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Stability Analysis and Dynamics Preserving Nonstandard Finite Difference Schemes for a Malaria Model

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STABILITY ANALYSIS AND DYNAMICS PRESERVING NONSTANDARD FINITE DIFFERENCE SCHEMES FOR A MALARIA MODEL

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When both human and mosquito populations vary, forward bifurcation occurs if the basic reproduction number $\mathbf{R}_0$ is less than one in the absence of disease-induced death. When the disease-induced death rate is large enough, $\mathbf{R}_0 = 1$ is a subcritical backward bifurcation point. The domain for the study of the dynamics is reduced to a compact and feasible region, where the system admits a specific algebraic decomposition into infective and non-infected humans and mosquitoes. Stability results are extended and the possibility of backward bifurcation is clarified. A dynamically consistent nonstandard finite difference scheme is designed.

***Keywords*:** bifurcation analysis; dynamic consistency; global asymptotic stability; malaria; nonstandard finite difference

1. INTRODUCTION

Malaria is caused by a protozoa of the genus plasmodium and is transmitted by the female anopheles mosquito (vector). In contrast to Macdonald (1957), Chitnis et al. (2008) introduced the model where the number of bites of mosquitoes per human depends on the population sizes of both mosquitoes and humans. First, we shall obtain an additional threshold number ξ and establish the global asymptotic stability of the disease-free equilibrium when $R_0 \leq \xi \leq 1$, making the interval $\xi < R_0 \leq 1$ the specific region where backward bifurcation occurs. The number ξ serves to check the stability of the infectious-related Metzler matrix which is involved in the decomposition. We shall design a nonstandard finite difference scheme as a

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reliable numerical method and demonstrate computationally that our scheme displays the backward bifurcation phenomenon when $\xi < R_0 \leq 1$.

2. THE MODEL

From Chitnis et al. (2006) the dynamics of malaria is:

$$S_h'(t) = \Lambda_h + \psi_h N_h(t) + \rho_h R_h(t) - c(N_h(t), N_v(t))\beta_{hv} I_v(t) S_h(t) - f_h(N_h(t)) S_h(t), \quad (1)$$

$$E_h'(t) = c(N_h(t), N_v(t))\beta_{hv} I_v(t) S_h(t) - \nu_h E_h(t) - f_h(N_h(t)) E_h(t), \quad (2)$$

$$I_h'(t) = \nu_h E_h(t) - (\gamma_h + f_h(N_h(t)) + \delta_h) I_h(t), \quad (3)$$

$$R_h'(t) = \gamma_h I_h(t) - \rho_h R_h(t) - f_h(N_h(t)) R_h(t), \quad (4)$$

$$S_v'(t) = \psi_v N_v(t) - c(N_h(t), N_v(t))(\beta_{vh} I_h(t) + \tilde{\beta}_{vh} R_h(t)) S_v(t) - f_v(N_v(t)) S_v(t), \quad (5)$$

$$E_v'(t) = c(N_h(t), N_v(t))\left(\beta_{vh} I_h(t) + \tilde{\beta}_{vh} R_h\right) S_v(t) - \nu_v E_v(t) - f_v(N_v(t)) E_v(t), \quad (6)$$

$$I_v'(t) = \nu_v E_v(t) - f_v(N_v(t)) I_v(t). \quad (7)$$

with

$$f_h = \mu_{1h} + \mu_{2h} N_h(t), \quad f_v = \mu_{1v} + \mu_{2v} N_v(t), \quad (8)$$

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t), \quad N_v(t) = S_v(t) + E_v(t) + I_v(t), \quad (9)$$

$$c(N_h(t), N_v(t)) = \frac{\sigma_v \sigma_h}{\sigma_h N_h(t) + \sigma_v N_v(t)}. \quad (10)$$

The flow diagram of the model is represented in Figure 1, the state variables are enumerated in Table 1, and the parameters in Table 2 given in Chitnis et al. (2006) are reproduced.

Table 2 presents three sets of parameters treated in Chitnis et al. (2006, 2008) and which are used in the numerical simulations of Section 4. The populations $N_v(t)$ and $N_h(t)$ satisfy:

$$N_v'(t) = (\psi_v - \mu_{1v} - \mu_{2v} N_v(t)) N_v(t), \quad (11)$$

and

$$N_h'(t) = \Lambda_h + (\psi_h - \mu_{1h} - \mu_{2h} N_h(t)) N_h(t) - \delta_h I_h(t). \quad (12)$$

Eq. (11) has a nontrivial equilibrium at:

$$N_v^* = \frac{\psi_v - \mu_{1v}}{\mu_{2v}}, \quad (13)$$

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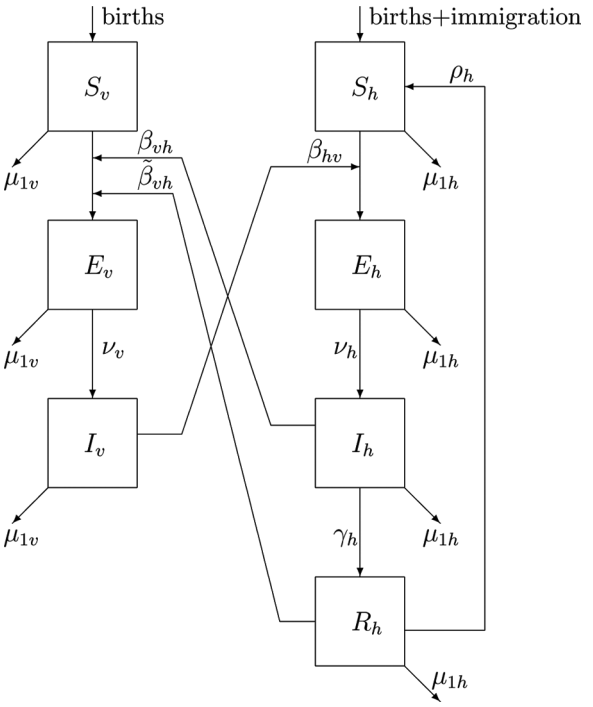


Figure 1. Compartmental flow diagram.

which is globally asymptotically stable on $N_v > 0$. The explicit solution of Eq. (11) is

$$N_v(t) = \frac{N_v^* N_v(0)}{N_v(0) + \left(N_v^* - N_v(0)\right)e^{-t\mu_{2v}N_v^*}}. \tag{14}$$

If $\delta_h = 0$ or the human population is disease-free ($I_h = 0$), then Eq. (12) is reduced to:

$$N_h' = \Lambda_h + (\psi_h - \mu_{1h} - \mu_{2h}N_h)N_h, \tag{15}$$

which is decoupled from the rest of the model. The nonnegative equilibrium in this case is

Table 1. The state variables of Eq. (1)–(7)

Humans	Mosquito
S_h: Number of susceptible humans	S_v: Number of susceptible mosquitoes
E_h: Number of exposed humans	E_v: Number of exposed mosquitoes
I_h: Number of infective humans	I_v: Number of infective mosquitoes
R_h: Number of recovered (immune and asymptomatic, but slightly infectious) humans	

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Table 2. Description of parameters and three sets of values used in the simulations

	Description	Set 1	Set 2	Set 3
Humans				
Λ_h	immigration rate	0.041	0.03285	0.033
ψ_h	relative birth rate	5.5×10^{-5}	7.666×10^{-5}	1.1×10^{-4}
μ_{1h}	density-independent force of mortality/ out-migration rate	8.8×10^{-6}	4.212×10^{-5}	1.6×10^{-5}
μ_{2h}	density-dependent force of mortality/ out-migration rate	2×10^{-7}	10^{-7}	3×10^{-7}
σ_h	bites tolerated by a human per unit time	4.3	18	19
β_{hv}	probability of transmission of infection from infective mosquito	0.022	0.02	0.022
$\frac{1}{\nu_h}$	average duration of the latent period	0.1	0.08333	0.1
γ_h	recovery rate	0.0035	0.003704	0.0035
ρ_h	loss of immunity rate	0.0027	0.0146	0.00055
δ_h	disease-induced death rate	1.8×10^{-5}	3.454×10^{-4}	9×10^{-5}
Mosquitoes				
ψ_v	relative birth rate	0.13	0.4	0.13
μ_{1v}	density-independent force of mortality	0.033	0.1429	0.033
μ_{2v}	density-dependent force of mortality	7×10^{-5}	2.279×10^{-4}	2×10^{-5}
σ_v	bites required by a mosquito per unit time	0.33	0.6	0.5
β_{vh}	probability of transmission of infection from infective human	0.24	0.8333	0.48
$\tilde{\beta}_{vh}$	probability of transmission of infection from recovered human	0.024	0.08333	0.048
$\frac{1}{\nu_v}$	average duration of the latent period	0.083	0.1	0.091

