential equations that describe the dynamics of the wild and sterile mosquito populations are formulated as shown below:

$$\begin{cases} \dfrac{d\omega}{dt} = \dfrac{a_v\omega}{1+\omega}\cdot\dfrac{\omega}{\omega+g} - \mu_v\omega, \\ \dfrac{dg}{dt} = b - \mu_g g. \end{cases} \tag{2.2}$$

By simple calculation of equation (2.2), it can be obtained that

$$\lim_{t\to\infty}\omega(t) = \frac{r_0}{\mu_v}, \qquad \lim_{t\to\infty} g(t) = \frac{b}{\mu_g}.$$

Let

$$\Omega := \{(\omega, g) : 0 \le \omega \le \frac{r_0}{\mu_v},\ 0 \le g \le \frac{b}{\mu_g}\},$$

where $r_0 = a_v - \mu_v > 0$, thus Ω is positively invariant for solutions of system (2.2).

2.1 Existence of equilibrium

In this section, for system (2.2), it is easy to see that there is only one boundary equilibrium $E_0 = (0, g_0)$, where $g_0 = \frac{b}{\mu_g}$. Then, we solve the equilibrium by setting the right-hand sides of (2.2) to zero and the system takes the form:

$$\begin{cases} \dfrac{a_v\omega}{1+\omega} \cdot \dfrac{\omega}{\omega + g} - \mu_v\omega = 0, \\ b - \mu_g g = 0. \end{cases} \tag{2.3}$$

Through direct calculations, with $g = \frac{b}{\mu_g}$, we have:

$$\mu_v\mu_g\omega^2 + (\mu_v b + \mu_v\mu_g - \mu_g a_v)\omega + \mu_v b = 0. \tag{2.4}$$

If $c = (a_v - \mu_v)\mu_g - \mu_v b$, then equation (2.4) has two solutions:

$$\omega^{\pm} = \frac{c \pm \sqrt{c^2 - 4\mu_v^2\mu_g b}}{2\mu_v\mu_g}. \tag{2.5}$$

We define

$$b_0 = \frac{(a_v - \mu_v)\mu_g}{\mu_v}.$$

Thus, we conclude that for the existence of a solution for equation (2.4):

(1) If $c < 0$, $b > b_0$, system (2.4) has no positive solution.
(2) If $c = 0$, $b = b_0$, system (2.4) has no solution.
(3) If $c > 0$, $b < b_0$, the properties of the solution for system (2.4) depend on its discriminant. If $\triangle < 0$, system (2.4) has no solution. If $\triangle = 0$, system (2.4) has a unique positive solution. If $\triangle > 0$, system (2.4) has two positive solutions.

It follows from equation (2.4) that we know its discriminant:

$$\begin{aligned} \triangle &= (a_v - \mu_v)^2\mu_g^2 + \mu_v^2 b^2 - 2\mu_v b\mu_g(a_v - \mu_v) - 4b\mu_v^2\mu_g \\ &= (a_v - \mu_v)^2\mu_g^2 + \mu_v^2 b^2 - 2\mu_v b\mu_g(a_v + \mu_v) \\ &= \mu_v^2 b^2 - 2\mu_v\mu_g(a_v + \mu_v)b + (a_v - \mu_v)^2\mu_g^2. \end{aligned}$$

Let the right-hand side of the above formula be $f(b)$. Obviously, f is a quadratic function of b. We also note that the discriminant of $f(b) = 0$ is greater than 0:

$$\triangle_1 = 4\mu_v^2\mu_g^2(a_v + \mu_v)^2 - 4\mu_v^2\mu_g^2(a_v - \mu_v)^2 > 0,$$

thus, equation $f(b) = 0$ has two positive solutions

$$b^{\pm} = \frac{\mu_g(a_v + \mu_v) \pm 2\mu_g\sqrt{a_v\mu_v}}{\mu_v}. \tag{2.6}$$

Through image analysis, we obtain, if $b^- < b < b^+, f(b) < 0$, system (2.4) has no solution. If $b \le b^-$ or $b \ge b^+, f(b) \ge 0$, system (2.4) has a solution. Since

$$\begin{aligned}\mu_v(b_0 - b^-) &= \mu_g(a_v - \mu_v) - \mu_g(a_v + \mu_v) + 2\mu_g\sqrt{a_v\mu_v} \\ &= 2\mu_g(\sqrt{a_v\mu_v} - \mu_v) > 0\end{aligned}$$

and

$$b^+ = \frac{\mu_g(a_v + \mu_v) + 2\mu_g\sqrt{a_v\mu_v}}{\mu_v} > \frac{\mu_g(a_v - \mu_v)}{\mu_v} = b_0,$$

we have $b^- < b_0 < b^+$. Respectively, if $b \ge b^+$, system (2.4) has no positive solution. If $b = b^-$, system (2.4) has a unique positive solution. If $b < b^-$, system (2.4) has two positive solutions.

As an immediate consequence of the above result, we present the main results on the equilibria of system (2.2):

Theorem 2.1

(i) *If $b > b^-$, system (2.2) has no positive equilibrium, and only has one boundary equilibrium $E_0(0, g_0)$;*

(ii) *If $b = b^-$, system (2.2) has a unique equilibrium $E_1(\frac{c}{2\mu_v\mu_g}, g_0)$ and boundary equilibrium $E_0(0, g_0)$;*

(iii) *If $b < b^-$, system (2.2) has two positive equilibrium $E_2(\omega^-, g_0)$, $E_3(\omega^+, g_0)$ and one boundary equilibrium $E_0(0, g_0)$, where $\omega^{\pm}$ is given by (2.5).*

2.2 Stability of equilibrium

In this section, we investigate the stability of boundary equilibrium E_0, positive equilibrium E_1, E_2, and E_3 of system (2.2).

To calculate the stability of boundary equilibrium $E_0(0, g_0)$, we need to linearize system (2.2) about steady-state E_0 and evaluate the resulting Jacobian matrix:

$$J_1 = \begin{pmatrix} -\mu_v & 0 \\ 0 & -\mu_g \end{pmatrix},$$

It is clear that the eigenvalues of J_1 are all negative. When $b > b^-$, the system has a unique boundary equilibrium E_0, and hence E_0 is global asymptotically stable. When $b \le b^-$, E_0 is locally asymptotically stable.

We now turn our attention to positive equilibrium. To calculate the stability, the linearization of (2.2) about a positive equilibrium point yields the Jacobian matrix:

$$J_2 = \begin{pmatrix} \frac{a_v\omega(g-\omega^2)}{(1+\omega)^2(\omega+g)^2} & -\frac{a_v\omega^2}{(1+\omega)(\omega+g)^2} \\ 0 & -\mu_g \end{pmatrix}.$$

Let $h(\omega,g)=\frac{a_v\omega(g-\omega^2)}{(1+\omega)^2(\omega+g)^2}$. At $E_1(\frac{c}{2\mu_v\mu_g},g_0)$, we obtain

$$a_v\omega(g-\omega^2)=\frac{a_vc}{2\mu_v\mu_g}\cdot\frac{4b\mu_v^2\mu_g-c^2}{4\mu_v^2\mu_g^2}=0.$$

Hence, $h(\omega,g)=0$. Furthermore, $detJ_2=0$, then E_1 is an unstable equilibrium.

