Evaluation of the Efficacy of Wolbachia Intervention on Dengue Burden in a Population: A Mathematical Insight

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Abstract—This paper discusses the development and analysis of a nonlinear mathematical model to describe the transmission dynamics and control of dengue disease within the interacting human and mosquito populations. The model, which is governed by a twelve-dimensional system of ordinary differential equations, captures the subpopulation of symptomatic infected human with severe dengue symptoms and Wolbachia-infected mosquito population. The dengue-free equilibrium of the model is obtained, and shown to be globally asymptotically stable with respect to the key dengue threshold, denoted by $\mathscr{R}_0$. Numerical simulations are carried out to investigate the effects of Wolbachia coverage and fraction of symptomatic infectious humans that will get dengue severe symptoms on the dynamical spread of dengue in the community. The impacts of various Wolbachia coverage levels on the disease spread are quantified by carrying out the efficiency analysis.

Index Terms—basic reproduction number, dengue fever, efficiency analysis, Wolbachia

I. Introduction

Globally, dengue has been recognized as the fastest spreading vector-borne infection and is endemic in more than 100 countries [1], particularly in the tropical and subtropical regions [2]. The disease is primarily caused by dengue virus (DENV) [1]. DENV is a single-stranded RNA virus belonging to the family Flaviviridae and genus Flavivirus consisting of four different serotypes, viz, DENV-1, DENV-2, DENV-3 and DENV-4 [2]. The virus is mainly transmitted by Aedes aegypti and Aedes albopictus mosquitoes. Aedes aegypti mosquitoes are known to be the primary vector for the transmission of DENV in urban regions, whereas Aedes albopictus mosquitoes are frequently seen in peri-urban and rural environments [3].

DENV is transmitted to humans upon the bite by infected female Aedes mosquitoes [2]. During bite, susceptible (healthy) mosquitoes acquire infection from an infected person, then transmit the infection to other susceptible humans during blood meals [3]. Clinical manifestations of DENV infection range from asymptomatic infection or dengue fever (DF), to the more life-threatening complications, dengue haemorrhagic fever (DHF) and dengue shock syndrome (DSS) [2], [4]. The typical symptoms of dengue infections include high fever, headache, pain behind the eyes, joint pains, nausea, and vomiting among others [3]. Over the last 5 decades, the worldwide incidence of dengue has increased by 30-fold [2], with about 100 to 400 million dengue cases reported annually on a global scale [5].

As of now, only one dengue vaccine, Dengvaxia (CYD-TDV), has received a licensure [4], [5], which has been marketed in Indonesia since 2016 [4]. However, due to the complex eligibility requirements amongst other factors [6], dengue vaccination is yet to be integrated into dengue control strategy in many other dengue-affected countries. At present, the widespread prevention and control of DF is limited to the avoidance of mosquito bites and vector control measures, primarily relied on insecticides (adulticide and/ or larvicide) and community engagement for environmental management initiatives. In the absence of licensed antiviral prophylactic or therapeutic treatments, treatment is mainly in the form of supportive care [6]. Among other dengue control activities, insecticide-based intervention plays a major role. However, the efficiency of current dengue control programs (including insecticide control) may be threatened by the resistance to these

insecticides in mosquito vector population [1]. Apart from the more traditional vector control methods stated above, innovative 'technologies' such as release of Wolbachia infection, which reduces the ability of Aedes Aegypti mosquitoes to transmit dengue, Zika, chikungunya, and yellow fever, are also under evaluation presently. Female mosquitoes infected with the bacteria can pass this to their progeny and spread Wolbachia vertically across the generations. It is evident that large-scale deployments of Wolbachia-infected mosquitoes is effective to substantively decrease dengue incidence in the population [6].

A number of mathematical models have been formulated and analysed to investigate the dynamical spread and control of dengue in the human population (see, for example, [3], [6]–[10] and some of the references therein). In [10], the authors developed and analysed a nonlinear mathematical model for dengue disease transmission dynamics in the presence of Wolbachia-carrying mosquitoes. Knerer et al. [6] conducted a similar study by developing a mathematical model describing the dynamical spread of dengue with the presence of an imperfect vaccination strategy and Wolbachia-infected mosquito population without presenting any theoretical analysis for it. Several simulations were carried out to determine the least costly and most effective of different control strategies involving the use of at least any one of the control measures. Xue et al. [3] proposed a mathematical model for the transmission dynamics of multi-strain DENV with cross-immunity. In [7], Abidemi et al. explored the impact of several combinations strategies of personal preventive measures, treatment therapy and insecticide control on the transmission dynamics of dengue within the interacting human and mosquito populations. An insightful result arising from the study is that the use of combined effort of human personal protection and insecticide control could be enough to eliminate dengue in the community. Musa et al. [9] developed and analysed a mathematical model including the asymptomatic and severe cases of DENV infection in the human population to assess the dynamics of transmission of DENV within the interacting human and mosquito populations. However, to the best of our knowledge, none of the mathematical investigation of Wolbachia intervention on dengue disease transmission and spread in a community captures the severe cases (those with DHF/DSS) of dengue infections in the human population. This is a research gap that this paper purposely fills. Hence, this paper considers the development and analysis of a nonlinear mathematical model which does not only include the severe infection phase of DENV but also features the Wolbachia-carrying mosquito population to assess the efficacy of applying Wolbachia-infected mosquitoes as a new dengue control strategy for dengue elimination in the population. The remainder of this paper is structured as follows: Section II presents the methodology employed in this work, ranging from model formulation to model theoretical analysis. Numerical simulations and efficiency analysis are considered in Section III. This is followed up by concluding remark in Section IV.

II. Methods

A. Model Formulation

With consideration of the nonlinear mathematical models for dengue disease transmission dynamics and control proposed by Knerer et al. [6] and Musa et al. [9], this section discusses the development of dengue epidemic model featuring the Wolbachia-infected mosquito population. The model stratifies the total population of human at time t, represented as $N_h(t)$, into six epidemiological classes namely, susceptible humans, exposed humans (infected but not infectious humans), asymptomatically infected humans (exposed humans who can progress and become infectious without showing any clinical symptoms), symptomatic infectious humans, symptomatic infectious humans with severe DENV (DHF/DSS), and recovered humans, which are respectively denoted by $S_h(t)$, $E_h(t)$, $A_h(t)$, $I_{hc}(t)$, $I_{hs}(t)$, and $R_h(t)$. Hence,

$$N_h(t) = S_h(t)+E_h(t)+A_h(t)+I_{hc}(t)+I_{hs}(t)+R_h(t). \quad (1)$$

The total population of non-Wolbachia-carrying mosquito at time t, denoted by $N_n(t)$, is divided into three sub-populations namely, susceptible mosquitoes ($S_n(t)$), exposed mosquitoes ($E_n(t)$), and infectious mosquitoes ($I_n(t)$). Thus,

$$N_n(t) = S_n(t) + E_n(t) + I_n(t). \quad (2)$$

Similarly, the total Wolbachia-carrying mosquito population at time t, denoted by $N_w(t)$, is split into three epidemiological classes namely, susceptible mosquitoes, $S_w(t)$, exposed mosquitoes, $E_w(t)$, and infectious mosquitoes, $I_w(t)$, so that