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$$N_h^* = \frac{\psi_h - \mu_{1h} + \left((\psi_h - \mu_{1h})^2 + 4\mu_{2h}\Lambda_h\right)^{1/2}}{2\mu_{2h}}. \tag{16}$$

Using Eq. (12), and the fact that $-\delta_h N_h \leq -\delta_h I_h \leq 0$, the population N_h, when considered independently of the model, satisfies the differential inequalities:

$$\begin{aligned}\Lambda_h + (\psi_h - \mu_{1h} - \mu_{2h}N_h(t))N_h(t) - \delta_h N_h(t) \leq N_h'(t) \leq \Lambda_h \\ + (\psi_h - \mu_{1h} - \mu_{2h}N_h(t))N_h(t).\end{aligned} \tag{17}$$

In the terminology of Mickens (2007), Eq. (11) and (17) are conservation laws. While the first conservation law Eq. (11) has the explicit solution given in Eq. (14), the situation is different for the second conservation law (17), from which we derive inequality (22) below.

Consider the lower bound equation from Eq. (17):

$$N_h'(t) = \Lambda_h + (\psi_h - \mu_{1h} - \mu_{2h}N_h(t))N_h(t) - \delta_h N_h(t), \tag{18}$$

and let $N_h^{\#}$ denote its nonnegative equilibrium:

$$N_h^{\#} = \frac{\psi_h - \mu_{1h} - \delta_h + \left((\psi_h - \mu_{1h} - \delta_h)^2 + 4\mu_{2h}\Lambda_h\right)^{1/2}}{2\mu_{2h}}. \tag{19}$$

We assume that the parameters are such that:

$$N_v^* > 0, \quad N_h^{\#} > 0 \quad \text{and} \quad N_h^* > 0. \tag{20}$$

Given the initial condition:

$$N_h(0) = N_h^0, \tag{21}$$

let $\overline{N}_h(t)$ and $\underline{N}_h(t)$ denote the solutions of Eq. (15) and (18), respectively. Using the monotonicity Theorem 8.XI in Walter (1970), the conservation law (17) implies that the solution of Eq. (12) with the initial condition (21) satisfies:

$$\underline{N}_h(t) \le N_h(t) \le \overline{N}_h(t). \tag{22}$$

The RHS inequality in Eq. (22) is often obtained by the Gronwall inequality, but the upper bound in Eq. (17) is not linear in N_h. Chitnis et al. (2006) showed that the epidemiological model Eq. (1)–(7) defines a dynamical system on the unbounded positive cone:

$$\mathcal{D} = \left\{(S_h, E_h, I_h, R_h, S_v, E_v, I_v) \in \mathbb{R}^7 \mid (S_h, E_h, I_h, R_h, S_v, E_v, I_v) \ge 0\right\} \tag{23}$$

with, in terms of Eq. (13) and (16), the disease-free equilibrium (DFE) being given by:

$$\mathcal{E}_0 \equiv DFE = (S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*) = (N_h^*, 0, 0, 0, N_v^*, 0, 0). \tag{24}$$

Consider the vector function:

$$F = \left(c(N_h,\, N_v)\beta_{hv} I_v S_h,\, 0,\, 0,\, c(N_h, N_v)\left(\beta_{vh} I_h + \tilde{\beta}_{vh} R_h\right) S_v,\, 0\right)^T, \tag{25}$$

representing the rate at which secondary infections increase the relevant disease compartments, while the vector function:

$$V = \begin{pmatrix} (\nu_h + f_h)E_h, (\gamma_h + f_h + \delta_h)I_h - \nu_h E_h, -\gamma_h I_h + (\rho_h + f_h)R_h, \\ (\nu_v + f_v)E_v, -\nu_v E_v + f_v)I_v \end{pmatrix}^T \tag{26}$$

with $f_h = f_h(N_h)$ and $f_v = f_v(N_v)$, represents the rate at which disease progression, death, and recovery decrease these compartments. Following Diekmann and Heesterbeek (2000) and van Driessche and Watmough (2008), the next generation matrix is $J_F J_V^{-1}$, where J_F and J_V are the Jacobian matrices of the vector-functions

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F and V evaluated at the DFE, and the basic reproduction number R_0 is defined as the spectral radius of $J_F J_V^{-1}$: $R_0 := \rho(J_F J_V^{-1})$. After computation, we obtain the result of Chitnis et al. (2006) rewritten as:

$$R_0 = c(N_h^*, N_v^*) \left(\frac{\beta_{hv}\nu_h\nu_v \left(\beta_{vh} + \frac{\gamma_h + \tilde{\beta}_{vh}}{\rho_h + f_h(N_h^*)}\right) N_h^* N_v^*}{f_v(N_v^*)(\nu_h + f_h(N_h^*))(\nu_v + f_v(N_v^*))(\gamma_h + f_h(N_h^*) + \delta_h)} \right)^{1/2}. \quad (27)$$

Theorem 1. *The disease-free equilibrium $\mathcal{E}_0$ is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. In the absence of disease-induced death ($\delta_h = 0$), the transcritical bifurcation at $R_0 = 1$ is forward supercritical.*

In the case when δ_h is large enough, Chitnis et al. (2006) conjectured that there is a subcritical backward bifurcation at $R_0 = 1$.

3. RESULTS

The region $\mathcal{D}$ on which Chitnis et al. (2006) studied the malaria model Eq. (1)–(7) as a dynamical system is unbounded. In view of the conservation laws (11) and (22), it makes biological sense to work with the much smaller region:

$$\mathcal{G} = \left\{ (S_h, E_h, I_h, R_h, S_v, E_v, I_v) \in \mathcal{D} \,|\, N_h^{\#} \le N_h \le N_h^*,\ N_v = N_v^* \right\}, \quad (28)$$

and to expect that the asymptotic behavior of the system on $\mathcal{D}$ is equivalently studied on $\mathcal{G}$. This fact would mean that the population dynamics does not affect significantly the long-term behavior of the epidemiological model. In this sense, the region $\mathcal{G}$ is biologically feasible. We recall some basic definitions related to LaSalle's Invariance Theory for dynamical systems (LaSalle, 1976).

Definition 2. A compact set $M \subset \mathcal{D}$ is called *stable* for a dynamical system defined on $\mathcal{D}$ if for every neighborhood U (in the topology on $\mathcal{D}$) of M there exists a neighborhood W of M such that every trajectory initiated at a point in W is in U for all $t \ge 0$.

Definition 3. A compact set $M \subset \mathcal{D}$ is called an *attractor* of a dynamical system defined on $\mathcal{D}$ if there exists a neighborhood U of M such that for every point $x \in U$ and neighborhood W of M there exists a time $t_{x,\,W} > 0$ such that the trajectory initiated at x belongs to W for $t > t_{x,\,W}$. The largest set U is called a *basin of attraction*. If $U = \mathcal{D}$ the set M is called a *global attractor*. A set M which is both stable and a global attractor is said to be *globally asymptotically stable* (GAS).

When the set M is a singleton, definitions 2 and 3 identify the usual properties of stability and attractiveness of equilibria.

Theorem 4. *The set $\mathcal{G}$ given in Eq. (28) is GAS for the dynamical system of Eq. (1)–(7) defined on $\mathcal{D}$.*

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As mentioned earlier, the fact that $\mathcal{G}$ is a globally asymptotically stable set reduces the study of the dynamical system of Eq. (1)–(7) from $\mathcal{D}$ to $\mathcal{G}$. For example, $\mathcal{G}$ contains the positive limit set of any trajectory of the dynamical system on $\mathcal{D}$.

