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▶ To cite this version:

Hamadjam Abboubakar, Jean Claude Kamgang, Daniel Tieudjo. Backward Bifurcation and Control in Transmission Dynamics of Arboviral Diseases. 2015. hal-01200471v3

HAL Id: hal-01200471 https://hal.science/hal-01200471v3

Preprint submitted on 2 Nov 2015

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Backward Bifurcation and Control in Transmission Dynamics of Arboviral Diseases

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Abstract

In this paper, we derive and analyze a compartmental model for the control of arboviral diseases 8 which takes into account an imperfect vaccine combined with individual protection and some vec-9 tor control strategies already studied in the literature such as the use of adulticides, destruction of 10 breeding site, and reduction of eggs and larvae through chemical interventions. After the formulation 11 of the model, a qualitative study based on stability analysis and bifurcation theory reveals that the 12 phenomenon of backward bifurcation may occur. The stable disease-free equilibrium of the model 13 coexists with a stable endemic equilibrium when the reproduction number, \mathcal{R}_0 , is less than unity. Us-14 ing Lyapunov functions theory, we prove that the trivial equilibrium is globally asymptotically stable; 15 when the disease-induced death is not considered, or/and, when the standard incidence is replaced 16 by the mass action incidence, the backward bifurcation does not occur. Under a certain threshold 17 condition, we establish the global asymptotic stability of the disease-free equilibrium of the full model. 18 Through sensitivity analysis, we determine the relative importance of model parameters for disease 19 transmission. Numerical simulations show that the combination of several control mechanisms would 20 significantly reduce the spread of the disease, if we maintain the level of each control high, and this, 21 over a long period. 22

Keywords: Compartmental model, Arboviral diseases, Vaccination, Vector control strategies,
 Stability, Backward bifurcation, Sensitivity analysis.

²⁵ AMS Subject Classification (2010): 34D20, 34D23, 37N25, 92D30.

26 1 Introduction

Arboviral diseases are affections transmitted by hematophagous arthropods. There are cur-27 rently 534 viruses registered in the International Catalog of Arboviruses and 25% of them have 28 caused documented illness in human populations [1, 2, 3]. Examples of those kinds of diseases 29 are Dengue, Yellow fever, Saint Louis fever, Encephalitis, West Nile fever and Chikungunya. 30 A wide range of arboviral diseases are transmitted by mosquito bites and constitute a public 31 health emergency of international concern. According to World Health Organisation (WHO), 32 Dengue, caused by any of four closely-related virus serotypes (DEN-1-4) of the genus Flavivirus, 33 causes 50–100 million infections worldwide every year, and the majority of patients worldwide 34 are children aged 9 to 16 years [4, 5, 6]. The dynamics of arboviral diseases like Dengue or 35

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Chikungunya are influenced by many factors such as human and mosquito behaviours. The virus itself (multiple serotypes of dengue virus [5, 6], and multiple strains of chikungunya virus [7, 8]), as well as the environment directly or indirectly affects all the present mechanisms of control [9, 10].

For all mentioned diseases, only yellow fever has a licensed vaccine. Nonetheless, consid-40 erable efforts are made to obtain the vaccines for other diseases. In the case of Dengue for 41 example, the scientists of French laboratory SANOFI have conducted different tries in Latin 42 America and Asia. Thus, a tetravalent vaccine could be quickly set up in the coming months. 43 The tries in Latin America have shown that vaccine efficacy was 64.7%. Serotype–specific vac-44 cine efficacy was 50.3% for serotype 1, 42.3% for serotype 2, 74.0% for serotype 3, and 77.7%45 for serotype 4 [11]. The tries in Asia have shown that efficacy was 30.2%, and differed by 46 serotype [12]. In any case, it is clear that this vaccine will be imperfect. 47

Host-vector models for arboviral diseases transmission were proposed in [13, 14, 15, 16,
17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30] with the focus on the construction of the
basic reproductive ratio and related stability analysis of the disease free and endemic equilibria.
Some of these works in the literature focus on modelling the spread of arboviral diseases and its
control using some mechanism of control like imperfect vaccines [23, 24, 30] and other control
tools like individual protection and vector control strategies [13, 14, 19, 25, 27, 28].

In [19], Dumont and Chiroleu proposed a compartmental model to study the impact of vector control methods used to contain or stop the epidemic of Chikungunya of 2006 in Réunion island. Moulay et *al.* [27] studied an optimal control based on protection and vector control strategies to fight against Chikungunya. In [24], Rodrigues et *al.* simulate an hypothetical vaccine as an extra protection to the human population against epidemics of Dengue, using the optimal control theory. In those models [19, 24, 27],

 $_{60}$ (i) the population is constant,

(ii) the disease-induced death in humans is not considered,

⁶² (iii) the complete stage progression of development of vectors is not considered,

(iv) none of the above mentioned models takes into account the combination of the mechanisms
 of control already studied in the literature, such as vaccination, individual protection and
 vector control strategies (destruction of breeding site, eggs and larvae reduction).

The aim of this work is to propose and study a arboviral disease control model which takes into account human immigration, disease-induced mortality in human communities, the complete stage structured model for vectors and a combination of human vaccination, individual protection and vector control strategies to fight against the spread of these kind of diseases.

We start with the formulation of a constant control model, which is an extension of the 70 previous model developed in [30]. We include the complete stage progression of development 71 of vectors, the waning vaccine, and four others controls (individual protection, the use of 72 adulticides, destruction of breeding site, and reduction of eggs and larvae through chemical 73 interventions). We compute the net reproductive number \mathcal{N} , as well as the basic reproduction 74 number, \mathcal{R}_0 , and investigate the existence and stability of equilibria. We prove that the trivial 75 equilibrium is globally asymptotically stable whenever $\mathcal{N} < 1$. When $\mathcal{N} > 1$ and $\mathcal{R}_0 < 1$, 76 we prove that the system exhibit the backward bifurcation phenomenon. The implication of 77 this occurrence is that the classical epidemiological requirement for effective eradication of the 78 disease, $\mathcal{R}_0 < 1$, is no longer sufficient, even though necessary. However, considering two 79 situations: the model without vaccination and the model with mass incidence rates, we prove 80 that the disease-induced death and the standard incidence functions, respectively, are the main 81

causes of the occurrence of backward bifurcation. We find that the disease-free equilibrium is globally asymptotically stable under certain threshold condition. Through local and global sensitivity analysis, we determine the relative importance parameters of the model on the disease transmission. By using the pulse control technique (the control is not continuous in time order is effective only one day every T days [19]) in numerical simulations, we evaluate the impact of different control combinations on the decrease of the spread of these diseases.

The paper is organized as follows. In Section 2 we present the transmission model and in Section 3 we carry out some analysis by determining important thresholds such as the net reproductive number \mathcal{N} and the basic reproduction number \mathcal{R}_0 , and different equilibria of the model. We then demonstrate the stability of equilibria and carry out bifurcation analysis. In section 4, both local and global sensitivity analysis are used to assess the important parameters in the spread of the diseases. Section 5 is devoted to numerical simulations. A conclusion rounds up the paper.

⁹⁵ 2 The formulation of the model

The model we propose here is an extension of the previous model studied in [30], and is based on the modelling approach given in [19, 20, 21, 22, 23, 27, 28]. It is assumed that the human and vector populations are divided into compartments described by time-dependent state variables. The compartments in which the populations are divided are the following ones:

-For humans, we consider susceptible (denoted by S_h), vaccinated (V_h) , exposed (E_h) , infectious (I_h) and resistant or immune (R_h) ; So that, $N_h = S_h + V_h + E_h + I_h + R_h$. Following Garba et al. [23] and Rodrigues et al. [24], we assume that the immunity, obtained by the vaccination process, is temporary. So, we denote by ω , the waning rate of vaccine. The recruitment in human population is at the constant rate Λ_h , and newly recruited individuals enter the susceptible compartment S_h . Are concerned by recruitment people that are totally naive from the disease. Each individual human compartment goes out from the dynamics at natural mortality rates μ_h . The human susceptible population is decreased following infection, which can be acquired via effective contact with an exposed or infectious vector at a rate

$$\lambda_h = \frac{a\beta_{hv}(\eta_v E_v + I_v)}{N_h}$$
[23],

where a is the biting rate per susceptible vector, β_{hv} is the transmission probability from an 100 infected vector $(E_v \text{ or } I_v)$ to a susceptible human (S_h) . The expression of λ_h is obtained as 101 follows: the probability that a vector chooses a particular human or other source of blood to bite 102 can be assumed as $\frac{1}{N_h}$. Thus, a human receives in average $a \frac{N_v}{N_h}$ bites per unit of times. Then, 103 the infection rate per susceptible human is given by $a\beta_{hv}\frac{N_v}{N_h}\frac{(\eta_v E_v + I_v)}{N_v}$. In expression of λ_h , 104 the modification parameter $0 < \eta_v < 1$ accounts for the assumed reduction in transmissibility 105 of exposed mosquitoes relative to infectious mosquitoes [23, 30] (see the references therein for 106 the specific sources). Latent humans (E_h) become infectious (I_h) at rate γ_h . Infectious humans 107 recover at a constant rate, σ or dies as consequence of infection, at a disease-induced death 108 rate δ . After infection, immune humans retain their immunity for life. 109

¹¹⁰ – Following [27], the stage structured model is used to describe the vector population dy-¹¹¹ namics, which consists of three main stages: embryonic (E), larvae (L) and pupae (P). Even ¹¹² if eggs (E) and immature stages (L and P) are all aquatic, it is important to dissociate them ¹¹³ because, for the control point of view, drying the breeding sites does not kill eggs, but only ¹¹⁴ larvae and pupae. Moreover, chemical interventions on the breeding sites has impact on the larvae population, but not on the eggs [27]. The number of laid eggs is assumed proportional
to the number of females. The system of stage structured model of aquatic phase development
of vector is given by (see [27] for details)

$$\begin{cases} \dot{E} = \mu_b \left(1 - \frac{E}{\Gamma_E} \right) (S_v + E_v + I_v) - (s + \mu_E) E \\ \dot{L} = sE \left(1 - \frac{L}{\Gamma_L} \right) - (l + \mu_L) L \\ \dot{P} = lL - (\theta + \mu_P) P \end{cases}$$

¹¹⁸ Unlike the authors of [27], we take into account the pupal stage in the development of the vector.

This is justified by the fact that they do not feed during this transitional stage of development, as they transform from larvae to adults [10, 31]. So, the control mechanisms cannot be applied to them.

With a rate θ , pupae become female Adults. Each individual vector compartment goes out from the dynamics at natural mortality rates μ_v . The vector susceptible population is decreased following infection, which can be acquired via effective contact with an exposed or infectious human at a rate

$$\lambda_v = \frac{a\beta_{vh}(\eta_h E_h + I_h)}{N_h} \ [23]$$

where β_{vh} is the probability of transmission of infection from an infectious human $(E_h \text{ or } I_h)$ to a susceptible vector (S_v) . The modification parameter $0 \leq \eta_h < 1$ accounts for the relative infectiousness of exposed humans in relation to infectious humans. Here too, it is assumed that susceptible mosquitoes can acquire infection from exposed humans [16, 23, 30]. Latent vectors (E_v) become infectious (I_v) at rate γ_v . The vector population does not have an immune class, since it is assumed that their infectious period ends with their death [21].

Then, we add new terms in the model to assess the different control tools studied:

(i) α_1 represents the efforts made to protect human from mosquitoes bites. It mainly consists to the use of mosquito nets or wearing appropriate clothes [28]. Thus we modify the infection term as follows:

$$\lambda_h^c = (1 - \alpha_1)\lambda_h$$
, and $\lambda_v^c = (1 - \alpha_1)\lambda_v$, with $0 \le \alpha_1 < 1$; (1)

(ii) η_1 and η_2 are respectively, egg and larval mortality rates induced by chemical intervention,

(iii) c_m is the additional mortality rate due to adulticide,

(iv) α_2 is the parameter associated with the efficacy of the mechanical control.

¹³⁵ The above assumptions lead to the following non-linear system of ordinary differential equations

$$\begin{pmatrix}
\dot{S}_{h} = \Lambda_{h} + \omega V_{h} - (\lambda_{h}^{c} + \xi + \mu_{h}) S_{h} \\
\dot{V}_{h} = \xi S_{h} - [(1 - \epsilon)\lambda_{h}^{c} + \omega + \mu_{h}] V_{h} \\
\dot{E}_{h} = \lambda_{h}^{c} [S_{h} + (1 - \epsilon)V_{h}] - (\mu_{h} + \gamma_{h})E_{h} \\
\dot{I}_{h} = \gamma_{h}E_{h} - (\mu_{h} + \delta + \sigma)I_{h} \\
\dot{R}_{h} = \sigma I_{h} - \mu_{h}R_{h} \\
\dot{S}_{v} = \theta P - \lambda_{v}^{c}S_{v} - (\mu_{v} + c_{m})S_{v} \\
\dot{E}_{v} = \lambda_{v}^{c}S_{v} - (\mu_{v} + \gamma_{v} + c_{m})E_{v} \\
\dot{I}_{v} = \gamma_{v}E_{v} - (\mu_{v} + c_{m})I_{v} \\
\dot{E} = \mu_{b} \left(1 - \frac{E}{\alpha_{2}\Gamma_{E}}\right) (S_{v} + E_{v} + I_{v}) - (s + \mu_{E} + \eta_{1})E \\
\dot{L} = sE \left(1 - \frac{L}{\alpha_{2}\Gamma_{L}}\right) - (l + \mu_{L} + \eta_{2})L \\
\dot{P} = lL - (\theta + \mu_{P})P
\end{cases}$$
(2)

¹³⁶ The description of state variables and parameters of model (2) are given in table 1 and table

¹³⁷ 2, respectively.

138 It is important to note that no intervention measure is performed to kill the pupae for two

¹³⁹ reasons: the first reason is the fact that at this stage, no food is absorbed by the insect, so

¹⁴⁰ it is impossible to make her ingested a toxic substance; the second reason is that the soluble

141 products in the water deposits by contact are not selective for mosquito nymphs and act on all aquatic wildlife.



Figure 1: A compartmental model for the transmission dynamics of vector-borne diseases, which takes into account a waning vaccine and the complete phase of aquatic development of vector.

142

Table 1: The state variables of model (2).

	Humans		Vectors
S_h :	Susceptible	E:	Eggs
V_h :	Vaccines	L:	Larvae
E_h :	Infected in latent stage	P:	Pupae
I_h :	Infectious	S_v :	Susceptible
R_h :	Resistant (immune)	E_v	Infected in latent stage
		I_v	Infectious

¹⁴³ 2.1 Well–posedness of the model

We now show that the system (2) is mathematically well defined and biologically feasible. Let us set

$$k_{1} := \xi + \mu_{h}; \ k_{2} := \omega + \mu_{h}; \ k_{3} := \mu_{h} + \gamma_{h}; \ k_{4} := \mu_{h} + \delta + \sigma;$$

$$k_{5} := s + \mu_{E} + \eta_{1}; \ k_{6} := l + \mu_{L} + \eta_{2}; \ k_{7} := \theta + \mu_{P}; \ k_{8} := \mu_{v} + c_{m};$$

$$k_{9} := \mu_{v} + \gamma_{v} + c_{m}; K_{E} := \alpha_{2}\Gamma_{E}; K_{L} := \alpha_{2}\Gamma_{L}; \pi := 1 - \epsilon, \tau := a(1 - \alpha_{1}).$$
(3)

 $_{146}$ System (2) can be rewritten in the following way

$$\frac{dX}{dt} = \mathbb{A}(X)X + F \tag{4}$$

¹⁴⁷ with $X = (S_h, V_h, E_h, I_h, R_h, S_v, E_v, I_v, E, L, P)^T$, $\mathbb{A}(X) = \begin{pmatrix} A_1(X) & 0 \\ 0 & A_4(X) \end{pmatrix}$ with

$$A_1(X) = \begin{pmatrix} -\lambda_h^c - k_1 & \omega & 0 & 0 & 0 \\ \xi & -\pi\lambda_h^c - k_2 & 0 & 0 & 0 \\ \lambda_h^c & \pi\lambda_h^c & -k_3 & 0 & 0 \\ 0 & 0 & \gamma_h & -k_4 & 0 \\ 0 & 0 & 0 & \sigma & -\mu_h \end{pmatrix}$$

and

148

149

$$A_2(X) = \begin{pmatrix} -(\lambda_v^c + k_8) & 0 & 0 & 0 & 0 & \theta \\ \lambda_v^c & -k_9 & 0 & 0 & 0 \\ 0 & \gamma_v & -k_8 & 0 & 0 & 0 \\ A_{96} & A_{96} & A_{96} & -A_{97} & 0 & 0 \\ 0 & 0 & 0 & A_{109} & -A_{10} & 0 \\ 0 & 0 & 0 & 0 & l & -k_7 \end{pmatrix}$$

where $A_{96} = \mu_b \left(1 - \frac{E}{K_E}\right)$, $A_{97} = \left(\frac{\mu_b N_v}{K_E} + k_5\right)$, $A_{109} = s \left(1 - \frac{L}{K_L}\right)$ and $A_{10} = \frac{sE}{K_L} + k_6$; and $F = (\Lambda_h, 0, 0, 0, 0, 0, 0, 0, 0, 0)^T$.

