Analysis of Dengue Fever Transmission Dynamics with Multiple Controls: A Mathematical Approach

1st Afeez Abidemi
Department of Mathematical Sciences
Federal University of Technology
Akure, Nigeria
aabidemi@futa.edu.ng
orcid: 0000-0003-1960-0658

2nd Hammed Olawale Fatoyinbo
School of Fundamental Sciences
Massey University
Palmerston North, New Zealand
h.fatoyinbo@massey.ac.nz
orcid: 0000-0002-6036-2957

3rd Joshua Kiddy K. Asamoah
Complex Systems Research Center
Shanxi University
Taiyuan 030006, China
topeljoshua@gmail.com
orcid: 0000-0002-7066-246X

2020 International Conference on Decision Aid Sciences and Application (DASA) | 978-1-7281-9677-0/20/$31.00 ©2020 IEEE | DOI: 10.1109/DASA51403.2020.9317064

***Abstract*—Dengue is a mosquito-borne viral infection caused by the dengue viruses of four serotypes, DENV-1,2,3,4. The disease is transmitted by the bites of infected female Aedes mosquitoes. This paper presents a compartmental deterministic model including human prevention and vector control interventions for the dynamics of dengue fever spread. Theoretical analysis of the model is conducted to obtain the associated dengue-free equilibrium. The next generation matrix method is used to calculate the effective reproduction number. The local stability analysis of the dengue-free equilibrium is presented. Numerical simulations of different strategies of control combination are considered, and how they impact the dynamical behaviour of the system are analysed. We found that dengue prevalence can be reduced in a community by implementing any control intervention which combines human prevention and vector control measures.**

***Index Terms*—autonomous system, control intervention, effective reproduction number, stability**

I. INTRODUCTION

Dengue virus (DENV) is a worldwide threat to global public health as it causes a variety of infections such as dengue fever (DF), the clinically more severe dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) [1]. Failure to provide a timely medical treatment for any dengue-related human infections, particularly DHF and DSS, can lead to death [2]. Annually, DENV is responsible for over 100 million infections and 20,000 deaths [3].

There are four virus serotypes causing dengue, namely, DENV-1, DENV-2, DENV-3 and DENV-4 [4]. Each of the viruses is primarily acquired through the bites of infected *Aedes* mosquitoes [5]. The process of DENV transmission is maintained in a cycle of infected humans–non-infected female *Aedes* mosquitoes–infected female *Aedes* mosquitoes–healthy humans [6]. After 3–14 days of the bite of infected mosquito, the symptoms of dengue become apparent. A dengue patient can acquire permanent immunity against the particular DENV serotype upon recovery from the infection, but the risk of getting infected with the other three strains is increased [7].

Currently, there is no available vaccine against dengue, although several candidate vaccines are in different phases of their clinical trials [8]. In particular, a live attenuated vaccine Dengvaxia was recently licensed, although the vaccine is only efficacious and safe in seropositive individuals [9]. Hence, vector control and personal protection against the infected mosquitoes bites remain the possible primary dengue prevention methods [5].

Mathematical models have become valuable tools in facilitating the understanding of the mechanisms involved in the transmission dynamics and control of dengue [4], [10]. Mathematically, dengue disease spread and control in the interacting human and mosquito populations has been described using compartmental models governed by autonomous systems of ordinary differential equations (ODEs) in many previous studies (see [2], [4], [5], [7], [11], [12] and some of the references therein). For instance, Carvalho *et al.* [4] evaluated the effect of three control strategies, namely, mechanical, chemical and vaccination control strategies in order to derive the effective way to eradicate dengue in a community. The study revealed that the use of combination of chemical and mechanical controls is much more efficient than their separate use, however, not enough to eliminate dengue disease in the population. Also, increasing rate of vaccine and its efficiency may lead to a delay in recurrence of dengue.

Srivastav and Ghosh [2] presented a compartmental model including treatment function to evaluate the effect of treatment of dengue infected individuals on the spread of the disease in a population. Similarly, compartmental model including three control parameters that account for personal protection, treatment and adulticide controls was formulated and analysed for dengue spread and control in [7]. The computer simulated results indicate that dengue prevalence can be reduced in a population using the three control interventions, where the implementation of their combined efforts shows more efficacy on the dynamics of the disease control.

In [5], a compartmental model was presented and analysed for the transmission dynamics and control of dengue disease using various control measures that target human population (personal protection, treatment and hypothetical vaccine) and vector population (larvicide, adulticide and ecological control). It was found that dengue can be effectively controlled using an integrated vector control strategy involving the combined efforts of human protection and vector control intervention measures. Also, Zhu *et al.* [11] developed and analysed

a spatial compartmental model incorporating vector control (larvicide and adulticide) strategy on the way to effectively curtail the spatiotemporal transmission of dengue.

It is a well-known fact that asymptomatic cases account for the higher proportion in dengue-related infections than the symptomatic cases [13]. A survey conducted in Central America among school children revealed the ratio of asymptomatic to symptomatic cases to be 13:1 [14]. However, consideration of the asymptomatic dengue infection carriers in compartmental dengue model formulation did not receive attention in any of the previous studies. Further, considering the efficacy of various vector control measures, a mathematical analysis of single-type control interventions carried out in [5] had shown that open space spray of insecticide (adulticide) is the most effective to contain dengue spread. One underlying idea is that this control strategy is sufficient to reduce the size of mosquito population to the level at which the spread of DENV between the interacting human and mosquito populations has been significantly slowed down. However, using only one control intervention may not be effective in stemming the transmission of dengue in a population because it is possible for the *Aedes* mosquitoes to survive and develop resistance against the used chemical for space spraying over time. Also, the use of only insecticide-treated bed nets (ITNs) as a preventive intervention against mosquito bites may be less effective to curtail DENV spread because mosquito can bite any time [15].

Hence, owing to the fact that combination of several control interventions are required to significantly control dengue disease spread [5], [12], this study focuses on analysing the effectiveness of using ITNs, two treatment control measures (one aiming at the latently infected individuals and the other targeting the symptomatic infectious individuals) and mosquito reduction effort using adulticide based on different combination intervention strategies such that at least three controls are implemented. To this end, a compartmental mathematical model capturing asymptomatic carriers of dengue infections, which also incorporates four control intervention parameters to gain insightful information on dengue disease spread and control is proposed in this work. Employing the next generation matrix (NGM) approach, the effective reproduction number of the model is calculated. Also, the local asymptotic behaviour of the model is examined based on the computed reproduction number.