Theorem 5. *Let a positive dynamical system, discrete or continuous, be defined on a set $\mathcal{D} \subseteq \mathbb{R}^n$ and let a compact set $\mathcal{E} \subset \mathcal{D}$ be globally asymptotically stable. Denote by M the largest invariant subset of $\mathcal{E}$. Then M is GAS on $\mathcal{D}$. In particular if $M = \{x^*\}$ where x^* is an equilibrium of the system with basin of attraction containing $\mathcal{E}$ then x^* is GAS of the system on $\mathcal{D}$.*

Theorem 5 is a form of LaSalle's Invariance Principle. The essential difference is that here we use the GAS of $\mathcal{E}$ instead of a Lyapunov function for defining $\mathcal{E}$. A compact set is stable if and only if there exists a Lyapunov function for it (Auslander and Seibert, 1964).

Motivated by Theorems 4 and 5, we consider the dynamical system of Eq. (1)–(7) on the smaller set $\mathcal{G}$. For the global asymptotic stability of the DFE on $\mathcal{G}$ (Castillo-Chavez et al., 2002; Kamgang and Sallet, 2008) we decompose the vector:

$$x := (S_h, E_h, I_h, R_h, S_v, E_v, I_v) \tag{29}$$

of dependent variables into the vectors:

$$x_s := (S_h, S_v)^T, \quad \text{and} \quad x_i := (E_h, I_h, R_h, E_v, I_v)^T, \tag{30}$$

which represent the noninfected and the infected humans and mosquitoes, respectively. The nonzero component of the disease-free equilibrium is:

$$x_s^* := \left(N_h^*, N_v^*\right)^T. \tag{31}$$

The original model is then written on the domain $\mathcal{G}$ in the matrix form:

$$x_s'(t) = A_1(x(t))(x_s(t) - x_s^*) + A_{12}(x)x_i(t), \tag{32}$$

$$x_i'(t) = A_2(x(t))x_i(t), \tag{33}$$

where

$$A_1(x) = \begin{pmatrix} \psi_h - c(N_h)\beta_{hv}I_v - \mu_{1h} - \mu_{2h}N_h^* - \mu_{2h}N_h & 0 \\ 0 & -c(N_h)(\beta_{vh}I_h + \tilde{\beta}_{vh}R_h) - \mu_{2h}N_v \end{pmatrix}, \tag{34}$$

$$A_{12}(x) = \begin{pmatrix} \psi_h - \mu_{2h}N_h^* & \psi_h - \mu_{2h}N_h^* & \psi_h - \mu_{2h}N_h^* + \rho_h & 0 & -c(N_h)N_h^* \\ 0 & -c(N_h)N_v^*\beta_{vh} & -c(N_h)N_v^*\tilde{\beta}_{vh} & \psi_v - \mu_{2h}N_v^* & \psi_v - \mu_{2h}N_v^* \end{pmatrix}, \tag{35}$$

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$$A_2(x)=\begin{pmatrix} -\nu_h-f_h(N_h) & 0 & 0 & 0 & c(N_h)\beta_{hv}S_h \\ \nu_h & -\gamma_h-\delta_h-f_h(N_h) & 0 & 0 & 0 \\ 0 & \gamma_h & -\rho_h-f_h(N_h) & 0 & 0 \\ 0 & c(N_h)\beta_{vh}S_v & c(N_h)\tilde{\beta}_{vh}S_v & -\nu_v-f_v(N_v^*) & 0 \\ 0 & 0 & 0 & \nu_v & -f_v(N_v^*) \end{pmatrix}. \tag{36}$$

For the entries of the matrices appearing in Eq. (32)–(33), we use the abbreviation $c(N_h) \equiv c(N_h, N_v^*) = \frac{\sigma_h\sigma_v}{\sigma_h N_h+\sigma_v N_v^*}$ because $N_v = N_v^* = \text{const}$ on $\mathcal{G}$.

Following Kamgang and Sallet (2008), in Eq. (32)–(33), the algebraic structure of A_1 and A_2 as Metzler matrices is essential. A matrix is called Metzler if its non-diagonal entries are nonnegative (Jacquez and Simons, 1993). The matrix A_2 must be irreducible, which explains why we further restrict the domain of the system to:

$$\tilde{\mathcal{G}} = \{x \in \mathcal{G} : x_s \neq 0\}. \tag{37}$$

The set $\tilde{\mathcal{G}}$ is positively invariant because only the initial point of any trajectory can have $x_s = 0$. From Eq. (1) and (5), we have $S_h' > 0$ and $S_v' > 0$ whenever $S_h = 0$ and $S_v = 0$, respectively. Thus:

$$A_2(x) \text{ is Metzler and irreducible for all } x \in \tilde{\mathcal{G}}.$$

The diagonal entries of $A_1(x)$ are negative because $\psi_h \leq \mu_{1h} + \mu_{2h}N_h^*$ in view of Eq. (16). Therefore,

$$x_S^* \text{ is a GAS equilibrium of the system reduced to the subdomain} \{x \in \tilde{\mathcal{G}} : x_i = 0\}. \tag{38}$$

Theorem 4.3 in Kamgang and Sallet (2008) gives the GAS of the equilibrium of a dissipative system of the form of Eq. (32)–(33), which satisfies Eq. (3) and (38) provided there exists a matrix $\overline{A}_2$ with the additional properties:

$$A_2(x) \leq \overline{A}_2,\ x \in \tilde{\mathcal{G}}, \tag{39}$$

$$\text{if } A_2(\overline{x}) = A_2 \text{ for some } \overline{x} = (\overline{x}_s\ \overline{x}_i)^T \in \tilde{\mathcal{G}} \text{ then } \overline{x}_i = 0, \tag{40}$$

$$\alpha(\overline{A}_2) \leq 0, \tag{41}$$

where $\alpha(A)$ denotes the largest real part of the eigenvalues of A. For Eq. (32)–(33) using the fact that:

$$f_h(N_h) \geq f_h(N_h^{\#}), \tag{42}$$

$$c(N_h) \leq c(N_h^{\#}), \tag{43}$$

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$$c(N_h)S_h \le c(N_h^{\#})N_h, \tag{44}$$

we obtain the upper bound of $A_2(x)$:

$$\overline{A}_2 = \begin{pmatrix} -\nu_h - f_h(N_h^{\#}) & 0 & 0 & 0 & c(N_h^*)\beta_{hv}N_h^* \\ \nu_h & -\gamma_h - \delta_h - f_h(N_h^{\#}) & 0 & 0 & 0 \\ 0 & \gamma_h & -\rho_h - f_h(N_h^{\#}) & 0 & 0 \\ 0 & c(N_h^{\#})\beta_{vh}N_v^* & c(N_h^{\#})\tilde{\beta}_{vh}N_v^* & -\nu_v - f_v(N_v^*) & 0 \\ 0 & 0 & 0 & \nu_v & -f_v(N_v^*) \end{pmatrix}. \tag{45}$$

The last entry in row 1 of A_2 is bounded as $c(N_h)\beta_{hv}S_h \le c(N_h)\beta_{hv}N_h \le c(N_h^*)\beta_{hv}N_h^*$ because $c(N_h)\beta_{hv}N_h$ is an increasing function of N_h. In the third row of $A_2 c(N_h) \le c(N_h^{\#})$ because $c(N_h)$ is a decreasing function of N_h.

The equality $A_2(x) = \overline{A}_2(x)$ is possible only when $S_h = N_h$ and $S_v = N_v^*$ which implies $x_i = 0$. Therefore both Eq. (39) and (40) hold.