At $E_2(\omega^-,g_0)$,

$$h(\omega^-,g_0)=\frac{a_v\omega(b-\mu_g\omega^2)}{\mu_g(1+\omega)^2(\omega+g)^2}.$$

Since

$$\begin{aligned}2\mu_v\mu_g(b\mu_v-\mu_g\mu_v\omega^2)&=2\mu_v\mu_g(2b\mu_v-c\omega^-)\\&=2\mu_v\mu_g(2b\mu_v-c\cdot\frac{c-\sqrt{c^2-4\mu_v^2\mu_gb}}{2\mu_v\mu_g})\\&=4b\mu_v^2\mu_g-c(c-\sqrt{c^2-4\mu_v^2\mu_gb})\\&=-\sqrt{c^2-4\mu_v^2\mu_g}b(\sqrt{c^2-4\mu_v^2\mu_gb}-c)>0,\end{aligned}$$

we have $h(\omega^-,g_0)>0$, which yields $detJ_2<0$, then E_2 is an unstable saddle point.

Similarly, at $E_3(\omega^+,g_0)$, we have $h(\omega^+,g_0)<0$, which yields $detJ_2>0$, then E_3 is a stable node point.

Consequently, we can use the stability information about the steady states to understand the asymptotic dynamics of our model and obtain the following results.

Theorem 2.2

(i) *If $b>b^-$, system (2.2) has no positive equilibrium, it only has a unique boundary equilibrium $E_0(0,g_0)$, which is globally asymptotically stable;*

(ii) *If $b=b^-$, system (2.2) has a unique positive equilibrium $E_1(\frac{c}{2\mu_v\mu_g},g_0)$, which is unstable, and boundary equilibrium $E_0(0,g_0)$, which is locally asymptotically stable;*

(iii) *If $b<b^-$, system (2.2) has a unstable saddle point $E_2(\omega^-,g_0)$, node point $E_3(\omega^+,g_0)$, which is locally asymptotically stable, and boundary equilibrium $E_0(0,g_0)$, which is locally asymptotically stable. Here, it is worth noting that the system approaches E_0 or E_3 depending on the initial value of the system.*

3 A malaria model with sterile release

3.1 The basic reproductive number

We follow the line in [22, 23, 29] to formulate our malaria model. To keep the model tractable in mathematical analysis, for the human population, we divide it into groups of susceptible, infective, and recovered individuals. We let $S_h(t)$ be the number of susceptible humans, $I_h(t)$ be the number of infective humans who are infected, and $R_h(t)$ be the number of humans who hare recovered from infection but have partly lost their immunity. Moreover, let $N_h(t)=S_h(t)+I_h(t)+R_h(t)$ be the total number of humans at time t. Note that if there is no infection, the human population has an asymptotically stable steady-state $\lim_{t\to\infty}S_h=\Lambda_h/\mu_h:=S_h^0$. Then, the differential equations that describe the dynamics of

Table 1 Definitions in the system

Symbols	Definitions
Λ_h	the input flow of the susceptible humans including birth
λ_h	the infection rate for humans
θ_h	the rate of immunity loss for humans
μ_h	the natural death rate of humans
δ_h	the disease-induced death rate for humans
η_h	the recovery rate of humans
λ_v	the infection rates for mosquitoes
μ_v	the natural death rate of wild mosquitoes
μ_g	the natural death rate of sterile mosquitoes

human are formulated as shown below:

$$\begin{cases} \dfrac{dS_h}{dt} = \Lambda_h - \lambda_h S_h + \theta_h R_h - \mu_h S_h, \\ \dfrac{dI_h}{dt} = \lambda_h S_h - (\mu_h + \delta_h + \eta_h) I_h, \\ \dfrac{dR_h}{dt} = \eta_h I_h - (\theta_h + \mu_h) R_h, \end{cases} \tag{3.1}$$

where the definitions $\Lambda_h, \lambda_h, \theta_h, \mu_h, \delta_h, \eta_h$ in the system are given in Table 1.

To account for the transmission dynamics between humans and mosquitoes, we divide the mosquito population into groups of susceptible and infective individuals, denoted by $S_v(t)$ and $I_v(t)$, respectively. The vector component of the model does not include an immune class as mosquitoes never recover from infection, that is, their infective period ends with their death due to their relatively short life-cycle. Thus, the immune class in the mosquito population is negligible and death occurs equally in all groups. Our model also excludes the immature mosquitoes since they do not participate in the infection cycle and thus in the waiting period, they limit the vector population growth. Consider the impact of limited resources on population reproduction. Similarly, let $N_v(t) = S_v(t) + I_v(t)$ be the total number of mosquitoes at time t, g be the sterile mosquito, and b be the release of sterile mosquitoes. Then, the differential equations that describe the dynamics of mosquito populations are formulated as shown below:

$$\begin{cases} \dfrac{dS_v}{dt} = \dfrac{a_v N_v}{N_v + g} \cdot \dfrac{N_v}{1 + N_v} - \lambda_v S_v - \mu_v S_v, \\ \dfrac{dI_v}{dt} = \lambda_v S_v - \mu_v I_v, \\ \dfrac{dg}{dt} = b - \mu_g g, \end{cases} \tag{3.2}$$

where the variables λ_v, μ_v, μ_g in the system are given in Table 1.

Note that the total population size of wild mosquitoes satisfies the following equation:

$$\frac{dN_v}{dt} = \frac{a_v N_v}{N_v + g} \cdot \frac{N_v}{1 + N_v} - \mu_v N_v.$$

Instead of system (3.1) and (3.2), we hereafter consider the following system:

$$\begin{cases} \dfrac{dS_h}{dt} = \Lambda_h - \lambda_h S_h + \theta_h R_h - \mu_h S_h, \\ \dfrac{dI_h}{dt} = \lambda_h S_h - (\mu_h + \delta_h + \eta_h) I_h, \\ \dfrac{dR_h}{dt} = \eta_h I_h - (\theta_h + \mu_h) R_h, \\ \frac{dN_v}{dt} = \frac{a_v N_v}{N_v + g} \cdot \frac{N_v}{1+N_v} - \mu_v N_v, \\ \dfrac{dI_v}{dt} = \lambda_v (N_v - I_v) - \mu_v I_v, \\ \dfrac{dg}{dt} = b - \mu_g g. \end{cases} \tag{3.3}$$

Observe that system (3.3) is a smooth system in the open set Γ of $\mathbb{R}^6_+$, given by

$$\Gamma := \{(S_h, I_h, R_h, N_v, I_v, g) \in \mathbb{R}^6 : N_h > 0\}.$$

It is easy to see that if $\phi(t)$ is a solution of system (3.3) with $\phi(0) \in \Gamma$, then it is defined for t in a maximal interval $[0, T^+)$ with $0 < T^+ < +\infty$, such that $\phi(t) \in \Gamma$ for all $t \in [0, T^+)$. We are only interested in the solutions of system (3.3) in the following subset $\mathcal{D}$ of Γ:

$$\mathcal{D} := \mathbb{R}^6_+ \backslash (\{N_h = 0\} \cup \{N_v = 0\}).$$

Furthermore, we conclude that $\mathcal{D}$ is the manifold on which both vectors and hosts have nonzero population sizes.

Define the set

$$\Omega := \{(N_h, N_v, g) : 0 \le N_h \le N_h^0, 0 \le N_v \le N_v^0, 0 \le g \le g_0\},$$

where $N_h^0 := \Lambda_h/\mu_h$, $N_v^0 = r_0/\mu_v$, $r_0 = a_v - \mu_v > 0$, $g_0 = b/\mu_g$ and let

$$\mathcal{D}_0 = \{I_h = R_h = I_v = 0\} \cap \mathcal{D}.$$

Then, $\mathcal{D}_0$ is a subset of $\mathcal{D}$, and every solution $\phi(t)$ of system (3.3) with $\phi(0) \in \mathcal{D} \backslash \mathcal{D}_0$ is defined and bounded for t in $[0, \infty)$, $\phi(t) \in int(\mathbb{R}^6_+)$, and its ω-limit set lies in the compact set Ω, which is positively invariant for solutions of system (3.3).