II. Method

A. Model Formulation

To formulate the model, the total host population at time t, represented as $N_h(t)$, is sub-grouped into five mutually exclusive epidemiological states: susceptible humans ($S_h(t)$), exposed humans ($E_h(t)$), asymptomatic infectious humans ($A_h(t)$), symptomatic infectious humans ($I_h(t)$), and recovered humans ($R_h(t)$). Thus,

$$N_h(t) = S_h(t) + E_h(t) + A_h(t) + I_h(t) + R_h(t).$$

Similarly, the population of *Aedes aegypti* female mosquito at time t, denoted as $N_v(t)$, is sub-grouped into three classes: susceptible mosquito ($S_v(t)$), exposed mosquito ($E_v(t)$), and infectious mosquito ($I_v(t)$). Then,

$$N_v(t) = S_v(t) + E_v(t) + I_v(t).$$

For the human population, let Λ_h be the constant recruitment rate and μ_h be the natural human death rate. Then, the newly recruited individuals enter susceptible human subpopulation S_h so that the rate of change of S_h is given by

$$\frac{dS_h(t)}{dt} = \Lambda_h - \frac{b\beta_h I_v S_h}{N_h} - \mu_h S_h,$$

where β_h is the probability of DENV transmission from I_v to S_h, and b is the biting rate of mosquito per S_v. It is assumed that mosquitoes cannot transfer DENV at latency period. Furthermore, the derivation of human force of infection $\lambda_h = \frac{b\beta_h I_v}{N_h}$ is described as follows: it can be assumed that the probability that a mosquito chooses a particular individual to bite is $\frac{1}{N_h}$. Thus, the number of bites per unit of times an individual receives on average is $\frac{bN_v}{N_h}$. Consequently, the infection rate per susceptible human is expressed as $b\beta_h \left(\frac{N_v}{N_h}\right) \frac{I_v}{N_v}$. Also, the rate of change of the subpopulation of exposed human is

$$\frac{dE_h(t)}{dt} = \frac{b\beta_h I_v S_h}{N_h} - \alpha_h E_h - \mu_h E_h,$$

where α_h is the rate of progression of humans from the exposed class E_h to the infected class A_h or I_h. It is assumed that the fractions ν and $1-\nu$ of exposed individuals move to A_h and I_h classes respectively. Here, the inflow rate is $\frac{b\beta_h I_v}{N_h}$ and the outflow rate is $\alpha_h + \mu_h$. Similarly, the rate of change of asymptomatic infectious human subpopulation is

$$\frac{dA_h(t)}{dt} = \nu\alpha_h E_h - \gamma_a A_h - \mu_h A_h,$$

where γ_a is the progression rate of humans in class A_h to the recovered human subpopulation R_h. Next, the rate of change of infectious human subpopulation I_h is

$$\frac{dI_h(t)}{dt} = (1-\nu)\alpha_h E_h - \gamma_i I_h - \mu_h I_h,$$

where γ_i is the rate at which humans in the subpopulation I_h move to the subpopulation R_h. The inflow rate is $(1-\nu)\alpha_h$ while $(\gamma_i I + \mu_h)$ is the outflow rate. Finally, the rate of change of the subpopulation of recovered individual is

$$\frac{dR_h(t)}{dt} = \gamma_a A_h + \gamma_i I_h - \mu_h R_h.$$

Turning to the mosquito population, let Λ_v be the constant mosquito recruitment rate and μ_v be the natural mosquito death rate. The newly recruited mosquitoes enter the susceptible mosquito subpopulation S_v so that the dynamics of S_v is described by

$$\frac{dS_v(t)}{dt} = \Lambda_v - \frac{b\beta_v(\eta A_h + I_h)S_v}{N_h} - \mu_v S_v,$$

where β_v is the DENV transmission probability from an infected human A_h or I_h to a susceptible mosquito S_v, b

is the mosquito biting rate per susceptible human S_h, and $0 \leq \eta \leq 1$ is the modification parameter representing the assumed reduction in transmissibility of asymptomatic infectious humans A_h relative to the symptomatic infectious humans I_h. Note that the description of the derivation of the mosquito force of infection, denoted as $\lambda_v = \frac{b\beta_v(\eta A_h + I_h)}{N_h}$, is similar to that of λ_h. Now, the rate of change of exposed mosquito subpopulation is given as

$$\frac{dE_v(t)}{dt} = \frac{b\beta_v(\eta A_h + I_h)S_v}{N_h} - \alpha_v E_v - \mu_v E_v,$$

where α_v of the outflow term $\alpha_v + \mu_v$ is the progression rate of mosquitoes in the exposed subpopulation E_v to the infectious mosquito subpopulation I_v, and $\frac{b\beta_v(\eta A_h + I_h)}{N_h}$ is the inflow rate. Similarly, the rate of change of infectious mosquito subpopulation is

$$\frac{dI_v(t)}{dt} = \alpha_v E_v - \mu_v I_v.$$

Following the above discussion, the mathematical model governing the dynamics of dengue fever population is presented by the system of non-linear ODEs in (1) as

$$\frac{dS_h}{dt} = \Lambda_h - \frac{b\beta_h I_v}{N_h} S_h - \mu_h S_h, \tag{1a}$$
$$\frac{dE_h}{dt} = \frac{b\beta_h I_v}{N_h} S_h - \alpha_h E_h - \mu_h E_h, \tag{1b}$$
$$\frac{dA_h}{dt} = \nu\alpha_h E_h - \gamma_a A_h - \mu_h A_h, \tag{1c}$$
$$\frac{dI_h}{dt} = (1-\nu)\alpha_h E_h - \gamma_i I_h - \mu_h I_h, \tag{1d}$$
$$\frac{dR_h}{dt} = \gamma_a A_h + \gamma_i I_h - \mu_h R_h, \tag{1e}$$
$$\frac{dS_v}{dt} = \Lambda_v - \frac{b\beta_v(\eta A_h + I_h)}{N_h} S_v - \mu_v S_v, \tag{1f}$$
$$\frac{dE_v}{dt} = \frac{b\beta_v(\eta A_h + I_h)}{N_h} S_v - \alpha_v E_v - \mu_v E_v, \tag{1g}$$
$$\frac{dI_v}{dt} = \alpha_v E_v - \mu_v I_v, \tag{1h}$$

with the initial conditions presented by Equation (2) as

$$S_h(0) = S_{0h},\ E_h(0) = E_{0h},\ A_h(0) = A_{0h},\ I_h(0) = I_{0h},$$
$$R_h(0) = R_{0h},\ S_v(0) = S_{0v},\ E_v(0) = E_{0v},\ I_v(0) = I_{0v}. \tag{2}$$