$$N_w(t) = S_w(t) + E_w(t) + I_w(t). \quad (3)$$

Following the above stratification of the human and mosquito populations, the mathematical model for the dynamics of dengue disease transmission between the interacting human and mosquito populations is governed by a twelve-dimensional system of non-linear ordinary differential equations given by

$$\frac{dS_h}{dt} = \Pi_h - a_n\beta_{nh}\frac{I_n}{N_h}S_h - a_w\beta_{wh}\frac{I_w}{N_h}S_h - \mu_h S_h, \quad (4a)$$

$$\frac{dE_h}{dt} = \phi\left(a_n\beta_{nh}\frac{I_n}{N_h} + a_w\beta_{wh}\frac{I_w}{N_h}\right)S_h - (\tau_h+\mu_h)E_h, \quad (4b)$$

$$\frac{dA_h}{dt} = (1-\phi)\left(a_n\beta_{nh}\frac{I_n}{N_h} + a_w\beta_{wh}\frac{I_w}{N_h}\right)S_h - (\alpha_1+\mu_h)A_h, \quad (4c)$$

$$\frac{dI_{hc}}{dt} = \tau_h E_h - (\alpha_2+\mu_h)I_{hc}, \quad (4d)$$

$$\frac{dI_{hs}}{dt} = (1-\sigma)\alpha_2 I_{hc} - (\alpha_3+\delta_h+\mu_h)I_{hs}, \quad (4e)$$

$$\frac{dR_h}{dt} = \sigma\alpha_2 I_{hc} + \alpha_3 I_{hs} + \alpha_1 A_h - \mu_h R_h, \tag{4f}$$

$$\frac{dS_n}{dt} = (1-\eta)\Pi_n - a_n\beta_{hn}\frac{A_h + I_{hc} + I_{hs}}{N_h}S_n - \mu_n S_n, \tag{4g}$$

$$\frac{dE_n}{dt} = a_n\beta_{hn}\frac{A_h + I_{hc} + I_{hs}}{N_h}S_n - (\tau_n + \mu_n)E_n, \tag{4h}$$

$$\frac{dI_n}{dt} = \tau_n E_n - \mu_n I_n, \tag{4i}$$

$$\frac{dS_w}{dt} = \eta\Pi_w - a_w\beta_{hw}\frac{A_h + I_{hc} + I_{hs}}{N_h}S_w - \mu_w S_w, \tag{4j}$$

$$\frac{dE_w}{dt} = a_w\beta_{hw}\frac{A_h + I_{hc} + I_{hs}}{N_h}S_w - (\tau_w + \mu_w)E_w, \tag{4k}$$

$$\frac{dI_w}{dt} = \tau_w E_w - \mu_w I_w, \tag{4l}$$

subject to the initial conditions presented by Eq. (5) as

$$(X(0) = X_0), \tag{5}$$

where $X = (S_h, E_h, A_h, I_{hc}, I_{hs}, R_h, S_n, E_n, I_n, S_w, E_w, I_w)$. Tables I and II, respectively, provide the variables and parameters associated with the dengue model (4).

B. Basic Qualitative Properties of the Dengue Model (4)

The basic properties of solutions of the dengue model (4) are provided in this section.

1) Positivity and Boundedness of Solutions: In view of the dengue model (4) describing the dynamics of human and mosquito (both non-Wolbachia and Wolbachia-carrying) populations during a dengue epidemic, the model parameters (as shown in Table II) are nonnegative. Also, it is important to prove that all the state variables of the model are nonnegative for all time.

Theorem 1. The state variables $S_h(t)$, $E_h(t)$, $A_h(t)$, $I_{hc}(t)$, $I_{hs}(t)$, $R_h(t)$, $S_n(t)$, $E_n(t)$, $I_n(t)$, $S_w(t)$, $E_w(t)$ and $I_w(t)$ of the dengue model (4) subject to the initial conditions, as appeared in Eq. (5), remain nonnegative for all time $t > 0$.

Proof. Consider Equation (4a) as

$$\begin{aligned}\frac{dS_h(t)}{dt} &= \Pi_h - (\Phi_h(t) + \mu_h)S_h(t),\\ &\geq -(\Phi_h(t) + \mu_h)S_h(t),\end{aligned}$$

where $\Phi_h(t) = \frac{a_n\beta_{nh}I_n + a_w\beta_{wh}I_w}{N_h}$, which, upon using the integrating factor method, becomes

$$\frac{d}{dt}\left(S_h(t)\exp\left\{\mu_h t + \int_0^t \Phi_h(u)du\right\}\right) \geq 0.$$

Thus,

$$S_h(t) \geq S_h(0)\exp\left\{-\left(\mu_h t + \int_0^t \Phi_h(u)du\right)\right\} > 0 \;\forall\; t > 0.$$

Using the same approach, it can be shown that other state variables $E_h(t)$, $A_h(t)$, $I_{hc}(t)$, $I_{hs}(t)$, $R_h(t)$, $S_n(t)$, $E_n(t)$, $I_n(t)$, $S_w(t)$, $E_w(t)$ and $I_w(t)$ are nonnegative for all $t > 0$. □

Next, consider the closed set expressed as

$$\mathfrak{D} = \mathfrak{D}_h \cup \mathfrak{D}_n \cup \mathfrak{D}_w \subset \mathbb{R}^6_+ \times \mathbb{R}^3_+ \times \mathbb{R}^3_+ \tag{6}$$

with

$$\begin{aligned}\mathfrak{D}_h &= \left\{(S_h(t), E_h(t), A_h(t), I_{hc}(t), I_{hs}(t), R_h(t)) \in \mathbb{R}^6_+ : N_h \leq \frac{\Pi_h}{\mu_h}\right\},\\ \mathfrak{D}_n &= \left\{(S_n(t), E_n(t), I_n(t)) \in \mathbb{R}^3_+ : N_n \leq \frac{(1-\eta)\Pi_n}{\mu_n}\right\},\\ \mathfrak{D}_w &= \left\{(S_w(t), E_w(t), I_w(t)) \in \mathbb{R}^3_+ : N_w \leq \frac{\eta\Pi_w}{\mu_w}\right\}.\end{aligned}$$

It can be shown that the closed set $\mathfrak{D}$ in Eq. (6) is positively invariant and attracting for the dengue model (4).

Theorem 2. The closed set $\mathfrak{D}$ defined in Eq. (6) is positively invariant and attracting in respect of the dengue model (4).