In the absence of infection, the model has a steady state, which is called the disease-free equilibrium. To establish the stability of this equilibrium, the Jacobian of system (3.3) is computed and evaluated at the disease-free equilibrium. The local stability of the disease-free equilibrium is then determined based on the signs of the eigenvalues of this Jacobian. The equilibrium is locally stable if the real parts of all these eigenvalues are negative. Furthermore, we derive a formula for the basic reproductive number by investigating the local stability of the disease-free equilibrium.

For system (3.3), there exists a disease-free equilibrium point $(S_h, I_h, R_h, I_v, N_v, g) = (S_h^0, 0, 0, 0, N_v^0, g_0)$, where $S_h^0 = \Lambda_h/\mu_h$, $g_0 = b/\mu_g$. Note that N_v^0 corresponds exactly to the positive equilibrium ω of system (2.2). That is, the disease-free equilibrium G_0, G_1, G_2, G_3 of system (3.3) corresponds to E_0, E_1, E_2, E_3 of system (2.2).

We shall use the techniques in [33, 34] to find the basic reproductive number $\Re_0$. From [29], we know that

$$\lambda_v = r\beta_h \frac{I_h}{N_h}, \qquad \lambda_h = r\beta_v \frac{I_v}{N_h},$$

where r is the average number of bites that a single mosquito makes on all human hosts, β_h is the transmission probability per bite to a susceptible mosquito, β_v is the transmission probability per bite to a susceptible human.

Note that the Jacobian matrix at disease-free equilibrium $(S_h^0, 0, 0, 0, N_v^0, g_0)$ has the form:

$$J = \begin{pmatrix} J_{31} & 0 & 0 \\ 0 & J_{32} & 0 \\ 0 & 0 & J_{33} \end{pmatrix}.$$

Here,

$$J_{31} = \begin{pmatrix} -\mu_h & \theta_h \\ 0 & -(\theta_h + \mu_h) \end{pmatrix},$$

$$J_{32} = \begin{pmatrix} -(\mu_h + \delta_h + \eta_h) & r\beta_v \\ r\beta_h \frac{N_v^0}{S_h^0} & -\mu_v \end{pmatrix},$$

$$J_{33} = \begin{pmatrix} \frac{a_v N_v (N_v g + N_v + 2g)}{(N_v+g)^2(1+N_v)^2} - \mu_v & -\frac{a_v N_v^2}{(N_v+g)^2(1+N_v)} \\ 0 & -\mu_g \end{pmatrix}.$$

At disease-free equilibrium G_0, where $N_v^0 = 0$, we have:

$$J_{32} = \begin{pmatrix} -(\mu_h + \delta_h + \eta_h) & r\beta_v \\ 0 & -\mu_v \end{pmatrix}, \quad J_{33} = \begin{pmatrix} -\mu_v & 0 \\ 0 & -\mu_g \end{pmatrix}.$$

Obviously, all the characteristic roots of J_{31}, J_{32}, J_{33} have negative real parts, then disease-free equilibrium G_0 is locally asymptotically stable. Since E_1 of system (2.2) is unstable, the disease-free equilibrium G_1 of system (3.3) is also unstable. At G_2, $detJ_{33} < 0$, and its characteristic root has a negative real part, then disease-free equilibrium G_2 is also unstable. At G_3, the characteristic roots of J_{31} and J_{33} have negative real parts. If the characteristic root of J_{32} also has a negative real part, then disease-free equilibrium G_3 is locally asymptotically stable. It is easily seen that:

$$|J_{32}| = \sigma_{1h}\mu_v - r^2\beta_v\beta_h \frac{N_v^0}{S_h^0} = \sigma_{1h}\mu_v\left(1 - \frac{r^2\beta_v\beta_h\mu_h\omega^+}{\sigma_{1h}\mu_v\Lambda_h}\right),$$

where $\sigma_{1h} = \mu_h + \delta_h + \eta_h$.

We define

$$\Re_0 = \sqrt{\frac{r^2\beta_v\beta_h\mu_h\omega^+}{(\mu_h + \delta_h + \eta_h)\mu_v\Lambda_h}}. \tag{3.4}$$

Furthermore, if $\Re_0 = 1$, we have

$$\frac{r^2\beta_v\beta_h\mu_h\omega^+}{\sigma_{1h}\mu_v\Lambda_h} = 1,$$

where,

$$\omega^+ = \frac{c + \sqrt{c^2 - 4\mu_v^2\mu_g b}}{2\mu_v\mu_g}$$

and

$$c = (a_v - \mu_v)\mu_g - \mu_v b.$$

Hence, $\Re_0^2$ can be represented as a function of b, and let $\Re_0^2 = l(b)$. Through a simple calculation, we know that there exists a unique positive root b_1 to equation $l(b) = 1$:

$$b_1 = \frac{\mu_g\sigma_{1h}\Lambda_h(a_v - \mu_v)r^2\beta_v\beta_h\mu_h - \mu_v^2\mu_g\sigma_{1h}^2\Lambda_h^2}{r^2\beta_v\beta_h\mu_h(r^2\beta_v\beta_h\mu_h + \mu_v\sigma_{1h}\Lambda_h)}. \tag{3.5}$$

If $b < b_1$, then $\Re_0 > 1$. If $b = b_1$, then $\Re_0 = 1$. If $b > b_1$, then $\Re_0 < 1$. Thus, the disease-free equilibrium G_3 of system (3.3) is locally asymptotically stable if $b > b_1$. Hence, the positive equilibrium E_3 of system (2.2) is locally asymptotically stable. However, as we obtained in the previous section, if $b > b^-$, there is no positive equilibrium of system (2.2), and hence $b_1 < b^-$.

Theorem 3.1

(i) *If $b > b^-$, system (3.3) has no endemic equilibrium, it only has a disease-free equilibrium G_0 that is locally asymptotically stable*;

(ii) *If $b = b^-$, system (3.3) has a unique unstable disease-free equilibrium G_1, and disease-free equilibrium G_0, which is locally asymptotically stable*;

(iii) *If $b_1 < b < b^-$, then $\Re_0 < 1$, and system (3.3) has an unstable disease-free equilibrium G_2, and two disease-free equilibrium G_0 and G_3, which are locally asymptotically stable. Solutions approach either the unstable or the stable disease-free equilibrium, depending on its initial values.*

(iv) *If $b < b_1 < b^-$, then $\Re_0 > 1$, and system (3.3) has a disease-free equilibrium G_0, which is locally asymptotically stable, and two disease-free equilibrium G_2 and G_3 that are unstable.*

3.2 Existence of endemic equilibrium and backward bifurcation

In this section, we investigate the existence of endemic equilibria of (3.1) and (3.2).