Table I describes the variables and parameters involved in the construction of model (1). Also, the flow diagram of model (1) is given by Fig. 1. Fig. 1 gives a clear view of the inter-relationships between the various compartments for the two interacting human and mosquito populations regarding to DENV spread in a community.

Next, we introduce four different control parameters that represent the use of ITNs (denoted as ε), treatment drug therapy of latently infected (or exposed) individuals (ϕ), chemotherapy or treatment of symptomatic infectious individuals (δ), and open space spraying of adulticide (ξ) into the basic model (1), so the disease transmission probabilities β_h and β_v are modified as $(1-\varepsilon)\beta_h$ and $(1-\varepsilon)\beta_v$, the

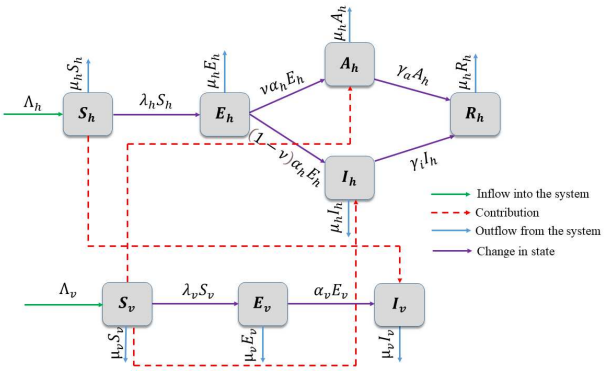


Fig. 1: Flow diagram of the dengue model (1), where $\lambda_h = \frac{b\beta_h I_v}{N_h}$ and $\lambda_v = \frac{b\beta_v(\eta A_h + I_h)}{N_h}$

exposed individuals recovered at a treatment control-dependent rate $\phi\alpha_h E_h$ (where α_h is the human infectiousness rate), the natural recovery rate of infectious individuals, γ_i, is increased by value $\tau_1\delta$ (where τ_1 measures the efficacy of control δ), and the mosquito per-capita recruitment rate Λ_v is reduced by a factor $1-\tau_2\xi$ (where τ_2 accounts for the efficacy of control ξ). Then, the basic model (1) becomes

$$\frac{dS_h}{dt} = \Lambda_h - \frac{b\beta_h(1-\varepsilon)I_v}{N_h} S_h - \mu_h S_h, \tag{3a}$$
$$\frac{dE_h}{dt} = \frac{b\beta_h(1-\varepsilon)I_v}{N_h} S_h - (\alpha_h + \mu_h)E_h, \tag{3b}$$
$$\frac{dA_h}{dt} = (1-\phi)\nu\alpha_h E_h - (\gamma_a + \mu_h)A_h, \tag{3c}$$
$$\frac{dI_h}{dt} = (1-\phi)(1-\nu)\alpha_h E_h - (\gamma_i + \tau_1\delta + \mu_h)I_h, \tag{3d}$$
$$\frac{dR_h}{dt} = \phi\alpha_h E_h + \gamma_a A_h + (\gamma_i + \tau_1\delta)I_h - \mu_h R_h, \tag{3e}$$
$$\frac{dS_v}{dt} = (1-\tau_2\xi)\Lambda_v - \frac{b\beta_v(1-\varepsilon)(\eta A_h + I_h)}{N_h} S_v - (\mu_v + \tau_2\xi)S_v, \tag{3f}$$
$$\frac{dE_v}{dt} = \frac{b\beta_v(1-\varepsilon)(\eta A_h + I_h)}{N_h} - (\alpha_v + \mu_v + \tau_2\xi)E_v, \tag{3g}$$
$$\frac{dI_v}{dt} = \alpha_v E_v - (\mu_v + \tau_2\xi)I_v, \tag{3h}$$

with initial conditions given at time $t = 0$.

B. *Qualitative analysis of model* (3)

1) Positivity of solutions: All the state variables of the dengue model (3) can be shown to have positive solutions. This will in turn establish the epidemiological meaningfulness of the model.

Theorem 1. *The solution*

$$X(t) = (S_h(t), E_h(t), A_h(t), I_h(t), R_h(t), S_v(t), E_v(t), I_v(t))$$

of the dengue model (3) *with* $X(0) \geq 0$ *is non-negative for all* $t > 0$. *Moreover,*

$$\limsup_{t\to\infty} N_h(t) \leq \frac{\Lambda_h}{\mu_h} \text{ and } \limsup_{t\to\infty} N_v(t) \leq \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v + \tau_2\xi)},$$

TABLE I: PARAMETER VALUES OF THE DENGUE MODEL (3)

