Deterministic Models in Dengue Transmission Dynamics

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Abstract

A deterministic model for monitoring the impact of treatment on the transmission dynamics of dengue in the human and vector populations is presented. In addition to having a locally-asymptotically stable disease-free equilibrium (DFE) whenever the basic reproduction number is less than unity, it is shown, using a Lyapunov function and LaSalle Invariance Principle that the DFE of both treatment-free and treatment model, in the absence of dengue-induced mortality, is globally-asymptotically stable whenever the reproduction number is less than unity. Each of the models has a unique endemic equilibrium whenever its reproduction number exceeds unity. Numerical simulations of the model show that for high treatment rates, the disease can be controlled within a community.

Introduction

Dengue hemorrhagic fever (DHF) was first recognized in the Philippines in 1953, and in Thailand in 1955 (Esteva [12], Gubler [19], WHO [32]). It has become the most important arthropod-borne viral disease of humans that is endemic in many countries in Southeast Asia, the Americas, the Africa, the Eastern Mediterranean, and the Western Pacific (Chowell et. al[8], Shekhar [28]). Currently, the annual estimations of dengue fever range from 50 to 100 million cases yearly (Monath [27]), with approximately 20,000 deaths globally (Shekhar [28]). Figures from the World Health Organization show that hundreds of thousands of cases of DHF are recorded annually (Blaney [3,4], WHO [33]). Cases of dengue range from asymptomatic to clinically non-specific flu-like symptoms to dengue fever (DF) to dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). DHF and DSS are the most severe form of dengue disease with an average case-fatality rate being approximately 17%. Many primary dengue infections are asymptomatic.

The disease is caused by any of four closely-related virus serotypes (DEN-1-4) of the genus Flavivirus, and is transmitted by its principle mosquito mainly Aedes aegypti. Aedes aegypti is a highly anthropophilic daytime feeder, living around densely populated human habitat (Chowell [8]). Susceptible female mosquitoes acquire the infection when feeding on infectious humans. Susceptible humans are infected when bitten by feeding infectious female (Yang [34]).

There is no specific treatment for dengue. Persons with dengue fever should rest and drink plenty of fluids. They should be kept away from mosquitoes for the protection of others. At present, the treatment strategy of dengue fever consists of the following: (i) The Hemopurifier, which has been designed to isolate and capture highly pathogenic viruses and emerging viral threats, it represents the only proposed treatment for OHF that simultaneously targets broad-strain clearance of dengue virus and also assists in the modulation of excessive cytokine activity. (ii) Antipyretics-aspirin and nonsteroidal anti-inflammatory drugs such as ibuprofen should be avoided so that platelet function will not be impaired. (iii) Monitoring of blood pressure, urine output, hematocrit, platelet count, and level of consciousness.

Numerous mathematical models have been developed in the literature to gain insights into the transmission dynamics of dengue in a community (see, for instance, Chowell et. al [8], Coutinho [9], Derouich [10], Esteva [11,12,13 and 14], Feng [15], Ferguson et. al [16], Garba [17, 18], Struchiner et. al [29], Tewa et. al [30], Yang [34]). While Chowell et al. [8] estimated the basic reproduction number of dengue using spatial epidemic data. Tewa et al. [30] established global asymptotic stability of the equilibria of a single-strain dengue model. Garba et al. [17] investigate the qualitative dynamics of a single strain dengue model in the presence of an imperfect vaccine, the authors [18] also consider the effect of cross-immunity on the transmission dynamics of two...
strains of dengue, and Struchiner et al. [29] gave a
detailed discussion on current research issues in
modelling mosquito-borne diseases.

This paper complement, and extends, the
aforementioned studies by considering a new
mathematical model which incorporates the
dynamics of individuals and vectors who are
asymptotically infected to the disease (that is,
individuals that are infected but not yet infectious
are assumed capable of transmitting the disease).