For system (3.1) and (3.2), if there exists endemic equilibria:

$$E^* = (S_h^*, I_h^*, R_h^*, I_v^*, N_v^*, g^*),$$

then E^* should satisfy equations (3.1) and (3.2), its coordinates should satisfy the conditions $S_h^* > 0$, $I_h^* > 0$, $R_h^* > 0$, $I_v^* > 0$, $N_v^* > 0$, and $g^* = b/\mu_g$. Assume the parameters are nonnegative and E^* is an endemic equilibrium of system (3.1) and (3.2), then we solve for

the equilibrium by setting the right-hand sides of (3.1)and (3.2) to zero and the system takes the form:

$$\begin{cases} \Lambda_h - \lambda_h^* S_h^* + \theta_h R_h^* - \mu_h S_h^* = 0, \\ \lambda_h^* S_h^* - (\mu_h + \delta_h + \eta_h) I_h^* = 0, \\ \eta_h I_h^* - (\theta_h + \mu_h) R_h^* = 0, \\ \dfrac{a_v N_v^*}{1 + N_v^*} \dfrac{N_v^*}{N_v^* + g^*} - \mu_v S_v^* - \lambda_v S_v^* = 0, \\ \lambda_v^* S_v^* - \mu_v I_v^* = 0, \\ b - \mu_g g^* = 0, \end{cases}$$

where

$$\lambda_h^* = \frac{r\beta_v I_v^*}{N_h^*}, \quad \lambda_v^* = \frac{r\beta_h I_h^*}{N_h^*} \tag{3.6}$$

and $N_h^* = S_h^* + I_h^* + R_h^*$. A straightforward computation shows that

$$S_h^* = \frac{\sigma_{1h}\sigma_{2h}\Lambda_h}{\sigma_{1h}\sigma_{2h}(\mu_h + \lambda_h^*) - \theta_h\eta_h\lambda_h^*} = \frac{\Lambda_h}{\mu_h + K_1\lambda_h^*}, \tag{3.7}$$

where, $K_1 = 1 - \frac{\theta_h\eta_h}{\sigma_{1h}\sigma_{2h}}$, $\sigma_{2h} = \mu_h + \theta_h$,

$$I_h^* = \frac{S_h^*}{\sigma_{1h}}\lambda_h^* = \frac{\Lambda_h\lambda_h^*}{\sigma_{1h}(\mu_h + K_1\lambda_h^*)}, \tag{3.8}$$

$$R_h^* = \frac{\eta_h S_h^*}{\sigma_{1h}\sigma_{2h}}\lambda_h^* = \frac{\eta_h\Lambda_h\lambda_h^*}{\sigma_{1h}\sigma_{2h}(\mu_h + K_1\lambda_h^*)}. \tag{3.9}$$

By equations (3.7), (3.8), and (3.9), we have

$$N_h^* = S_h^* + I_h^* + R_h^* = (1 + K_2\lambda_h^*)\frac{\Lambda_h}{\mu_h + K_1\lambda_h^*}, \tag{3.10}$$

where, $K_2 = \frac{\sigma_{2h}+\eta_h}{\sigma_{1h}\sigma_{2h}}$.

Substituting I_h^* of equation (3.8) and N_h^* of equation (3.10) into λ_v^* of equation (3.6) yields:

$$\lambda_v^* = \frac{r\beta_h\lambda_h^*}{\sigma_{1h}(1 + K_2\lambda_h^*)}. \tag{3.11}$$

It follows from the second equation of (3.2) that:

$$I_v^* = \frac{\lambda_v^*}{\mu_v}S_v^*, \tag{3.12}$$

then

$$N_v^* = S_v^* + I_v^* = \frac{\lambda_v^* + \mu_v}{\mu_v}S_v^*, \tag{3.13}$$

Define $t = \frac{\lambda_v^* + \mu_v}{\mu_v}$, then $N_v^* = tS_v^*$. Substituting the first equation of system (3.2), and $g^* = b/\mu_g$, we have

$$(\lambda_v^* + \mu_v)t^2(S_v^*)^2 + [(\lambda_v^* + \mu_v)(1 + g^*)t - a_v t^2]S_v^* + (\lambda_v^* + \mu_v)g^* = 0. \tag{3.14}$$

Let $t_1 = a_v t^2 - (\lambda_v^* + \mu_v)(1 + g^*)t$. Since $a_v - \mu_v > g^*\mu_v$, then

$$\begin{aligned} t_1/t &= a_v t - (\lambda_v^* + \mu_v)(1 + g^*) \\ &= a_v \frac{\lambda_v^* + \mu_v}{\mu_v} - (\lambda_v^* + \mu_v)(1 + g^*) \\ &= (\lambda_v^* + \mu_v)\frac{a_v - \mu_v}{\mu_v} - g^*(\lambda_v^* + \mu_v) \\ &= (\lambda_v^* + \mu_v)\frac{a_v - \mu_v - g^*\mu_v}{\mu_v} > 0. \end{aligned}$$

Thus, $t_1 > 0$, moreover, $t_1^2 - 4(\lambda_v^* + \mu_v)^2 t^2 g^* > 0$. Hence, equation (3.14) has positive solutions in the range of real numbers. Consequently, S_v^* can be represented by λ_v^*.

Hence, substituting I_v^* in (3.12) and N_h^* in (3.10) into λ_h^* of (3.6) simplifies to the following:

$$\lambda_h^* = \frac{r\beta_v\mu_h(1 + K_3\lambda_h^*)}{\mu_v\Lambda_h(1 + K_2\lambda_h^*)}\lambda_v^* S_v^*, \tag{3.15}$$

where, $K_3 = K_1/\mu_h$.

Then, substituting λ_v^* in (3.11) into λ_h^* in (3.15), it is easily seen that λ_h^* satisfies

$$\lambda_h^* = \frac{r^2\beta_v\beta_h\mu_h(1 + K_3\lambda_h^*)\lambda_h^*}{\mu_v\Lambda_h(1 + K_2\lambda_h^*)^2\sigma_{1h}}S_v^*, \tag{3.16}$$

which is equivalent to

$$1 = \frac{r^2\beta_v\beta_h\mu_h(1 + K_3\lambda_h^*)}{\mu_v\Lambda_h(1 + K_2\lambda_h^*)^2\sigma_{1h}}S_v^*. \tag{3.17}$$

Since

$$N_v^* = \frac{\lambda_v^* + \mu_v}{\mu_v}S_v^*,$$

then equation (3.17) is equivalent to

$$1 = \frac{r^2\beta_v\beta_h\mu_h(1 + K_3\lambda_h^*)N_v^*}{\sigma_{1h}\mu_v\Lambda_h(1 + K_2\lambda_h^*)[\mu_v + (M_1 + \mu_v K_2)\lambda_h^*]},$$

where $M_1 = \frac{r\beta_h}{\sigma_{1h}}$. From the previous section, the reproductive number

$$\Re_0 = \sqrt{\frac{r^2\beta_v\beta_h\mu_h\omega^+}{\sigma_{1h}\mu_v\Lambda_h}}.$$

Hence,

$$1 = \Re_0^2 \frac{(1 + K_3\lambda_h^*)N_v^*\mu_v}{(1 + K_2\lambda_h^*)[\mu_v + (M_1 + \mu_v K_2)\lambda_h^*]\omega^+}.$$

Defining

$$F(\lambda_h^*, N_v^*) = K_2(M_1 + \mu_v K_2)(\lambda_h^*)^2 + (M_1 + \mu_v(2K_2 - \Re_0^2 K_3\frac{N_v^*}{\omega^+}))\lambda_h^* + (1 - \Re_0^2\frac{N_v^*}{\omega^+})\mu_v,$$

then a positive root of equation $F(\lambda_h^*, N_v^*) = 0$ corresponds to a positive endemic equilibrium for system (3.1) and (3.2). From Theorem 2.2, we obtain if $b < b_1$, E_2 is an unstable saddle point, so its corresponding endemic equilibrium must also be unstable. Hence, if $N_v^* = \omega^+$, we have

$$g(\lambda_h^*) = K_2(M_1 + \mu_v K_2)(\lambda_h^*)^2 + (M_1 + \mu_v(2K_2 - \Re_0^2 K_3))\lambda_h^* + (1 - \Re_0^2)\mu_v.$$

Let $K_4 = \frac{M_1}{\mu_v} + K_2$, then $g(\lambda_h^*) = 0$ is shown below:

$$K_2K_4(\lambda_h^*)^2 + K_3(\frac{K_2 + K_4}{K_3} - \Re_0^2)\lambda_h^* + (1 - \Re_0^2) = 0. \tag{3.18}$$

When $\Re_0 > 1, 1 - \Re_0^2 < 0$, equation (3.18) has a unique positive root $\lambda_h^* = \frac{K_3 - K_2 - K_4}{K_2K_4}$ if and only if $K_2 + K_4 < K_3$, then if $\Re_0 > 1$, there exists a unique endemic equilibrium for system (3.1) and (3.2).