Parameter	Description	Value	Source
Λ_h	Human recruitment rate	120.2407	Estimated [16]
μ_h	Human lifespan (per day)	$\frac{1}{74\times365}$	[17]
b	Mosquito biting rate	0.66272	[16]
β_h	Transmission probability of dengue virus from I_v to S_h	0.75	[18]
β_v	Transmission probability of dengue virus from I_h and A_h to S_v	0.75	[18]
γ_a	Progression rate from class A_h to class R_h	0.328833	[18]
γ_i	Recovery rate of individuals in class I_h	0.328833	[18]
α_h	Progression rate from either class A_h or I_h	0.12899	[16]
Λ_v	Mosquito recruitment rate	231978.5714	Estimated [16]
η	Modification parameter that accounts for the reduced infectiousness of humans in the A class when compared to humans in the I_h class	0.6000	Assumed
α_v	Rate of progression of exposed mosquitoes to become infectious	0.00396	[16]
μ_v	Lifespan of the female mosquitoes (per day)	$\frac{1}{42}$	[16]
ν	Fraction of new infectious humans that are asymptomatic	0.5000	Assumed
τ_1	Proportion of effective treatment	0.3	[19]
τ_2	Killing efficacy of adulticide control	$[0.2, 0.8]$	[19]
ε	Personal protection using insecticide-treated bed nets (ITNs) or mosquito-repellent lotion	$[0, 1]$	[5]
ϕ	treatment drug therapy for latently infected humans, E_h	$[0, 1]$	Assumed
δ	Chemotherapy or treatment of individuals in class I_h	$[0, 1]$	[5]
ξ	Mosquito reduction effort using open space spray of insecticide (adulticide)	$[0, 1]$	[5]

where $N_h(t) = S_h(t) + E_h(t) + A_h(t) + I_h(t) + R_h(t)$ *and* $N_v(t) = S_v(t) + E_v(t) + I_v(t)$.

Proof. Following [5], [20], we use a relevant approach to prove Theorem 1. Let $t_s = \sup\{t > 0 : X(t) > 0\}$. Clearly, $t_s > 0$. Consider Equation (3a),

$$\frac{dS_h(t)}{dt} = \Lambda_h - \lambda_h(t)S_h(t) - \mu_h S_h(t), \tag{4}$$

where $\lambda_h(t) = \frac{b\beta_h(1-\varepsilon)I_v(t)}{N_h(t)}$. Then,

$$\frac{dS_h(t)}{dt} = [\lambda_h(t) + \mu_h]\, S_h(t) = \Lambda_h. \tag{5}$$

Solving Equation (5) yields

$$\frac{d}{dt}\left[S_h(t)\exp\left\{\mu_h t + \int_0^t \lambda_h(\zeta)d\zeta\right\}\right] = \Lambda_h \exp\left\{\mu_h t + \int_0^t \lambda_h(\zeta)d\zeta\right\}.$$

Thus,

$$S_h(t_s)\exp\left\{\mu_h t_s + \int_0^{t_s} \lambda_h(\zeta)d\zeta\right\} - S_h(0) = \int_0^{t_s} \Lambda_h \exp\left\{\mu_h \psi + \int_0^{\psi} \lambda_h(\epsilon)d\epsilon\right\} d\psi.$$

Therefore,

$$\begin{aligned} S_h(t_s) &= S_h(0)\exp\left\{-\left(\mu_h t_s + \int_0^{t_s} \lambda_h(\zeta)d\zeta\right)\right\} \\ &\quad + \exp\left\{-\left(\mu_h t_s + \int_0^{t_s} \lambda_h(\zeta)d\zeta\right)\right\} \\ &\quad \times \int_0^{t_s} \Lambda_h \exp\left\{\mu_h \psi + \int_0^{\psi} \lambda_h(\epsilon)d\epsilon\right\} d\psi, \\ &> 0. \end{aligned}$$

Similarly, it can be shown that $E_h(t_s) > 0$, $A_h(t_s) > 0$, $I_h(t_s) > 0$, $R_h(t_s) > 0$, $S_v(t_s) > 0$, $E_v(t_s) > 0$, and $I_v(t_s) > 0$. Hence, the solution $X(t) > 0 \;\forall\; t > 0$.

To verify the later part of the proof, note that $0 < S_h(0) \leq N_h(t)$, $0 \leq E_h(0) \leq N_h(t)$, $0 \leq A_h(0) \leq N_h(t)$, $0 \leq I_h(0) \leq N_h(t)$, $0 \leq R_h(0) \leq N_h(t)$, $0 < S_v(0) \leq N_v(t)$, $0 \leq E_v(0) \leq N_v(t)$, and $0 \leq I_v(0) \leq N_v(t)$. We obtain the rates of change of $N_h(t)$ and $N_v(t)$ with respect to time by adding the components of human and mosquito populations of the dengue model (3) as

$$\begin{aligned} \frac{dN_h(t)}{dt} &= \Lambda_h - \mu_h N_h(t), \\ \frac{dN_v(t)}{dt} &= \Lambda_v(1-\tau_2\xi) - (\mu_v + \tau_2\xi)N_v(t). \end{aligned}$$

Hence,

$$\limsup_{t\to\infty} N_h(t) \leq \frac{\Lambda_h}{\mu_h}, \quad \limsup_{t\to\infty} N_v(t) \leq \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v+\tau_2\xi)}$$

as required to show. □

2) Invariant region: Let $\mathcal{M}_h = \left\{(S_h(t), E_h(t), A_h(t), I_h(t)R_h(t)) \in \mathbb{R}^5_+ : N_h(t) \leq \frac{\Lambda_h}{\mu_h}\right\}$ and $\mathcal{M}_v = \left\{(S_v(t), E_v(t), I_v(t)) \in \mathbb{R}^3_+ : N_v(t) \leq \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v+\tau_2\xi)}\right\}$ so that

$$\mathcal{M} = \mathcal{M}_h \times \mathcal{M}_v \subset \mathbb{R}^5_+ \times \mathbb{R}^3_+. \tag{6}$$

Theorem 2. *The biologically feasible region* $\mathcal{M}$ *of the dengue model* (3) *is positively invariant.*

Proof. It follows from Equations (3a)–(3e) that

$$\frac{dN_h(t)}{dt} = \Lambda_h - \mu_h N_h(t), \tag{7}$$

and summing up Equations (3f)–(3h) leads to

$$\frac{dN_v(t)}{dt} = (1-\tau_2\xi)\Lambda_v - (\mu_v + \tau_2\xi)N_v(t). \tag{8}$$

Thus, from Equations (7) and (8) respectively,

$$N_h(t) = N_h(0)e^{-\mu_h t} + \frac{\Lambda_h}{\mu_h}\left(1 - e^{-\mu_h t}\right),$$
$$N_v(t) = N_v(0)e^{-(\mu_v+\tau_2\xi)t} + \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v+\tau_2\xi)}\left(1 - e^{-(\mu_v+\tau_2\xi)}\right).$$

Clearly, $N_h(t) \to \frac{\Lambda_h}{\mu_h}$ and $N_v(t) \to \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v+\tau_2\xi)}$ as $t \to \infty$. In particular, $N_h(t) \leq \frac{\Lambda_h}{\mu_h}$ if the total population at time $t = 0$, $N_h(0) \leq \frac{\Lambda_h}{\mu_h}$. Similarly, $N_v(0) \leq \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v+\tau_2\xi)}$. Therefore, $\mathcal{M}$ is positively invariant. □

Hence, it suffices to analyse the dynamical behaviours of dengue governed by model (3) in the region $\mathcal{M}$ where the model is biologically and mathematically makes sense.