Proof. Using the expression

$$\begin{aligned}\frac{dN_h}{dt} = \frac{\partial N_h}{\partial S_h}\frac{dS_h}{dt} + \frac{\partial N_h}{\partial E_h}\frac{dE_h}{dt} + \frac{\partial N_h}{\partial A_h}\frac{dA_h}{dt} + \frac{\partial N_h}{\partial I_{hc}}\frac{dI_{hc}}{dt}\\ + \frac{\partial N_h}{\partial I_{hs}}\frac{dI_{hs}}{dt} + \frac{\partial N_h}{\partial R_h}\frac{dR_h}{dt},\end{aligned}$$

the rate of change of the total human population with respect to time t is obtained from summing the components of Equations (4a) to (4f) as

$$\begin{aligned}\frac{dN_h(t)}{dt} &= \Pi_h - \mu_h N_h(t) - \delta_h I_{hs},\\ &\leq \Pi_h - \mu_h N_h(t).\end{aligned} \tag{7}$$

Thus, by a standard comparison theorem [11], Equation (7) leads to

$$N_h(t) \leq N_h(0)\exp\{-\mu_h t\} + \frac{\Pi_h}{\mu_h}(1 - \exp\{-\mu_h t\}).$$

So, $N_h(t) \leq \frac{\Pi_h}{\mu_h}$ if $N_h(0) \leq \frac{\Pi_h}{\mu_h}$, which implies that the region $\mathfrak{D}$ is positively invariant in respect of the dengue model (4). In addition, if $N_h(0) > \frac{\Pi_h}{\mu_h}$, then either the solution of the model enters the region $\mathfrak{D}$ in definite time or $N_h(t)$ converges to $\frac{\Pi_h}{\mu_h}$ while the dengue infected humans approach zero as $t \to \infty$.

Similarly, the summation of the components of Equations (4g) to (4i) produces the rate of change of the total population of non-Wolbachia-carrying mosquito as

$$\frac{dN_n}{dt} = (1-\eta)\Pi_n - \mu_n N_n, \tag{8}$$

so that by a standard comparison theorem [11],

$$N_n(t) \leq \frac{(1-\eta)\Pi_n}{\mu_n} + \left(N_n(0) - \frac{(1-\eta)\Pi_n}{\mu_n}\right)\exp\{-\mu_n t\}.$$

Consequently, $N_n(t) \leq \frac{(1-\eta)\Pi_n}{\mu_n}$ provided that $N_n(0) \leq \frac{(1-\eta)\Pi_n}{\mu_n}$, indicating that the region $\mathfrak{D}$ is positively invari-

TABLE I Description of the variables in the dengue model (4)

Variable	Description
S_h	Susceptible human subpopulation
E_h	Exposed human subpopulation
A_h	Asymptomatic human subpopulation
I_{hc}	Symptomatic human with clinical symptoms of dengue virus subpopulation
I_{hs}	Symptomatic human with severe clinical symptoms of dengue virus subpopulation
R_h	Recovered human subpopulation
N_h	Human total population
S_n	Susceptible non-Wolbachia-carrying mosquitoes
E_n	Exposed non-Wolbachia-carrying mosquitoes
I_n	Infectious non-Wolbachia-carrying mosquitoes
N_n	Total population of non-Wolbachia-carrying mosquito
S_w	Susceptible Wolbachia-carrying mosquitoes
E_w	Exposed Wolbachia-carrying mosquitoes
I_w	Infectious Wolbachia-carrying mosquitoes
N_w	Total population of Wolbachia-carrying mosquito

ant in respect of the dengue model (4). In addition, if $N_n(0) > \frac{(1-\eta)\Pi_n}{\mu_n}$, then either the solution of model (4) enters the region $\mathfrak{D}$ in definite time or $N_n(t)$ converges to $\frac{(1-\eta)\Pi_n}{\mu_n}$ while the dengue infected non-Wolbachia-carrying mosquitoes approach zero as $t \to \infty$.

Lastly, the rate of change of total Wolbachia-carrying mosquito population is obtained as

$$\frac{dN_w}{dt} = \eta\Pi_w - \mu_w N_w \tag{9}$$

by summing all the components of Eqs. (4j) to (4l). Thus, by a standard comparison theorem [11],

$$N_w(t) \leq \frac{\eta\Pi_w}{\mu_w} + \left(N_w(0) - \frac{\eta\Pi_w}{\mu_w}\right)\exp\{-\mu_w t\}.$$

Hence, $N_w(t) \leq \frac{\eta\Pi_w}{\mu_w}$ if $N_w(0) \leq \frac{\eta\Pi_w}{\mu_w}$, suggesting that the region $\mathfrak{D}$ is positively invariant in respect of model (4). Furthermore, if $N_w(0) > \frac{\eta\Pi_w}{\mu_w}$, then either the solution of the dengue model (4) enters the region $\mathfrak{D}$ in definite time or $N_w(t)$ converges to $\frac{\eta\Pi_w}{\mu_w}$ while the dengue infected Wolbachia-carrying mosquitoes approach zero as $t \to \infty$. Therefore, the region $\mathfrak{D}$ is attracting, meaning that every solution in $\mathbb{R}^{12}_+$ enters $\mathfrak{D}$ in the long run. □

In light of Theorems 1 and 2, consideration of the dynamics of the dengue model (4) in the region $\mathfrak{D}$, as defined in Eq. (6), is sufficient, and hence, the model is considered to be mathematically well-posed in this region [12], [13].

C. Stability Analysis

We explore the long-term asymptotic behaviour of the solution trajectories of the dengue model (4) around the associated equilibrium points with the model in this section. Notably, the stability analysis of the model is limited to that around the dengue-free equilibrium (DFE) in this paper.

1) Existence of Dengue-Free Equilibrium: By DFE of the dengue model (4), it means a steady state solution of the model when no incidence of dengue takes place in the population. Thus, at this equilibrium point, $E_h = A_h = I_{hc} = I_{hs} = E_n = I_n = E_w = I_w = 0$. Consequently, the DFE of the dengue model (4), denoted by $\mathfrak{E}^*$, is obtained as

$$\begin{aligned}\mathfrak{E}^* &= (S_h^*, E_h^*, A_h^*, I_{hc}^*, I_{hs}^*, R_h^*, S_n^*, E_n^*, I_n^*, S_w^*, E_w^*, I_w^*)\\ &= \left(\frac{\Pi_h}{\mu_h}, 0, 0, 0, 0, 0, \frac{(1-\eta)\Pi_n}{\mu_n}, 0, 0, \frac{\eta\Pi_w}{\mu_w}, 0, 0\right).\end{aligned} \tag{10}$$

2) Computation of Dengue Threshold: The dengue threshold, which is also referred to as the dengue basic reproduction number, denoted as $\mathscr{R}_0$, can be defined as the measure of the potential spread of dengue in a wholly susceptible population. In other words, the threshold quantity $\mathscr{R}_0$ is a representation of the number of secondary dengue infections transmitted from either the infected humans (individuals in classes A_h, I_{hc} and I_{hs}), infected non-Wolbachia-carrying mosquitoes (I_n) or infected Wolbachia-carrying mosquitoes (I_w) in a population that is completely susceptible. To derive the dengue threshold $\mathscr{R}_0$ for model (4), the next generation matrix (NGM) approach and the standard notations as appeared in [14] are employed as follows: Here, are taken as the infected compartments at DFE so that the Jacobian matrices F and V are given by

$$F = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & \phi a_n\beta_{nh} & 0 & \phi a_w\beta_{wh} \\ 0 & 0 & 0 & 0 & 0 & \pi a_n\beta_{nh} & 0 & \pi a_w\beta_{wh} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & F_1 & F_1 & F_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & F_2 & F_2 & F_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