When $\Re_0 < 1, 1 - \Re_0^2 > 0$, if $K_2 + K_4 \geq K_3$, then equation (3.18) has no positive root. If $K_2 + K_4 < K_3$ and $\Re_0^2 > \frac{K_2 + K_4}{K_3}$, letting

$$\begin{aligned}\Delta =&(K_2 + K_4 - K_3\Re_0^2)^2 - 4K_2K_4(1 - \Re_0^2)\\ =&K_3^2(\Re_0^2)^2 + [4K_2K_4 - 2K_3(K_2 + K_4)]\Re_0^2 + (K_2 - K_4)^2 = 0\end{aligned}$$

we obtain that the critical value of $\Re_0$ and denote it as $\Re_0^*$. Letting

$$K_5 = K_3(K_2 + K_4) - 2K_2K_4 + 2\sqrt{K_2K_4(K_2 - K_3)(K_4 - K_3)},$$

then

$$\Re_0^* = \frac{\sqrt{K_5}}{K_3}. \tag{3.19}$$

Through analysis, it can be concluded if $\sqrt{\frac{K_2 + K_4}{K_3}} < \Re_0 < \Re_0^*$, $\Delta < 0$, if $\Re_0 = \Re_0^*$, $\Delta = 0$, if $\Re_0 > \Re_0^*$, $\Delta > 0$.

It should be noted that $K_2 + K_4 < K_3$, which is equal to

$$\frac{2(\sigma_{2h} + \eta_h)}{\sigma_{1h}\sigma_{2h}} + \frac{r\beta_h}{\sigma_{1h}\mu_v} < \frac{1}{\mu_h}(1 - \frac{\theta_h\eta_h}{\sigma_{1h}\sigma_{2h}}),$$

or

$$\sigma_{2h}\mu_v\mu_h + \eta_h\mu_v\mu_h + r\beta_h\sigma_{2h}\mu_h < \delta_h\sigma_{2h}\mu_v,$$

that is,

$$\delta_h > \mu_h\left(1 + \frac{\eta_h}{\sigma_{2h}} + \frac{r\beta_h}{\mu_v}\right) := \delta_h^*. \tag{3.20}$$

As an immediate consequence of the above result, we present the main results on the endemic equilibria of system (3.1) and (3.2).

Theorem 3.2 *For system* (3.1) *and* (3.2), *if* $b < b_1$,

(i) *If* $\Re_0 > 1$, *there exists a unique endemic equilibrium*;

(ii) *When* $0 \le \delta_h \le \delta_h^*$, $\Re_0 \le 1$, *there exists no endemic equilibrium*;

(iii) *When* $\delta_h > \delta_h^*$, *if* $\Re_0 < \Re_0^* < 1$, *there exists no endemic equilibrium*; *if* $\Re_0^* < \Re_0 < 1$, *there exists the endemic equilibrium*.

Note that, if $0 < b < b_1$, we have $\Re_0 > 1$. If $0 < b < b^-$,

$$N_v^0 = \frac{c + \sqrt{c^2 - 4\mu_v^2\mu_g b}}{2\mu_v\mu_g},$$

where, $c = (a_v - \mu_v)\mu_g - \mu_v b$, since

$$f(b) = c^2 - 4\mu_v^2\mu_g b = \mu_v^2 b^2 - 2\mu_v\mu_g(a_v + \mu_v)b + (a_v - \mu_v)^2\mu_g^2.$$

Thus, if $0 < b < b^-$, $f(b) > 0$ and $f(b)$ is a monotonically decreasing function of b, then by the expression for c, c is also a nonnegative and monotonically decreasing function of b. Hence, $\Re_0$ is a monotonically decreasing function of b. That is to say, the more sterile mosquitoes that are released, the smaller the reproductive number of system (3.1) and (3.2).

It follows from the fourth equation of system (3.3) that:

$$\lim_{t\to\infty} N_v(t) = N_v^0.$$

Then, system (3.3) takes the form:

$$\begin{cases} \dfrac{dS_h}{dt} = \Lambda_h - r\beta_v\dfrac{I_v}{N_h}S_h + \theta_h R_h - \mu_h S_h, \\ \dfrac{dI_h}{dt} = r\beta_v\dfrac{I_v}{N_h}S_h - (\mu_h + \delta_h + \eta_h)I_h, \\ \dfrac{dR_h}{dt} = \eta_h I_h - (\theta_h + \mu_h)R_h, \\ \dfrac{dI_v}{dt} = r\beta_h\dfrac{I_h}{N_h}(N_v^0 - I_v) - \mu_v I_v, \\ \dfrac{dg}{dt} = b - \mu_g g. \end{cases} \tag{3.21}$$

Define $S_h = x_1, I_h = x_2, R_h = x_3, I_v = x_4, g = x_5, x = (x_1, x_2, x_3, x_4, x_5)^T$, and $f = (f_1, f_2, f_3, f_4, f_5)^T$, then system (3.21) is equivalent to

$$\frac{dx}{dt} = f(x, \beta_v),$$

where,

$$\begin{cases} f_1 = \Lambda_h - r\beta_v \dfrac{x_4}{x_1+x_2+x_3} x_1 + \theta_h x_3 - \mu_h x_1, \\ f_2 = r\beta_v \dfrac{x_4}{x_1+x_2+x_3} x_1 - (\mu_h + \delta_h + \eta_h) x_2, \\ f_3 = \eta_h x_2 - (\theta_h + \mu_h) x_3, \\ f_4 = r\beta_h \dfrac{x_2}{x_1+x_2+x_3} (N_v^0 - x_4) - \mu_v x_4, \\ f_5 = b - \mu_g x_5. \end{cases} \tag{3.22}$$

If $\Re_0 = 1$, $\beta_v = \beta_v^* = \frac{\sigma_{1h}\mu_v\Lambda_h}{r^2\beta_h\mu_h S_v^0}$, the Jacobian matrix at the disease-free equilibrium $A_0 = (\frac{\Lambda_h}{\mu_h}, 0, 0, 0, g^*)$ of equation (3.22) has the form:

$$J(A_0, \beta_v) = \begin{pmatrix} -\mu_h & 0 & \theta_h & -r\beta_v & 0 \\ 0 & -\sigma_{1h} & 0 & r\beta_v & 0 \\ 0 & \eta_h & -\sigma_{2h} & 0 & 0 \\ 0 & r\beta_h \frac{S_v^0\mu_h}{\Lambda_h} & 0 & -\mu_v & 0 \\ 0 & 0 & 0 & 0 & -\mu_g \end{pmatrix}. \tag{3.23}$$