3) Stability of dengue-free equilibrium $\mathcal{E}_0$: Here, we show that the dengue model (3) has a dengue-free equilibrium (DFE) denoted as $\mathcal{E}_0$. Setting the right hand sides of Equations (3a)–(3h) to zero, $\mathcal{E}_0$ is obtained as

$$\begin{aligned}\mathcal{E}_0 &= \left(S_h^0, 0, 0, 0, 0, S_v^0, 0, 0\right) \\ &= \left(\frac{\Lambda_h}{\mu_h}, 0, 0, 0, 0, \frac{\Lambda_v(1-\tau_2\xi)}{(\mu_v+\tau_2\xi)}, 0, 0\right).\end{aligned} \tag{9}$$

To establish the stability of the dengue model (3), it is necessary to first derive the control-induced basic reproduction number, denoted as $\mathcal{R}_c$, for the model using the NGM operator on system (3). Considering $E_h(t)$, $A_h(t)$, $I_h(t)$, $E_v(t)$ and $I_v(t)$ as the infected classes and then applying the NGM notation in [21], the Jacobian matrices F including the new infectious terms and the transition matrix V denoting the remaining terms can be obtained, so that the control-induced reproduction number $\mathcal{R}_c$ is

$$\mathcal{R}_c = \rho\left(FV^{-1}\right),$$
$$\mathcal{R}_c = \sqrt{\frac{(1-\varepsilon)^2 b^2 \beta_h \beta_v (1-\phi)\alpha_h(k_3\eta\nu + k_2(1-\nu))\alpha_v S_v^0}{k_1 k_2 k_3 k_4 k_5 S_h^0}}, \tag{10}$$

where ρ is the spectra radius and $k_1 = \alpha_h + \mu_h$, $k_2 = \gamma_a + \mu_h$, $k_3 = \gamma_i + \tau_1\delta + \mu_h$, $k_4 = \alpha_v + \mu_v + \tau_2\xi$, and $k_5 = \mu_v + \tau_2\xi$.

It follows from the expression of $\mathcal{R}_c$ in (10) that the basic reproduction number, $\mathcal{R}_0$, of the basic dengue model (1) is

$$\mathcal{R}_0 = \sqrt{\frac{b^2\beta_h\beta_v\alpha_h(l_1\eta\nu + k_2(1-\nu))\alpha_v S_v^1}{k_1 k_2 l_1 l_2 \mu_v S_h^0}}, \tag{11}$$

where $S_v^1 = \frac{\Lambda_v}{\mu_v}$, $l_1 = \gamma_i + \mu_h$, $l_2 = \alpha_v + \mu_v$.

The expression $\mathcal{R}_c$ accounts for the number of secondary infections owing to the infections by one dengue-infected individual introduced into a completely susceptible population in the presence of control interventions. Further, by the standard technique in the literature, calculating the basic reproduction number using the NGM operator automatically proves the local asymptotic stability of DFE. This was summarized in Theorem 2 of [21]. Thus, the following result is verified:

Theorem 3. *If $\mathcal{R}_c < 1$, then DFE $\mathcal{E}_0$ of the dengue model* (3) *is locally asymptotically stable (LAS), and unstable if $\mathcal{R}_c > 1$.*

C. Analysis of the impacts of controls ε, ϕ, δ and ξ

Here, the impacts of using ITNs (ε), treatment on latently infected humans (ϕ), treatment on symptomatic dengue infection carriers (δ) and adulticide (ξ) in decreasing dengue burden is determined. To do achieve this, derivative of the effective reproduction number $\mathcal{R}_c$ is taken with respect to each control parameter. The results obtained are as given in Equations (12)–15:

$$\frac{\partial\mathcal{R}_c}{\partial\varepsilon} = -\sqrt{\frac{\Sigma}{k_1k_2k_3k_4k_5^2\Lambda_h}} \leq 0, \tag{12}$$

$$\frac{\partial\mathcal{R}_c}{\partial\phi} = -\frac{1}{2}\sqrt{\frac{(1-\varepsilon)^2\Sigma}{k_1k_2k_3k_4k_5^2(1-\phi)^2\Lambda_h}} \leq 0, \tag{13}$$

$$\begin{aligned}\frac{\partial\mathcal{R}_c}{\partial\delta} = -\frac{1}{2}\Bigg[&\frac{(1-\varepsilon)^2\tau_1\Sigma}{k_1k_2k_3^2k_4k_5^2\Lambda_h} \\ &- \frac{(1-\varepsilon)^2\tau_1\eta\nu\Sigma}{k_1k_2k_3k_4k_5^2\Lambda_h(k_3\eta\nu + k_2(1-\nu))}\Bigg] \\ &\times \frac{1}{\sqrt{\frac{(1-\varepsilon)^2\Sigma}{k_1k_2k_3k_4k_5^2\Lambda_h}}} \leq 0,\end{aligned} \tag{14}$$

$$\begin{aligned}\frac{\partial\mathcal{R}_c}{\partial\xi} = -\frac{1}{2}\Bigg[&\frac{(1-\varepsilon)^2\tau_2\Sigma}{k_1k_2k_3k_4k_5^2\Lambda_h(1-\tau_2\xi)} \\ &+ \frac{(1-\varepsilon)^2\tau_2\Sigma}{k_1k_2k_3k_4^2k_5^2\Lambda_h} + \frac{2(1-\varepsilon)^2\tau_2}{k_1k_2k_3k_4k_5^3\Lambda_h}\Bigg] \\ &\times \frac{1}{\sqrt{\frac{(1-\varepsilon)^2\Sigma}{k_1k_2k_3k_4k_5^2\Lambda_h}}} \leq 0,\end{aligned} \tag{15}$$

where

$$\Sigma = b^2\beta_v\beta_h\alpha_h(1-\phi)\alpha_v\mu_h(k_3\eta\nu + k_2(1-\nu))\Lambda_v(1-\tau_2\xi).$$