TABLE II Description of parameters of the dengue model (4) and their numerical values

Parameter	Description	Value	Source
Π_h	Rate of recruitment into susceptible human subpopulation	120.2407	Estimated from [7]
a_n	Biting rate of non-Wolbachia-carrying mosquitoes	0.66272	[7]
β_{nh}	non-Wolbachia-carrying vector to host transmission probability	0.186	[6]
a_w	Wolbachia-carrying mosquitoes biting rate	$0.95 \times a_n$	Assumed in view of [6]
β_{wh}	Infected Wolbachia-carrying vector to host transmission probability	$0.5 \times \beta_{nh}$	[6]
μ_h	Natural death rate of humans	$1/(74 \times 365)$	[7]
ϕ	Fraction of infected individuals who are exposed	0.18	[9]
$1-\phi$	Fraction of infected individuals who are asymptomatic	0.82	[9]
τ_h	Rate at which the exposed individuals progress and become infectious individuals with clinical symptoms	1/7	[6]
$\alpha_1, \alpha_2, \alpha_3$	Rate at which infectious individuals recover in class A_h, I_{hc}, I_{hs}, respectively	1/6, 1/6, 1/6	[Assumed, [9], Assumed]
σ	Fraction of infected individuals that will not get a severe symptom	0.1	[9]
$1-\sigma$	Fraction of infected individuals that will get a severe symptom	0.9	[9]
δ_h	Disease-induced death rate of humans	0.001	[9]
η	Wolbachia release coverage	$[0, 1]$	[6]
Π_n	Recruitment rate of non-Wolbachia-carrying susceptible mosquitoes	$\mu_n \times N_n(0)$	Assumed
β_{hn}	Infected humans to susceptible non-Wolbachia-carrying mosquitoes transmission probability	0.186	[6]
τ_n	Average extrinsic incubation rate of non-Wolbachia-carrying mosquitoes	1/9	[6]
μ_n	Non-Wolbachia-carrying mosquitoes natural mortality rate	1/12	[6]
Π_w	Recruitment rate of Wolbachia-carrying susceptible mosquitoes	$\mu_w \times N_w(0)$	Assumed
β_{hw}	Infected humans to susceptible Wolbachia-carrying mosquitoes transmission probability	0.186	[6]
τ_w	Average extrinsic incubation rate of Wolbachia-carrying mosquitoes	1/9	[6]
μ_w	Mortality rate of Wolbachia-carrying mosquitoes	$1.10 \times \mu_n$	[6]

where $F_1 = \frac{a_n \beta_{hn} \mu_h (1-\eta) \Pi_n}{\Pi_h \mu_n}$, $F_2 = \frac{a_w \beta_{hw} \mu_h \eta \Pi_w}{\Pi_h \mu_w}$, $\pi = (1-\phi)$, and

$$V = \begin{pmatrix} n_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & n_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\tau_h & 0 & n_3 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -\pi_1 \alpha_2 & n_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & n_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\tau_n & \mu_n & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & n_6 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\tau_w & \mu_w \end{pmatrix},$$

where $\pi_1 = (1-\sigma)$, $n_1 = \tau_h + \mu_h$, $n_2 = \alpha_1 + \mu_h$, $n_3 = \alpha_2 + \mu_h$, $n_4 = \alpha_3 + \delta_h + \mu_h$, $n_5 = \tau_n + \mu_n$, and $n_6 = \tau_w + \mu_w$. Thus, $\mathscr{R}_0 = \rho\left(FV^{-1}\right)$, where ρ is the spectral radius of the NGM $G = FV^{-1}$, and is obtained as

$$\mathscr{R}_0^2 = \frac{\Delta}{\Pi_h n_1 n_2 n_3 n_4 n_5 n_6 \mu_n^2 \mu_w^2}, \tag{11}$$

where

$$\begin{aligned} \Delta = {} & (a_n \beta_{hn} \tau_n (1-\eta) \Pi_n n_6 a_n \beta_{nh} \\ & + a_w \beta_{hw} \eta \Pi_w \tau_w n_5 \mu_n^2 a_w \beta_{wh}) \\ & \times \mu_h (n_1 n_3 n_4 (1-\phi) + \phi \alpha_2 \tau_h (1-\sigma) n_2 + \phi \tau_h n_2 n_4), \end{aligned}$$

which can be expressed as

$$\mathscr{R}_0^2 = \mathscr{R}_{nh} \mathscr{R}_{hn} + \mathscr{R}_{wh} \mathscr{R}_{hw}, \tag{12}$$

where

$$\mathscr{R}_{nh} = \frac{a_n \beta_{nh} \mu_h}{\Pi_h} \left[\frac{(1-\phi)}{n_2} + \frac{\phi \alpha_2 \tau_h (1-\sigma)}{n_1 n_3 n_4} + \frac{\phi \tau_h}{n_1 n_3} \right],$$

$$\mathscr{R}_{hn} = \frac{a_n\beta_{hn}\tau_n(1-\eta)\Pi_n}{\mu_n^2 n_5},$$
$$\mathscr{R}_{wh} = \frac{a_w\beta_{wh}\mu_h}{\Pi_h}\left[\frac{(1-\phi)}{n_2} + \frac{\phi\alpha_2\tau_h(1-\sigma)}{n_1n_3n_4} + \frac{\phi\tau_h}{n_1n_3}\right],$$
$$\mathscr{R}_{hw} = \frac{a_w\beta_{hw}\tau_w\eta\Pi_w}{\mu_w^2 n_6},$$

and with $n_1 = \tau_h + \mu_h$, $n_2 = \alpha_1 + \mu_h$, $n_3 = \alpha_2 + \mu_h$, $n_4 = \alpha_3 + \delta_h + \mu_h$, $n_5 = \tau_n + \mu_n$, and $n_6 = \tau_w + \mu_w$.

The local and global asymptotic behaviours of the dengue model (4) can be investigated around the DFE in terms of $\mathscr{R}_0$. These are what considered next. Based on Theorem 2 in [14], the following result of local asymptotic dynamics of the dengue model (4) around the DFE is established.

Theorem 3. The DFE $\mathfrak{E}^*$ of the dengue model (4) is locally asymptotically stable (LAS) if $\mathscr{R}_0 < 1$ and unstable if $\mathscr{R}_0 > 1$.

The epidemiological insight from Theorem 3 is that it is possible to reduce or eliminate dengue disease governed by model (4) from the population whenever an influx by dengue infected humans and mosquitoes is small such that the dengue threshold $\mathscr{R}_0$ is below unity.

Also, for the elimination of the dengue disease spread described by model (4) to be independent of the initial sizes of the sub-populations contained in the model, there is a need to establish the global asymptotic stability of the DFE of model (4) given by (10). The idea of Agusto et al. [15] is helpful in doing this. Now, consider the feasible region

$$\mathfrak{D}_1 = \{X \in \mathfrak{D} : S_h \leq S_h^*, S_n \leq S_n^*, S_w \leq S_w^*\}, \qquad (13)$$

where $X = (S_h, E_h, A_h, I_{hc}, I_{hs}, R_h, S_n, E_n, I_n, S_w, E_w, I_w)$.