Obviously, two of the eigenvalues of (3.23) are $\lambda_1 = -\mu_h$ and $\lambda_2 = -\mu_g$, the remaining eigenvalues are the roots of equation

$$\begin{vmatrix} \lambda + \sigma_{1h} & 0 & -r\beta_v \\ -\eta_h & \lambda + \sigma_{2h} & 0 \\ -r\beta_h \frac{S_v^0\mu_h}{\Lambda_h} & 0 & \lambda + \mu_v \end{vmatrix} = 0,$$

then we have:

$$(\lambda + \sigma_{2h})(\lambda^2 + (\sigma_{1h} + \mu_v)\lambda + \sigma_{1h}\mu_v - \frac{r^2\beta_v\beta_h\mu_h S_v^0}{\Lambda_h}) = 0.$$

Hence, the eigenvalues of (3.23) are:

$$\lambda_3 = -\sigma_{2h}, \quad \lambda_4 = -(\sigma_{1h} + \mu_v), \quad \lambda_5 = 0.$$

Hence, 0 is the single eigenvalue of $J(A_0, \beta_v)$, and all other eigenvalues of $J(A_0, \beta_v)$ have negative real parts.

To apply the Castillo-Chavez and Song Theorem [35], we essentially have to compute two quantities, labeled a and b, which depend on the higher-order terms in the Taylor expansion of the system. Let $\omega = (\omega_1, \omega_2, \omega_3, \omega_4, \omega_5)^T$ be the nonnegative right eigenvector corresponding to the zero eigenvalue with respect to $J(A_0, \beta_v)$, it is easy to show that

$$\omega = (\frac{-\mu_h(\sigma_{1h} + \theta_h) - \theta_h\delta_h}{\sigma_{2h}\mu_h}\omega_2, \omega_2, \frac{\eta_h}{\sigma_{2h}}\omega_2, \frac{rS_v^0\beta_h\mu_h}{\mu_v\Lambda_h}\omega_2, 0)^T.$$

Let $\nu = (\nu_1, \nu_2, \nu_3, \nu_4, \nu_5)$ be the nonnegative left eigenvector corresponding to the zero eigenvalue with respect to $J(A_0, \beta_v)$, then

$$\nu = (0, \nu_2, 0, \frac{\Lambda_h \sigma_{1h}}{rS_v^0 \beta_h \mu_h} \nu_2, 0).$$

Since $\nu \cdot \omega = 1$, namely, $\nu_2\omega_2 + \frac{\sigma_{1h}}{\mu_v}\nu_2\omega_2 = 1$. we have:

$$\omega_2 = \frac{\mu_v}{\sigma_{1h}}, \qquad \nu_2 = \frac{\sigma_{1h}}{\sigma_{1h} + \mu_v}.$$

Here, the Taylor-expansion system (3.22) is represented by the $f_i(A_0, \beta_v)(i = 1, 2, 3, 4, 5)$, and we have

$$\begin{aligned}
&\frac{\partial^2 f_1}{\partial x_4 \partial x_2} = \frac{\partial^2 f_1}{\partial x_4 \partial x_3} = \frac{\partial^2 f_1}{\partial x_2 \partial x_4} = \frac{\partial^2 f_1}{\partial x_3 \partial x_4} = r\beta_v \frac{\mu_h}{\Lambda_h}, \\
&\frac{\partial^2 f_2}{\partial x_4 \partial x_2} = \frac{\partial^2 f_2}{\partial x_4 \partial x_3} = \frac{\partial^2 f_2}{\partial x_2 \partial x_4} = \frac{\partial^2 f_2}{\partial x_3 \partial x_4} = -r\beta_v \frac{\mu_h}{\Lambda_h}, \\
&\frac{\partial^2 f_4}{\partial x_2 \partial x_1} = \frac{\partial^2 f_4}{\partial x_1 \partial x_2} = \frac{\partial^2 f_4}{\partial x_3 \partial x_2} = \frac{\partial^2 f_4}{\partial x_2 \partial x_3} = -\frac{rS_v^0 \beta_h \mu_h^2}{\Lambda_h^2}, \\
&\frac{\partial^2 f_4}{\partial x_4 \partial x_2} = \frac{\partial^2 f_4}{\partial x_2 \partial x_4} = -\frac{r\beta_h \mu_h}{\Lambda_h}.
\end{aligned}$$

These second partial derivatives have the same result after switching the order of derivation, since

$$\frac{\partial^2 f_4}{\partial x_2^2} = -\frac{2rS_v^0 \beta_h \mu_h^2}{\Lambda_h^2}.$$

In addition, all other derivatives are equal to zero. Consequently, we can readily compute the following quantity by substituting the vectors ω and ν and the respective partial derivatives into the expression:

$$\begin{aligned}
a &= \sum_{k,i,j=1}^{5} \nu_k \omega_i \omega_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(A_0, \beta_v) \\
&= 2\nu_2\omega_2^2\left(\frac{rS_v^0 \beta_h \mu_h}{\mu_v \Lambda_h} + \frac{rS_v^0 \beta_h \eta_h \mu_h}{\sigma_{2h} \mu_v \Lambda_h}\right)\left(-\frac{r\beta_v \mu_h}{\Lambda_h}\right) \\
&\quad + 2\nu_2\omega_2^2\left(-\frac{\Lambda_h \sigma_{1h}}{rS_v^0 \beta_h \mu_h} \cdot \frac{\mu_h(\sigma_{1h} + \theta_h) + \theta_h \delta_h}{\sigma_{2h} \mu_h}\right. \\
&\quad \left. + \frac{\Lambda_h \sigma_{1h} \eta_h}{rS_v^0 \beta_h \mu_h \sigma_{2h}}\right)\left(-\frac{rS_v^0 \beta_h \mu_h^2}{\Lambda_h^2}\right) + 2\nu_2\omega_2^2\left(-\frac{r\beta_h \sigma_{1h} \mu_h}{\mu_v \Lambda_h}\right) + 2\nu_2\omega_2^2\left(-\frac{\sigma_{1h} \mu_h}{\Lambda_h}\right) \\
&= 2\nu_2\omega_2^2\left(-\frac{\sigma_{1h}\mu_h}{\Lambda_h} - \frac{\eta_h \mu_h \sigma_{1h}}{\sigma_{2h} \Lambda_h} + \frac{\sigma_{1h}(\mu_h(\sigma_{1h} + \theta_h) + \theta_h \delta_h)}{\sigma_{2h} \Lambda_h}\right. \\
&\quad \left. - \frac{\sigma_{1h} \eta_h \mu_h}{\sigma_{2h} \Lambda_h} - \frac{r\beta_h \sigma_{1h} \mu_h}{\mu_v \Lambda_h} - \frac{\sigma_{1h} \mu_h}{\Lambda_h}\right) \\
&= \frac{2\mu_v^2}{\mu_v + \sigma_{1h}}\left(-\frac{2\mu_h}{\Lambda_h} - \frac{2\eta_h \mu_h}{\sigma_{2h} \Lambda_h} + \frac{\mu_h(\mu_h + \delta_h + \eta_h) + \theta_h(\mu_h + \delta_h)}{\sigma_{2h} \Lambda_h} - \frac{r\beta_h \mu_h}{\mu_v \Lambda_h}\right)
\end{aligned}$$

$$= \frac{2\mu_v^2\mu_h}{\Lambda_h(\sigma_{1h}+\mu_v)}\left(\frac{\delta_h}{\mu_h} - 1 - \frac{\eta_h}{\sigma_{2h}} - \frac{r\beta_h}{\mu_v}\right).$$

Note that $\frac{\partial^2 f_2}{\partial x_4 \partial \beta_v} = 1$, and all other derivatives $\frac{\partial^2 f_k}{\partial x_i \partial \beta_v}$ are equal to zero. Hence, we can calculate b by substituting the vector ω, v, and the respective partial derivatives into the expression:

$$b = \sum_{k,i=1}^{5} v_k \omega_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_v}(A_0, \beta_v) = v_2\omega_4 = \frac{rS_v^0\beta_h\mu_h}{\Lambda_h(\mu_v+\sigma_{1h})}.$$

Clearly, $b > 0$. Furthermore, we have:

$$\delta_h^* = \left(1 + \frac{\eta_h}{\sigma_{2h}} + \frac{r\beta_h}{\mu_v}\right)\mu_h,$$

then when $\delta_h > \delta_h^*$, we obtain $a > 0$. Thus, the backward bifurcation of system (3.3) occurs.