From Equations (12)–(15), it is observed that all the four control measures have a positive impact in lowering $\mathcal{R}_c$. Thus, the disease burden can be reduced in a population by implementing the control measures. Hence, in agreement with [5], the application of combined efforts of multiple controls (ε, ϕ, δ, and ξ) that have directly impact $\mathcal{R}_c$ will yield a more significant result in curtailing dengue disease spread in a population compare to the control strategy analysed in the previous studies [2], [7], [8].

III. Numerical Simulations, Results and Discussions

To numerically demonstrate the impact of using five different combinations (interventions A–E) of the four control parameters consider in the dengue model (3) on the transmission of dengue in interacting human and mosquito populations, the model parameter values used are as given in Table I. The initial

conditions are taken as $S_h(0) = 3247503$, $E_h(0) = 120$, $A_h(0) = 40$, $I_h(0) = 37$, $R_h(0) = 0$, $S_v(0) = 12990600$, $E_v(0) = 100$, and $I_v(0) = 100$ in considerations with the values previously used in [16]. All the controls are considered on a sub-interval $\varepsilon, \delta, \phi, \xi \in [0, 0.15)$. For this outbreak, the calculated $\mathcal{R}_0$ value in the case of no control is approximately $\mathcal{R}_0 = 3.2856$. The simulated results are demonstrated in Figs. 2–3. Also, the impact of using each control strategy on $\mathcal{R}_c$ is illustrated in Table II.

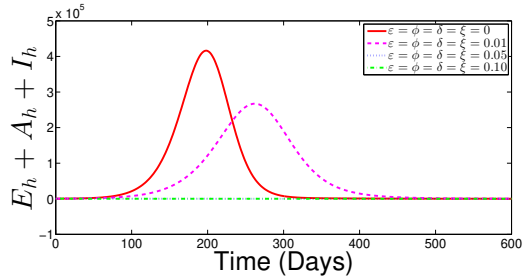
TABLE II: IMPACT OF CONTROL INTERVENTIONS A–E ON $\mathcal{R}_c$ OF THE DENGUE MODEL (3)

Control Level	Intervention	Control Parameter Value	$\mathcal{R}_c$ Value
I	A	$\varepsilon = \phi = \delta = \xi = 0.01$	2.3774
	B	$\phi = \delta = \xi = 0.01$	2.4014
	C	$\varepsilon = \delta = \xi = 0.01$	2.3894
	D	$\varepsilon = \phi = \xi = 0.01$	2.3841
	E	$\varepsilon = \phi = \delta = 0.01$	3.2273
II	A	$\varepsilon = \phi = \delta = \xi = 0.05$	0.9694
	B	$\phi = \delta = \xi = 0.05$	1.0205
	C	$\varepsilon = \delta = \xi = 0.05$	0.9946
	D	$\varepsilon = \phi = \xi = 0.05$	0.9829
	E	$\varepsilon = \phi = \delta = 0.05$	3.0004
III	A	$\varepsilon = \phi = \delta = \xi = 0.10$	0.4627
	B	$\phi = \delta = \xi = 0.10$	0.5141
	C	$\varepsilon = \delta = \xi = 0.10$	0.4878
	D	$\varepsilon = \phi = \xi = 0.10$	0.4753
	E	$\varepsilon = \phi = \delta = 0.10$	2.7310
IV	A	$\varepsilon = \phi = \delta = \xi = 0.15$	0.2640
	B	$\phi = \delta = \xi = 0.15$	0.3106
	C	$\varepsilon = \delta = \xi = 0.15$	0.2864
	D	$\varepsilon = \phi = \xi = 0.15$	0.2746
	E	$\varepsilon = \phi = \delta = 0.15$	2.4760

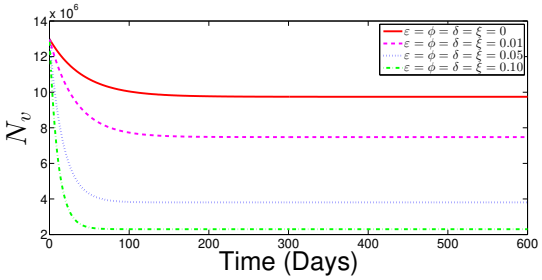
It is seen in Table II that for all the various levels of control implementation, intervention A most impacts $\mathcal{R}_c$, followed by intervention D, then intervention C, intervention B, and lastly intervention E.

A. Intervention A: Use of ε, ϕ, δ and ξ

Fig. 2 demonstrates the dynamical behaviours of dengue prevalence (that total number of infected individuals) in human population and the total mosquito population without and with the implementation of combined efforts of controls ε, ϕ, δ and ξ. It is seen from Fig. 2a that, the use of about 5% of each control is enough to sustain the total number of human infections at zero throughout the intervention period. Also, with the same level of controls, the size of the total female mosquito population decreases by 75% at the 50th day, and the size is consistently maintained over the remaining intervention period as shown in Fig. 2b. Hence, using this intervention strategy, it is possible to flatten the dengue epidemic curve if about 5% of the population comply with the use of ITNs, exposed individuals are early detected and timely treatment is given to about 5% of the latent patients, about 5% of the symptomatic dengue infection carriers is given timely treatment, and open space spray of adulticide is conducted at about 5% of the residential areas in a community. The use of the intervention could also lead to the eradication of female Aedes aegypti mosquitoes.