Note that $\mathbb{A}(X)$ is a Metzler matrix, i.e. a matrix such that off diagonal terms are non negative [33, 34], for all $X \in \mathbb{R}^{11}_+$. Thus, using the fact that $F \ge 0$, system (4) is positively invariant in \mathbb{R}^{11}_+ , which means that any trajectory of the system starting from an initial state in the positive orthant \mathbb{R}^{11}_+ , remains forever in \mathbb{R}^{11}_+ . The right-hand side is Lipschitz continuous: there exists a unique maximal solution.

By adding the first four equations of model system (2), it follows that

$$N_h(t) = \Lambda_h - \mu_h N_h - \delta I_h \le \Lambda_h - \mu_h N_h$$

Parameter	Description	Baseline value/range	Sources
Λ_h	Recruitment rate of humans	$2.5 \ day^{-1}$	[23]
μ_h	Natural mortality rate	$\frac{1}{(67 \times 365)} day^{-1}$	[23]
	in humans		
ξ	Vaccine coverage	Variable	
ω	Vaccine waning rate	Variable	
ϵ	The vaccine efficacy	Variable	
a	Average number of bites	$1 \ day^{-1}$	[13, 23]
eta_{hv}	Probability of transmission of	$0.1, 0.75 \ day^{-1}$	[13, 23]
	infection from an infected vector		
	to a susceptible human	[1]], 1	
γ_h	Progression rate from E_h to I_h	$\begin{bmatrix} \frac{1}{15}, \frac{1}{3} \end{bmatrix} day^{-1}$	[19, 32]
0	Disease-induced death rate	$10^{-3} day^{-1}$	[23]
σ	Recovery rate for humans	$0.1428 \ day^{-1}$	[13, 23]
η_h, η_v	Modifications parameter	$\begin{bmatrix} 0, 1 \end{bmatrix}$	[23]
μ_v	Natural mortality rate of vectors	$\begin{bmatrix} \overline{30}, \overline{14} \end{bmatrix} aay^{-1}$	[13, 23]
γ_v	Progression rate from E_v to I_v Probability of transmission of	$\begin{bmatrix} \overline{21}, \overline{2} \end{bmatrix} aay$	[19, 32] [12, 32]
$ ho_{vh}$	infection from an infected human	0.1, 0.15 <i>auy</i>	[13, 23]
	to a susceptible vector		
Α	Maturation rate from pupae	$0.08 dau^{-1}$	[10 27 28]
0	to adult	0.00 <i>aug</i>	[13, 21, 20]
114	Number of eggs at each deposit	$6 dau^{-1}$	[19 27 28]
Γ_E	Carrying capacity for eggs	10^3 , 10^6	[13, 27]
Γ_L^L	Carrying capacity for larvae	$5 \times 10^2, 5 \times 10^5$	[13, 27]
μ_E	Eggs death rate	0.2 or 0.4	[28]
μ_L	Larvae death rate	0.2 or 0.4	[28]
μ_P	Pupae death rate	0.4	Assumed
s	Transfer rate from eggs to larvae	$0.7 \ day^{-1}$	[28]
l	Transfer rate from larvae to pupae	$0.5 \ day^{-1}$	[27]
η_1,η_2	Eggs and larvae mortality rates	0.001, 0.3	[28]
	induced by chemical intervention		
α_1	Human protection rate	[0,1)	Assumed
α_2	Efficacy of the mechanical control	(0,1]	[19]
c_m	Adulticide killing rate	[0, 0.8]	[19]

Table 2: Description and baseline values/range of parameters of model (2).

So that

$$0 \le N_h(t) \le \frac{\Lambda_h}{\mu_h} + \left(N_h(0) - \frac{\Lambda_h}{\mu_h}\right) e^{-\mu_h t}$$

Thus, at $t \to \infty$, $0 \le N_h(t) \le \frac{\Lambda_h}{\mu_h}$. By adding the equations in S_v , E_v and I_v of system (2), it follows that

$$\dot{N}_v(t) = \theta P - \mu_v N_v$$

So that

$$0 \le N_v(t) = \frac{\theta P}{\mu_v} + \left(N_v(0) - \frac{\theta P}{\mu_v}\right) e^{-\mu_v t}$$

Thus, at $t \to \infty$, $0 \le N_v(t) \le \frac{\theta l K_L}{\mu_v k_7}$ since $P \le \frac{l K_L}{k_7}$.

Therefore, all feasible solutions of model system (2) enter the region:

$$\mathcal{D} = \left\{ (S_h, V_h, E_h, I_h, R_h, S_v, E_v, I_v, E, L, P) \in \mathbb{R}_+^{11} : N_h \le \frac{\Lambda_h}{\mu_h}; E \le K_E; L \le K_L; P \le \frac{lK_L}{k_7}; N_v \le \frac{\theta lK_L}{k_7 k_8} \right\},$$

which is a positively invariant set of system (2).

Furthermore, the model (2) is well-posed epidemiologically and we will consider dynamic behaviour of model (2) on \mathcal{D} .

¹⁶¹ **3** Mathematical analysis

In this section, we focus on the qualitative analysis of our model. We determine the different 162 equilibrium points which are governed by two epidemiological thresholds, the net reproductive 163 number denoted by \mathcal{N} and the basic reproduction number denoted by \mathcal{R}_0 . Then, with respect 164 on the values of these thresholds, we study the stability (local as well as global) of the different 165 equilibrium points, and also we test the occurrence of the backward bifurcation phenomenon. 166 These stability analysis are also done for the different corresponding models (model without 167 vaccination and model with mass-action incidences), to determine the causes of the occurrence 168 of backward bifurcation phenomenon. 169

¹⁷⁰ 3.1 The disease–free equilibria and its stability

$$S_{h}^{0} = \frac{\Lambda_{h}k_{2}}{\mu_{h}(k_{2}+\xi)}, \quad V_{h}^{0} = \frac{\xi\Lambda_{h}}{\mu_{h}(k_{2}+\xi)}, \quad N_{v}^{0} = \frac{K_{E}K_{L}k_{5}k_{6}(\mathcal{N}-1)}{\mu_{b}(K_{E}s+k_{6}K_{L})}, \\ P = \frac{K_{E}K_{L}k_{5}k_{6}k_{8}(\mathcal{N}-1)}{\mu_{b}\theta(K_{E}s+k_{6}K_{L})}, \quad L = \frac{K_{E}K_{L}k_{5}k_{6}k_{7}k_{8}(\mathcal{N}-1)}{\mu_{b}\theta l(K_{E}s+k_{6}K_{L})}, \\ E = \frac{K_{E}K_{L}k_{5}k_{6}k_{7}k_{8}(\mathcal{N}-1)}{s(\mu_{b}lK_{L}\theta+k_{5}k_{7}k_{8}K_{E})}.$$
(5)

where \mathcal{N} is the net reproductive number [27, 35, 36] given by

$$\mathcal{N} = \frac{\mu_b \theta l s}{k_5 k_6 k_7 k_8} \tag{6}$$

177 3.1.1 Local stability of disease–free equilibria

The local asymptotic stability result of equilibria \mathcal{E}_0 and \mathcal{E}_1 is given in the following.

Theorem 1. Define the basic reproductive number [37, 38]

$$\mathcal{R}_{0} = \sqrt{\frac{a^{2}(1-\alpha_{1})^{2}\beta_{hv}\beta_{vh}\mu_{h}k_{5}k_{6}\left(\gamma_{h}+k_{4}\eta_{h}\right)\left(\gamma_{v}+k_{8}\eta_{v}\right)\left(\pi\xi+k_{2}\right)\alpha_{2}\Gamma_{E}\Gamma_{L}(\mathcal{N}-1)}{k_{3}k_{4}k_{8}k_{9}\mu_{b}\Lambda_{h}\left(\xi+k_{2}\right)\left(k_{6}\Gamma_{L}+s\Gamma_{E}\right)}}$$
(7)

180 Then,

(i) if $\mathcal{N} \leq 1$, the trivial equilibrium \mathcal{E}_0 is locally asymptotically stable in \mathcal{D} ;

(ii) if $\mathcal{N} > 1$, the trivial equilibrium is unstable and the disease-free equilibrium \mathcal{E}_1 is locally asymptotically stable in \mathcal{D} whenever $\mathcal{R}_0 < 1$.

¹⁸⁴ *Proof.* See appendix **B**.

The basic reproduction number of a disease is the average number of secondary cases that one infectious individual produces during his infectious period in a totally susceptible population. The epidemiological implication of Theorem 1 is that, in general, when the basic reproduction number, \mathcal{R}_0 is less than unity, a small influx of infectious vectors into the community would not generate large outbreaks, and the disease dies out in time (since the DFE is locally asymptotically stable) [23, 37, 38, 39]. However, we will show in the subsection 3.2 that the disease may still persist even when $\mathcal{R}_0 < 1$.

¹⁹² 3.1.2 Global stability of the trivial equilibrium

¹⁹³ The global stability of the trivial equilibrium is given by the following result:

- **Theorem 2.** If $\mathcal{N} \leq 1$, then \mathcal{E}_0 is globally asymptotically stable on \mathcal{D} .
- ¹⁹⁵ *Proof.* To prove the global asymptotic stability of the trivial disease–free equilibrium \mathcal{E}_0 , we ¹⁹⁶ use the direct Lyapunov method. To this aim, we set Y = X - TE with
- ¹⁹⁷ $X = (S_h, V_h, E_h, I_h, R_h, S_v, E_v, I_v, E, L, P)^T$ and rewrite (2) in the following manner

$$\frac{dY}{dt} = \mathcal{B}(Y)Y.$$

The global asymptotic stability of \mathcal{E}_0 is achieved by considering the following Lyapunov function $\mathcal{L}(Y) = \langle g, Y \rangle$ where

$$g = \left(1, 1, 1, 1, 1, 1, 1, 1, \frac{k_8}{\mu_b}, \frac{k_5 k_8}{\mu_b s}, \frac{k_5 k_6 k_8}{\mu_b s l}\right)$$

¹⁹⁸ See appendix C for the details.

¹⁹⁹ 3.1.3 Global stability of the disease–free equilibrium

We now turn to the global stability of the disease-free equilibrium \mathcal{E}_1 . we prove that the diseasefree equilibrium \mathcal{E}_1 is globally asymptotically stable under a certain threshold condition. To this aim, we use a result obtained by Kamgang and Sallet [40], which is an extension of some results given in [38]. Using the property of \mathcal{E}_1 , it is possible to rewrite (2) in the following manner

$$\begin{cases} \dot{X}_S = \mathcal{A}_1(X)(X_S - X_{DFE}) + \mathcal{A}_{12}(X)X_I \\ \dot{X}_I = \mathcal{A}_2(X)X_I \end{cases}$$
(8)

where X_S is the vector representing the state of different compartments of non transmitting individuals $(S_h, V_h, R_h, S_v, E, L, P)$ and the vector X_I represents the state of compartments of different transmitting individuals (E_h, I_h, E_v, I_v) . Here, we have $X_S = (S_h, V_h, R_h, S_v, E, L, P)^T$, $X_I = (E_h, I_h, E_v, I_v)^T$, $X = (X_S, X_I)$ and $X_{DFE} := \mathcal{E}_1 = (S_h^0, V_h^0, 0, 0, 0, N_v^0, 0, 0, E, L, P)^T$,

$$\mathcal{A}_{1}(X) = \begin{pmatrix} \mathcal{A}_{1}^{(1)} & \mathcal{A}_{1}^{(2)} \\ \mathcal{A}_{1}^{(3)} & \mathcal{A}_{1}^{(4)} \end{pmatrix},$$

A direct computation shows that the eigenvalues of $\mathcal{A}_1(X)$ have negative real parts. Thus the system $\dot{X}_S = \mathcal{A}_1(X)(X_S - X_{DFE})$ is globally asymptotically stable at X_{DFE} . Note also that $\mathcal{A}_2(X)$ is a Metzler matrix.

208 We now consider the bounded set \mathcal{G} :

$$\mathcal{G} = \left\{ (S_h, V_h, E_h, I_h, R_h, S_v, E_v, I_v, E, L, P) \in \mathbb{R}_+^{11} : S_h \le N_h, V_h \le N_h, E_h \le N_h, I_h \le N_h, R_h \le N_h, N_h \le N_h,$$

Let us recall the following theorem [40] (See [40] for a proof in a more general setting).

²¹⁰ Theorem 3. Let $\mathcal{G} \subset \mathcal{U} = \mathbb{R}^7 \times \mathbb{R}^4$. The system (2) is of class C^1 , defined on \mathcal{U} . If

- 211 (1) \mathcal{G} is positively invariant relative to (8).
- (2) The system $\dot{X}_S = \mathcal{A}_1(X)(X_S X_{DFE})$ is Globally asymptotically stable at X_{DFE} .
- 213 (3) For any $x \in \mathcal{G}$, the matrix $\mathcal{A}_2(x)$ is Metzler irreducible.
- 214 (4) There exists a matrix $\bar{\mathcal{A}}_2$, which is an upper bound of the set
- $\mathcal{M} = \{\mathcal{A}_2(x) \in \mathcal{M}_4(\mathbb{R}) : x \in \mathcal{G}\} \text{ with the property that if } \mathcal{A}_2 \in \mathcal{M}, \text{ for any } \bar{x} \in \mathcal{G}, \text{ such that } \mathcal{A}_2(\bar{x}) = \bar{\mathcal{A}}_2, \text{ then } \bar{x} \in \mathbb{R}^7 \times \{0\}.$

- 217 (5) The stability modulus of $\bar{\mathcal{A}}_2$, $\alpha(\mathcal{A}_2) = \max_{\lambda \in sp(\mathcal{A}_2)} \mathcal{R}\mathbf{e}(\lambda)$ satisfied $\alpha(\mathcal{A}_2) \leq 0$.
- ²¹⁸ Then the DFE is GAS in \mathcal{G} .

For our model system (2), conditions (1–3) of the theorem 3 are satisfied. An upper bound of the set of matrices \mathcal{M} , which is the matrix $\bar{\mathcal{A}}_2$ is given by

$$\bar{\mathcal{A}}_{2} = \begin{pmatrix} -k_{3} & 0 & \frac{\tau\beta_{hv}\eta_{v}(S_{h}^{0} + \pi V_{h}^{0})}{\bar{N}_{h}} & \frac{\tau\beta_{hv}(S_{h}^{0} + \pi V_{h}^{0})}{\bar{N}_{h}} \\ \gamma_{h} & -k_{4} & 0 & 0 \\ \frac{\tau\beta_{vh}\eta_{h}S_{v}^{0}}{\bar{N}_{h}} & \frac{\tau\beta_{vh}S_{v}^{0}}{\bar{N}_{h}} & -k_{9} & 0 \\ 0 & 0 & \gamma_{v} & -k_{8} \end{pmatrix},$$

²¹⁹ where $\bar{N}_h = \frac{\Lambda_h}{(\mu_h + \delta)}$.

To check condition (5) in theorem 3, we will use the useful lemma [40] in appendix A. To this aim, let

222
$$A = \begin{pmatrix} -k_3 & 0\\ \gamma_h & -k_4 \end{pmatrix}, B = \begin{pmatrix} \frac{\tau \beta_{hv} \eta_v (S_h^0 + \pi V_h^0)}{\bar{N}_h} & \frac{\tau \beta_{hv} (S_h^0 + \pi V_h^0)}{\bar{N}_h} \\ 0 & 0 \end{pmatrix},$$
223
$$C = \begin{pmatrix} \frac{\tau \beta_{vh} \eta_h S_v^0}{\bar{N}_h} & \frac{\tau \beta_{vh} S_v^0}{\bar{N}_h} \\ 0 & 0 \end{pmatrix}, \text{ and } D = \begin{pmatrix} -k_9 & 0\\ \gamma_v & -k_8 \end{pmatrix}.$$

²²⁴ Clearly, A is a stable Metzler matrix. Then, after some computations, we obtain $D-CA^{-1}B$ ²²⁵ is a stable Metzler matrix if and only if

$$\mathcal{R}_c \le 1 \tag{9}$$

226 where

$$\mathcal{R}_{c} = \sqrt{\frac{a^{2}(1-\alpha_{1})^{2}\beta_{hv}\beta_{vh}k_{5}k_{6}\left(\gamma_{h}+k_{4}\eta_{h}\right)\left(\gamma_{v}+k_{8}\eta_{v}\right)K_{E}K_{L}(k_{2}+\pi\xi)(\mathcal{N}-1)}{k_{3}k_{4}k_{8}k_{9}\mu_{b}(k_{2}+\xi)(k_{6}K_{L}+K_{E}s)\Lambda_{h}}}\frac{(\mu_{h}+\delta)^{2}}{\mu_{h}}}{(10)}$$

227

228 We claim the following result

Theorem 4. If $\mathcal{N} > 1$ and $\mathcal{R}_c \leq 1$, then the disease-free equilibrium \mathcal{E}_1 is globally asymptotically stable in \mathcal{G} .