Theorem 3.3 *If $b < b_1$ and $\delta_h > \delta_h^*$, then the backward bifurcation of system* (3.3) *occurs at* $\Re_0 = 1$.

4 Simulations and biological explanations

In this section, we give examples to illustrate the validity of our results. In order to interpret the conclusions from a quantitative perspective, the dynamics of the malaria model with sterile mosquito populations by numerical simulations will be analyzed in the following. We find the numerical solutions of the model (3.3) and analyze the effect of threshold b^-, b_1 and the basic reproductive number $\Re_0$.

Example 4.1 Let the parameters be given by:

$$\mu_g = 0.6,\ a_v = 20,\ \mu_v = 0.5.$$

It follows from equation (2.6) that $b^- = 17$. With the initial values $(200, 180)$, when $b = 25 > b^-$, system (2.2) has no positive equilibrium, only a unique boundary equilibrium $E_0 = (0, 41.6677)$ that is globally asymptotically stable. That is to say, wild mosquitoes eventually become extinct. When $b = 16 < b^-$, there exists a positive equilibrium $E_3 = (9.5374, 26.6669)$, which is locally asymptotically stable, if the initial conditions are given by $(w, g) = (10, 180)$, the boundary equilibrium $E_0 = (0, 26.6671)$, which is locally asymptotically stable. as shown in Fig. 1.

Example 4.2 Let the parameters be given by:

$$\beta_h = 0.2,\ \beta_v = 0.24,\ r = 10,\ \Lambda_h = 10,\ \theta_h = 0.5,\ \mu_h = 0.02,$$

$$\delta_h = 0.5,\ \eta_h = 0.07,\ a_v = 10,\ \mu_v = 0.5,\ \mu_g = 0.6,\ b = 10.$$

It follows from equations (2.6) that $b^- = 7.2334$. As $b = 10 > b^-$, with the initial values $(200, 180, 100, 100, 300, 200)$, the solution approaches the disease-free equilibrium $G_0 = (271.2709, 0, 0, 0, 0, 16.6667)$, which is locally asymptotically stable, the disease finally disappears. Here, only I_h, R_h, I_v, and g are shown for visual convenience, as shown in Fig. 2.

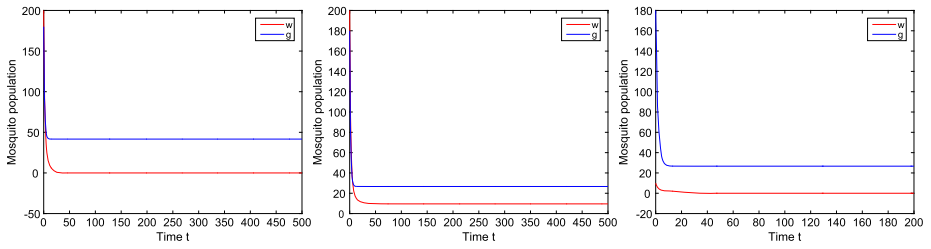

Figure 1 The red and green curves correspond to the wild and sterile mosquitoes, respectively. With the parameter values given in Example 4.1, $b^- = 17$. If the initial conditions are given by $(w, g) = (200, 180)$, when $b = 25 > b^-$, system (2.2) has no positive equilibrium, only a unique boundary equilibrium $E_0 = (0, 41.6677)$, which is globally asymptotically stable. When $b = 16 < b^-$, there exists a positive equilibrium $E_3 = (9.5374, 26.6669)$, which is locally asymptotically stable, if the initial conditions are given by $(w, g) = (10, 180)$, the boundary equilibrium $E_0 = (0, 26.6671)$, which is locally asymptotically stable, as shown in Fig. 1

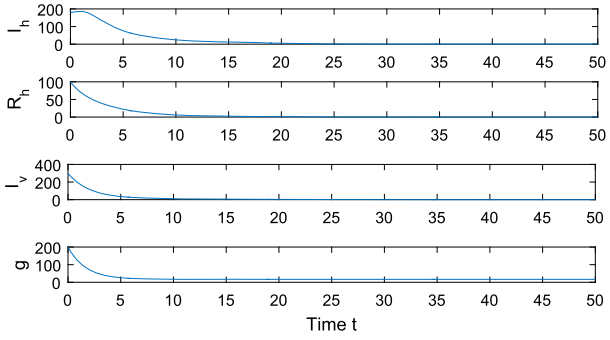

Figure 2 With the parameter values given in Example 4.2, $b^- = 7.2334$. The initial conditions are given by $(200, 180, 100, 100, 300, 200)$, when $b = 10 > b^-$, system (3.1) and (3.2) has no endemic equilibrium, when $t \to \infty$, the solution of system approaches the disease-free equilibrium $G_0 = (271.2709, 0, 0, 0, 0, 16.6667)$, which is locally asymptotically stable, the disease finally disappears. Here, only I_h, R_h, I_v and g are shown for visual convenience

Example 4.3 Let the parameters be given by:

$$\beta_h = 0.25,\ \beta_v = 0.4,\ r = 20,\ \Lambda_h = 10,\ \theta_h = 0.5,\ \mu_h = 0.2,$$

$$\delta_h = 0.5,\ \eta_h = 0.07,\ a_v = 10,\ \mu_v = 0.5,\ \mu_g = 0.6,\ b = 2.$$

It follows from equations (2.6), (3.4), and (3.5) that

$$b^- = 7.2334,\ \Re_0 = 1.6999,\ b_1 = 3.61.$$

Note that $0 < b < b_1$ and $\Re_0 > 1$, and there only exists the endemic equilibrium (2.4630, 19.0374, 2.5627, 13.7171, 15.4509, 3.3333), then the disease will persist, as shown in Fig. 3.