Basic model

The basic dengue treatment model to be designed is
based on subdividing the total human population at
time $t$, denoted by $N_h(t)$, into a number of
mutually-exclusive compartments namely,
susceptible ($S_h(t)$), asymptotically infected
($A_h(t)$), symptomatic infected ($I_h(t)$), treated
individuals ($T_h(t)$) and individuals in whom
treatment fails ($F_h(t)$), so that

$$N_h(t) = S_h(t) + A_h(t) + I_h(t) + T_h(t) + F_h(t).$$

Similarly, the total vector population at time $t$,
denoted by $N_v(t)$, is split into susceptible ($S_v(t)$),
exposed ($E_v(t)$), and infectious mosquitoes ($I_v(t)$), so that

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

The susceptible human population is increased by
the recruitment of individuals into the population at
a rate $\Pi_h$. These individuals acquire infection,
following contact with exposed or infectious
vectors in the $E_v$ and $I_v$ classes, at a rate $\lambda_h$
where

$$\lambda_h = C_{hv} \left( N_h(t), N_v \right) \frac{\eta_v E_v(t) + I_v(t)}{N_v(t)}.$$  \hspace{2cm} (1)

The parameter $C_{hv}$ is the effective contact rate
between the susceptible humans and infectious
mosquitoes, while $\eta_v$ is the modification
parameter $0 < \eta_v < 1$ accounts for the assumed
reduction in transmissibility of exposed mosquitoes
relative to infectious mosquitoes. Noting that for
the number of bites to be conserved, the following
equation must hold (Garba [17]),

$$C_{hv} N_v = C_{hv} \left( N_h(t), N_v \right) N_v.$$  \hspace{2cm} (2)

where $C_{hv}$ is the effective contact rate between
infectious humans and susceptible mosquitoes, so that,

$$N_v = \frac{C_{hv} \left( N_h(t), N_v \right) N_v}{C_{hv} N_v}.$$  \hspace{2cm} (3)

Thus, substituting (3) in (1), gives

$$\lambda_h = C_{hv} \frac{\eta_v E_v(t) + I_v(t)}{N_v(t)}.$$  \hspace{2cm} (4)

Similarly, it can be shown that the rate at which
mosquitoes become infected denoted by $\lambda_v$ is
given by,

$$\lambda_v = C_{hv} \frac{\eta_h A_h(t) + I_h(t) + \eta_h F_h(t)}{N_v(t)}.$$  \hspace{2cm} (5)

The parameter $0 \leq \eta_i \leq 1$ accounts for the assumed
reduced infectiousness of asymptotically infected
individuals, while $\eta_v \geq 0$ is the relative
risk of infectiousness of individuals who fail
treatment. It is assumed that newly-infected
individuals are asymptotically infected before
clinical symptoms, after which they become
symptomatically infected (Yang [34]). It is worth
stating that since the focus of the paper is to
evaluate treatment strategies of dengue that target
individuals who are symptomatically infected,
transition to or from $A_h$ to $T_h$ is not incorporated;
this is needed to help keep track of the infection
and treatment stages. It is assumed that the
population of symptomatically infected humans is
generated by the infection of susceptible humans
(at the rate $\lambda_h$) and diminished by development
of clinical symptoms (at a rate $\sigma_h$) and natural
death (at a rate $\mu_h$). Symptomatically infected individuals
are generated via the development of symptoms by
asymptotically infected humans (at the rate $\eta_h$),
these population is reduced following
treatment (at a rate $\beta_h$) and moved to the treated
class ($T_h$), while those who fail treatment move to
the class ($F_h$) (at a rate $\gamma_h$). All human population
suffer natural death (at the rate $\mu_h$). Furthermore,
infected individuals in the $I_h$ and $F_h$ class suffer
an additional dengue disease-induced death (at a
rate $\alpha_h$). It is assumed that treated individuals
acquire lifelong immunity against re-infection (so
that they do not acquire infection again). Individuals in
$F_h$ class fail treatment for various reason including non-compliance to the treatment
or development of resistance. In other words,
individuals in $F_h$ class may have (and can
transmit) dengue resistant strain. For mathematical convenience, we are not considering multiple strain dynamics.