Theorem 6. *The matrix $\overline{A}_2$ is a Metzler matrix which satisfies stability condition Eq. (41) whenever the basic reproduction number in Eq. (27) satisfies the inequality:*

$$R_0 \le \xi, \tag{46}$$

where the additional threshold number ξ is given by:

$$\xi = \left(\frac{\sigma_h N_h^{\#} + \sigma_v N_v^*}{\sigma_h N_h^* + \sigma_v N_v^*} \times \frac{\nu_h + \mu_{1h} + \mu_{2h} N_h^{\#}}{\nu_h + \mu_{1h} + \mu_{2h} N_h^*} \times \frac{\gamma_h + \delta_h + \mu_{1h} + \mu_{2h} N_h^{\#}}{\gamma_h + \delta_h + \mu_{1h} + \mu_{2h} N_h^*} \times \frac{\beta_{vh} + \tilde{\beta}_{vh} \frac{\gamma_h}{\rho_h + \mu_{1h} + \mu_{2h} N_h^*}}{\beta_{vh} + \tilde{\beta}_{vh} \frac{\gamma_h}{\rho_h + \mu_{1h} + \mu_{2h} N_h^{\#}}} \right)^{1/2}. \tag{47}$$

We apply Theorem 4.3 in Kamgang and Sallet (2008) and conclude that under condition (46), the disease-free equilibrium $(x_s^*, 0)$ is GAS on $\tilde{\mathcal{G}}$. From Eq. (37) for the points of $\mathcal{G}$ where $x_s = 0$, and from Eq. (46):

$$\text{the disease-free equilibrium is GAS on } \mathcal{G}. \tag{48}$$

Combining Theorem 4, Theorem 5, and Eq. (48) leads to:

Theorem 7. *If the values of the parameters of Eq. (1)–(7) are such that Eq. (20) and (46) hold, then the disease-free equilibrium is GAS on $\mathcal{D}$.*

Using the fact that $N_h^{\#} \le N_h^*$, we have $\xi \le 1$. Therefore, the result in Theorem 7 is consistent with the bifurcation analysis in Chitnis et al. (2006) who proved that if $\delta_h = 0$, the bifurcation at $R_0 = 1$ is forward supercritical. If $\delta_h = 0$, then $N_h^{\#} = N_h^*$ and

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Table 3. Threshold numbers for the three sets of parameter values and the stability of DFE

	Set 1	Set 2	Set 3
R_0	0.9503	0.9898	4.4402
ξ	0.9583	0.4124	not relevant
Threshold condition	$R_0 \leq \xi$	$\xi < R_0 < 1$	$R_0 > 1$
Stability of DFE	GAS	asymptotically stable (possibly co-exists with endemic equilibrium)	unstable

$\xi = 1$. This means that the DFE is GAS whenever $R_0 \leq 1$, which also implies that in this case the DFE is the unique equilibrium (no co-existence with an endemic equilibrium-EE). If $\delta_h > 0$, $\xi < 1$, then it is possible to have co-existence with an EE for $R_0 \in (\xi, 1]$. To confirm whether or not the backward phenomenon occurs in this case, one can use the center manifold theory, which provides sufficient conditions (Carr, 1981; Castillo-Chavez and Song, 2004; Garba et al., 2011). The three sets of values of the parameters given in Table 2 represent three qualitatively different cases with respect to the values of the threshold parameters (Table 3). Numerical simulations in Section 4 show the stability property of DFE in these three cases.

In particular, when $\xi < R_0 < 1$ the DFE may co-exist with two endemic equilibria (EE), one asymptotically stable and one unstable.

4. A NONSTANDARD FINITE DIFFERENCE SCHEME

We design a nonstandard finite difference (NSFD) scheme, which is consistent with the dynamics of the continuous malaria model of Eq. (1)–(7). For the numerical approximation of the model of Eq. (1)–(7), we replace the continuous time variable $t \in [0, \infty)$ by discrete nodes $t_n = n\Delta t$, $n \in \mathbb{Z}$ where Δt is the step size. We wish to find approximate solutions S_h^n, E_h^n, I_h^n, R_h^n, S_v^n, E_v^n, I_v^n, N_h^n, and N_v^n of S_h, E_h, I_h, R_h, S_v, E_v, I_v, N_h, and N_v at the time $t = t_n$. Our NSFD scheme reads as:

$$\frac{S_h^{n+1} - S_h^n}{\phi(\Delta t)} = \Lambda_h + \psi_h N_h^n + \rho_h R_h^{n+1} - c(N_h^n, N_v^n)\beta_{hv} I_v^n S_h^{n+1} - f_h(N_h^n) S_h^{n+1}, \tag{49}$$

$$\frac{E_h^{n+1} - E_h^n}{\phi(\Delta t)} = c(N_h^n, N_v^n)\beta_{hv} I_v^n S_h^{n+1} - \nu_h E_h^{n+1} - f_h(N_h^n) E_h^{n+1}, \tag{50}$$

$$\frac{I_h^{n+1} - I_h^n}{\phi(\Delta t)} = \nu_h E_h^{n+1} - (\gamma_h + f_h(N_h^n) + \delta_h) I_h^{n+1}, \tag{51}$$

$$\frac{R_h^{n+1} - R_h^n}{\phi(\Delta t)} = \gamma_h I_h^{n+1} - \rho_h R_h^{n+1} - f_h(N_h^n) R_h^{n+1}, \tag{52}$$

$$\frac{S_v^{n+1} - S_v^n}{\phi(\Delta t)} = \psi_v N_v^n - c(N_h^n, N_v^n)(\beta_{vh} I_h^n + \tilde{\beta}_{vh} R_h^n) S_v^{n+1} - f_v(N_v^n) S_v^{n+1}, \tag{53}$$

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$$\frac{E_v^{n+1}-E_v^n}{\phi(\Delta t)} = c(N_h^n, N_v^n)(\beta_{vh} I_h^n + \tilde{\beta}_{vh} R_h^n) S_v^{n+1} - \nu_v E_v^{n+1} - f_v(N_v^n) E_v^{n+1}, \tag{54}$$

$$\frac{I_v^{n+1}-I_v^n}{\phi(\Delta t)} = \nu_v E_v^{n+1} - f_v(N_v^n) I_v^{n+1}. \tag{55}$$

The numerical scheme of Eq. (49)–(55) is called a nonstandard finite difference method (Mickens, 1994; Anguelov and Lubuma, 2001, 2003) because nonlinear terms are approximated in a nonlocal way by using more than one mesh point: for instance $c(N_h,\ N_v)\beta_{hv} I_v S_h$ is approximated by $c(N_h^n, N_v^n)\beta_{hv} I_v^n S_h^{n+1}$ instead of $c(N_h^n, N_v^n)\beta_{hv} I_v^n S_h^n$, and because the standard denominator Δt of the discrete derivatives is replaced by a more complex function positive $\phi(\Delta t)$ which satisfies the condition:

$$\phi \equiv \phi(\Delta t) = \Delta t + O((\Delta t)^2). \tag{56}$$

The denominator function should reflect the essential qualitative features of the original continuous model. The NSFD scheme of Eq. (49)–(55) is inspired by the family of schemes that Anguelov et al. (2009a, 2009b, 2010a, 2011, 2012) designed for the basic MSEIR compartmental model. Eq. (49)–(55) are implicit but at every step they only require the solution of the linear system:

$$\begin{aligned} &A(x^n)\left(S_h^{n+1},\ E_h^{n+1},\ I_h^{n+1},\ R_h^{n+1},\ S_v^{n+1},\ E_v^{n+1},\ I_v^{n+1}\ \right)^T \\ &\quad = \left(S_h^n + \phi(\Delta t)(\Lambda_h + \psi_h N_h^n),\ E_h^n,\ I_h^n,\ R_h^n,\ S_v^n + \phi(\Delta t)\psi_v N_v^n,\ E_v^n,\ I_v^n\right)^T, \end{aligned} \tag{57}$$

where

$$A(x^n) = \begin{pmatrix} A_{11}(x^n) & 0 \\ 0 & A_{22}(x^n) \end{pmatrix}, \tag{58}$$

$$A_{11}(x^n) = \begin{pmatrix} 1+\phi(c^n\beta_{hv} I_v^n + f_h^n) & 0 & 0 & -\phi\rho_h \\ -\phi c^n \beta_{hv} I_v^n & 1+\phi(\nu_h + f_h^n) & 0 & 0 \\ 0 & -\phi\nu_h & 1+\phi(\gamma_h + f_h^n + \delta_h) & 0 \\ 0 & 0 & -\phi\gamma_h & 1+\phi(\rho_h + f_h^n) \end{pmatrix}, \tag{59}$$

$$A_{22}(x^n) = \begin{pmatrix} 1+\phi(c^n(\beta_{vh} I_h^n + \tilde{\beta}_{vh} R_h^n) + f_v^n) & 0 & 0 \\ -\phi c^n(\beta_{vh} I_h^n + \tilde{\beta}_{vh} R_h^n) & 1+\phi(\nu_v + f_v^n) & 0 \\ 0 & -\phi\nu_v & 1+\phi f_v^n \end{pmatrix}, \tag{60}$$

and we use the abbreviations $c^n = c(N_h^n, N_v^n)$, $f_h^n = f_h(N_h^n)$, $f_v^n = f_v(N_v^n)$, $\phi = \phi(\Delta t)$.