(a) Dengue prevalence in human population



(b) Total mosquito population

Fig. 2: Simulated results of the dengue model (3) showing the effect of combined use of controls ε, ϕ, δ and ξ

B. Intervention B: Use of controls ϕ, δ and ξ

This strategy implements the combined efforts of controls ϕ, δ and ξ to reduce the spread of dengue in interacting human and mosquito populations. The behaviours of the graphical results obtained for the dengue prevalence in human population and the total mosquito population are similar to those given in Figs. 2a and 2b respectively, and are therefore omitted. Using 5% of each controls involved in this intervention strategy is sufficient for dengue elimination in the population.

C. Intervention C: Use of controls ε, δ and ξ

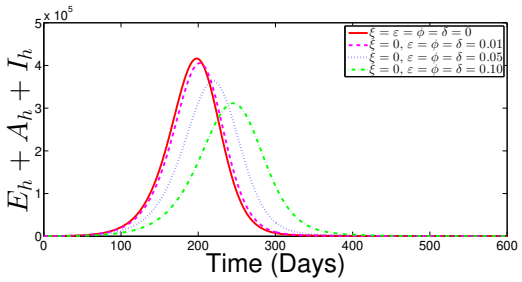
To curtail the transmission of dengue in a community, an intervention strategy which simultaneously apply controls ε, δ and ξ is considered. Similar to the results provided in Figs. 2a and 2b are obtained for the total numbers of infected humans and mosquitoes. Therefore, the graphical solutions and their discussions for this strategy are not presented here. Implementing 5% effort of each controls considered for this intervention strategy is sufficient to eliminate dengue prevalence in the population.

D. Intervention D: Use of controls ε, ϕ and ξ

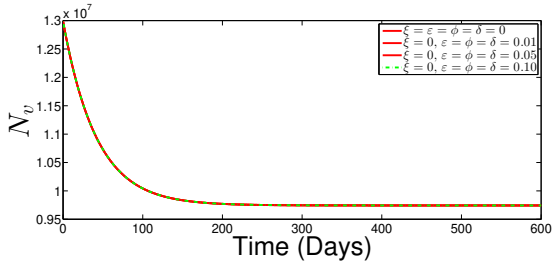
Effect of applying the combined efforts of controls ε, ϕ and ξ in controlling dengue spread in interacting human and mosquito populations is examined in this case. The graphical solutions of the total number of infected human and mosquito population are similar to the results presented for intervention

A (as shown in Figs. 2a and 2b respectively). For this reason, the results obtained for this intervention are omitted. Following the simultaneous implementation of the controls considered in this intervention strategy, dengue prevalence is eliminated in the population.

E. Intervention E: Use of controls ε, ϕ and δ



(a) Dengue prevalence in human population



(b) Total mosquito population

Fig. 3: Simulated results of the dengue model (3) showing the effect of combined use of controls ε, ϕ and δ

The behaviours of the number of infected humans and total mosquito population with and without implementing the control intervention which combines the efforts of controls ε, ϕ and δ is illustrated in Fig. 3. From Fig. 3a, it is observed that the peak of dengue prevalence in human population is continuously reduced with increased effort of each control and the time needed for the disease to peak is also delayed, but not enough to flatten dengue epidemic curve by implementing this control intervention. Furthermore, Fig. 3b shows that this control intervention strategy (which excludes any control efforts that aim at mosquito reduction) has no significant effect on the dynamics of the total mosquito population. Consequently, female *Aedes aegypti* mosquitoes could not be eradicated leading to the slow response and insufficiency of the control intervention in eliminating dengue prevalence in the population as DENV remains in the human population.

It follows from the results of this intervention strategy (as shown in Fig. 3) that the use of the strategy is not as effective as applying any of interventions A–D (see Fig. 2). This indicates the importance of including a vector control intervention (adulticide) that directly targets the reduction of mosquito population in dengue control plan.

F. Efficiency analysis

To compare the control interventions A–E, efficiency analysis is performed. This helps us in our decision making on the best control intervention strategy. Following [4], we compare the effects of various possible strategies in reducing dengue prevalence (including exposed, asymptomatic and symptomatic infected individuals) in a population. To this aim, the efficiency index is defined as [4]:

$$\Delta = \left(1 - \frac{\Delta_1}{\Delta_2}\right) \times 100, \tag{16}$$

where $\Delta_1 = \int_0^{t_f} (E_h + A_h + I_h)dt$ and $\Delta_2 = \int_0^{t_f} (E_h + A_h + I_h)dt$ measure the cumulated number of infected individuals (dengue prevalence) in the time interval $[0, t_f]$ with and without any control intervention respectively. So, a control intervention with the biggest Δ value will be the best intervention strategy [4].

Using the results obtained from the numerical implementations of interventions A–E (as shown in Figs. 2 and 3), and considering the control parameter values $\varepsilon = \delta = \phi = \xi = 0.10$, the results of effectiveness analysis are summarized in Table III.

TABLE III: EFFICIENCY INDEX

Intervention	Δ_1	Δ (%)
No control	3.5285×10^7	0
A	9.4846×10^3	99.9731
B	1.1076×10^4	99.9686
C	1.0049×10^4	99.9715
D	9.7552×10^3	99.9724
E	3.3850×10^7	4.0669

From Table III, it follows that intervention strategy A (combination of controls ε, ϕ, δ, and ξ) most averts/reduces the number of dengue infections in the population, followed by intervention strategy D (combination of controls ε, ϕ, and ξ), then intervention strategy C (combination of controls ε, δ, and ξ), intervention strategy B (combined efforts of controls ϕ, δ, and ξ), and finally intervention strategy E (combination of controls ε, ϕ and δ). This ranking of the five intervention strategies in terms of their efficacy is consistent with their impacts on $\mathcal{R}_c$ as shown in Table II.

IV. Conclusion

In this work, an autonomous system governing dengue disease transmission and control, which includes four different control parameters accounting for treatment rates for exposed and infectious individuals, the use of ITNs, and the effort of spraying insecticide has been developed and analysed to gain insight into the impact of using various control combination strategies in a way to effectively reduce dengue in a community.