The feasible region $\mathfrak{D}_1$ is positively invariant for the dengue model (4).

Proof. From Equation (4a) (where $S_h^* = \Pi_h/\mu_h$), we have

$$\frac{dS_h}{dt} = \Pi_h - \frac{a_n\beta_{nh}I_n + a_w\beta_{wh}I_w}{N_h}S_h - \mu_h S_h,$$
$$\leq \Pi_h - \mu_h S_h = \mu_h\left(\frac{\Pi_h}{\mu_h} - S_h\right) = \mu_h\left(S_h^* - S_h\right).$$

Thus,

$$S_h(t) \leq S_h^* - [S_h^* - S_h(0)]\exp\{-\mu_h t\}.$$

Therefore, if $N_h^* = \Pi_h/\mu_h$ and $S_h(0) \leq S_h^*$ for all $t \geq 0$, then $S_h(t) \leq S_h^*$ for all $t \geq 0$.

Similarly, we have from Equation (4g) (with $S_n^* = (1-\eta)\Pi_n/\mu_n$) that

$$\frac{dS_n}{dt} = (1-\eta)\Pi_n - a_n\beta_{hn}\frac{A_h + I_{hc} + I_{hs}}{N_h}S_n - \mu_n S_n,$$
$$\leq (1-\eta)\Pi_n - \mu_n S_n = \mu_n\left(\frac{(1-\eta)\Pi_n}{\mu_n} - S_n\right),$$
$$= \mu_n\left(S_n^* - S_n\right).$$

Hence,

$$S_n(t) \leq S_n^* - [S_n^* - S_n(0)]\exp\{-\mu_n t\}.$$

So, if $N_n^* = (1-\eta)\Pi_n/\mu_n$ and $S_n(0) \leq S_n^*$ for all $t \geq 0$, then $S_n(t) \leq S_n^*$ for all $t \geq 0$.

Finally, from Equation (4j) (with $S_w^* = \eta\Pi_w/\mu_w$), one obtains

$$\frac{dS_w}{dt} = \eta\Pi_w - a_w\beta_{hw}\frac{A_h + I_{hc} + I_{hs}}{N_h}S_w - \mu_w S_w,$$
$$\leq \eta\Pi_w - \mu_w S_w = \mu_w\left(\frac{\eta\Pi_w}{\mu_w} - S_w\right),$$
$$= \mu_w\left(S_w^* - S_w\right).$$

Thus,

$$S_w(t) \leq S_w^* - [S_w^* - S_w(0)]\exp\{-\mu_w t\}.$$

Hence, if $N_w^* = \eta\Pi_w/\mu_w$ and $S_w(0) \leq S_w^*$ for all $t \geq 0$, then $S_w(t) \leq S_w^*$ for all $t \geq 0$. Therefore, it has been established that the region $\mathfrak{D}_1$ is positively invariant and attracting all the solutions in $\mathbb{R}_+^{12}$ for the dengue model (4). □

Theorem 4. The DFE, $\mathfrak{E}^*$, of the dengue model (4) as given in Equation (10), is globally asymptotically stable (GAS) in $\mathfrak{D}_1$ defined in Equation (13) whenever $\mathscr{R}_0 \leq 1$.

Proof. The global asymptotic stability of the DFE of the dengue model (4) will be established by following the approach used in the previous works [15].

Let $Y = (S_h, R_h, S_n, S_w)$ and $Z = (E_h, A_h, I_{hc}, I_{hs}, E_n, I_n, E_w, I_w)$ and group the system (4) as

$$\frac{dY}{dt} = G(Y, 0),$$
$$\frac{dZ}{dt} = H(Y, Z),$$

where $G(Y,0)$ is the right-hand side of S_h, R_h, S_n and S_w with $E_h = A_h = I_{hc} = I_{hs} = E_n = I_n = E_w = I_w = 0$ and $H(Y,Z)$ is the right-had side of E_h, A_h, I_{hc}, I_{hs}, E_n, I_n, E_w and I_w.

Next, consider the reduced system $dY/dt = G(Y,0)$ given as

$$\frac{dS_h}{dt} = \Pi_h - \mu_h S_h, \qquad (14a)$$
$$\frac{dR_h}{dt} = -\mu_h R_h, \qquad (14b)$$
$$\frac{dS_n}{dt} = (1-\eta)\Pi_n - \mu_n S_n, \qquad (14c)$$
$$\frac{dS_w}{dt} = \eta\Pi_w - \mu_w S_w. \qquad (14d)$$

Let $Y^* = (S_h^*, R_h^*, S_n^*, S_w^*) = \left(\frac{\Pi_h}{\mu_h}, 0, \frac{(1-\eta)\Pi_n}{\mu_n}, \frac{\eta\Pi_w}{\mu_w}\right)$ be an equilibrium of the reduced system (14), we show that Y^* is a globally stable equilibrium of (14). This gives

$$S_h(t) = S_h(0)\exp\{-\mu_h t\} + \frac{\Pi_h}{\mu_h}\left[1 - \exp\{-\mu_h t\}\right]. \qquad (15)$$

and

$$R_h(t) = R_h(0)\exp\{-\mu_h t\}. \tag{16}$$

Taking the limit of $S_h(t)$ in Equation (15) and $R_h(t)$ in Equation (16) as $t \to \infty$, we have

$$\lim_{t\to\infty} S_h(t) = \frac{\Pi_h}{\mu_h} \text{ and } \lim_{t\to\infty} R_h(t) = 0.$$

Next, solving Equations (14c) and (14d) for $S_n(t)$ and $S_w(t)$ generates

$$S_n(t) = S_n(0)\exp\{-\mu_n t\} + \frac{(1-\eta)\Pi_n}{\mu_n}\left[1-\exp\{-\mu_n t\}\right] \tag{17}$$

and

$$S_w(t) = S_w(0)\exp\{-\mu_w t\} + \frac{\eta\Pi_w}{\mu_w}\left[1-\exp\{-\mu_w t\}\right]. \tag{18}$$

Taking the limit of $S_n(t)$ in Equation (17) and $S_w(t)$ in Equation (18) as $t \to \infty$ yields

$$\lim_{t\to\infty} S_n(t) = \frac{(1-\eta)\Pi_n}{\mu_n} \text{ and } \lim_{t\to\infty} S_w(t) = \frac{\eta\Pi_w}{\mu_w}.$$

Clearly, these asymptotic dynamics are non initial conditions-dependent in the feasible region $\mathfrak{D}$, implying that the convergence of solutions of the subsystem (14) is global in the closed set $\mathfrak{D}_1$. Next, in line with the ideas in many previous works [8], [15], [16], it requires to show that $H(Y,Z)$ satisfies the following two stated conditions:

i. $H(Y,0) = 0$.
ii. $H(Y,Z) = D_Z H(Y^*,0)Z - \tilde{H}(Y,Z)$, $\tilde{H}(Y,Z) \geq 0$, where $(Y^*,0) = \left(\frac{\Pi_h}{\mu_h}, 0, \frac{(1-\eta)\Pi_n}{\mu_n}, \frac{\eta\Pi_w}{\mu_w}, 0,0,0,0,0,0,0,0\right)$ and $D_Z H(Y^*,0)$ is the Jacobian of $H(Y,Z)$ taken in respect of $(E_h, A_h, I_{hc}, I_{hs}, E_n, I_n, E_w, I_w)$ and evaluated at $(Y^*,0)$, which is an M-matrix (a matrix with nonnegative diagonal entries).