First, using the sign structure of the matrices A_{11} and A_{22} and the fact that their columns are strictly diagonally dominated, we deduce that A_{11} and A_{22} are M-matrices for $x^n \in \mathcal{D}$. This implies that $A_{11}^{-1} \geq 0$ and $A_{22}^{-1} \geq 0$. Therefore, the scheme of Eq. (49)–(55) preserves the nonnegativity of the solutions of the continuous model. In particular, Eq. (49)–(55) define a discrete dynamical system on the domain $\mathcal{D}$.

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Second, by adding Eq. (49)–(52) we obtain the discrete scheme for the human population:

$$\frac{N_h^{n+1} - N_h^n}{\phi(\Delta t)} = \Lambda_h + \psi_h N_h - f_h(N_h^n) N_h^{n+1} - \delta_h I_h^{n+1}, \tag{61}$$

or, equivalently:

$$(1 + \phi(\Delta t) f_h(N_h^n)) N_h^{n+1} + \phi(\Delta t)\delta_h I_h^{n+1} = (1 + \phi(\Delta t)\psi_h) N_h^n + \phi(\Delta t)\Lambda_h. \tag{62}$$

Hence the sequence (N_h^n) satisfies the inequalities:

$$\underline{F}_h(N_h^n) \le N_h^{n+1} \le \overline{F}_h(N_h^n) \tag{63}$$

where

$$\underline{F}_h(y) = \frac{(1 + \phi(\Delta t)\psi_h) y + \phi(\Delta t)\Lambda_h}{1 + \phi(\Delta t) f_h(y) + \phi(\Delta t)\delta_h},$$
$$\overline{F}_h(y) = \frac{(1 + \phi(\Delta t)\psi_h) y + \phi(\Delta t)\Lambda_h}{1 + \phi(\Delta t) f_h(y)}.$$

N_h^* is a fixed point of $\overline{F}_h$ while $N_h^\#$ is a fixed point of $\underline{F}_h$. The positivity property is preserved with the standard denominator Δt in place of $\phi(\Delta t)$. However, for the preservation of other properties including a discrete conservation law, we use a denominator function satisfying Eq. (56) as well as:

$$\phi(\Delta t) \le (\Lambda_h \mu_{2h})^{-\frac{1}{2}}. \tag{64}$$

If $\Lambda_h = 0$ or $\mu_{2h} = 0$, the function $\phi(\Delta t)$ need not be bounded. We take:

$$\phi(\Delta t) = (\Lambda_h \mu_{2h})^{-\frac{1}{2}} \left(1 - e^{-\Delta t (\Lambda_h \mu_{2h})^{\frac{1}{2}}}\right).$$

Under Eq. (64), we have:

$$\frac{d\underline{F}_h}{dy} = \frac{(1 + \phi(\Delta t)\psi_h)(1 + \phi(\Delta t)(\mu_{1h} + \delta_h)) - \phi^2(\Delta t)\Lambda_h \mu_{2h}}{(1 + \phi(\Delta t) f_h(y) + \phi(\Delta t)\delta_h)^2} > 0,$$
$$\frac{d\overline{F}_h}{dy} = \frac{(1 + \phi(\Delta t)\psi_h)(1 + \phi(\Delta t)\mu_{1h}) - \phi^2(\Delta t)\Lambda_h \mu_{2h}}{(1 + \phi(\Delta t) f_h(y))^2} > 0.$$

Using Theorems 1, 2, and 3 in Anguelov and Lubuma (2003), we obtain that the difference schemes:

$$N_h^{n+1} = \overline{F}_h(N_h^n), \tag{65}$$

$$N_h^{n+1} = \underline{F}_h(N_h^n), \tag{66}$$

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replicate correctly the behavior of the solutions of differential Eq. (15) and (18) they approximate. They preserve the monotonicity of the solutions, the equilibria, and their basins of attraction. In this case we actually have replication of all topological dynamical properties of the original dynamical system, a concept which in Anguelov et al. (2011) is referred to as topological dynamic consistency. In particular, denoting by $(\overline{N}_h^n)$ and $(\underline{N}_h^n)$ the solutions of Eq. (65) and (66) respectively, the solution of Eq. (62) satisfies the analogue of the conservation law, Eq. (22):

$$\underline{N}_h^n \leq N_h^n \leq \overline{N}_h^n, \quad n \in \mathbb{N} \tag{67}$$

provided that the sequences are initialed at the same point. Using similar techniques in the simpler case of the vector population we obtain that the sequence $(N_v^n)_{n\in\mathbb{N}}$ satisfies the difference equation:

$$N_v^{n+1} = F_v(N_v^n), \tag{68}$$

where

$$F_v(y) = \frac{(1+\phi(\Delta t)\psi_v)y}{1+\phi(\Delta t)f_v(y)}, \tag{69}$$

which is topologically dynamically consistent and hence replicates correctly the dynamics of the continuous dynamical Eq. (11). The next theorem is obtained by using the dynamic consistency of Eq. (65), (66), and (68) as well as inequalities (67). The proof is similar to the proof of Theorem 4.

Theorem 8. *The set $\mathcal{G}$ given in Eq. (28) is GAS for the discrete dynamical system (49)–(55) defined on $\mathcal{D}$ under the condition (64).*

In view of Theorem 8 and of the analogue of Theorem 5 for discrete dynamical systems, the analysis of the asymptotic behavior of the solutions of Eq. (49)–(55) is restricted to the compact set $\mathcal{G}$. Using a discrete equivalent of the theorem of Kamgang and Sallet established in Anguelov et al. (2010a), we obtain:

Theorem 9. *If the values of the parameters of Eq. (1)–(7) are such that Eq. (20) and (46) hold, then the DFE is a GAS equilibrium of the discrete dynamical system (49)–(55), with Eq. (64), on $\mathcal{D}$.*

For numerical simulations we use the nonstandard scheme (49)–(55) due to the established consistency with Eq. (1)–(7). Standard numerical methods fail to preserve the dynamics of continuous models. We consider the three sets of data shown on Table 2. Figure 2 represents the coordinates related to the human population in a solution. After a short initial period the rate of change of the compartments is comparable with the rate of change of the total population (plot on the left). The solution approaches the DFE but due to the relatively slow change in the population size due to its vital dynamics (births, deaths, migration) it takes relatively longer to reach a close proximity of the DFE. The total population always remains between $\underline{N}_h$ and $\overline{N}_h$ in this case, being practically indistinguishable from $\overline{N}_h$ (plot on the right).

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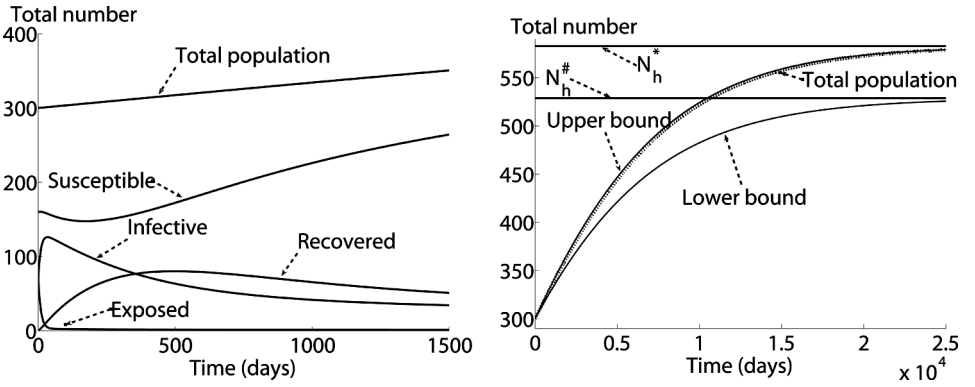


Figure 2. Human population for parameter values from Set 1 in Table 2. Left: by compartment; right: total population, its lower bound $\underline{N}_h$ and its upper bound $\overline{N}_h$ in terms of Eq. (22) (right).