231 Remark 1.

(i) From (10), we have $\mathcal{R}_c = \frac{(\mu_h + \delta)}{\mu_h} \mathcal{R}_0 > \mathcal{R}_0$, showing that \mathcal{R}_c is not necessarily an optimal threshold parameter.

(ii) Note that inequality (9) is equivalent to

$$\mathcal{R}_0 \le \mathcal{R}_G = \left(\frac{\mu_h}{\mu_h + \delta}\right) < 1,$$
(11)

which means that for

 $\mathcal{R}_0 \le \mathcal{R}_G,\tag{12}$

the disease-free equilibrium \mathcal{E}_1 is the unique equilibrium (no co-existence with endemic equilibria). If

$$\mathcal{R}_G < \mathcal{R}_0 \le 1,\tag{13}$$

then it is possible to have co-existence with endemic equilibria and thus, the occurrence of the backward bifurcation phenomenon.

(iii) Note that in the absence of disease-induced death, i.e. $\delta = 0$, inequalities (9) and (11) become

$$\mathcal{R}_0 \le 1. \tag{14}$$

This suggests that the disease-induced death may be a cause of the instability of the disease-free equilibrium \mathcal{E}_1 when $\mathcal{R}_0 < 1$, and thus, one cause of the occurrence of the backward bifurcation phenomenon.

Remark 2. The above results show that if, at any time, through appropriate interventions (eg the destruction of breeding sites, massive spraying, personal protection, vaccination, effective treatment,...), we are able to reduce \mathcal{N} or \mathcal{R}_0 and \mathcal{R}_c less than 1 for a sufficiently long period, then, the disease may disappear. The same remark is done in [19].

The backward bifurcation phenomenon, in epidemiological systems, indicate the possibility 249 of existence of at least two endemic equilibria when \mathcal{R}_0 is less than unity. Thus, the classical 250 requirement of $\mathcal{R}_0 < 1$ is, although necessary, no longer sufficient for disease elimination [23, 251 41, 42, 43]. In some epidemiological models, it has been shown that the backward bifurcation 252 phenomenon is caused by factors such as non-linear incidence (the infection force), disease-253 induced death and vaccine (perfect or not) [23, 43, 44, 45, 46, 47]. To confirm whether or not 254 the backward bifurcation phenomenon occurs in this case, one could use the approach developed 255 in [38, 46, 48], which is based on the general centre manifold theorem [49]. We will explore this 256 method in the next section. 257

²⁵⁸ 3.2 Endemic equilibria and bifurcation analysis

²⁵⁹ 3.2.1 Existence of endemic equilibria

We turn now to the existence of endemic equilibria. Let us introduce the following quantity $\mathcal{R}_1 = \mathcal{R}_{0,\delta=0}$. We prove the following result

²⁶² Theorem 5. We assume that $\mathcal{N} > 1$, then

(i) In the absence of disease-induced death in human population ($\delta = 0$), model system (2) have

- 265 1. A unique endemic equilibrium whenever $\mathcal{R}_1 > 1$.
- 266 2. No endemic equilibrium otherwise.
- ²⁶⁷ (ii) In presence of disease-induced death in human population ($\delta > 0$), model system (2) could ²⁶⁸ have
- 269 3. At least one endemic equilibrium whenever $\mathcal{R}_0 > 1$.
- 4. Zero, one or more than one endemic equilibrium whenever $\mathcal{R}_0 < 1$.
- ²⁷¹ *Proof.* See appendix D.

Note that case 4 of Theorem 5 indicate the possibility of existence of at least one endemic equilibrium for $\mathcal{R}_0 < 1$ and hence the potential occurrence of a backward bifurcation phenomenon.

Backward bifurcation analysis 3.2.2275

In the following, we use the centre manifold theory [25, 38, 46, 48] to explore the possibility of 276 backward bifurcation in (2). To do so, a bifurcation parameter β_{hv}^* is chosen, by solving for β_{hv} 277 from $\mathcal{R}_0 = 1$, giving 278

$$\beta_{hv}^{*} = \frac{k_{3}k_{4}k_{8}k_{9}\mu_{b}\Lambda_{h}\left(\xi + k_{2}\right)\left(k_{6}K_{L} + sK_{E}\right)}{a^{2}(1 - \alpha_{1})^{2}\beta_{vh}\mu_{h}k_{5}k_{6}\left(\gamma_{h} + k_{4}\eta_{h}\right)\left(\gamma_{v} + k_{8}\eta_{v}\right)\left(\pi\xi + k_{2}\right)K_{E}K_{L}(\mathcal{N} - 1)}.$$
(15)

Let $J_{\beta_{hv}^*}$ denotes the Jacobian of the system (2) evaluated at the DFE (\mathcal{E}_1) and with $\beta_{hv} = \beta_{hv}^*$. 279 Thus, 280

$$J_{\beta_{hv}^*} = \begin{pmatrix} J_1 & J_2 \\ J_3 & J_4 \end{pmatrix}, \tag{16}$$

where 281

285
$$K_4 = \left(k_6 + \frac{sE^*}{K_L}\right).$$

Note that the system (2), with $\beta_{hv} = \beta^*_{hv}$, has a hyperbolic equilibrium point (i.e., the 286 linearised system (2) has a simple eigenvalue with zero real part and all other eigenvalues 287 have negative real part). Hence, the centre manifold theory [49, 50] can be used to analyze 288 the dynamics of the model (2) near $\beta_{hv} = \beta_{hv}^*$. The technique in Castillo-Chavez and Song 289 (2004) [48] entails finding the left and right eigenvectors of the linearised system above as 290 follows. 291

The left eigenvector components of $J_{\beta_{hv}^*}$, which correspond to the uninfected states are zero (see Lemma 3 in [38]). Thus a non-zero components correspond to the infected states. It follows that the matrix $J_{\beta_{hv}^*}$ has a left eigenvector given by $\mathbf{v} = (v_1, v_2, \dots, v_{11})$, where

$$v_{1} = v_{2} = v_{5} = v_{6} = v_{9} = v_{10} = v_{11} = 0; \quad v_{3} = \frac{k_{8}N_{h}^{0}}{a(1-\alpha_{1})\beta_{hv}^{*}H^{0}}v_{8};$$
$$v_{4} = \frac{a(1-\alpha_{1})\beta_{vh}S_{v}^{0}(\eta_{v}k_{8}+\gamma_{v})}{k_{4}k_{9}N_{h}^{0}}v_{8}, \quad v_{7} = \frac{(\eta_{v}k_{8}+\gamma_{v})}{k_{9}}v_{8}, \quad v_{8} > 0.$$

The system (2) has a right eigenvector given by $\mathbf{w} = (w_1, w_2, \dots, w_{11})^T$, where

$$\begin{split} w_{11} &> 0, \quad w_8 > 0, \\ w_{10} &= \frac{k_7}{l} w_{11}, w_9 = \frac{K_1 \theta}{k_5 k_8} w_{11}, \quad w_7 = \frac{k_8}{\gamma_v} w_8, \quad w_6 = \frac{\theta}{k_8} w_{11} - \frac{k_9}{\gamma_v} w_8, \\ w_5 &= \frac{\gamma_h \sigma k_8 k_9 N_h^0}{a(1-\alpha_1) \beta_{vh} \mu_h \gamma_v S_v^0 (\eta_h k_4 + \gamma_h)} w_8, \quad w_4 = \frac{\mu_h}{\sigma} w_5, \quad w_3 = \frac{k_4}{\gamma_h} w_4, \\ w_2 &= -\frac{a(1-\alpha_1) \beta_{hv}^* (\eta_v k_8 + \gamma_v)}{\gamma_v N_h^0 (k_1 k_2 - \xi \omega)} (\xi S_h^0 + k_1 V_h^0) w_8, \\ w_1 &= \frac{\omega}{k_1} w_2 - \frac{a(1-\alpha_1) \beta_{hv}^* S_h^0}{k_1 N_h^0} (\eta_v w_7 + w_8) \,. \end{split}$$

Theorem 4.1 in Castillo-Chavez and Song [48] is then applied to establish the existence of backward bifurcation in (2). To apply such a theorem, it is convenient to let f_k represent the right-hand side of the k^{th} equation of the system (2) and let x_k be the state variables whose derivative is given by the k^{th} equation for k = 1, ..., 11. The local bifurcation analysis near the bifurcation point ($\beta_{hv} = \beta_{hv}^*$) is then determined by the signs of two associated constants, denoted by \mathcal{A}_1 and \mathcal{A}_2 , defined by

$$\mathcal{A}_1 = \sum_{k,i,j=1}^n v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j} \qquad and \qquad \mathcal{A}_2 = \sum_{k,i=1}^n v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_i \partial \phi} \tag{17}$$

with $\phi = \beta_{hv} - \beta_{hv}^*$. It is important to note that in $f_k(0,0)$, the first zero corresponds to the disease-free equilibrium, \mathcal{E}_1 , for the system (2). Since $\beta_{hv} = \beta_{hv}^*$ is the bifurcation parameter, it follows from $\phi = \beta_{hv} - \beta_{hv}^*$ that $\phi = 0$ when $\beta_{hv} = \beta_{hv}^*$ which is the second component in $f_k(0,0)$.

It follows then, after some algebraic computations, that

$$\mathcal{A}_1 = \Gamma_1 - \Gamma_2$$

with

$$\Gamma_1 = \frac{\tau \beta_{hv}^* (2V_h^0 w_1 + \pi S_h^0 w_2)}{(N_h^0)^2} (\eta_v w_7 + w_8) v_3 + \frac{\tau \beta_{vh} S_v^0}{N_h^0} \left[(\eta_h w_3 + w_4) \frac{1}{S_v^0} + \left(\eta_h w_3 + \frac{1}{S_v^0} w_4 \right) \right] w_6 v_7$$

$$\Gamma_2 = 2 \frac{\tau \beta_{vh} S_v^0}{(N_h^0)^2} \left(\sum_{i=1}^5 w_i \right) (\eta_h w_3 + w_4) v_7 + \frac{\tau \beta_{hv}^* (S_h^0 + \pi V_h^0) (N_h^0 + 1)}{(N_h^0)^2} \left(\sum_{i=3}^5 w_i \right) (\eta_v w_7 + w_8) v_3,$$

and

$$\mathcal{A}_2 = \frac{a(S_h^0 + \pi V_h^0)}{N_h^0} \left(\eta_v w_7 + w_8\right) v_3.$$

Note that the coefficient A_2 is always positive. Thus, using Theorem 4.1 in [48], the following result is established.

Theorem 6. The model (2) exhibits a backward bifurcation at $\mathcal{R}_0 = 1$ whenever $\mathcal{A}_1 > 0$. If the reversed inequality holds, then the bifurcation at $\mathcal{R}_0 = 1$ is forward.

The associated bifurcation diagrams are depicted in Figures 2 and 3. Parameter values used in figure 2 correspond to those in Table 3, except $\Lambda_h = 10$, $\epsilon = 1$, $\beta_{vh} = 0.8$, $\eta_h = 1$, $\eta_v = 1$, $\sigma = 0.01428$, $\delta = 1$, $\alpha_1 = 0.001$, $\alpha_2 = 1$, $c_m = 0.0001$, $\Gamma_E = 10^5$, $\Gamma_L = 50000$. In this case the conditions required by Theorem 6, are satisfied: $\mathcal{A}_1 = 0.0114 > 0$ and $\mathcal{A}_2 = 1.1393 > 0$.

Parameter values used in figure 3 correspond to those in Table 3, except $\Lambda_h = 10$, $\beta_{vh} = 0.8$, $\eta_h = \eta_v = 0 = \delta = c_m = \alpha_1 = 0$, $\alpha_2 = 1$, $\Gamma_E = 10^5$, $\Gamma_L = 50000$. We also have $\mathcal{A}_1 = -2.4223 < 0$ and $\mathcal{A}_2 = 0.8333 > 0$.



Figure 2: The backward bifurcation curves for model system (2) in the (\mathcal{R}_0, E_h^*) , and (\mathcal{R}_0, E_v^*) planes. The parameter β_{hv} is varied in the range [0, 0.2810] to allow \mathcal{R}_0 to vary in the range [0, 1.5]. Two endemic equilibrium points coexist for values of \mathcal{R}_0 in the range (0.2894, 1) (corresponding to the range (0.0105, 0.1249) of β_{hv}). The notation EE and DFE stand for endemic equilibrium and disease-free equilibrium, respectively. Solid lines represent stable equilibria and dash lines stand for unstable equilibria.



Figure 3: The forward bifurcation curves for model system (2) in the (\mathcal{R}_0, E_h^*) , and (\mathcal{R}_0, E_v^*) planes. Solid lines represent stable equilibria and dash lines stand for unstable disease-free equilibrium.

The occurrence of the backward bifurcation can be also seen in Figure 4. Here, \mathcal{R}_0 is less than the transcritical bifurcation threshold ($\mathcal{R}_0 = 0.29 < 1$), but the solution of the model 2 can approach either the endemic equilibrium point or the disease-free equilibrium point, depending on the initial condition.



Figure 4: Solutions of model (2) of the number of infected humans, E_h , and the number of infected vectors, E_v , for parameter values given in the bifurcation diagram in Figure 2 with $\beta_{hv} = 0.0105$. So $\mathcal{R}_0 = 0.29 < 1$, for two different set of initial conditions. The first set of initial conditions (corresponding to the solid trajectory) is $S_h = 700$, $V_h = 10$, $E_h = 220$, $I_h = 100$, $R_h = 60$, $S_v = 3000$, $E_v = 400$, $I_v = 120$, E = 10000, L = 5000 and P = 3000. The second set of initial conditions (corresponding to the dotted trajectory) is $S_h = 489100$, $V_h = 10$, $E_h = 220$, $I_h = 100$, $R_h = 60$, $S_v = 3000$, $E_v = 400$, $I_v = 120$, E = 10000, L = 5000 and P = 3000. The solution for initial condition 1 approaches the locally asymptotically stable endemic equilibrium point, while the solution for initial condition 2 approaches the locally asymptotically stable DFE.

317 3.3 The different causes of the backward bifurcation

From theorem 5, item (i), it follows that the disease-induced death in human (δ) may be a cause of the occurrence of the backward bifurcation phenomenon. In the following, we prove that the backward bifurcation phenomenon is caused by the disease-induced death in human and/or the standard incidence functions (λ_h^c and λ_v^c). To this aim, we will consider, in this section, two variants of the model (2): the corresponding model without vaccination and the corresponding model with mass action incidence.

324 3.3.1 Analysis of the model without vaccination

³²⁵ The model without vaccination is given by

$$\begin{cases}
S_{h} = \Lambda_{h} - (\lambda_{h}^{c} + \mu_{h}) S_{h} \\
\dot{E}_{h} = \lambda_{h}^{c} S_{h} - (\mu_{h} + \gamma_{h}) E_{h} \\
\dot{I}_{h} = \gamma_{h} E_{h} - (\mu_{h} + \delta + \sigma) I_{h} \\
\dot{R}_{h} = \sigma I_{h} - \mu_{h} R_{h} \\
\dot{S}_{v} = \theta P - \lambda_{v}^{c} S_{v} - (\mu_{v} + c_{m}) S_{v} \\
\dot{E}_{v} = \lambda_{v}^{c} S_{v} - (\mu_{v} + \gamma_{v} + c_{m}) E_{v} \\
\dot{I}_{v} = \gamma_{v} E_{v} - (\mu_{v} + c_{m}) I_{v} \\
\dot{E} = \mu_{b} \left(1 - \frac{E}{\alpha_{2} \Gamma_{E}} \right) (S_{v} + E_{v} + I_{v}) - (s + \mu_{E} + \eta_{1}) E \\
\dot{L} = sE \left(1 - \frac{L}{\alpha_{2} \Gamma_{L}} \right) - (l + \mu_{L} + \eta_{2}) L \\
\dot{P} = lL - (\theta + \mu_{P}) P
\end{cases}$$
(18)

where λ_h^c and λ_v^c are given at (1). Model system (18) is defined in the positively-invariant set

$$\mathcal{D}_{1} = \left\{ (S_{h}, E_{h}, I_{h}, R_{h}, S_{v}, E_{v}, I_{v}, E, L, P) \in \mathbb{R}^{10} : N_{h} \le \Lambda_{h}/\mu_{h}; E \le K_{E}; L \le K_{L}; P \le \frac{lK_{L}}{k_{7}}; N_{v} \le \frac{\theta lK_{L}}{k_{7}k_{8}} \right\}$$

Without lost of generality, we assume that $\mathcal{N} > 1$. The corresponding disease-free equilibria of model (18) are given by $\mathcal{E}_0^{nv} = (N_h^0, 0, 0, 0, 0, 0, 0, 0, 0)$ which correspond to the trivial equilibrium and $\mathcal{E}_1^{nv} = (N_h^0, 0, 0, 0, N_v^0, 0, 0, E, L, P)$ which correspond to the disease-free equilibrium, with $N_h^0 = \frac{\Lambda_h}{\mu_h}$ and N_v^0 , E, L and P are the same, given by (5). The associated next generation matrices, F_1 and V_1 , are, respectively, given by

$${}_{332} \quad F_1 = \begin{pmatrix} 0 & 0 & \tau \beta_{hv} \eta_v & \tau \beta_{hv} \\ 0 & 0 & 0 & 0 \\ \frac{\tau \beta_{vh} \eta_v N_v^0}{N_h^0} & \frac{\tau \beta_{vh} N_v^0}{N_h^0} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } V_1 = \begin{pmatrix} k_3 & 0 & 0 & 0 \\ -\gamma_h & k_4 & 0 & 0 \\ 0 & 0 & k_9 & 0 \\ 0 & 0 & -\gamma_v & k_8 \end{pmatrix}$$

It follows that the basic reproduction number for the model without vaccination, denoted by $\mathcal{R}_{nv} = \rho(F_1 V_1^{-1})$, is given by

$$\mathcal{R}_{nv} = \sqrt{\frac{a^2(1-\alpha_1)^2 \beta_{hv} \beta_{vh} (\gamma_h + k_4 \eta_h) (\gamma_v + k_8 \eta_v) N_v^0}{k_3 k_4 k_8 k_9 N_h^0}}.$$
(19)

Using Theorem 2 of [38], we establish the following result:

Theorem 7. Assumed that $\mathcal{N} > 1$. For basic arboviral model without vaccination, given by (18), the corresponding disease-free equilibrium is locally asymptotically stable (LAS) if $\mathcal{R}_{nv} < 1$, and unstable if $\mathcal{R}_{nv} > 1$.