So,

$$D_Z H(Y^*,0) = \begin{pmatrix} D_1 & D_2 \\ D_3 & D_4 \end{pmatrix},$$

where

$$D_1 = \begin{pmatrix} -n_1 & 0 & 0 & 0 \\ 0 & -n_2 & 0 & 0 \\ \tau_h & 0 & -n_3 & 0 \\ 0 & 0 & (1-\sigma)\alpha_2 & -n_4 \end{pmatrix},$$

$$D_2 = \begin{pmatrix} 0 & \phi a_n \beta_{nh}\frac{S_h^*}{N_h^*} & 0 & \phi a_w \beta_{wh}\frac{S_h^*}{N_h^*} \\ 0 & \pi a_n \beta_{nh}\frac{S_h^*}{N_h^*} & 0 & \pi a_w \beta_{wh}\frac{S_h^*}{N_h^*} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$D_3 = \begin{pmatrix} 0 & a_n \beta_{hn}\frac{S_n^*}{N_h^*} & a_n \beta_{hn}\frac{S_n^*}{N_h^*} & a_n \beta_{hn}\frac{S_n^*}{N_h^*} \\ 0 & 0 & 0 & 0 \\ 0 & a_w \beta_{hw}\frac{S_w^*}{N_h^*} & a_w \beta_{hw}\frac{S_w^*}{N_h^*} & a_w \beta_{hw}\frac{S_w^*}{N_h^*} \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$D_4 = \begin{pmatrix} -n_5 & 0 & 0 & 0 \\ \tau_n & -\mu_n & 0 & 0 \\ 0 & 0 & -n_6 & 0 \\ 0 & 0 & \tau_w & -\mu_w \end{pmatrix},$$

where $\pi = (1-\phi)$ in D_2. It follows from condition (ii) above that

$$\tilde{H}(Y,Z) = D_Z H(Y^*,0)Z - H(Y,Z).$$

Then,

$$D_Z H(Y^*,0)Z = \begin{pmatrix} \phi a_n \beta_{nh} I_n \frac{S_h^*}{N_h^*} + \phi a_w \beta_{wh} I_w \frac{S_h^*}{N_h^*} - n_1 E_h \\ \pi a_n \beta_{nh} I_n \frac{S_h^*}{N_h^*} + \pi a_w \beta_{wh} I_w \frac{S_h^*}{N_h^*} - n_2 A_h \\ \tau_h E_h - n_3 I_{hc} \\ (1-\sigma)\alpha_2 I_{hc} - n_4 I_{hs} \\ a_n \beta_{hn}\left(A_h + I_{hc} + I_{hs}\right)\frac{S_n^*}{N_h^*} - n_5 E_n \\ \tau_n E_n - \mu_n I_n \\ a_w \beta_{hw}\left(A_h + I_{hc} + I_{hs}\right)\frac{S_w^*}{N_h^*} - n_6 E_w \\ \tau_w E_w - \mu_w I_w \end{pmatrix},$$

where $\pi = (1-\phi)$, and

$$H(Y,Z) = \begin{pmatrix} \phi a_n \beta_{nh} I_n \frac{S_h}{N_h} + \phi a_w \beta_{wh} I_w \frac{S_h}{N_h} - n_1 E_h \\ \pi a_n \beta_{nh} I_n \frac{S_h}{N_h} + \pi a_w \beta_{wh} I_w \frac{S_h}{N_h} - n_2 A_h \\ \tau_h E_h - n_3 I_{hc} \\ (1-\sigma)\alpha_2 I_{hc} - n_4 I_{hs} \\ a_n \beta_{hn}\left(A_h + I_{hc} + I_{hs}\right)\frac{S_n}{N_h} - n_5 E_n \\ \tau_n E_n - \mu_n I_n \\ a_w \beta_{hw}\left(A_h + I_{hc} + I_{hs}\right)\frac{S_w}{N_h} - n_6 E_w \\ \tau_w E_w - \mu_w I_w \end{pmatrix},$$

where $\pi = (1-\phi)$. Thus,

$$\tilde{H}(Y,Z) = \begin{pmatrix} \phi\theta_n I_n + \phi\theta_w I_w \\ (1-\phi)\theta_n I_n + (1-\phi)\theta_w I_w \\ 0 \\ 0 \\ \frac{a_n \beta_{hn} S_n^*}{N_h^*}\left(A_h + I_{hc} + I_{hs}\right)\left(1 - \frac{S_n}{N_h}\frac{N_h^*}{S_n^*}\right) \\ 0 \\ \frac{a_w \beta_{hw} S_w^*}{N_h^*}\left(A_h + I_{hc} + I_{hs}\right)\left(1 - \frac{S_w}{N_h}\frac{N_h^*}{S_w^*}\right) \\ 0 \end{pmatrix},$$

where $\theta_n = \frac{a_n \beta_{nh} S_h^*}{N_h^*}\left(1 - \frac{S_h}{N_h}\frac{N_h^*}{S_h^*}\right)$ and $\theta_w = \frac{a_w \beta_{wh} S_h^*}{N_h^*}\left(1 - \frac{S_h}{N_h}\frac{N_h^*}{S_h^*}\right)$. Moreover, $S_h^* = \frac{\Pi_h}{\mu_h}$, $N_h^* = S_h^* + R_h^* = S_h^*$, $S_n^* = \frac{(1-\eta)\Pi_n}{\mu_n}$ and $S_w^* = \frac{\eta\Pi_w}{\mu_w}$. Since $S_h \leq S_h^*$, $S_n \leq S_n^*$ and $S_w \leq S_w^*$ in $\mathfrak{D}_1$, thus $N_h \leq N_h^*$. Therefore, if the population of human is at the DFE, then $\left(1 - \frac{S_h}{N_h}\frac{N_h^*}{S_h^*}\right) > 0$, $\left(1 - \frac{S_n}{N_h}\frac{N_h^*}{S_n^*}\right) > 0$ and $\left(1 - \frac{S_w}{N_h}\frac{N_h^*}{S_w^*}\right) > 0$, and thus, $\tilde{H}(Y,Z) \geq 0$. It therefore follows that