Similarly, the plots in Figure 3 are obtained for the model with values of the parameters from Set 2. Two solutions are represented, one converging to the DFE (bottom) and one converging to an EE (top). In both cases the conservation law

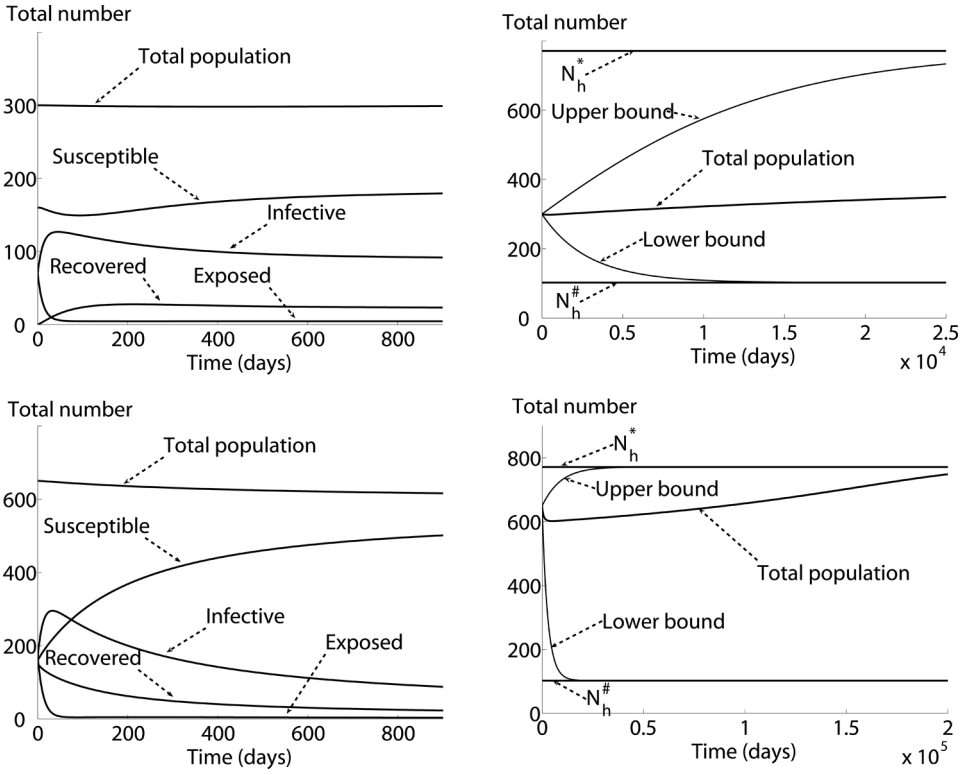


Figure 3. Human population for parameter values from Table 2, Set 2: by compartment (left); total population, its lower bound $\underline{N}_h$ and its upper bound $\overline{N}_h$ in terms of Eq. (22) (right); converging to EE (top); converging to DFE (bottom).

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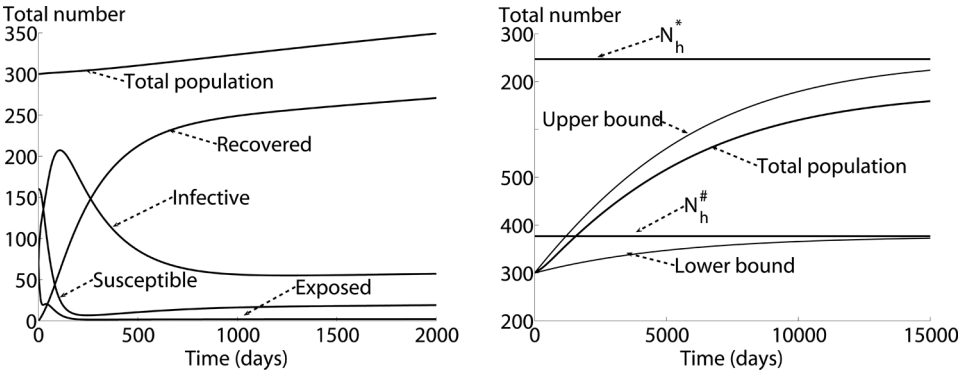


Figure 4. Human population for parameter values from 2, Set 3: by compartment (left); total population, its lower bound $\underline{N}_h$ and its upper bound $\overline{N}_h$ in terms of Eq. (22) (right).

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(22) is preserved (plots on the right). The initial dip in the total population size occurs when the solution approaches the DFE (bottom, right).

Figure 4 shows a solution obtained by parameter values from Set 3 and initialed at a point outside the disease-free manifold ($E_h = I_h = R_h = E_h = I_h = 0$). All such solutions converge to an EE.

Figures 5, 6, and 7 provide phase diagrams on the indicated plane with each of the three sets of parameter values. The five pointed stars indicate the initial points of the trajectories. The shaded area is the projection of the set $\mathcal{G}$. An invariant manifold of one dimension less is indicated on each Figure. The EE and the DFE co-exist on Figure 6. There are two asymptotically stable equilibria, denoted by circled stars and an unstable equilibrium denoted by a circle, all within region $\mathcal{G}$. This unstable

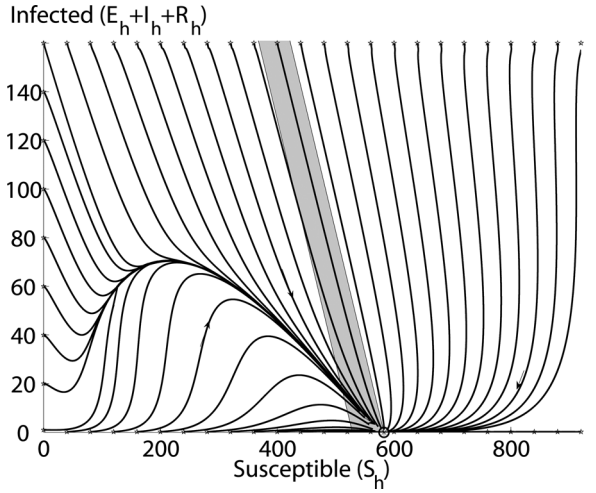


Figure 5. GAS of DFE: Phase diagram of Infected ($E_h + I_h + R_h$) versus Susceptible (S_h) for the model with parameter values from Table 2, Set 1.

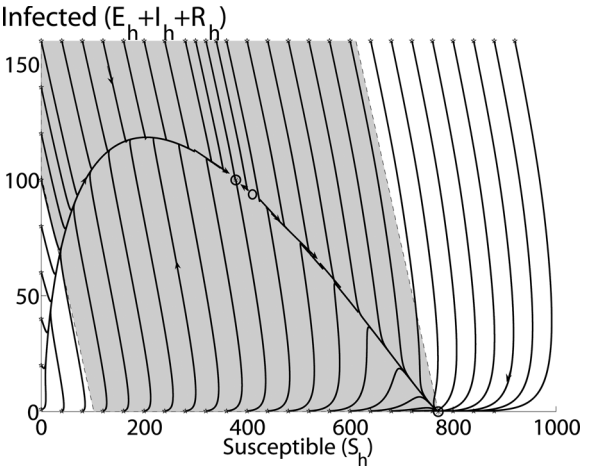


Figure 6. Backward bifurcation: Phase diagram of Infected ($E_h + I_h + R_h$) versus Susceptible (S_h) for the model with parameter values from Table 2, Set 2.