Existence of endemic equilibria. Here, the existence of endemic equilibria of the model
 (18) will be explored. Let us set the following coefficients

$$\mathcal{R}_{c_{1}} = \sqrt{\frac{\{2k_{8}(k_{3}k_{4} - \delta\gamma_{h}) + (\eta_{h}k_{4} + \gamma_{h})a\mu_{h}(1 - \alpha_{1})\beta_{vh}\}}{k_{3}k_{4}k_{8}}},$$

$$d_{2} = -k_{9}\mu_{b}\Lambda_{h}(sK_{E} + k_{6}K_{L})(k_{3}k_{4} - \delta\gamma_{h})((\eta_{h}k_{4} + \gamma_{h})a\mu_{h}(1 - \alpha_{1})\beta_{vh} + (k_{3}k_{4} - \delta\gamma_{h})k_{8}) < 0,$$

$$d_{1} = k_{3}^{2}k_{4}^{2}k_{8}k_{9}(sK_{E} + k_{6}K_{L})\mu_{b}\Lambda_{h}\mu_{h}(\mathcal{R}_{nv}^{2} - \mathcal{R}_{c_{1}}^{2}),$$

$$d_{0} = k_{3}^{2}k_{4}^{2}k_{8}k_{9}(sK_{E} + k_{6}K_{L})\mu_{b}\Lambda_{h}\mu_{h}^{2}(\mathcal{R}_{nv}^{2} - 1)).$$
(20)

³⁴¹ We claim the following:

³⁴² Theorem 8. The arboviral diseases model without vaccination (18) has:

- (i) A unique endemic equilibrium if $d_0 > 0 \Leftrightarrow \mathcal{R}_{nv} > 1$;
- (ii) A unique endemic equilibrium if $d_1 > 0$, and $d_0 = 0$ or $d_1^2 4d_2d_0 = 0$;
- 345 (iii) Two endemic equilibria if $d_0 < 0$ ($\mathcal{R}_{nv} < 1$), $d_1 > 0$ ($\mathcal{R}_{nv} > \mathcal{R}_{c_1}$) and $d_1^2 4d_2d_0 > 0$;
- 346 *(iv)* No endemic equilibrium otherwise.
- ³⁴⁷ Proof. Solving the equations in the model (18) in terms of $\lambda_h^{c,*}$ and $\lambda_v^{c,*}$, gives

$$S_{h}^{*} = \frac{\Lambda_{h}}{\mu_{h} + \lambda_{h}^{c,*}}, \quad E_{h}^{*} = \frac{\lambda_{h}^{c,*}S_{h}^{*}}{k_{3}}, \quad I_{h}^{*} = \frac{\gamma_{h}\lambda_{h}^{c,*}S_{h}^{*}}{k_{3}k_{4}}, \quad R_{h}^{*} = \frac{\sigma\gamma_{h}\lambda_{h}^{c,*}S_{h}^{*}}{\mu_{h}k_{3}k_{4}}, \tag{21}$$

348 and

$$S_{v}^{*} = \frac{\theta P}{(\lambda_{v}^{c,*} + k_{8})}, \quad E_{v}^{*} = \frac{\theta P \lambda_{v}^{c,*}}{k_{9}(\lambda_{v}^{c,*} + k_{8})}, \quad I_{v}^{*} = \frac{\gamma_{v}\theta P \lambda_{v}^{c,*}}{k_{8}k_{9}(\lambda_{v}^{c,*} + k_{8})}, \quad E = \frac{\mu_{b}\theta K_{E}P}{(k_{5}k_{8}K_{E} + \mu_{b}\theta P)}, \quad L = \frac{\mu_{b}\theta s K_{E}K_{L}P}{k_{6}K_{L}(k_{5}k_{8}K_{E} + \mu_{b}\theta P) + s\mu_{b}\theta K_{E}P}, \quad (22)$$

Substituting (21) and (22) into the expression of $\lambda_h^{c,*}$ and $\lambda_v^{c,*}$ and simplifying, lead the nonzero equilibria of the model without vaccination satisfy the quadratic equation

$$d_2(\lambda_h^{c,*})^2 + d_1\lambda_h^{c,*} + d_0 = 0$$
(23)

³⁵¹ where d_i , i = 0, 1, 2, are given by (20).

Clearly, $d_2 < 0$ and $d_0 > 0$ (resp. $d_0 < 0$) if $\mathcal{R}_{nv} > 1$ (resp. $\mathcal{R}_{nv} < 1$). Thus Theorem 8 is established.

It is clear that cases (ii) and (iii) of theorem 8 indicate the possibility of backward bifurcation (where the locally-asymptotically stable DFE co-exists with a locally asymptotically stable endemic equilibrium when $\mathcal{R}_{nv} < 1$) in the model without vaccination (18).

This is illustrated by numerical simulation of the model with the following set of parameter 357 values (it should be noted that these parameters are chosen for illustrative purpose only, and 358 may not necessarily be realistic epidemiologically): $\Lambda_h = 5, \beta_{hv} = 0.03, \eta_h = \eta_v = 1, \delta = 1, \sigma = 1$ 359 0.01, $c_m = 0.1$, $\beta_{vh} = 0.4$, $\alpha_1 = 0.7$ and $\alpha_2 = 0.5$. All other parameters are as in Table 3. With 360 this set of parameters, $\mathcal{R}_{c_1} = 0.0216 < 1$, $\mathcal{R}_{nv} = 0.2725 < 1$ (so that $\mathcal{R}_{c_1} < \mathcal{R}_{nv} < 1$). It follows: 361 $d_2 = -0.0263 < 0, d_1 = 4.8763 \times 10^{-4} \text{ and } d_0 = -3.5031 \times 10^{-7}, \text{ so that } d_1^2 - 4d_2d_0 = 2.0093 \times 10^{-7}$ 362 $10^{-7} > 0$. The resulting two endemic equilibria $\mathcal{E}^{nv} = (S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*, E, L, P)$, are: 363 $\mathcal{E}_1^{nv} = (281, 70, 5, 1207, 5739, 182, 44, 22180, 10201, 9977)$ which is locally stable and 364

 $\mathcal{E}_{2}^{nv} = (6333, 67, 4, 1147, 5936, 37, 2, 22180, 10201, 9977)$ which is unstable.

The associated bifurcation diagram is depicted in figure 5. This clearly shows the coexistence of two locally-asymptotically stable equilibria when $\mathcal{R}_{nv} < 1$, confirming that the model without vaccination (18) undergoes the phenomenon of backward bifurcation too. Thus, the following result is established.

Lemma 1. The model without vaccination (18) undergoes backward bifurcation when Case (iii) of Theorem 8 holds.



Figure 5: The backward bifurcation curves for model system (18) in the $(\mathcal{R}_{nv}, E_h^*)$ and $(\mathcal{R}_{nv}, E_v^*)$ planes. The parameter β_{hv} varied in the range [0, 0.9090] to allow \mathcal{R}_0 to vary in the range [0, 1.5]. Two endemic equilibrium points coexist for values of \mathcal{R}_0 in the range (0.2286, 1) (corresponding to the range (0.0211, 0.4040) of β_{hv}). The notation EE and DFE stand for endemic equilibrium and disease–free equilibrium, respectively. Solid lines represent stable equilibria and dash lines stand for unstable equilibria.

³⁷² Non-existence of endemic equilibria for $\mathcal{R}_{nv} < 1$ and $\delta = 0$. In this case, we have the ³⁷³ following result.</sup>

Lemma 2. The model (18) without disease-induced death ($\delta = 0$) has no endemic equilibrium when $\mathcal{R}_{nv,\delta=0} \leq 1$, and has a unique endemic equilibrium otherwise.

Proof. Considering the model (18) without disease-induced death in human, and applying the same procedure, we obtain that the non-zero equilibria of the model without vaccination satisfy

the linear equation 378

$$p_1\lambda_h^{c,*} + p_0 = 0$$

where $p_1 = k_9 k_{10} K_{12} a \mu_b \Lambda_h \mu_h (1 - \alpha_1) \beta_{vh} + k_3 (\mu_h + \sigma) k_8 k_9 K_{12} \mu_b \Lambda_h$ and 379

 $p_0 = -\mu_h k_3 k_4 k_8 k_9 K_{12} \mu_b \Lambda_h \left(\mathcal{R}_{nv,\delta=0}^2 - 1 \right).$ 380

Clearly, $p_1 > 0$ and $p_0 \ge 0$ whenever $R_{nv,\delta=0} \le 1$, so that $\lambda_h^{c,*} = -\frac{p_0}{p_1} \le 0$. Therefore, 381 the model (18) without disease-induced death in human, has no endemic equilibrium whenever 382 $\mathcal{R}_{nv,\delta=0} \leq 1.$ 383

The above result suggests the impossibility of backward bifurcation in the model (18) with-384 out disease-induced death, since no endemic equilibrium exists when $\mathcal{R}_{nv,\delta=0} < 1$ (and backward 385 bifurcation requires the presence of at least two endemic equilibria when $\mathcal{R}_{nv,\delta=0} < 1$ [23, 43]. 386 To completely rule out backward bifurcation in model (18), we use the direct Lyapunov method 387 to prove the global stability of the DFE. 388

Global stability of the DFE of (18) for $\delta = 0$. 389

Define the positively-invariant and attracting region 390

$$\mathcal{D}_{2} = \left\{ (S_{h}, E_{h}, I_{h}, R_{h}, S_{v}, E_{v}, I_{v}, E, L, P) \in \mathcal{D}_{1} : S_{h} \leq N_{h}^{0}; S_{v} \leq N_{v}^{0} \right\}.$$

We claim the following result. 391

Theorem 9. The DFE, \mathcal{E}_1^{nv} , of model (18) without disease-induced death ($\delta = 0$), is globally 392 asymptotically stable (GAS) in \mathcal{D}_2 if $\mathcal{R}_{nv,\delta=0} < 1$. 393

Proof. See appendix E. 394

3.3.2Analysis of the model with mass action incidence 395

Consider the model (2) with mass action incidence. Thus, the associated forces of infection, λ_{b}^{c} 396 and λ_v^c , respectively, reduce to 397

$$\lambda_{mh} = C_h(\eta_v E_v + I_v) \quad \text{and} \quad \lambda_{mv} = C_v(\eta_h E_h + I_h), \tag{24}$$

where, $C_h = a(1 - \alpha_1)\beta_{hv}$ and $C_v = a(1 - \alpha_1)\beta_{vh}$. The resulting model (mass action model), obtained by using (24) in (2), has the same disease-free equilibria given by (5). Without lost of generality, we consider that $\mathcal{N} > 1$. The associated next generation matrices, F_m and V_m are given by

$$F_m = \begin{pmatrix} 0 & 0 & C_h \eta_v H^0 & C_h H^0 \\ 0 & 0 & 0 & 0 \\ C_v \eta_v S_v^0 & C_v S_v^0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \ V_m = \begin{pmatrix} k_3 & 0 & 0 & 0 \\ -\gamma_h & k_4 & 0 & 0 \\ 0 & 0 & k_9 & 0 \\ 0 & 0 & -\gamma_v & k_8 \end{pmatrix},$$

where $H^0 = S_h^0 + \pi V_h^0$. It follows that the associated reproduction number for the mass action 398 model, denoted by $\mathcal{R}_{0,m} = \rho(F_m V_m^{-1})$, is given by 399

$$\mathcal{R}_{0,m} = \sqrt{\mathcal{R}_{hv}^m \mathcal{R}_{vh}^m},\tag{25}$$

400

where $\mathcal{R}_{hv}^{m} = \left(\frac{C_{h}\Lambda_{h}\left(\gamma_{h} + k_{4}\eta_{h}\right)\left(\pi\xi + k_{2}\right)}{\mu_{h}k_{3}k_{4}\left(\xi + k_{2}\right)}\right)$ and $\mathcal{R}_{vh}^{m} = \left(\frac{C_{v}\left(\gamma_{v} + k_{8}\eta_{v}\right)\theta P}{k_{8}^{2}k_{9}}\right)$. Using Theorem 2 of [38], the following result is established: 401

402

Theorem 10. Assume that $\mathcal{N} > 1$. For the arboviral disease model with mass action incidence, 403 given by (2) with (24), the DFE, \mathcal{E}_1 , is LAS if $\mathcal{R}_{0,m} < 1$, and unstable if $\mathcal{R}_{0,m} > 1$. 404

⁴⁰⁵ Existence of endemic equilibria. Solving the equations in the model (2) with (24) in terms ⁴⁰⁶ of λ_{mh}^* and λ_{mv}^* , gives

$$S_{mh}^{*} = \frac{\Lambda_{h}(\pi\lambda_{mh}^{c,*} + k_{2})}{\lambda_{mh}^{c,*}(k_{2} + \pi(k_{1} + \lambda_{mh}^{c,*})) + k_{1}k_{2} - \omega\xi}, \quad V_{mh}^{*} = \frac{\xi S_{mh}^{*}}{k_{2} + \pi\lambda_{mh}^{c,*}},$$

$$E_{mh}^{*} = \frac{\lambda_{mh}^{c,*}S_{mh}^{*}}{k_{3}}, \quad I_{mh}^{*} = \frac{\gamma_{h}\lambda_{h}^{c,*}S_{mh}^{*}}{k_{3}k_{4}}, \quad R_{mh}^{*} = \frac{\sigma\gamma_{h}\lambda_{mh}^{c,*}S_{mh}^{*}}{\mu_{h}k_{3}k_{4}},$$
(26)

407 and

$$S_{mv}^{*} = \frac{\theta P}{(\lambda_{mv}^{c,*} + k_8)}, \quad E_{mv}^{*} = \frac{\theta P \lambda_{mv}^{c,*}}{k_9 (\lambda_{mv}^{c,*} + k_8)}, \quad I_{mv}^{*} = \frac{\gamma_v \theta P \lambda_{mv}^{c,*}}{k_8 k_9 (\lambda_{mv}^{c,*} + k_8)}.$$
 (27)

Substituting (26) and (27) in the expression of λ_{mh}^* and λ_{mv}^* and simplifying, shows that the nonzero equilibria of the model (2) with (24) satisfy the quadratic equation

$$e_2(\lambda_{mh}^{c,*})^2 + e_1\lambda_{mh}^{c,*} + e_0 = 0, \qquad (28)$$

410 where e_i , i = 0, 1, 2, are given by

$$e_{2} = k_{8}k_{9}\pi \left[\left(\gamma_{h} + k_{4}\eta_{h} \right) C_{v}\Lambda_{h} + k_{3}k_{4}k_{8} \right]$$

$$e_{1} = \frac{k_{3}k_{4}k_{8}^{2}k_{9}\kappa\pi}{(\pi\xi + k_{2})} \left(\mathcal{R}_{cm}^{2} - \mathcal{R}_{0,m}^{2} \right),$$

$$e_{0} = k_{3}k_{4}k_{8}^{2}k_{9}\kappa \left(1 - \mathcal{R}_{0,m}^{2} \right),$$

with $\kappa = k_1 k_2 - \xi \omega > 0$ and

$$\mathcal{R}_{cm} = \sqrt{\frac{\left[(\gamma_h + k_4 \eta_h) \left(\pi \xi + k_2\right) \Lambda_h C_v + (k_1 \pi + k_2) k_3 k_4 k_8\right] (\pi \xi + k_2)}{k_3 k_4 k_8 \kappa \pi}}.$$

 e_2 is always positive and e_0 is positive (resp. negative) whenever $\mathcal{R}_{0,m}$ is less (resp. greater) than 411 unity. Thus, the mass action model admits only one endemic equilibrium whenever $\mathcal{R}_{0,m} > 1$. 412 Now, we consider the case $\mathcal{R}_{0,m} < 1$. The occurrence of backward bifurcation phenomenon 413 depend of the sign of coefficient e_1 . The coefficient e_1 is always positive if and only if $\mathcal{R}_{0,m} < c_1$ 414 \mathcal{R}_{cm} . It follows that the disease-free equilibrium is the unique equilibrium when $\mathcal{N} > 1$ and 415 $\mathcal{R}_{cm} < 1$. Now if $\mathcal{R}_{cm} < \mathcal{R}_{0,m} < 1$, then in addition to the DFE \mathcal{E}_1 , there exists two endemic 416 equilibria whenever $\Delta_m = e_1^2 - 4e_2e_0 > 0$. However, $\mathcal{R}_{cm} < \mathcal{R}_{0,m} < 1 \Rightarrow \mathcal{R}_{cm} < 1 \Leftrightarrow$ 417 $\beta_{vh} < -\frac{k_3 k_4 k_8 (\xi \omega \pi + k_1 \pi^2 \xi + k_2 (\pi \xi + k_2))}{a(1 - \alpha_1) (\gamma_h + k_4 \eta_h) (\pi \xi + k_2) (\pi \xi + k_2) \Lambda_h} < 0.$ Since all parameter of model are non-negative, we conclude that the condition $\mathcal{R}_{cm} < \mathcal{R}_{0,m} < 1$ does not hold. And thus, the model 418 419 with mass-action incidence does not admit endemic equilibria for $\mathcal{R}_{0,m} < 1$. We claim the 420 following: 421

422 Lemma 3. The arboviral diseases model (2) with mass-action incidences (24) has:

(i) a unique endemic equilibrium if $\mathcal{R}_{0,m} > 1$;

424 *(ii)* no endemic equilibrium otherwise.