Qualitative analysis of the model indicates that the model admits one DFE, $\mathcal{E}_0$, which is LAS if the effective reproduction number $\mathcal{R}_c$ satisfies $\mathcal{R}_c < 1$, and unstable if $\mathcal{R}_c > 1$. The

numerical values obtained for $\mathcal{R}_c$ show that $\mathcal{R}_c$ considerably decreases with increasing levels of the four control intervention measures analysed. The simulated results show that implementation of any of the control interventions considered in this paper can lead to the elimination of dengue prevalence in the population (particularly when adulticide is integrated into the control plan), where $\mathcal{R}_c$ is mostly decreased using intervention A (which combines the efforts of ITNs, treatment controls of exposed and infectious humans, and open space spray of adulticide), followed by interventions D (which combines ITNs control with efforts of treatment of exposed humans and adulticide controls), C (including the use of ITNs, treatment of infectious humans and use of adulticide), B (which combines treatment of exposed and infectious humans and adulticide controls), and E (which combines the efforts of controls ITNs and treatment of exposed and infectious humans). We therefore conclude that a control strategy that considers both human prevention and vector control measures may be sufficient to eliminate dengue in a population.

In the present study, it has been shown that application of combined control interventions may be the highest promise for successful long-term dengue control strategy. To this end, we aim to develop a non-autonomous version of the dengue model proposed in this work to obtain the optimal combination of control strategies to effectively minimize dengue spread in a population by employing optimal control theory in the future work.

REFERENCES

[1] M. Zhu, Z. Lin, and L. Zhang, "Spatial-temporal risk index and transmission of a nonlocal dengue model," *Nonlinear Analysis: Real World Applications*, vol. 53, p. 103076, 2020.

[2] A. K. Srivastav and M. Ghosh, "Assessing the impact of treatment on the dynamics of dengue fever: A case study of india," *Applied Mathematics and Computation*, vol. 362, p. 124533, 2019.

[3] K. O. Douglas, S. K. Dutta, B. Martina, F. Anfasa, T. Samuels, and M. G.-S. Hilaire, "Dengue fever and severe dengue in Barbados, 2008–2016," *Tropical Medicine and Infectious Disease*, vol. 5, no. 2, p. 68, 2020.

[4] S. A. Carvalho, S. O. da Silva, and I. da Cunha Charret, "Mathematical modeling of dengue epidemic: control methods and vaccination strategies," *Theory in Biosciences*, vol. 138, no. 2, pp. 223–239, 2019.

[5] A. Abidemi, M. I. Abd Aziz, and R. Ahmad, "The impact of vaccination, individual protection, treatment and vector controls on dengue," *Engineering Letters*, vol. 27, no. 3, pp. 613–622, 2019.

[6] N.-F. Mazlan, L. L. Tan, M. I. H. Reza, G. C. Ta, N. H. Abd Karim, and L. Y. Heng, "Managing dengue disaster: Uncovering paramount community elements for dna sensory tool accessibility in Malaysia," *Sains Malaysiana*, vol. 49, no. 4, pp. 743–754, 2020.

[7] G. R. Phaijoo and D. B. Gurung, "Mathematical model of dengue disease transmission dynamics with control measures," *Journal of Advances in Mathematics and Computer Science*, vol. 23, no. 3, pp. 1–12, 2017.

[8] I. Ghosh, P. K. Tiwari, and J. Chattopadhyay, "Effect of active case finding on dengue control: Implications from a mathematical model," *Journal of Theoretical Biology*, vol. 464, pp. 50–62, 2019.

[9] WHO, "Dengue and severe dengue," Accessed 10 August 2020. [Online]. Available: https://www.who.int/en/news-room/fact-sheets/detail/dengue-and-severe-dengue

[10] O. J. Brady and S. I. Hay, "The global expansion of dengue: How aedes aegypti mosquitoes enabled the first pandemic arbovirus," *Annual Review of Entomology*, vol. 65, pp. 191–208, 2020.

[11] G. Zhu, T. Liu, J. Xiao, B. Zhang, T. Song, Y. Zhang, L. Lin, Z. Peng, A. Deng, W. Ma *et al.*, "Effects of human mobility, temperature and mosquito control on the spatiotemporal transmission of dengue," *Science of the Total Environment*, vol. 651, pp. 969–978, 2019.

[12] H. Abboubakar, J. C. Kamgang, and D. Tieudjo, "Backward bifurcation and control in transmission dynamics of arboviral diseases," *Mathematical Biosciences*, vol. 278, pp. 100–129, 2016.

[13] Q. Jing and M. Wang, "Dengue epidemiology," *Global Health Journal*, vol. 3, no. 2, pp. 37–45, 2019.

[14] G. G. Baaten, G. J. Sonder, H. L. Zaaijer, T. van Gool, J. A. Kint, and A. van den Hoek, "Travel-related dengue virus infection, the netherlands, 2006–2007," *Emerging Infectious Diseases*, vol. 17, no. 5, pp. 821–827, 2011.

[15] Y. S. Kusuma, D. Burman, R. Kumari, A. S. Lamkang, and B. V. Babu, "Impact of health education based intervention on community's awareness of dengue and its prevention in delhi, india," *Global Health Promotion*, vol. 26, no. 1, pp. 50–59, 2019.

[16] A. Abidemi and N. A. B. Aziz, "Optimal control strategies for dengue fever spread in Johor, Malaysia," *Computer Methods and Programs in Biomedicine*, vol. 196, p. 105585, 2020.

[17] Ministry of Health Malaysia, "Health facts 2014," Accessed 15 March 2019. [Online]. Available: http://www.moh.gov.my

[18] R. Jan, M. A. Khan, and J. F. Gómez-Aguilar, "Asymptomatic carriers in transmission dynamics of dengue with control interventions," *Optimal Control Applications and Methods*, vol. 41, no. 2, pp. 430–447, 2020.

[19] H. Abboubakar, J. C. Kamgang, L. N. Nkamba, and D. Tieudjo, "Bifurcation thresholds and optimal control in transmission dynamics of arboviral diseases," *Journal of Mathematical Biology*, vol. 76, no. 1-2, pp. 379–427, 2018.

[20] F. B. Agusto and M. C. A. Leite, "Optimal control and cost-effective analysis of the 2017 meningitis outbreak in Nigeria," *Infectious Disease Modelling*, vol. 4, pp. 161–187, 2019.

[21] P. van den Driessche and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission," *Mathematical Biosciences*, vol. 180, no. 1, pp. 29–48, 2002.