$H(Y,Z) =$

$$\begin{pmatrix} 0 & 0 & 0 & 0 & 0 & \phi\theta_n I_n & 0 & \phi\theta_w I_w \\ 0 & 0 & 0 & 0 & 0 & \pi\theta_n I_n & 0 & \pi\theta_w I_w \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \tilde{\theta}_n A_h & \tilde{\theta}_n I_{hc} & \tilde{\theta}_n I_{hs} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \tilde{\theta}_w A_h & \tilde{\theta}_w I_{hc} & \tilde{\theta}_w I_{hs} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

where $\pi = (1-\phi)$, $\theta_n = \frac{a_n\beta_{nh}S_h^*}{N_h^*}\left(1-\frac{S_h}{N_h}\frac{N_h^*}{S_h^*}\right)$, $\theta_w = \frac{a_w\beta_{wh}S_h^*}{N_h^*}\left(1-\frac{S_h}{N_h}\frac{N_h^*}{S_h^*}\right)$, $\tilde{\theta}_n = \frac{a_n\beta_{hn}S_n^*}{N_h^*}\left(1-\frac{S_n}{N_h}\frac{N_h^*}{S_n^*}\right)$, and $\tilde{\theta}_w = \frac{a_w\beta_{hw}S_w^*}{N_h^*}\left(1-\frac{S_w}{N_h}\frac{N_h^*}{S_w^*}\right)$. Therefore, by the theorem in [16], the DFE $\mathfrak{E}^*$ given in Equation (10) is GAS. □

The result in Theorem 4 suggests that dengue will be eliminated from the community if the dengue threshold quantity $\mathscr{R}_0$ can be brought to a value less than unity.

D. Assessing the Impact of Wolbachia Release Coverage, η, on Dengue Burden

This section explores the impact of Wolbachia release coverage, η, on dengue disease burden in the population in the sense of [7]. For our results to remain tractable, we decided to work with $\mathscr{R}_0^2$ as expressed in Equation (12). It is important to state that this decision does not alter the conclusion when the actual expression of the dengue threshold, $\mathscr{R}_0$, is used. Thus, the partial derivative of $\mathscr{R}_0^2$ in Equation (12) with respect to the Wolbachia release coverage, η, gives

$$\begin{aligned} \frac{\partial\mathscr{R}_0^2}{\partial\eta} &= \frac{(A_1-A_2)\mu_h[n_2\phi\alpha_2\pi_1\tau_h+\pi n_3 n_1 n_4+\phi\tau_h n_2 n_4]}{\Pi_h\mu_n^2\mu_w^2 n_1 n_2 n_3 n_4 n_5 n_6}, \\ &= -\frac{(A_2-A_1)\mu_h[n_2\phi\alpha_2\pi_1\tau_h+\pi n_3 n_1 n_4+\phi\tau_h n_2 n_4]}{\Pi_h\mu_n^2\mu_w^2 n_1 n_2 n_3 n_4 n_5 n_6}, \\ &< 0, \end{aligned} \tag{19}$$

where $\pi = (1-\phi)$, $\pi_1 = 1-\sigma$, $A_1 = a_w^2\beta_{hw}\beta_{wh}\Pi_w\tau_w n_5\mu_n^2$, $A_2 = a_n^2\beta_{hn}\beta_{nh}\Pi_n\tau_n n_6\mu_w^2$). The result in Equation (19) indicates that $\mathscr{R}_0^2$ is a decreasing function of the parameter η (which can be clearly seen when compared the two expressions in Equations (11) and (19), see also Table III). Thus, the reduction (or even elimination) of dengue disease burden in the population is possible with an increasing coverage of Wolbachia release in the community.

III. Numerical simulations and efficiency analysis

A. Numerical simulations

In this section, the numerical simulation of the dengue model (4) is explored to investigate the impacts of the varying Wolbachia coverage, η, and the fraction of symptomatic infectious individuals in class I_{hc} to progress to the class I_{hs}, accounted by $1-\sigma$, on the dynamical behaviours of dengue spread and transmission in the population. All the simulations are carried out in MATLAB with ode45 routine. The initial conditions of model (4) are estimated as follows: The total human population is taken as $N_h(0) = 3247700$ as in [7] with $E_h(0) = 420$, $A_h(0) = 120$, $I_{hc}(0) = 30$, $I_{hs}(0) = 7$, $R_h(0) = 0$ so that $S_h(0) = 3247700-(420+120+30+7) = 3247123$. It is assumed that the total numbers of non-Wolbachia-carrying and Wolbachia-carrying mosquitoes are $N_n(0) = p\times N_h(0)$ and $N_w(0) = q\times N_h(0)$, where $p = 10$ and $q = 4$ are proportionality constants accounting for the average non-Wolbachia-infected and Wolbachia-infected mosquitoes to human ratio, so that $E_n(0) = 700$, $I_n(0) = 330$, $S_n(0) = N_n(0)-E_n(0)-I_n(0) = 32475970$, $E_w(0) = 100$, $I_w(0) = 100$, and $S_w(0) = E_w(0)-I_w(0) = 12990600$. Whereas the parameter values used are as defined in Table II.

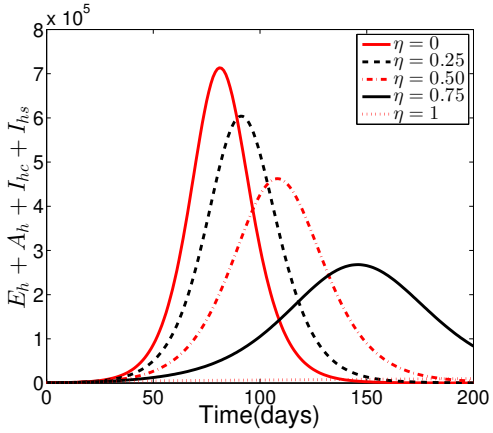
In Fig. 1, the varying effect of Wolbachia coverage, η, on the dynamic behaviour of dengue spread among the interacting human, non-Wolbachia-carrying mosquito, and Wolbachia-carrying mosquito populations is illustrated. The disease prevalence in human population decreases as η increases as Fig. 1a shows. It is also observed that the size of non-Wolbachia-carrying mosquito population considerably declines as η increases, whereas the size of the Wolbachia-carrying mosquito population increases as η is increased as shown in Figs. 1b and 1c, respectively. The physical interpretation of this is that the more the Wolbachia-infected mosquitoes are released into the community, the less the number of non-Wolbachia-infected mosquito and dengue prevalence in the human population. An insightful result arising from this is that elimination of dengue in the population is possible if a required level of Wolbachia coverage is successfully attained with time.

Moreover, in Table III, we demonstrate the effect of different levels of Wolbachia coverage on the dengue threshold $\mathscr{R}_0$. It is seen that the basic reproduction number $\mathscr{R}_0$ decreases with an increasing η. This reaffirms the positive impact of η on $\mathscr{R}_0$ as illustrated in Equation (19).