425 Global stability of the DFE for the model with mass action incidence.

Since the DFE of the model with mass action incidence is the unique equilibrium whenever the corresponding basic reproduction number $\mathcal{R}_{0,m}$ is less than unity, it remains to show that the DFE is GAS. To this aim, we use the direct Lyapunov method. Let us define the following positive constants:

$$p_1 = \frac{1}{k_3}, p_2 = \frac{C_h H^0(\eta_v k_8 + \gamma_v)}{k_8 k_9} \frac{C_v S_v^0}{k_3 k_4}, \ p_3 = p_1 C_h H^0 \frac{(\eta_v k_8 + \gamma_v)}{k_8 k_9}, \ p_4 = \frac{C_h H^0}{k_3 k_8}$$

430 Consider the Lyapunov function

$$\mathcal{L} = p_1 E_h + p_2 I_h + p_3 E_v + p_4 I_v$$

431 The derivative of \mathcal{L} is given by

$$\begin{aligned} \dot{\mathcal{L}} &= p_1 \dot{E}_h + p_2 \dot{I}_h + p_3 \dot{E}_v + p_4 \dot{I}_v \\ &= (p_1 C_h \eta_v H + p_4 \gamma_v - p_3 k_9) E_v + (p_1 C_h H - p_4 k_8) I_v \\ &+ (p_3 C_v \eta_h S_v + p_2 \gamma_h - p_1 k_3) E_h + (p_3 C_v S_v - p_2 k_4) I_h \end{aligned}$$

Replacing p_i , i = 1, ..., 4, by their respective term, and using the fact that $H = (S_h + \pi V_h) \leq H^0 = (S_h^0 + \pi V_h^0)$ and $S_v \leq N_v^0$ in

$$\mathcal{D}_{3} = \left\{ (S_{h}, V_{h}, E_{h}, I_{h}, R_{h}, S_{v}, E_{v}, I_{v}, E, L, P) \in \mathcal{D} : N_{h} \le \frac{\Lambda_{h}}{\mu_{h}}, S_{v} \le N_{v}^{0} = \theta P, E \le K_{E}, L \le K_{L}, P \le \frac{lK_{L}}{k_{7}k_{8}} \right\},$$

434 we obtain $\dot{\mathcal{L}} \leq \left(\mathcal{R}^2_{0,m} - 1\right) E_h.$

We have $\dot{\mathcal{L}} \leq 0$ if $\mathcal{R}_{0,m} \leq 1$, with $\dot{\mathcal{L}} = 0$ if $\mathcal{R}_{0,m} = 1$ or $E_h = 0$. Whenever $E_h = 0$, we also have $I_h = 0$, $E_v = 0$ and $I_v = 0$. Substituting $E_h = I_h = E_v = I_v = 0$ in the first, fourth and fifth equation of Eq. (2) with mass action incidence (24) gives $S_h(t) \to S_h^0$, $V_h(t) \to V_h^0$, $R_h(t) \to 0$, and $S_v(t) \to S_v^0 = N_v^0$ as $t \to \infty$. Thus

$$[S_h(t), V_h(t), E_h(t), I_h(t), R_h(t), S_v(t), E_v(t), I_v(t), E(t), L(t), P(t)] \to (S_h^0, V_h^0, 0, 0, 0, N_v^0, 0, 0, E, L, P)$$

as $t \to \infty$.

It follows from the LaSalle's invariance principle [51, 52, 53], that every solution of (2) with mass action incidence, with initial conditions in \mathcal{D}_3 converges to the DFE, as $t \to \infty$. Hence, the DFE, \mathcal{E}_1 , of the model with mass action incidence, is GAS in \mathcal{D}_3 if $\mathcal{R}_{0,m} \leq 1$.

442 Thus, we claim the following result.

Theorem 11. The DFE, \mathcal{E}_1 , of the model (2) with mass action incidence, is globally asymptotically stable (GAS) in \mathcal{D}_3 if $\mathcal{R}_{0,m} < 1$.

Thus, the substitution of standard incidence with mass action incidence in the arboviral model (2) removes the backward bifurcation phenomenon of the model. It should be mentioned that a similar situation was reported by Garba *et al.* in [23] and by Sharomi *et al.* in [43].

448 We summarize the previous analysis of subsection 3.3 as follows:

Lemma 4. The main causes of occurrence of backward bifurcation phenomenon in models (2) and (18) are the disease-induced death and the standard incidence rates.

451 4 Sensitivity analysis

As shown in the previous sections, model (2) may admit single or multiple steady states according to the value of the basic reproduction number \mathcal{R}_0 . In turn, \mathcal{R}_0 depends on the parameters of the model. The various uncertainties encountered in data collection and the estimated values lead us to evaluate the robustness of the model predictions with the parameter values and, in particular, to estimate the effect on \mathcal{R}_0 of varying single parameter. To this aim, we use sensitivity analysis and calculate the sensitivity indices of \mathcal{R}_0 to the parameters in the model using both local and global methods.

Parameter	value	Parameter	value	Parameter	value
c_m	0.01	s	0.7	eta_{vh}	0.75
μ_b	6	η_2	0.3	Γ_E	10000
μ_P	0.4	μ_E	0.2	Γ_L	5000
heta	0.08	ϵ	0.61	$lpha_2$	0.5
l	0.5	Λ_h	2.5	μ_h	$\frac{1}{67*365}$
a	1	β_{hv}	0.75	η_v	0.35
μ_v	$\frac{1}{30}$	μ_L	0.4	σ	0.1428
γ_h	$\frac{1}{14}$	η_h	0.35	γ_v	$\frac{1}{21}$
ξ	0.5	ω	0.05	η_1	0.001
δ	0.001	α_1	0.2		

Table 3: Parameter values using to compute the sensitivity indices of \mathcal{R}_0 .

459 4.1 Local sensitivity analysis

The local sensitivity analysis, based on the *normalised sensitivity index* of \mathcal{R}_0 (see [54]), is given by

$$S_{\Psi} = \frac{\Psi}{\mathcal{R}_0} \frac{\partial \mathcal{R}_0}{\partial \Psi}$$

where Ψ denotes the generic parameter of (2).

This index indicates how sensitive \mathcal{R}_0 is to changes of parameter Ψ . Clearly, a positive (resp. negative) index indicates that an increase in the parameter value results in an increase (resp. decrease) in the \mathcal{R}_0 value [54].

For instance, the computation of the sensitivity index of \mathcal{R}_0 with respect to a is given by

$$S_a = \frac{a}{\mathcal{R}_0} \frac{\partial \mathcal{R}_0}{\partial a} = 1 > 0.$$

This shows that \mathcal{R}_0 is an increasing function of a and the parameter a has an influence on the spread of disease.

We tabulate the indices of the remaining parameters in Table 2 using parameter values on Table 3. The results are displayed in Table 4 and Figure 7a. The parameters are arranged from most sensitive to least. The model system (2) is most sensitive to a, the average number of mosquitoes bites, followed by μ_v , ϵ , s, Λ_h , β_{hv} , β_{vh} , Γ_E , Γ_L and α_2 . It is important to note that increasing (decreasing) a by 10% increases (decreases) \mathcal{R}_0 by 10%. However, increasing (decreasing) the parameters μ_v by 10% decreases (increases) \mathcal{R}_0 by 9.190%. The same reasoning can be done for other parameters.

476 4.2 Uncertainty and global sensitivity analysis

Local sensitivity analysis assesses the effects of individual parameters at particular points in parameter space without taking into account of the combined variability resulting from considering all input parameters simultaneously. Here, we perform a global sensitivity analysis to examine the model's response to parameter variation within a wider range in the parameter space.

Following the approach by Marino *et al.* [55] and Wu *et al.* [56], partial rank correlation coefficients (PRCC) between the basic reproduction number \mathcal{R}_0 and each parameter are derived from 5,000 runs of the Latin hypercube sampling (LHS) method [57]. The parameters are

Parameter	Index	Parameter	Index	Parameter	Index
a	+1	σ	-0.2911	ξ	-0.0566
μ_v	-0.9190	c_m	-0.2757	ω	+0.0565
ϵ	-0.6223	α_1	-0.25	μ_E	-0.0171
s	+0.5172	η_h	+0.2067	δ	-0.0020
Λ_h	-0.5	γ_h	-0.2064	η_1	-0.0000858
$\beta_{hv}, \beta_{vh}, \Gamma_E, \Gamma_L, \alpha_2$	+0.5	η_v	+0.1207		
μ_h	+0.4996	γ_v	+0.1174		
μ_P	-0.4810	μ_L	-0.1026		
heta	+0.4810	μ_b	+0.0772		
l	+0.4489	η_2	-0.0770		

Table 4: Sensitivity indices of \mathcal{R}_0 to parameters of model (2), evaluated at the baseline parameter values given in Table 3.

assumed to be random variables with uniform distributions with their mean value listed in Table 3.

With these 5,000 runs of LHS, the derived distribution of \mathcal{R}_0 is given in Figure 6. This sampling shows that the mean of \mathcal{R}_0 is 2.0961 and the standard deviation is 2.7910. This implies that for the mean of parameter values given in Table 3, we may be confident that the model predicts an endemic state. The probability that $\mathcal{R}_0 > 1$ (the disease-free equilibrium is unstable and there is exactly one endemic equilibrium point) is 55.60%. We also evaluate the probabilities that condition in Theorem 4 and inequalities (11), (12) and (13) are satisfied. Let us set $\mathbb{P}[X]$ the probability of X, and the sets of parameter values for which ($\mathcal{N} > 1$) is true by Φ ,

$$\mathbb{P}\left[\neg\Phi\right] = \mathbb{P}\left[\mathcal{N} \le 1\right] = 0.0096,\tag{29a}$$

$$\mathbb{P}\left[\Phi \quad \text{and} \quad (\mathcal{R}_0 \le 1)\right] = 0.4440, \tag{29b}$$

$$\mathbb{P}\left[\Phi \quad \text{and} \quad (\mathcal{R}_0 \leq \mathcal{R}_G)\right] = 0.0220,$$
(29c)

$$\mathbb{P}\left[\Phi \quad \text{and} \quad (\mathcal{R}_G < \mathcal{R}_0 \le 1)\right] = 0.4220. \tag{29d}$$

Therefore, the probability that the trivial disease-free equilibrium is locally asymptotically 487 stable is 0.0096 (from (29a)), the probability that the disease free equilibrium point is locally 488 asymptotically stable is 0.440 (from (29b)), the probability that the disease free equilibrium 489 point is locally asymptotically stable and (i) there are no endemic equilibrium points is 0.0220 490 ((29c)); and (ii) there are two endemic equilibrium points is 0.4220 (from (29d)). This implies 491 that for the ranges of parameter values given in Table 3, the disease-free equilibrium point is 492 likely to be locally asymptotically stable but, the probability of co-existence of a locally asymp-493 totically stable endemic equilibrium point (occurrence of backward bifurcation phenomenon) is 494 very significant. 495

We now use sensitivity analysis to analyze the influence of each parameter on the basic reproductive number. From the previously sampled parameter values, we compute the PRCC between \mathcal{R}_0 and each parameter of model (2). The parameters with large PRCC values (> 0.5 or < -0.5) statistically have the most influence [56]. The results, displayed in Table 5 and Figure 7 (b), show that the parameter α_1 , the human protection rate, has the highest influence on \mathcal{R}_0 . This suggests that individual protection may potentially be the most effective strategy to reduce \mathcal{R}_0 . The other parameters with an important effect are α_2 , β_{hv} , β_{vh} and θ .



Figure 6: Sampling distribution of \mathcal{R}_0 from 5,000 runs of Latin hypercube sampling. The mean of \mathcal{R}_0 is 2.0961 and the standard deviation is 2.7910. Furthermore, $\mathbb{P}(\mathcal{R}_0 > 1) = 0.5560$.

We note that the order of the most important parameters for \mathcal{R}_0 from the local sensitivity analysis does not match that of the global sensitivity analysis, showing that the local results are not robust, and depend of the parameters values. So, for this kind of situation, we must to consider the results of the global sensitivity analysis.

Parameter	Correlation	Parameter	Correlation	Parameter	Correlation
	Coefficients		Coefficients		Coefficients
α_1	-0.6125	l	0.3767	γ_v	0.0378
$lpha_2$	0.5960	ϵ	-0.3348	μ_L	-0.0357
β_{hv}	0.5817	s	0.2945	c_m	-0.0271
β_{vh}	0.5815	σ	-0.1808	η_h	0.0178
θ	0.5078	μ_P	-0.1594	η_1	-0.0161
a	0.4810	μ_h	0.1306	μ_E	-0.0113
μ_v	-0.3911	γ_h	-0.0605	ξ	-0.0109
Γ_L	0.4195	η_v	0.0578	δ	-0.0077
Γ_E	0.3888	μ_b	0.0439	η_2	0.0037
Λ_h	-0.3876	ω	0.0410		

Table 5: Partial Rank Correlation Coefficients between \mathcal{R}_0 and each parameters of model (2).

507 5 Numerical simulations

In the previous model [30], we have shown that the use of a vaccine with efficacy of about 60%, should be accompanied by other control measures such as means of individual protection (spanning wearing clothes during hours of vector activity, use of repellents,...), vector control (combining the use of adulticide to kill adult vectors, chemical control with use of larvicide to



(b) Partial rank correlation coefficients for \mathcal{R}_0

Figure 7: Local (a) and global (b) sensitivity indices for \mathcal{R}_0 against model parameters show that the order of the most important parameters for \mathcal{R}_0 from the local sensitivity analysis does not match those from the global sensitivity analysis.

kill the eggs and larvae, and mechanical control to reduce the number of breeding sites at least near habited areas) [19]. Here, we investigate and compare numerical results, with the different scenario. We use the following initial state variables $S_h(0) = 700$, $V_h(0) = 10$, $E_h(0) = 220$, $I_h(0) = 100$, $R_h(0) = 60$, $S_v(0) = 3000$, $E_v(0) = 400$, $I_v(0) = 120$, E(0) = 10000, L = 5000, P = 3000.

517 5.1 Strategy A: Vaccination combined with individual protection 518 only

In this strategy, we consider the model (2) without vector control. we set $\alpha_2 = 1$ and $c_m = \eta_1 = \eta_2 = 0$ and vary the parameter related to individual protection, namely α_1 , between 0 and 0.8. The values of other parameters are given in Table 3. Figure 8 shows that the increase of the individual protection level, permit to reduce the total number of infected humans, and the total number of infected vectors, but has no impact on the populations of eggs and larvae. However, from this figure, it is clear that, this reduction is significant if the level of protection must turn around 80% at least, and this, over a long period. Thus, continuous education campaigns of ⁵²⁶ local populations, on how to protect themselves individually, are important in the fight against the spread of arboviral diseases.



Figure 8: Simulations results showing how the total number of infected humans and the total number of infected vectors decrease when the individual protection increase. All others parameters values are in Table 3.

527

528 5.2 Strategy B: Vaccination combined with adulticide

Nowadays, *Deltamethrin* is the most used insecticide for impregnation of bednets, because it is 529 a highly effective compound on mosquitoes, and this, at of very low doses [58]. However, when 530 sprayed in an open environment, *Deltamethrin* seems to be effective only during a couple of 531 hours [19, 59, 60]. Also, its use over a long period and continuously, leads to strong resistance of 532 the wild populations of *Aedes aegypti*, for example [58]. The mortality of the mosquitoes after 533 spraying varied between 20% and 80%. To be more realistic, we will consider the technique 534 called "pulse control" (the control is not continuous in time order is effective only one day every 535 T days) [19]. To this aim, we consider that spraying is done once a week, and this, for 100 π 536 days. We set $\alpha_1 = \eta_1 = \eta_2 = 0$ and $\alpha_2 = 1$. 537

Simulation results on figure 9 show that a mortality rate induced by the use of larvicide, c_m , greater than 60% has a significant impact on the decrease of the total number of infected humans and vectors, and on the decrease of eggs and larvae.