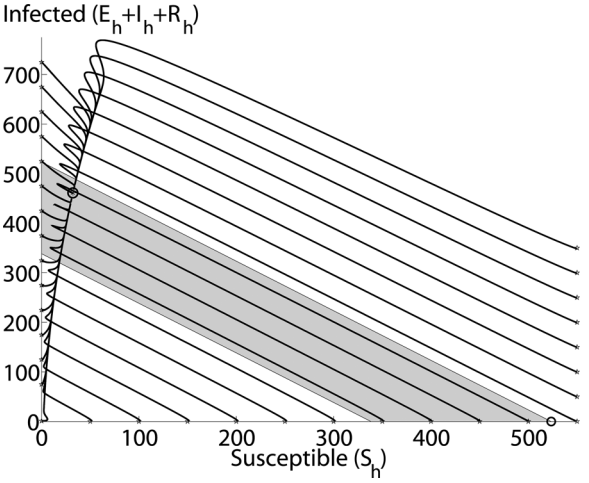


Figure 7. Unstable DFE: Phase diagram of Infected ($E_h + I_h + R_h$) versus Susceptible (S_h) for the model with parameter values from Table 2, Set 3.

equilibrium, which is a saddle point, actually accounts for the dip in the population size observed on Figure 3.

5. CONCLUSION

We have proved the global asymptotic stability of the disease-free equilibrium in the Chitnis et al. (2006, 2008) model and specified the region of its backward bifurcation. We have designed a nonstandard finite difference scheme that is dynamically consistent with the original model. A possible extension of this work is in the setting of the sterile insect technique (Dumont and Tchuenche, 2012).

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6. APPENDIX: PROOFS OF MAIN RESULTS

Proof of Theorem 4. With Eq. (15) and (18) appended with initial condition (21), we associate Eq. (11) with the initial condition:

$$N_v(0) = N_v^0. \tag{70}$$

For $\varepsilon > 0$, denote:

$$B_\varepsilon(\mathcal{G}) = \Big\{ (S_h, E_h, I_h, R_h, S_v, E_v, I_v) \in \mathcal{D} | N_h^\# - \varepsilon < N_h < N_h^* + \varepsilon, \\ N_v^* - \varepsilon < N_v < N_v^* + \varepsilon \Big\}. \tag{71}$$

The collection of sets $\{B_\varepsilon(\mathcal{G})\colon \varepsilon > 0\}$ is a complete neighborhood system of the compact set $\mathcal{G}$ in the relative topology of $\mathcal{D}$. This means that for the neighborhood sets in Definitions 2 and 3, it is enough to consider the sets in this collection. Consider an arbitrary $\varepsilon > 0$. The points N_v^*, N_h^*, and $N_h^\#$ are globally asymptotically stable equilibria of the dynamical systems defined by Eq. (11), (15), and (18) respectively on the interval $(0, +\infty)$. For any initial point of Eq. (1)–(7), $N_h^0 \in (0, +\infty)$ and $N_v^0 \in (0, +\infty)$. Therefore there exists $t_\varepsilon > 0$ such that for any $t > t_\varepsilon$ we have:

$$N_h^\# - \varepsilon < \underline{N}_h(t) \le N_h(t) \le \overline{N}_h(t) < N_h^* + \varepsilon, \tag{72}$$

$$N_v^* - \varepsilon < N_v(t) < N_v^* + \varepsilon \tag{73}$$

or, equivalently:

$$(S_h(t),\, E_h(t),\, I_h(t),\, R_h(t),\, S_v(t),\, E_v(t),\, I_v(t)) \in B_\varepsilon(\mathcal{G}). \tag{74}$$

This proves that $\mathcal{G}$ is a global attractor. Due to the monotonicity of $\underline{N}_h(t)$, $\overline{N}_h(t)$, and $N_v(t)$ we have:

$$\begin{cases} N_h^\# - \varepsilon < N_h^0 < N_h^* + \varepsilon \\ N_v^* - \varepsilon < N_v^0 < N_v^* + \varepsilon \end{cases} \Rightarrow \begin{cases} N_h^\# - \varepsilon < \underline{N}_h(t) \le N_h(t) \le \overline{N}_h(t) < N_h^* + \varepsilon \\ N_v^* - \varepsilon < N_v(t) < N_v^* + \varepsilon \end{cases} \tag{75}$$

This means that any solution of Eq. (1)–(7) which starts from a point in $B_\varepsilon(\mathcal{G})$ remains in $B_\varepsilon(\mathcal{G})$. This shows that the set $\mathcal{G}$ is stable. □

Proof of Theorem 5. The proofs are similar for discrete and continuous dynamical systems. In the case of continuous dynamical system defined on $\mathcal{D}$ by a system of ODEs:

$$y' = f(y), \tag{76}$$

the set M considered in the theorem is closed and therefore compact because the closure of an invariant set is also an invariant set. For $y(y_0, t)$ a solution of Eq. (76) satisfying $y(y_0, 0) = y_0$, denote by $\Omega(y^0)$ the positive limit set of $y(y_0, t)$ (LaSalle, 1976):

$$\Omega(y^0) = \bigcap_{0<T<+\infty} \text{closure}(\{y(y_0, t) : t \ge T\}).$$

As $\Omega(y^0) \subseteq \mathcal{E}$, using the properties of limit sets in chs. 2.4 and 2.5 of LaSalle (1976), $\Omega(y_0)$ is an invariant set. Therefore, $\Omega(y_0) \subset M$. The set $\Omega(y_0)$ is closed, it is also compact. The fact that any neighborhood of $\Omega(y_0)$ contains $y(y_0, t)$ for t sufficiently large implies the same property for any neighborhood of M. Hence M is a global attractor. The proof of the stability is based on the same approach as in LaSalle (1968), though not using a Lyapunov function. Assume that M is not stable. Then, there exists a neighborhood W of M such that given any positive integer n there exist y_n and $\tau_n > 0$ satisfying $\text{dist}(y_n, M) < \frac{1}{n}$ and $y(y_n, \tau_n) \in \partial W$. Using compactness, we assume without loss of generality that the sequences (y_n) and (τ_n) are such that $\lim_{n\to\infty} y_n = \hat{y} \in M$ and $\lim_{n\to\infty} y(y_n, \tau_n) = q \in \partial W$. With the fixed sequence (y_n), we associate the set:

$$\gamma^+ = \{z : \exists (t_n) : \lim_{n\to\infty} y(y_n, t_n) = z,\ z \notin M\}, \tag{77}$$

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which is nonempty because $q \in \gamma^+$. Let $z \in \gamma^+$ and let (t_n) be a corresponding sequence. For each such time sequence we have $\lim_{n\to\infty} t_n = +\infty$. Because if (t_n) has a subsequence (t_{n_j}) which converges to some $\tilde{t} \in (0, +\infty)$ then $\lim_{n\to\infty} y(y_n, t_n) = y(\hat{y}, \tilde{t}) \in M$, which is a contradiction. For any $t \in (-\infty, +\infty)$, the sequence $(y(y_n, t_n + t))$ is defined for sufficiently large n because we are dealing with a positive dynamical system. In view of the semigroup property of the solution operator, we have $\lim_{n\to\infty} y(y_n, t_n + t) = \lim_{n\to\infty} y(y(y_n, t_n), t) = y(z, t)$. The set M being invariant and $z \notin M$, $y(z, t) \notin M$. Therefore $y(z, t) \in \gamma^+$ with $(t_n + t)$ as an associated time sequence. This implies that γ^+ is both a positive and a negative invariant set of the dynamical system on $\mathcal{D}$. Then we use the stability of $\mathcal{E}$ to show that $\gamma^+ \subset \mathcal{E}$. Let U be an arbitrary neighborhood of $\mathcal{E}$. From the stability of $\mathcal{E}$ there exists a neighborhood $\hat{U}$ of $\mathcal{E}$ such that $y(y_0, t) \in U$ for all $t \geq 0$ whenever $y_0 \in \hat{U}$. Due to the fact that dist $(y_n, \mathcal{E}) \leq \text{dist}(y_n, M) \to 0$, $y_n \in \hat{U}$ for sufficiently large n. This implies that $y(y_n, t) \in U$ for sufficiently large n. Therefore, for every $z \in \gamma^+$, $z = \lim_{n\to\infty} y(y_n, t_n) \in$ closure (U). Because U is arbitrary and due to the compactness of $\mathcal{E}$, $z \in \mathcal{E}$. Hence $\gamma^+ \subseteq \mathcal{E}$. Because M is the largest invariant subset of $\mathcal{E}$ we have $\gamma^+ \subseteq M$, which contradicts the definition of the set γ^+ in Eq. (77). This completes the proof of Theorem 5. □