Example 4.4 Let the parameters be given by:

$$\beta_h = 0.02,\ \beta_v = 0.8,\ r = 15,\ \Lambda_h = 100,\ \theta_h = 0.5,\ \mu_h = 0.12,$$

$$\delta_h = 0.7,\ \eta_h = 0.07,\ a_v = 10,\ \mu_v = 0.2,\ \mu_g = 0.6,\ b = 8.$$

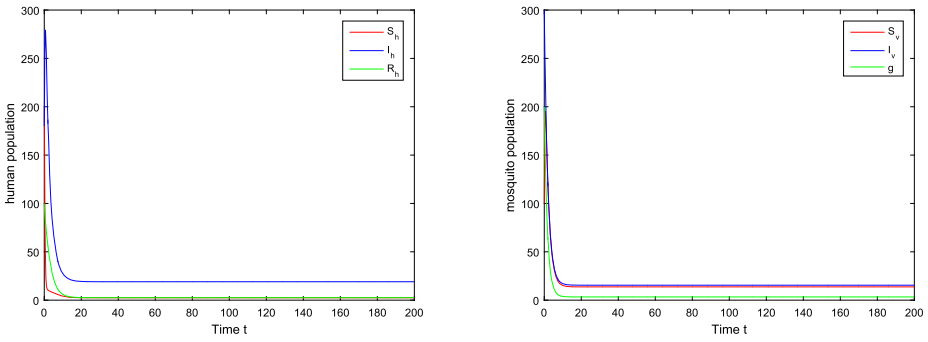

Figure 3 With the parameter values given in Example 4.3 and the initial values (200, 180, 100, 400, 300, 200), then $b^{-} = 7.2334$, $b_1 = 3.61$ and the reproductive number $\Re_0 = 1.6999$ of system (3.3). As $0 < b < b_1$ and $\Re_0 > 1$, there exists the endemic equilibrium (2.4630, 19.0374, 2.5627, 13.7171, 15.4509, 3.3333)

It follows from equations (3.4), (3.19), and (3.20) that:

$$\Re_0 = 0.9254, \quad \Re_0^* = 0.8782, \quad \delta_h^* = 0.3135.$$

Note that $\delta_h > \delta_h^*$, $\Re_0^* < \Re_0 < 1$, though $\Re_0 < 1$, we still have $(I_h, I_v) = (99.3414, 35.2888)$, the disease still persists. as shown in the left of Fig. 4. Here, only I_h, I_v are shown for visual convenience.

With the parameters given by:

$$\beta_h = 0.02,\ \beta_v = 0.8,\ r = 65,\ \Lambda_h = 50,\ \theta_h = 0.5,\ \mu_h = 0.12,$$
$$\delta_h = 0.8,\ \eta_h = 0.7,\ a_v = 10,\ \mu_v = 0.32,\ \mu_g = 0.6,\ b = 18.$$

It follows from equations (3.4), (3.19), and (3.20) that:

$$\Re_0 = 0.9363, \quad \Re_0^* = 0.9981, \quad \delta_h^* = 0.7430.$$

Note that $\delta_h > \delta_h^*$, $\Re_0 < \Re_0^* < 1$, then the disease disappears, as shown in the right of Fig. 4. Here, only I_h, I_v are shown for visual convenience.

For model (3.3), we show that it may undergo backward bifurcation, where the stable disease-free equilibrium coexists with the stable endemic equilibrium. Moreover, we give a more through mathematical analysis in Sect. 3.2 and derive a formula for the quantity δ_h^* that is explicitly given by (3.20). Then, we give a complete determination condition whether backward bifurcation occurs in Theorem 3.3, namely, $\delta_h > \delta_h^*$. In other words, when $0 \le \delta_h \le \delta_h^*$, system (3.3) has no endemic equilibria if $\Re_0 \le 1$ and backward bifurcation cannot occur. Solutions approach either the disease-free equilibrium, or the stable endemic equilibrium, depending on their initial values. Furthermore, we obtain a through analysis about the existence of backward bifurcation by applying a center manifold. It is worth noting that owing to the existence of backward bifurcation, even small fluctuation of parameters can produce a completely different result.

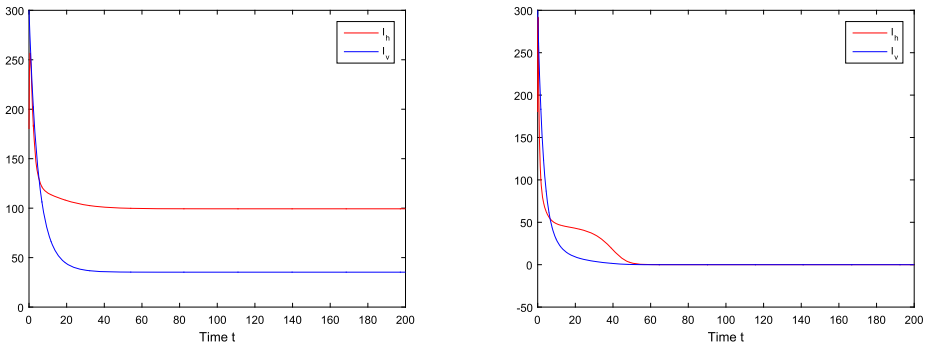

Figure 4 With the parameter values given in Example 4.4 and the initial values (200, 180, 100, 400, 300, 200), when $\delta_h > \delta_h^*$, if $\Re_0^* < \Re_0 < 1$, though $\Re_0 < 1$, $(I_h, I_v) = (99.3414, 35.2888)$, the disease still persists, as shown in the left of the figure. If $\Re_0 < \Re_0^* < 1$, then the disease disappears. as shown in the right of the figure. Here, only I_h, I_v are shown for visual convenience

5 Conclusions

Malaria and other mosquito-borne diseases are transmitted by wild mosquitoes. To prevent the transmission of mosquito-borne diseases, an effective way is to reduce or eradicate wild mosquitoes. In recent years, the sterile-insect technique has been applied in experiments. Hence, it is crucial to study the dynamic of mosquitoes and humans, and devise effective and realistic methods for controlling mosquito populations in communities. As is known, the dynamic of mosquitoes is closely related to the environment and resources in a region. Hence, to obtain a more realistic model, it will be considered by taking into account the impact of limited resources of mosquito populations. Thus, we establish and study a malaria-transmission dynamic model of releasing sterile mosquitoes, which focuses on the mosquito populations affected by the impact of limited resource. In this study, we first analyze a two-dimensional model that contains only wild and sterile mosquitoes, through qualitative analysis, the existence, stability of the equilibrium, and the threshold b^- of releasing sterile mosquitoes are obtained. When $b \geq b^-$, the wild-mosquito population eventually becomes extinct. When $b < b^-$, system (2.2) has a boundary equilibrium that is locally asymptotically stable and nodes. In other words, sterile mosquitoes and wild mosquitoes may coexist. System (2.2) approaches either the extinction equilibrium or the stable equilibrium depending on the initial values. Then, human and mosquito populations with sterile release were combined into one system, and we assume that the release rate of sterile mosquitoes is a constant, and derive a formula for the reproductive number $\Re_0$ for model (3.3). For system (3.3), there exists the disease-free equilibrium that is locally asymptotically stable if $\Re_0 < 1$, and there exists a unique endemic equilibrium if $\Re_0 > 1$. When $\Re_0 = 1$, a release threshold b_1 for sterile mosquitoes is obtained, and there exists the disease-free equilibrium, which is locally asymptotically stable if $b \geq b_1$, in other words, the disease disappears. When $b_1 < b < b^-$, there exist two disease-free equilibria that are locally asymptotically stable, and there exists endemic equilibrium if $b < b_1 < b^-$. Based on this threshold, malaria transmission can be better controlled in the presence of wild and sterile mosquitoes. Finally, we show that a backward bifurcation may occur under certain condition for system (3.1) and (3.2). The existence of backward bifurcation can make the disease more difficult to control, we should pay more attention to the initial sizes of the involved populations. If only the basic reproductive number is controlled to less than 1, the

disease may still spread. Here, we conclude that $\Re_0$ is a monotonically decreasing function of b. With the increase of releasing sterile mosquito populations, the basic reproductive number will decrease. Therefore, releasing sterile mosquitoes is conducive for controlling malaria.

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Author contributions
All authors contributed equally to the manuscript and typed, read, and approved the final manuscript.

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Data availability
Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study.

Declarations

Competing interests
The authors declare that they have no competing interests.

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