Figure 9: Simulations results showing how the total number of infected vectors, eggs and larvae populations decrease when the aldulticide control parameter c_m increase. All others parameters values are in Table 3.

541 5.3 Strategy C: Vaccination combined with larvicide

Since the efficacy and the duration of a larvicide (Bti=Bacillus thuringiensis var. israelensis) strongly depend on several factors like water quality, exposure, and even the type of breeding sites, we thus consider, to be more realistic, that the duration can vary between a couple of days and two weeks [19, 61]. We consider that the larvicide spraying happens once every 15 days, and this, on a period of 100 days. We set $\alpha_1 = c_m = 0$ and $\alpha_2 = 1$.

The figure 10 shows that the use of larvicide has no significant impact on the decrease of 547 total number of infected humans and vectors, as well as on the number of eggs and larvae. This 548 can be justified by the fact that the use of conventional larvicides requires certain constraints 549 on their use: they can not be used continuously, their duration of action decreases with time. 550 In addition, eggs of certain populations of vectors such as *Aedes albopictus*, come into prolonged 551 hibernation when conditions in the breading sites are not conducive to their good growth (this 552 is justified by the control rate value $\eta_1 = 0.001$). Also, the pupae do not consume anything, 553 until reaching the mature stage. 554

555 5.4 Strategy D: Vaccination combined with mechanical control

The effectiveness of this type of control depends largely on awareness campaigns of local people in the sense that, to reduce the proliferation of vectors, people should destroy and systematically,



Figure 10: Simulations results showing how the total number of infected humans, the total number of infected vectors, and the eggs and larvae populations decrease with the larvicide control associated parameters η_1 and η_2 . All others parameters values are in Table 3.

potential breeding sites. Thus, we consider that this type of control can be achieved by local populations, and this, daily. We set $\alpha_1 = c_m = 0 = \eta_1 = \eta_2$.

The figure 11 shows that this type of control is appropriate in the fight against the proliferation of vectors. This can only be possible by the multiplication of local populations awareness campaigns.

563 5.5 Strategy E: Combining vaccination, individual protection and 564 adulticide

In this strategy, we consider the model (2) without larvicide and mechanical control. we set $\alpha_2 = 1$ and $\eta_1 = \eta_2 = 0$ and vary the parameter related to individual protection and the use of adulticide, namely α_1 and c_m , respectively, between 0 and 0.8. The values of other parameters are given in Table 3. Figure 12 shows that the use of the combination of these controls decreases significantly the total number of infected humans, infected vectors as well as the number of eggs and larvae, when its associated rates, namely α_1 and c_m , are greater than 0.3 and 0.2, respectively.



Figure 11: Simulations results showing how the total number of infected vectors, eggs and larvae populations decrease with the mechanical control associated parameter α_2 . All others parameters values are in Table 3.

572 5.6 Strategy F: Combining vaccination, individual protection and 573 mechanical control

Like for strategy E, the simulations results on figure 13 show that the combined use of these three types of controls has a positive impact in the vector control.

576 6 Conclusion

In this paper, we have derived and analyzed a deterministic model for the transmission of arboviral diseases with non linear form of infection and complete stage structured model for vectors, which takes into account a vaccination with waning immunity, individual protection and vector control strategies.

⁵⁸¹ We have begun by calculate the net reproductive number \mathcal{N} and the basic reproduction ⁵⁸² number, \mathcal{R}_0 , and investigate the existence and stability of equilibria. The stability analysis ⁵⁸³ revealed that for $\mathcal{N} \leq 1$, the trivial equilibrium is globally asymptotically stable. When ⁵⁸⁴ $\mathcal{N} > 1$ and $\mathcal{R}_0 < 1$, the disease-free equilibrium is locally asymptotically stable. Under certain ⁵⁸⁵ threshold condition, the disease-free equilibrium is also globally asymptotically stable. We ⁵⁸⁶ have found that the model exhibits backward bifurcation. The epidemiological implication of ⁵⁸⁷ this phenomenon is that for effective eradication and control of diseases, \mathcal{R}_0 should be less than



Figure 12: Simulations results showing the advantage that we have to combine vaccination, individual protection and adulticide.

a critical values less than one. Thus, we have proved, that the disease-induced death is the principal cause of the backward bifurcation phenomenon in the full model and the corresponding model without vaccination. However, the substitution of the standard incidences with the mass action incidences removed the backward bifurcation phenomenon.

We have proved that the model admits at least one endemic equilibrium, and only one endemic equilibrium point in the model without disease-induced death, and in the model with mass action incidences, whenever the basic reproduction number is great than unity.

Using parameters value of Chikungunya and Dengue fever, we have calculated the sensitivity 595 indices of the basic reproduction number, \mathcal{R}_0 , to the parameters in the model using both local 596 and global methods. Local sensitivity analysis showed that the model system is most sensitive 597 to a, the average number of mosquitoes bites, followed by μ_v , the natural mortality rate of 598 vectors. Considering that all input parameters vary simultaneously, we have used the Latin 599 Hypercube Sampling (LHS) to estimate statistically the mean value of the basic reproduction 600 number. The result showed that the model is in an endemic state, since the mean of \mathcal{R}_0 is 601 greater than unity. We also estimated the probability that the model predicts the occurrence 602 of backward bifurcation phenomenon and of the likely stability of the disease-free equilibrium 603 point. 604

⁶⁰⁵ Then, using global sensitivity analysis, we have computed the Partial Rank Correlation ⁶⁰⁶ Coefficients between \mathcal{R}_0 and each parameter of the model. Unlike the local sensitivity analysis, ⁶⁰⁷ the global analysis showed that the parameters α_1 , the human protection rate, has the highest



Figure 13: Simulations results showing the advantage that we have to combine vaccination, individual protection and mechanical control.

⁶⁰⁸ influence on \mathcal{R}_0 . The other parameters with an important effect are α_2 , the efficacy of the ⁶⁰⁹ mechanical control, β_{hv} , the probability of transmission of infection from an infected vector to ⁶¹⁰ a susceptible human, β_{vh} , the probability of transmission of infection from an infected human ⁶¹¹ to a susceptible vector, and θ , the maturation rate from pupae to adult vectors. This showed ⁶¹² that the order of the most important parameters for \mathcal{R}_0 from the local sensitivity analysis does ⁶¹³ not match those from the global sensitivity analysis. So, the local sensitivity results are not ⁶¹⁴ robust.

To assess the impact of combination of different controls, we have conducted several sim-615 ulations, using the called "pulse control" technique. According to the numerical results, we 616 conclude that the use of an imperfect vaccine with low efficacy combined with high individual 617 protection and good vector control strategy (reduction of breeding sites by local populations 618 action, chemical action using adulticides and larvicides), can effectively reduce the transmission 619 of the pathogen and the proliferation of vector populations. However, due to lack of resources to 620 implement these control mechanisms, developing countries should focus on the education of the 621 local populations. Because, unlike diseases such as malaria whose breeding sites of Anophe-622 les mosquitoes are known, those of Aedes (aegypti and albopictus) and Culex, for example, 623 are smaller (old tires, flower pots, vases and other hollow...) and unknown for many local 624 populations, which favour the development of vectors. 625

Thus, pending the development of a high efficacy vaccine and long-acting, individual protection and the various vector control methods are effective ways to combat the spread of arboviral diseases, for developing countries. In addition, the realization of the combination of these controls may be too expensive, because it means that, for constant controls, we must keep them at high levels, and this, for a long time. Thus it is important to know what happens when, instead of the constant controls, we use time dependent controls, in optimal control theory. This represents a perspective of this work.

Acknowledgement

⁶³⁴ The first author (H. A) thanks the Direction of UIT of Ngaoundere for their financial assistance ⁶³⁵ in the context of research missions in 2015.

⁶³⁶ A Useful result.

⁶³⁷ We use the following result, which is the characterization of Metzler matrices, to compute the ⁶³⁸ threshold \mathcal{R}_c , obtained at Eq. (10).

Lemma 5 ([40]). Let M be a square Metzler matrix written in block form $\begin{pmatrix} A & B \\ C & D \end{pmatrix}$ with Aand D square matrices. M is Metzler stable if and only if matrices A and $D - CA^{-1}B$ are Metzler stable.

$_{642}$ B Proof of Theorem 1.

⁶⁴³ The Jacobian matrix of f at the Trivial equilibrium is given by

$$Df(\mathcal{E}_0) = \begin{pmatrix} Df_1 & Df_2 \\ Df_3 & Df_4 \end{pmatrix}.$$
 (30)

644 where

and $H^0 = S_h^0 + \pi V_h^0$. The characteristic polynomial of $Df(\mathcal{E}_0)$ is given by:

$$P(\lambda) = -(\lambda + k_3) (\lambda + k_4) (\lambda + k_8) (\lambda + k_9) (\lambda + \mu_h) \phi_1(\lambda) \phi_2(\lambda)$$

where $\phi_{1}(\lambda) = \lambda^{2} + (k_{2} + k_{1})\lambda + \mu_{h}(k_{2} + \xi) \text{ and } \phi_{2}(\lambda) = \lambda^{4} + A_{1}\lambda^{3} + A_{2}\lambda^{2} + A_{3}\lambda + A_{4}.$ we have set $A_{1} = k_{5} + k_{6} + k_{7} + k_{8}, \quad A_{2} = k_{8}(k_{5} + k_{6} + k_{7}) + k_{7}(k_{5} + k_{6}) + k_{5}k_{6},$ $A_{3} = k_{5}k_{6}k_{7} + k_{8}(k_{5}k_{6} + k_{7}(k_{5} + k_{6})), \quad A_{4} = k_{5}k_{6}k_{7}k_{8}(1 - \mathcal{N}).$

The roots of $P(\lambda)$ are $\lambda_1 = -\mu_h$, $\lambda_1 = -k_1$, $\lambda_2 = -k_3$, $\lambda_3 = -k_4$, $\lambda_4 = -k_8$, $\lambda_4 = -k_9$, and the others roots are the roots of $\phi_1(\lambda)$ and $\phi_2(\lambda)$. The real part of roots of $\phi_1(\lambda)$ are negative. Since $\mathcal{N} < 1$, it is clear that all coefficients of $\phi_2(\lambda)$ are always positive. Now we just have to verify that the Routh-Hurwitz criterion holds for polynomial $\phi_2(\lambda)$. To this aim, setting

$$\begin{array}{ccc} {}_{655} & H_1 = A_1, \ H_2 = \begin{vmatrix} A_1 & 1 \\ A_3 & A_2 \end{vmatrix}, \ H_3 = \begin{vmatrix} A_1 & 1 & 0 \\ A_3 & A_2 & A_1 \\ 0 & A_4 & A_3 \end{vmatrix}, \ H_4 = \begin{vmatrix} A_1 & 1 & 0 & 0 \\ A_3 & A_2 & A_1 & 1 \\ 0 & A_4 & A_3 & A_2 \\ 0 & 0 & 0 & A_4 \end{vmatrix} = A_4 H_3.$$

⁶⁵⁶ The Routh-Hurwitz criterion of stability of the trivial equilibrium \mathcal{E}^0 is given by

$$\begin{cases}
H_1 > 0 \\
H_2 > 0 \\
H_3 > 0 \\
H_4 > 0
\end{cases} \Leftrightarrow
\begin{cases}
H_1 > 0 \\
H_2 > 0 \\
H_3 > 0 \\
A_4 > 0
\end{cases}$$
(31)

657 We have $H_1 = A_1 = k_5 + k_6 + k_7 + k_8 > 0$,

$$H_{2} = A_{1}A_{2} - A_{3}$$

= $(k_{7} + k_{6} + k_{5})k_{8}^{2} + (k_{7}^{2} + (2k_{6} + 2k_{5})k_{7} + k_{6}^{2} + 2k_{5}k_{6} + k_{5}^{2})k_{8}$
+ $(k_{6} + k_{5})k_{7}^{2} + (k_{6}^{2} + 2k_{5}k_{6} + k_{5}^{2})k_{7} + k_{5}k_{6}^{2} + k_{5}^{2}k_{6}$

$$\begin{split} H_{3} &= A_{1}A_{2}A_{3} - A_{1}^{2}A_{4} - A_{3}^{2} \\ &= (k_{6} + k_{5}) \left(k_{7}^{2} + (k_{6} + k_{5}) k_{7} + k_{5}k_{6}\right) k_{8}^{3} \\ &+ \left(\mu_{b}ls\theta + (k_{6} + k_{5}) k_{7}^{3} + 2(k_{6} + k_{5})^{2}k_{7}^{2} + \left(k_{6}^{3} + 4k_{5}k_{6}^{2} + 4k_{5}^{2}k_{6} + k_{5}^{3}\right) k_{7} + k_{5}k_{6}^{3} + 2k_{5}^{2}k_{6}^{2} + k_{5}^{3}k_{6}\right) k_{8}^{2} \\ &+ \left[(2k_{7} + 2k_{6} + 2k_{5}) \mu_{b}ls\theta + \left(k_{6}^{2} + 2k_{5}k_{6} + k_{5}^{2}\right) k_{7}^{3} + \left(k_{6}^{3} + 4k_{5}k_{6}^{2} + 4k_{5}^{2}k_{6} + k_{5}^{3}\right) k_{7}^{2} \\ &+ \left(2k_{5}k_{6}^{3} + 4k_{5}^{2}k_{6}^{2} + 2k_{5}^{3}k_{6}\right) k_{7} + k_{5}^{2}k_{6}^{3} + k_{5}^{3}k_{6}^{2} \right] k_{8} + \left(k_{7}^{2} + (2k_{6} + 2k_{5}) k_{7} + k_{6}^{2} + 2k_{5}k_{6} + k_{5}^{2}\right) \mu_{b}ls\theta \\ &+ \left(k_{5}k_{6}^{2} + k_{5}^{2}k_{6}\right) k_{7}^{3} + \left(k_{5}k_{6}^{3} + 2k_{5}^{2}k_{6}^{2} + k_{5}^{3}k_{6}\right) k_{7}^{2} + \left(k_{5}^{2}k_{6}^{3} + k_{5}^{3}k_{6}^{2}\right) k_{7} \\ \end{split}$$

We always have $H_1 > 0$, $H_2 > 0$, $H_3 > 0$ and $H_4 > 0$ if $\mathcal{N} < 1$. Thus, the trivial equilibrium \mathcal{E}_0 is locally asymptotically stable whenever $\mathcal{N} < 1$.

We assume the net reproductive number $\mathcal{N} > 1$. Following the procedure and the notation in [38], we may obtain the basic reproduction number \mathcal{R}_0 as the dominant eigenvalue of the *next-generation matrix* [37, 38]. Observe that model (2) has four infected populations, namely E_h, I_h, E_v, I_v . It follows that the matrices F and V defined in [38], which take into account the new infection terms and remaining transfer terms, respectively, are given by $\zeta = \frac{\tau \beta_{hv} n_v H^0}{\tau \beta_{hv} m_v} \frac{\tau \beta_{hv} H^0}{\tau} \lambda$

$${}_{666} \quad F = \left(\begin{array}{ccccc} 0 & 0 & \frac{\tau \beta_{hv} \eta_v H^*}{N_h^0} & \frac{\tau \beta_{hv} H^*}{N_h^0} \\ 0 & 0 & 0 & 0 \\ \frac{\tau \beta_{vh} \eta_v S_v^0}{N_h^0} & \frac{\tau \beta_{vh} S_v^0}{N_h^0} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{array} \right), \text{ and } V = \left(\begin{array}{ccccc} k_3 & 0 & 0 & 0 \\ -\gamma_h & k_4 & 0 & 0 \\ 0 & 0 & k_9 & 0 \\ 0 & 0 & -\gamma_v & k_8 \end{array} \right).$$

⁶⁶⁷ The dominant eigenvalue of the next-generation matrix FV^{-1} is given by (7). The local ⁶⁶⁸ stability of the disease-free equilibrium \mathcal{E}_1 is a direct consequence of Theorem 2 in [38]. This ⁶⁶⁹ ends the proof.

⁶⁷⁰ C Proof of Theorem 2.