Proof of Theorem 6. We write the matrix $\overline{A}_2$ defined in Eq. (45) in a block form:

$$\overline{A}_2 = \begin{pmatrix} B & C \\ D & E \end{pmatrix}, \tag{78}$$

where B is a 3×3 matrix and E is a 2×2 matrix. Using Kamgang and Sallet (2008) or Lemma 5 in Dumont et al. (2008), $\overline{A}_2$ is a stable Metzler matrix if and only if B and $E - DB^{-1}C$ are stable Metzler matrices. The matrix B is lower triangular with negative diagonal entries. Hence it is a stable Metzler matrix. Moreover, its inverse being:

$$B^{-1} = -\begin{pmatrix} \frac{1}{\nu_h + f_h(N_h^\#)} & 0 & 0 \\ \frac{\nu_h(\rho_h + f_h(N_h^\#))}{d} & \frac{1}{\gamma_h + \delta_h + f_h(N_h^\#)} & 0 \\ \frac{\nu_h \gamma_h}{d} & \frac{\gamma_h(\nu_h + f_h(N_h^\#))}{d} & \frac{1}{\rho_h + f_h(N_h^\#)} \end{pmatrix}, \tag{79}$$

where $d = |\det(B)| = (\nu_h + f_h(N_h^\#))(\gamma_h + \delta_h + f_h(N_h^\#))(\rho_h + f_h(N_h^\#))$, we have:

$$B^{-1}C = -\begin{pmatrix} 0 & \frac{c(N_h^*)\beta_{hv}N_h^*}{\nu_h + f_h(N_h^\#)} \\ 0 & \frac{c(N_h^*)\beta_{hv}N_h^*\nu_h(\rho_h + f_h(N_h^\#))}{d} \\ 0 & \frac{c(N_h^*)\beta_{hv}N_h^*\nu_h\gamma_h}{d} \end{pmatrix}, \tag{80}$$

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$$DB^{-1}C = -\begin{pmatrix} 0 & \frac{c(N_h^*)\beta_{hv}N_h^*c(N_h^{\#})N_v^*\nu_h(\beta_{vh}(\rho_h+f_h(N_h^{\#}))+\tilde{\beta}_{vh}\gamma_h)}{d} \\ 0 & 0 \end{pmatrix}, \tag{81}$$

and

$$E - DB^{-1}C = \begin{pmatrix} -\nu_v - f_v(N_v^*) & \frac{c(N_h^*)\beta_{hv}N_h^*c(N_h^{\#})N_v^*\nu_h(\beta_{vh}(\rho_h+f_h(N_h^{\#}))+\tilde{\beta}_{vh}\gamma_h)}{d} \\ \nu_v & -f_v(N_v^*) \end{pmatrix}. \tag{82}$$

Using the fact that $\mathrm{tr}(E - DB^{-1}C) < 0$, we have:

$$\alpha(E - DB^{-1}C) \leq 0 \text{ if and only if } \det(E - DB^{-1}C) \leq 0, \tag{83}$$

or, equivalently:

$$(\nu_v + f_v(N_v^*)f_v(N_v^*) - \nu_v \frac{c(N_h^*)\beta_{hv}N_h^*c(N_h^{\#})N_v^*\nu_h(\beta_{vh}(\rho_h + f_h(N_h^{\#})) + \tilde{\beta}_{vh}\gamma_h)}{(\nu_h + f_h(N_h^{\#}))(\gamma_h + \delta_h + f_h(N_h^{\#}))(\rho_h + f_h(N_h^{\#}))} \leq 0, \tag{84}$$

which means that:

$$\frac{c(N_h^*)N_h^*c(N_h^{\#})N_v^*\nu_h\nu_v\beta_{hv}\left(\beta_{vh} + \tilde{\beta}_{vh}\frac{\gamma_h}{\rho_h+f_v(N_h^{\#})}\right)}{(\nu_h + f_h(N_h^{\#}))(\gamma_h + \delta_h + f_h(N_h^{\#}))(\nu_v + f_v(N_v^*))f_v(N_v^*)} \leq 1. \tag{85}$$

With the basic reproduction number in Eq. (27), the threshold inequality (85) is equivalent to inequality (46). □

Proof of Theorem 9. We consider here only the case $R_0 < \xi$ or equivalently:

$$\alpha(\overline{A}_2) < 0. \tag{86}$$

The proof is based on an application of Theorem 3 in Anguelov et al. (2010a). We write the system in a form similar to Eq. (32)–(33) as:

$$x_s^{n+1} = g(x_s^n, x_i^n), \tag{87}$$

$$P(N_h^n)x_i^{n+1} = Q(x_s^{n+1})x_i^n, \tag{88}$$

where

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$$P(N^n)=\begin{pmatrix} 1+\phi(\nu_h+f_h^n) & 0 & 0 & 0 & 0 \\ -\phi\nu_h & 1+\phi(\gamma_h+f_h^n+\delta_h) & 0 & 0 & 0 \\ 0 & -\phi\gamma_h & 1+\phi(\rho_h+f_h^n) & 0 & 0 \\ 0 & 0 & 0 & 1+\phi(\nu_v+f_v^*) & 0 \\ 0 & 0 & 0 & -\phi\nu_v & 1+\phi f_v^* \end{pmatrix},$$

and

$$Q(x_s^{n+1})=\begin{pmatrix} 1 & 0 & 0 & 0 & \phi c^{n*}\beta_{hv}S_h^{n+1} \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & \phi c^{n*}\beta_{vh}S_v^{n+1} & \phi c^{n*}\tilde{\beta}_{vh}S_v^{n+1} & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix},$$

with the abbreviations $f_v^*=f_v(N_v^*)$, $c^{n*}=c(N_h^n,N_v^*)$, $\phi=\phi(\Delta t)$. Similarly to Eq. (32), an explicit expression for g in Eq. (87) is not needed. What is required is that the point $x_s^*=(N_h^*,N_v^*)$ is a GAS equilibrium of the corresponding subsystem whenever $x_i=0$. It is true, after substituting $x_i^n=x_i^{n+1}=0$ in Eq. (49) and (53). We have $(P(N^n))^{-1}\geq 0$ because $P(N^n)$ is an M-matrix. Hence the transition matrix $B(x^n):=(P(N_h^n))^{-1}Q(x_s^{n+1})$ in the explicit form:

$$x_i^{n+1}=(P(N_h^n))^{-1}Q(x_s^{n+1})x_i^n \tag{89}$$

of Eq. (88) is nonnegative. Theorem 3 in Anguelov et al. (2010a) yields the GAS of the DFE provided that the matrix $B(x^n)=(P(N_h^n))^{-1}Q(x_s^{n+1})$ has an irreducible upper bound $\overline{B}$ such that $\rho(\overline{B})<1$. Here, the matrix $B(x^n)$ is upper bounded on the compact set $\mathcal{G}$ given in Eq. (28) by the matrix $\overline{B}=(P(N_h^{\#}))^{-1}Q(x_s^*)$, which thanks to $Q(x_s^*)-P(N_h^{\#})=\phi\overline{A}_2$ for the matrix $\overline{A}_2$ in Eq. (45), can be written of the form:

$$\overline{B}=I+\phi(P(N_h^{\#}))^{-1}\overline{A}_2.$$

Like $\overline{A}_2$, the matrix $\overline{B}$ is irreducible. Moreover, by using the properties of nonnegative matrices (Berman and Plemmons, 1979; Dumont and Chiroleu, 2010) and by assumption (86) we deduce that $\rho(\overline{B})<1$. Therefore, the DFE is a GAS equilibrium of the discrete dynamical system defined by Eq. (49)–(55). □

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