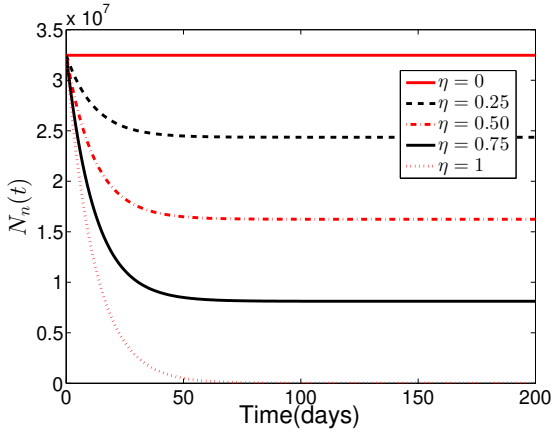
TABLE III Illustration of the basic reproduction number $\mathscr{R}_0$ versus different Wolbachia coverage levels

Wolbachia coverage, $\eta(\%)$	$\mathscr{R}_0$ value
0	2.694
25	2.393
50	2.049
75	1.634
100	1.068

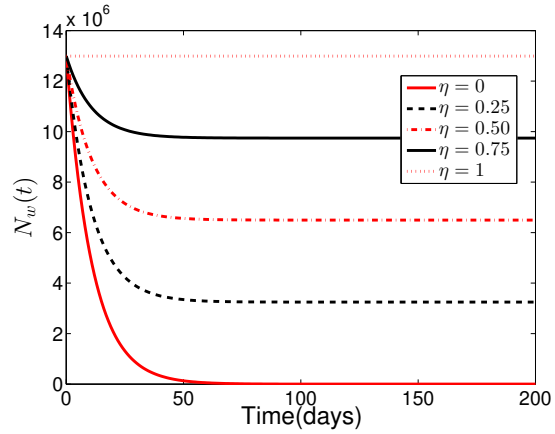
Further, the effect of variation in the fraction of symptomatically infected humans with mild symptoms that progress and become symptomatically infected with severe DHF/DSS, $1-\sigma$, on the dynamics of dengue disease transmission and spread in the population is investigated. In particular, the dynamics of dengue prevalence in human population is illustrated as $1-\sigma$ varies (see Fig. 2). It is seen that there are different epidemic peaks for different



(a) Disease prevalence in human population



(b) Population of non-Wolbachia-carrying mosquito



(c) Population of Wolbachia-carrying mosquito

Fig. 1 Time series plot showing how different levels of η affects the dynamics of model (4)

values of $1-\sigma$ by which dengue burden decreases in human population as the fraction $1-\sigma$ decreases. This suggests that the less the fraction of individuals in class I_{hc} progressing and entering the class I_{hs}, the less the size of dengue prevalence in the human population, and vice-versa. The epidemiological insight from this result is that the burden of dengue can be significantly reduced in the population if the fraction of symptomatic infected individuals with mild disease symptoms to become symptomatic infected with severe DHF/DSS is considerably reduced. This can be achieved by providing a timely treatment for symptomatic infected individuals with mild clinical symptoms to aid their quick recovery.

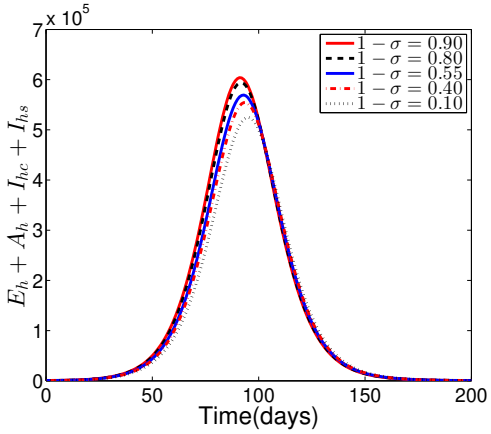


Fig. 2 Simulations of the dengue model (4) with $1-\sigma = (0.90, 0.80, 0.55, 0.40, 0.10)$ and with fixed $\eta = 0.25$

B. Efficiency analysis

To quantify the efficacy of the implemented Wolbachia control at varying level of coverage, η, on the dynamics of dengue disease spread in the population as demonstrated by the time series plots shown in Fig. 1, it is important to carry out the efficiency analysis on the five different coverage levels considered. Thus, the idea from previous studies is helpful to define the efficiency index, denoted by $\mathfrak{I}_e$, as in [7]:

$$\mathfrak{I}_e = 100 \times \left(\frac{\mathfrak{P}_n - \mathfrak{P}_w}{\mathfrak{P}_n} \right) \%, \tag{20}$$

where $\mathfrak{P}_w$ and $\mathfrak{P}_n$ are the cumulative numbers of infected humans in the presence and absence of Wolbachia-carrying mosquitoes, respectively, which are obtained from

$$\int_0^{200} (E_h(t) + A_h(t) + I_{hc}(t) + I_{hs}(t))dt.$$

According to this analysis, the value of η that produces the highest efficiency index is considered as most efficient [7]. Notably, $\mathfrak{P}_n$ is obtained using MATLAB by setting η and the state variable $S_w(t)$, $E_w(t)$ and $I_w(t)$ to zero in model (4) as $\mathfrak{P}_w = 2.6716 \times 10^7$. The values of $\mathfrak{P}_w$ for different η and the associated efficiency index $\mathfrak{I}$ are tabulated in Table IV. The highest Wolbachia coverage ($\eta = 100\%$) has the highest efficiency index value, whereas the least coverage level ($\eta = 0\%$) gives the efficiency index with the least value as Table IV shows. In other words, there is a direct relationship between the Wolbachia coverage and

TABLE IV Efficiency indices for various values Wolbachia coverage

Wolbachia coverage, $\eta(\%)$	$\mathfrak{P}_w(\times 10^6)$	$\mathfrak{I}_e(\%)$
0	23.579	11.7420
25	23.466	12.1650
50	22.999	13.9130
75	19.374	27.4817
100	1.1321	95.7625

its efficiency index. This is physically interpreted as the higher the Wolbachia coverage, the higher the efficiency index. This further justifies the results in Fig. 1a.

IV. Conclusion

This paper considered the development and analysis of twelve-dimensional nonlinear mathematical model for dengue disease spread. The model features symptomatic infected human with severe DHF/DSS subpopulation and Wolbachia-infected mosquito population to investigate the efficacy of the application of Wolbachia intervention on the spread and transmission of the disease in the population. The disease-free state solution of the model is obtained. The dengue threshold quantity (the basic reproduction number), $\mathscr{R}_0$, is obtained. By employing the comparison theorem, it is shown that the model has a GAS DFE whenever $\mathscr{R}_0 < 1$. Theoretically, it was shown that $\mathscr{R}_0$ is a decreasing function of Wolbachia coverage level, η. This is complemented with numerical simulation. Furthermore, numerical evaluation of the impact of η on the dynamics dengue disease transmission in the population shows that dengue disease burden can significantly reduced in the population with an increasing Wolbachia coverage level in the community. Numerical results also show that dengue prevalence in the population reduces as the fraction of symptomatic infected individuals with mild clinical symptoms to become symptomatic infected with severe DHF/DSS reduces. These results suggest that the use of Wolbachia control could be helpful in curtailing the community spread of dengue, and provision of timely treatment (hospitalization) for symptomatic infected individuals with mild clinical symptoms to aid their quick recovery also has a positive response in the fight against the disease.

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