Setting Y = X - TE with $X = (S_h, V_h, E_h, I_h, R_h, S_v, E_v, I_v, E, L, P)^T$, $H^0 = (S_h^0 + \pi V_h^0)$, $A_{99} = \left(k_5 + \mu_b \frac{S_v + E_v + I_v}{K_E}\right)$, and $A_{10} = \left(k_6 + s \frac{E}{K_L}\right)$. we can rewrite (2) in the following manner $\frac{dY}{dt} = \mathcal{B}(Y)Y$ (32)

It is clear that Y = (0, 0, 0, 0, 0, 0, 0, 0, 0, 0) is the only equilibrium. Then it suffices to consider the following Lyapunov function $\mathcal{L}(Y) = \langle g, Y \rangle$ were $g = \left(1, 1, 1, 1, 1, 1, 1, 1, \frac{k_8}{\mu_b}, \frac{k_5 k_8}{\mu_b s}, \frac{k_5 k_6 k_8}{\mu_b sl}\right)$. Straightforward computations lead that

$$\begin{aligned} \dot{\mathcal{L}}(Y) &= \langle g, \dot{Y} \rangle \stackrel{\text{def}}{=} \langle g, \mathcal{B}(Y)Y \rangle \\ &= -\mu_h Y_1 - \mu_h Y_2 - \mu_h Y_3 - (\mu_h + \delta)Y_4 - \mu_h Y_5 \\ &- \frac{k_8}{K_E} (Y_6 + Y_7 + Y_8) - \frac{k_5 k_8}{\mu_b K_L} Y_9 Y_{10} + \theta \left(1 - \frac{1}{\mathcal{N}}\right) Y_{11} \end{aligned}$$

We have $\dot{\mathcal{L}}(Y) < 0$ if $\mathcal{N} \leq 1$ and $\dot{\mathcal{L}}(Y) = 0$ if $Y_i = 0, i = 1, 2, ..., 11$ (i.e. $S_h = S_h^0, V_h = V_h^0$ and $E_h = I_h = R_h = S_v = E_v = I_v = E = L = P = 0$). Moreover, the maximal invariant set contained in $\left\{ \mathcal{L} | \dot{\mathcal{L}}(Y) = 0 \right\}$ is (0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0). Thus, from Lyapunov theory, we deduce that (0, 0, 0, 0, 0, 0, 0, 0, 0, 0) and thus, \mathcal{E}_0 , is GAS if and only if $\mathcal{N} \leq 1$.

$_{665}$ D Proof of Theorem 5.

In order to determine the existence of endemic equilibria, i.e., equilibria with all positive components, say

$$\mathcal{E}^{**} = (S_h^*, V_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*, E, L, P)$$

we have to look for the solution of the algebraic system of equations obtained by equating the 688 right sides of system (2) to zero. In this way we consider two case: 689

(i) Special case: Absence of disease-induced death in human ($\delta = 0$). 690

Note that in the absence of disease-induced death in human population, we have $N_h^* =$ 691 $N_h^0 = \Lambda_h / \mu_h$. Let 692

$$\lambda_h^{c,*} = \frac{a(1-\alpha_1)\beta_{hv}(\eta_v E_v^* + I_v^*)}{N_h^*}, \quad \lambda_v^{c,*} = \frac{a(1-\alpha_1)\beta_{vh}(\eta_h E_h^* + I_h^*)}{N_h^*}$$
(33)

be the forces of infection of humans and vectors at steady state, respectively. Solving the 693 equations in (2) at steady state gives 694

$$S_{h}^{*} = \frac{\Lambda_{h}(\pi\lambda_{h}^{c,*} + k_{2})}{\mu_{h}(k_{2} + \xi) + \lambda_{h}^{c,*}(\pi\lambda_{h}^{c,*} + \pi k_{1} + k_{2})}, \quad V_{h}^{*} = \frac{\xi S_{h}^{*}}{(\pi\lambda_{h}^{c,*} + k_{2})},$$

$$E_{h}^{*} = \frac{\lambda_{h}^{c,*}(S_{h}^{*} + \pi V_{h}^{*})}{k_{3}}, \quad I_{h}^{*} = \frac{\gamma_{h}\lambda_{h}^{c,*}(S_{h}^{*} + \pi V_{h}^{*})}{k_{3}k_{4}}, \quad R_{h}^{*} = \frac{\sigma\gamma_{h}\lambda_{h}^{c,*}(S_{h}^{*} + \pi V_{h}^{*})}{\mu_{h}k_{3}k_{4}},$$
(34)

and 695

$$S_{v}^{*} = \frac{\theta P}{(\lambda_{v}^{c,*} + k_{8})}, \quad E_{v}^{*} = \frac{\theta P \lambda_{v}^{c,*}}{k_{9}(\lambda_{v}^{c,*} + k_{8})}, \quad I_{v}^{*} = \frac{\gamma_{v}\theta P \lambda_{v}^{c,*}}{k_{8}k_{9}(\lambda_{v}^{c,*} + k_{8})},$$

$$E = \frac{\mu_{b}\theta K_{E}P}{(k_{5}k_{8}K_{E} + \mu_{b}\theta P)}, \quad L = \frac{\mu_{b}\theta s K_{E}K_{L}P}{k_{6}K_{L}(k_{5}k_{8}K_{E} + \mu_{b}\theta P) + s\mu_{b}\theta K_{E}P},$$
(35)

where P is solution of the following equation 696

$$f(P) = -k_7 P \left[\mu_b \theta (sK_E + k_6 K_L) P + k_5 k_6 k_8 K_E K_L (\mathcal{N} - 1) \right] = 0$$
(36)

A direct resolution of the above equation give P = 0 or $P = \frac{k_5 k_6 k_8 K_E K_L (\mathcal{N} - 1)}{\mu_b \theta (sK_E + k_6 K_L)}$. Note that P = 0 corresponds to the trivial equilibrium \mathcal{E}_0 . Now we consider P > 0 i.e. 697

698 $\mathcal{N} > 1$. Replacing (34) and (35) in (33) give 699

$$\lambda_h^{c,*} = \frac{a(1-\alpha_1)\beta_{hv}\mu_h}{\Lambda_h} \left(\eta_v \frac{\theta P \lambda_v^*}{k_9(\lambda_v^* + k_8)} + \frac{\gamma_v \theta P \lambda_v^*}{k_8 k_9(\lambda_v^* + k_8)}\right)$$
(37)

700

$$\lambda_{v}^{c,*} = \frac{a(1-\alpha_{1})\beta_{vh}\mu_{h}}{\Lambda_{h}} \left(\eta_{h}\frac{\lambda_{h}^{*}(S_{h}^{*}+\pi V_{h}^{*})}{k_{3}} + \frac{\gamma_{h}\lambda_{h}^{*}(S_{h}^{*}+\pi V_{h}^{*})}{k_{3}k_{4}}\right)$$
(38)

Substuting (38) in (37) give 701

$$(k_6 K_L + s K_E) \lambda_h^* \left[a_2 (\lambda_h^*)^2 + a_1 \lambda_h^* + a_0 \right] = 0$$
(39)

where a_2 , a_1 and a_0 are given by 702

$$\mathcal{R}_{b} = \sqrt{\frac{(\pi\xi + k_{2})}{\pi(\xi + k_{2})}} \left(\frac{(k_{1}\pi + k_{2})}{\mu_{h}} + \frac{a(1 - \alpha_{1})\beta_{vh}(\gamma_{h} + k_{4}\eta_{h})(\pi\xi + k_{2})}{k_{3}k_{4}k_{8}} \right),$$

$$a_{2} = (a(1 - \alpha_{1})\beta_{vh}\mu_{h}(\gamma_{h} + k_{4}\eta_{h}) + k_{3}k_{4}k_{8})k_{9}\mu_{b}\Lambda_{h}\pi,$$

$$a_{1} = \frac{k_{3}k_{4}k_{8}k_{9}\mu_{b}\Lambda_{h}(\xi + k_{2})\mu_{h}\pi}{(\pi\xi + k_{2})}(\mathcal{R}_{b} - \mathcal{R}_{1}),$$

$$a_{0} = \mu_{h}k_{3}k_{4}k_{8}k_{9}\mu_{b}\Lambda_{h}(\xi + k_{2})(1 - \mathcal{R}_{1}).$$
(40)

The trivial solution $\lambda_h^* = 0$ of (39) corresponds to the disease-free equilibrium \mathcal{E}_1 . Now, we 703 just look the equilibria when $\lambda_h^* > 0$. Note that coefficient a_2 is always positive and a_0 is 704

negative (resp. positive) if and only if $\mathcal{R}_1 > 1$ (resp. $\mathcal{R}_1 < 1$). Thus model system (2), 705 in absence of disease-induced death in human population ($\delta = 0$), admits only one endemic 706 equilibrium whenever $\mathcal{R}_1 > 1$. Since the sign of coefficient a_1 depend of the value of parameter, 707 we investigate the possibility of occurrence of backward bifurcation phenomenon when $\mathcal{R}_1 < 1$. 708 Furthermore, consider the inequality 709

$$\mathcal{R}_1 < \mathcal{R}_b. \tag{41}$$

Since a_2 is always positive and a_0 is always positive whenever $\mathcal{R}_1 < 1$, then, the occur-710 rence of backward bifurcation phenomenon depend of the sign of coefficient a_1 . The co-711 efficient a_1 is always positive if and only if condition (41) holds (i.e $\mathcal{R}_1 < \mathcal{R}_b$). It fol-712 lows that the disease-free equilibrium is the unique equilibrium when $\mathcal{N} > 1$ and $\mathcal{R}_1 < 1$. 713 Now if $\mathcal{R}_b < \mathcal{R}_1 < 1$, then in addition to the DFE \mathcal{E}_1 , there exists two endemic equi-714 libria whenever $\Delta = a_1^2 - 4a_2a_0 > 0$. However, $\mathcal{R}_b < \mathcal{R}_1 < 1 \Rightarrow \mathcal{R}_b < 1 \Leftrightarrow \beta_{vh} < \delta_{vh} < 0$ 715 $\frac{[\pi^{2}\xi^{2} + (\mu_{h}\pi^{2} + (2\omega + \mu_{h})\pi)\xi + (\omega + \mu_{h})^{2}]k_{3}k_{4}k_{8}}{[\pi^{2}\xi^{2} + (\mu_{h}\pi^{2} + (2\omega + \mu_{h})\pi)\xi + (\omega + \mu_{h})^{2}]k_{3}k_{4}k_{8}} < 0.$ Since all parameter of model (2) 716 $\frac{-a(1-\alpha_1)\mu_h(\pi\xi+k_2)^2(\gamma_h+k_4\eta_h)}{\alpha_{\rm re}} < 0. \text{ Since an parameter of model (2)}$ are nonnegative, we conclude that the condition $\mathcal{R}_b < \mathcal{R}_1 < 1$ does not hold. And thus, the 717 backward bifurcation never occurs in the absence of disease-induced death in human.

(ii) Presence of disease induced death in human ($\delta \neq 0$). 719

In this case, we have $N_h^* = \frac{\Lambda_h - \delta I_h^*}{\mu_h}$. Applying the same procedure as case (i), we obtain 720 that λ_h^* at steady state is solution of the following equation 721

$$f(\lambda_h^*) = \lambda_h^* \left[c_4 (\lambda_h^*)^4 + c_3 (\lambda_h^*)^3 + c_2 (\lambda_h^*)^2 + c_1 \lambda_h^* + c_0 \right] = 0,$$
(42)

where 722

$$c_4 = -\pi^2 k_9 K_{12} \mu_b \Lambda_h \left(k_3 k_4 - \delta \gamma_h \right) \left(k_{10} a \mu_h (1 - \alpha_1) \beta_{vh} + k_8 (k_3 k_4 - \delta \gamma_h) \right),$$

723

718

$$c_3 = \pi (k_3 k_4 k_5 k_6 k_{10} k_{11} a^2 \mu_h^2 (1 - \alpha_1)^2 \beta_{hv} n \pi \beta_{vh} K_E K_L + 2k_9 k_{10} K_{12} a \mu_b \delta \Lambda_h \mu_h \gamma_h \pi (1 - \alpha_1) \beta_{vh} \xi$$

$$-k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\pi(1-\alpha_{1})\beta_{vh}\xi - 2k_{8}k_{9}K_{12}\mu_{b}\delta^{2}\Lambda_{h}\gamma_{h}^{2}\pi\xi + 2k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h}\pi\xi$$

 $-k_{1}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\pi(1-\alpha_{1})\beta_{vh}+2k_{2}k_{9}k_{10}K_{12}a\mu_{b}\delta\Lambda_{h}\mu_{h}\gamma_{h}(1-\alpha_{1})\beta_{vh}$

$$-2k_{2}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}(1-\alpha_{1})\beta_{vh}+2k_{1}k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h}\pi-2k_{1}k_{3}^{2}k_{4}^{2}k_{8}k_{9}K_{12}\mu_{b}\Lambda_{h}\pi$$

$$-2k_2k_8k_9K_{12}\mu_b\delta^2\Lambda_h\gamma_h^2+4k_2k_3k_4k_8k_9K_{12}\mu_b\delta\Lambda_h\gamma_h-2k_2k_3^2k_4^2k_8k_9K_{12}\mu_b\Lambda_h)$$

724

$$= k_3 k_4 k_5 k_6 k_{10} k_{11} a^2 \mu_h^2 (1 - \alpha_1)^2 \beta_{hv} n \pi^2 \beta_{vh} \xi K_E K_L$$

$$+k_1k_3k_4k_5k_6k_{10}k_{11}a^2\mu_h^2(1-\alpha_1)^2\beta_{hv}n\pi^2\beta_{vh}K_EK_L$$

 $+2k_{2}k_{3}k_{4}k_{5}k_{6}k_{10}k_{11}a^{2}\mu_{h}^{2}(1-\alpha_{1})^{2}\beta_{hv}n\pi\beta_{vh}K_{E}K_{L}+k_{9}k_{10}K_{12}a\mu_{b}\delta\Lambda_{h}\mu_{h}\gamma_{h}\pi^{2}(1-\alpha_{1})\beta_{vh}\xi^{2}$

 $-k_{8}k_{9}K_{12}\mu_{b}\delta^{2}\Lambda_{h}\gamma_{h}^{2}\pi^{2}\xi^{2}-k_{1}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\pi^{2}(1-\alpha_{1})\beta_{vh}\xi$

$$+ k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\omega\pi(1-\alpha_{1})\beta_{vh}\xi + 2k_{2}k_{9}k_{10}K_{12}a\mu_{b}\delta\Lambda_{h}\mu_{h}\gamma_{h}\pi(1-\alpha_{1})\beta_{vh}\xi$$

$$-k_{2}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\pi(1-\alpha_{1})\beta_{vh}\xi+2k_{1}k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h}\pi^{2}\xi$$

$$-2k_3k_4k_8k_9K_{12}\mu_b\delta\Lambda_h\gamma_h\omega\pi\xi+2k_3^2k_4^2k_8k_9K_{12}\mu_b\Lambda_h\omega\pi\xi-2k_2k_8k_9K_{12}\mu_b\delta^2\Lambda_h\gamma_h^2\pi\xi$$

$$+ 2k_2k_3k_4k_8k_9K_{12}\mu_b\delta\Lambda_h\gamma_h\pi\xi - 2k_1k_2k_3k_4k_9k_{10}K_{12}a\mu_b\Lambda_h\mu_h(1-\alpha_1)\pi\beta_{vh}$$

$$+k_{2}^{2}k_{9}k_{10}K_{12}a\mu_{b}\delta\Lambda_{h}\mu_{h}\gamma_{h}(1-\alpha_{1})\beta_{vh}-k_{2}^{2}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}(1-\alpha_{1})\beta_{vh}$$

 $-k_2^2k_8k_9K_{12}\mu_b\delta^2\Lambda_h\gamma_h^2+2k_2^2k_3k_4k_8k_9K_{12}\mu_b\delta\Lambda_h\gamma_h-k_2^2k_3^2k_4^2k_8k_9K_{12}\mu_b\Lambda_h,$

725

$$\begin{aligned} c_{1} &= \left((k_{1}k_{3}k_{4}k_{5}k_{6}k_{10}k_{11}a^{2}\mu_{h}^{2}(1-\alpha_{1})\beta_{hv}n\pi^{2} + k_{3}k_{4}k_{5}k_{6}k_{10}k_{11}a^{2}\mu_{h}^{2}(1-\alpha_{1})^{2}\beta_{hv}n(k_{2}-\omega)\pi \right)\beta_{vh}\xi \\ &+ (2k_{1}k_{2}k_{3}k_{4}k_{5}k_{6}k_{10}k_{11}a^{2}\mu_{h}^{2}(1-\alpha_{1})\beta_{hv}n\pi + k_{2}^{2}k_{3}k_{4}k_{5}k_{6}k_{10}k_{11}a^{2}\mu_{h}^{2}(1-\alpha_{1})\beta_{hv}n)(1-\alpha_{1})\beta_{vh} \right)K_{E}K_{L} \\ &+ (k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\omega\pi(1-\alpha_{1})\beta_{vh} - 2k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h}\omega\pi)\xi^{2} \\ &+ ((k_{2}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\omega - k_{1}k_{2}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}\pi)(1-\alpha_{1})\beta_{vh} \\ &+ (2k_{1}k_{3}^{2}k_{4}^{2}k_{8}k_{9}K_{12}\mu_{b}\Lambda_{h}\omega + 2k_{1}k_{2}k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h})\pi \\ &+ (2k_{2}k_{3}^{2}k_{4}^{2}k_{8}k_{9}K_{12}\mu_{b}\Lambda_{h} - 2k_{2}k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h})\omega\xi \\ &- k_{1}k_{2}^{2}k_{3}k_{4}k_{9}k_{10}K_{12}a\mu_{b}\Lambda_{h}\mu_{h}(1-\alpha_{1})\beta_{vh} - 2k_{1}^{2}k_{2}k_{3}^{2}k_{4}^{2}k_{8}k_{9}K_{12}\mu_{b}\Lambda_{h}\pi \\ &+ 2k_{1}k_{2}^{2}k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h} - 2k_{1}k_{2}^{2}k_{3}^{2}k_{4}^{2}k_{8}k_{9}K_{12}\mu_{b}\Lambda_{h}\pi \\ &+ 2k_{1}k_{2}^{2}k_{3}k_{4}k_{8}k_{9}K_{12}\mu_{b}\delta\Lambda_{h}\gamma_{h} - 2k_{1}k_{2}^{2}k_{3}^{2}k_{4}^{2}k_{8}k_{9}K_{12}\mu_{b}\Lambda_{h}, \end{aligned}$$

726

$$c_0 = k_3^2 k_4^2 k_8 k_9 K_{12} \mu_b \Lambda_h \mu_h^2 (k_2 + \xi)^2 \left(\mathcal{R}_0^2 - 1 \right),$$

with $k_{10} = \gamma_h + \eta_h k_4$, $k_{11} = \gamma_v + \eta_v k_8$, $K_{12} = (sK_E + k_6K_L)$ and $n = \mathcal{N} - 1$. Notes that c_4 is always negative and c_0 is positive (resp. negative) if \mathcal{R}_0 is greater (resp. less) that the unity. It follows, depending of the sign of coefficients c_3 , c_2 and c_1 , that the model system (2) admits at least one endemic equilibrium whenever $\mathcal{R}_0 > 1$ and the phenomenon of backward (resp. forward) bifurcation can occurs when $\mathcal{R}_0 < 1$ (resp. $\mathcal{R}_0 > 1$). This ends the proof.

E Proof of Theorem 9

733 Consider the Lyapunov function

$$\mathcal{G} = q_1 E_h + q_2 I_h + q_3 E_v + q_4 I_v,$$

734 where

$$q_1 = \frac{1}{k_3}; \ q_3 = \frac{\zeta_1 S_h^0}{k_3 k_8} \frac{(\gamma_v + k_8 \eta_v)}{k_9}, \ q_2 = \frac{\zeta_1 S_h^0}{k_3 k_8} \frac{(\gamma_v + k_8 \eta_v) \zeta_2 S_v^0}{k_4 k_9}, \ q_4 = \frac{\zeta_1 S_h^0}{k_3 k_8} \frac{(\gamma_v + k_8 \eta_v) \zeta_2 S_v^0}{k_4 k_9},$$

and we have set $\zeta_1 = \frac{\tau \mu_h \beta_{hv}}{\Lambda_h}$ and $\zeta_2 = \frac{\tau \mu_h \beta_{vh}}{\Lambda_h}$. The derivative of \mathcal{G} is given by

Replacing q_i , i = 1, ..., 4, by their value gives after straightforward simplifications

$$\dot{\mathcal{G}} \le \left(\mathcal{R}_{nv,\delta=0}^2 - 1\right) E_h$$

⁷³⁷ We have $\dot{\mathcal{G}} \leq 0$ if $\mathcal{R}_{nv,\delta=0} \leq 1$, with $\dot{\mathcal{G}} = 0$ if $\mathcal{R}_{nv,\delta=0} = 1$ or $E_h = 0$. Whenever $E_h = 0$, we also ⁷³⁸ have $I_h = 0$, $E_v = 0$ and $I_v = 0$. Substituting $E_h = I_h = E_v = I_v = 0$ in the first, fourth and ⁷³⁹ fifth equation of Eq. (18) with $\delta = 0$ gives $S_h(t) \to S_h^0 = N_h^0$, $R_h(t) \to 0$, and $S_v(t) \to S_v^0 = N_v^0$ ⁷⁴⁰ as $t \to \infty$. Thus

$$[S_h(t), E_h(t), I_h(t), R_h(t), S_v(t), E_v(t), I_v(t), E(t), L(t), P(t)] \to (N_h^0, 0, 0, 0, N_v^0, 0, 0, E, L, P)$$

as $t \to \infty$.

It follows from the LaSalle's invariance principle [51, 52, 53] that every solution of (18) (when

 $\mathcal{R}_{nv,\delta=0} \leq 1$), with initial conditions in \mathcal{D}_2 converges to \mathcal{E}_1^{nv} , as $t \to \infty$. Hence, the DFE, \mathcal{E}_1^{nv} , of model (18) without disease-induced death, is GAS in \mathcal{D}_2 if $\mathcal{R}_{nv,\delta=0} \leq 1$.

744 **References**

- [1] A. Chippaux, Généralités sur arbovirus et arboviroses overview of arbovirus and arbovirus
 rosis, Med. Maladies Infect. 33 (2003) 377–384.
- [2] N. Karabatsos, International Catalogue of Arboviruses, including certain other viruses of
 vertebrates, San Antonio, TX. 1985, 2001 update.
- [3] D. J. Gubler, Human arbovirus infections worldwide, Ann. N. Y. Acad. Sci. 951 (2001)
 13-24.
- [4] SANOFI PASTEUR, Dengue vaccine, a priority for global health (2013).
- [5] World Health Organization, Dengue and severe dengue, www.who.int/mediacentre/
 factsheets/fs117/en (Updated September 2013).
- [6] World Health Organization, Dengue and dengue haemorhagic fever, www.who.int/
 mediacentre/factsheets/fs117/en (2009).
- [7] Djamila Moulay, Modélisation et analyse mathématique de systèmes dynamiques en
 épidémiologie. application au cas du chikungunya., Ph.D. thesis, Université du Havre
 (2011).
- [8] P. Parola, X. de Lamballerie, J. Jourdan, C. Rovery, V. Vaillant, P. Minodier, P. Brouqui,
 A. Flahault, D. Raoult, R. N. Charrel, Novel chikungunya virus variant in travelers returning from indian ocean islands, Emerging Infectious Diseases 12 (10) (Octobre 2006)
 1-12.
- [9] Anthony Brasseur, Analyse des pratiques actuelles destinées á limiter la propagation
 d'aedes albopictus dans la zone sud est de la france et propositions d'amélioration, Ph.D.
 thesis, Écoles des Hautes Études en Santé Publique (EHESP) (2011).
- [10] S. A. Carvalho, S. O. da Silva, I. da Cunha Charret, Mathematical modeling of dengue
 epidemic: Control methods and vaccination strategies, arXiv:1508.00961v1 (2015) 1–11.
- [11] L. Villar, G. H. Dayan, J. L. Arredondo-García, D. M. Rivera, R. Cunha, C. Deseda,
 H. Reynales, M. S. Costa, J. O. Morales-Ramrez, G. Carrasquilla, L. C. Rey, R. Dietze,
 K. Luz, E. Rivas, M. C. M. Montoya, M. C. Supelano, B. Zambrano, E. Langevin, M. Boaz,
 N. Tornieporth, M. Saville, F. Noriega, Efficacy of a tetravalent dengue vaccine in children
 in latin america, The New England Journal of Medicine 372 (2) (2015) 113–123.
- [12] A. Sabchareon, D. Wallace, C. Sirivichayakul, K. Limkittikul, P. Chanthavanich, S. Suvannadabba, V. Jiwariyavej, W. Dulyachai, K. Pengsaa, T. Anh Wartel, A. Moureau, M. Saville, A. Bouckenooghe, S. Viviani, N. G. Tornieporth, J. Lang, Protective efficacy of the recombinant, live-attenuated, cyd tetravalent dengue vaccine in thai schoolchildren: a randomised, controlled phase 2b trial, Lancet 380 (2012) 1559–1567.
- [13] D. Aldila, T. Götz, E. Soewono, An optimal control problem arising from a dengue disease
 transmission model, Mathematical Biosciences 242 (2013) 9–16.
- [14] M. Antonio, T. Yoneyama, Optimal and sub-optimal control in dengue epidemics, Optim.
 Control Appl. Methods 63 (22) (2001) 63-73.

- [15] J. R. Cannon, D. J. Galiffa, An epidemiology model suggested by yellow fever, Math.
 Methods Appl. Sci. 35 (2012) 196–206.
- [16] F. A. B. Coutinho, M. N. Burattini, L. F. Lopez, E. Massad, Threshold conditions for a non-autonomous epidemic system describing the population dynamics of dengue, Bulletin of Mathematical Biology 68 (2006) 2263–2282.
- [17] G. Cruz-Pacheco, L. Esteva, C. Vargas, Seasonality and outbreaks in west nile virus infec tion, Bull. Math. Biol. 71 (2009) 1378–1393.
- [18] M. Derouich, A. Boutayeb, Dengue fever: mathematical modelling and computer simula tion, Applied Mathematics and Computation 177 2 (2006) 528-544.
- [19] Y. Dumont, F. Chiroleu, Vector control for the chikungunya disease, Math. Biosci. Eng. 7
 (2010) 313–345.
- [20] L. Esteva, C. Vargas, Analysis of a dengue disease transmission model, Math. Biosci. 150
 (1998) 131–151.
- [21] L. Esteva, C. Vargas, A model for dengue disease with variable human population, J.
 Math. Biol. 38 (1999) 220-240.
- [22] Z. Feng, V. Velasco-Hernadez, Competitive exclusion in a vector-host model for the dengue fever, J. Math. Biol. 35 (1997) 523-544.
- [23] S. M. Garba, A. B. Gumel, M. R. A. Bakar, Backward bifurcations in dengue transmission dynamics, Math. Biosci. 215 (2008) 11–25.
- ⁸⁰¹ [24] H. S. Rodrigues, M. T. T. Monteiro, D. F. M. Torres, Vaccination models and optimal ⁸⁰² control strategies to dengue, Mathematical Biosciences 247 (2014) 1–12.
- [25] K. W. Blayneha, A. B. Gumel, S. Lenhart, T. Clayton, Backward bifurcation and optimal
 control in transmission dynamics of west nile virus, Bulletin of Mathematical Biology 72
 (2010) 1006–1028. doi:10.1007/s11538-009-9480-0.
- [26] N. A. Maidana, H. M. Yang, Dynamic of west nile virus transmission considering several
 coexisting avian populations, Math. Comput. Modelling 53 (2011) 1247–1260.
- ⁸⁰⁸ [27] D. Moulay, M. A. Aziz-Alaoui, M. Cadivel, The chikungunya disease: Modeling, vector ⁸⁰⁹ and transmission global dynamics, Math. Biosci. 229 (2011) 50–63.
- [28] D. Moulay, M. A. Aziz-Alaoui, K. Hee-Dae, Optimal control of chikungunya disease: larvae
 reduction,treatment and prevention, Mathematical Biosciences and Engineering 9 (2) (April 2012) 369–393.
- [29] P. Poletti, G. Messeri, M. Ajelli, R. Vallorani, C. Rizzo, S. Merler, Transmission potential
 of chikungunya virus and control measures: the case of italy, PLoS One 6 (e18860) (2011)
 1-12.
- [30] Hamadjam Abboubakar, Jean C. Kamgang, Léontine N. Nkamba, Daniel Tieudjo, Lucas
 Emini, Modeling the dynamics of arboviral diseases with vaccination perspective, Biomath
 4 (2015).

- [31] C. Oliva, études biologiques et comportementales de deux espèces de moustiques (aedes albopictus et anopheles arabiensis) vectrices de maladies en vue du développement de la technique de linsecte stérile (tis) contre ces vecteurs à l'ile de la réunion, HAL Id: tel-00965525 (2014) 1–224.
- [32] T. W. Scott, A. C. Morrison, Vector dynamics and transmission of dengue virus: implications for dengue surveillance and prevention strategies: vector dynamics and dengue prevention, Current Topics in Microbiology and Immunology 338 (2010) 115–128.
- [33] A. Berman, R. J. Plemons, Nonnegative matrices in the mathematical sciences, 1994.
- [34] J. A. Jacquez, Qualitative theory of compartmental systems, SIAM Rev. 35 (1993) 43–79.
- [35] J. M. Cushing, An Introduction to Structured Population Dynamics, SIAM, Philadelphia,
 1998.
- ⁸³⁰ [36] J. M. Cushing, Z. Yicang, The net reproductive value and stability in matrix population ⁸³¹ models, Nat. Resour. Model. 8 (1994) 297–333.
- [37] O. Diekmann, J. A. P. Heesterbeek, Mathematical Epidemiology of Infectious Diseases.
 Model building, analysis and interpretation, John Wiley & Sons, Chichester, 2000.
- [38] P. van den Driessche, J. Watmough, Reproduction numbers and the sub-threshold endemic
 equilibria for compartmental models of disease transmission, Math. Biosci. 180 (2002) 29–
 48.
- ⁸³⁷ [39] G. Cruz-Pacheco, L. Esteva, J. A. Montaño-Hirose, C. Vargas, Modelling the dynamics of ⁸³⁸ west nile virus, Bulletin of Mathematical Biology 67 (2005) 1157–1172.
- [40] J. C. Kamgang, G. Sallet, Computation of threshold conditions for epidemiological models
 and global stability of the disease-free equilibrium (dfe), Mathematical Biosciences 213
 (2008) 1–12.
- [41] J. Arino, C. C. McCluskey, P. van den Driessche, Global results for an epidemic model with
 vaccination that exhibits backward bifurcation, SIAM Journal on Applied Mathematics 64
 (2003) 260–276.
- [42] F. Brauer, Backward bifurcations in simple vaccination models, J. Math. Anal. Appl. 298
 (2004) 418–431.
- [43] O. Sharomi, C. Podder, A. Gumel, E. Elbasha, J. Watmough, Role of incidence function in vaccine-induced backward bifurcation in some hiv models, Mathematical Biosciences 210 (2007) 436-463.
- ⁸⁵⁰ [44] B. Buonomo, D. Lacitignola, On the backward bifurcation of a vaccination model with ⁸⁵¹ nonlinear incidence, Nonlinear Analysis: Modelling and Control 16 (1) (2011) 30–46.
- ⁸⁵² [45] B. Buonomo, A note on the direction of the transcritical bifurcation in epidemic models,
 ⁸⁵³ Nonlinear Analysis: Modelling and Control 20 (2015) 38–55.
- ⁸⁵⁴ [46] J. Dushoff, W. Huang, C. Castillo-Chavez, Backward bifurcations and catastrophe in sim-⁸⁵⁵ ple models of fatal diseases, J. Math. Biol. 36 (1998) 227–248.
- ⁸⁵⁶ [47] M. Safan, M. Kretzschmar, K. P. Hadeler, Vaccination based control of infections in sirs ⁸⁵⁷ models with reinfection: special reference to pertussis, J. Math. Biol. 67 (2013) 1083–1110.

- [48] C. Castillo-Chavez, B. Song, Dynamical models of tuberculosis and their applications,
 Math. Biosci. Eng. 1 (2004) 361–404.
- [49] J. Guckenheimer, P. Holmes, Dynamical Systems and Bifurcations of Vector Fields, Non linear Oscillations, 1983.
- ⁸⁶² [50] J. Carr, Applications of Centre Manifold Theory, Springer, New York, 1981.
- ⁸⁶³ [51] J. K. Hale, Ordinary Differential Equations, John Wiley and Sons, 1969.
- ⁸⁶⁴ [52] J. P. LaSalle, Stability theory for ordinary differential equations, J. Differ. Equ. (1968)
 ⁸⁶⁵ 57-65.
- ⁸⁶⁶ [53] J. P. LaSalle, The stability of dynamical systems, Society for Industrial and Applied Math ⁸⁶⁷ ematics, Philadelphia, Pa., 1976.
- ⁸⁶⁸ [54] N. Chitnis, J. M. Hyman, J. M. Cushing, Determining important parameters in the spread
 ⁸⁶⁹ of malaria through the sensitivity analysis of a mathematical model, Bull. Math. Biol. 70
 ⁸⁷⁰ (2008) 1272–1296.
- [55] S. Marino, I. B. Hogue, C. J. Ray, D. E. Kirschner, A methodology for performing global uncertainty and sensitivity analysis in systems biology, Journal of Theoretical Biology 254 (2008) 178–196.
- ⁸⁷⁴ [56] J. Wu, R. Dhingra, M. Gambhir, J. V. Remais, Sensitivity analysis of infectious disease
 ⁸⁷⁵ models: methods, advances and their application, Journal of the Royal Society Interface
 ⁸⁷⁶ 10 (2013) 1–14.
- ⁸⁷⁷ [57] M. Stein, Large sample properties of simulations using latin hypercube sampling, Techno-⁸⁷⁸ metrics 29 (1987) 143–151.
- ⁸⁷⁹ [58] F. Darriet, S. Marcombe, V. Corbel, Insecticides larvicides et adulticides alternatifs pour
 les opérations de démonstication en france, synthèse bibliographique, IRD (2007) 1–46.
- ⁸⁸¹ [59] P. Bosc, V. Boullet, M. Echaubard, M. L. Corre, S. Quilici, J. P. Quod, J. Rochat,
 ⁸⁸² S. Ribes, M. Salamolard, E. Thybaud, Premier Bilan sur les Impacts des Traitements
 ⁸⁸³ Anti-moustiques, dans le cadre de la lutte Contre le Chikungunya, sur les Espèces et les
 ⁸⁸⁴ Milieux de l'île de la Réunion (Juin 2006).
- [60] Helena Sofia Ferreira Rodrigues, Optimal control and numerical optimization applied to
 epidemiological models, Ph.D. thesis, Universidade de Aveiro Departamento de Matemat ica (2012).
- 888 [61] S. Licciardi, personal communication.