The susceptible mosquitoes are generated by birth (at a rate \( \Pi_f \)) and diminished by infection, following effective contact with infectious human (at the rate \( \lambda_f \)), and due to natural death (at a rate \( \mu_f \)). All vectors suffer natural death (at the rate \( \mu_v \)), and infectious vector suffer additional dengue disease-induced death (at a rate \( \delta_v \)). Finally, the insecticide to eliminate the adult mosquitoes, which is applied inside and surrounding houses (in severe epidemic situations heavy duty application of insecticide can be used), is assessed by the additional mortality rate to all vectors population (at a rate \( \nu_v \)). The model is given by the following system of differential equations (see Figure 1 for a flow diagram)

\[\begin{align*}
\frac{dS_H}{dt} &= \Pi_H - \lambda_H S_H - \mu_H S_H, \\
\frac{dA_H}{dt} &= \lambda_H S_H - (\sigma_H + \mu_H) A_H, \\
\frac{dI_H}{dt} &= \sigma_H A_H - (\epsilon_H + \mu_H + \delta_H) I_H, \\
\frac{dR_H}{dt} &= \epsilon_H I_H - (\mu_H + \delta_H) R_H, \\
\frac{dS_V}{dt} &= \Pi_V - \lambda_V S_V - (\mu_V + \nu_V) S_V, \\
\frac{dA_V}{dt} &= \lambda_V S_V - (\sigma_V + \mu_V + \nu_V) A_V, \\
\frac{dI_V}{dt} &= \sigma_V A_V - (\epsilon_V + \mu_V + \nu_V + \delta_V) I_V, \\
\frac{dR_V}{dt} &= \epsilon_V I_V - (\mu_V + \nu_V + \delta_V) R_V.
\end{align*}\]

It is assumed that all the parameters and stated variables of the model are non-negative (since the model monitors human and vector populations) for all \( t \geq 0 \).

**Basic properties**

In this section, the basic dynamical features of the model will be explored. We claim the following: The closed set

\[D = \left\{ (S_H, A_H, I_H, T_H, F_H, S_V, A_V, I_V) \in \mathbb{R}^8 : \begin{array}{l}
S_H + A_H + I_H + T_H + F_H \leq \frac{\Pi_H}{\mu_H} - \frac{\Pi_V}{\mu_V + \nu_V}, \\
S_V + A_V + I_V \leq \frac{\Pi_V}{\mu_V + \nu_V},
\end{array} \right\}
\]

is positively-invariant and attracting with respect to the basic model.

Thus, in \( D \), the model is well-posed epidemiologically and mathematically (Hethcote [20]). Hence, it is sufficient to study the dynamics of the basic model in \( D \).

**Treatment-free model**

Before analyzing the full model, we first consider the treatment-free model, obtained by setting \( \tau_H = \tau_H = T_H = F_H = 0 \) in (5). Further, since data suggest that the dengue-induced mortality in human is negligible (Kawaguchi [22]), we set the mortality parameter to zero (i.e., \( \delta_H = 0 \)). Thus,

\[\frac{dN_H}{dt} = \Pi_H - \mu_H N_H, \]

so that the total human population is constant at steady-state give the following reduced model.

\[\begin{align*}
\frac{dS_H}{dt} &= \Pi_H - \lambda_H S_H - \mu_H S_H, \\
\frac{dA_H}{dt} &= \lambda_H S_H - (\sigma_H + \mu_H) A_H, \\
\frac{dI_H}{dt} &= \sigma_H A_H - (\epsilon_H + \mu_H) I_H, \\
\frac{dR_H}{dt} &= \epsilon_H I_H - (\mu_H + \delta_H) R_H, \\
\frac{dS_V}{dt} &= \Pi_V - \lambda_V S_V - (\mu_V + \nu_V) S_V, \\
\frac{dA_V}{dt} &= \lambda_V S_V - (\sigma_V + \mu_V + \nu_V) A_V, \\
\frac{dI_V}{dt} &= \sigma_V A_V - (\epsilon_V + \mu_V + \nu_V + \delta_V) I_V, \\
\frac{dR_V}{dt} &= \epsilon_V I_V - (\mu_V + \nu_V + \delta_V) R_V.
\end{align*}\]

It can be shown that the biologically-relevant region

\[\Gamma = \left\{ (S_H, A_H, I_H, S_V, A_V, I_V) \in \mathbb{R}^6 : \begin{array}{l}
S_H + A_H + I_H \leq \frac{\Pi_H}{\mu_H}, \\
S_V + A_V + I_V \leq \frac{\Pi_V}{\mu_V + \nu_V}
\end{array} \right\}
\]

is positively-invariant and attracting with respect to treatment-free model.

**Disease-free equilibrium (DFE)**

The disease-free equilibrium (DFE) of treatment-free model (5) is given by

\[E_0 = (S_H, A_H, I_H, S_V, A_V, I_V) = \left[ \begin{array}{c}
\frac{\Pi_H}{\mu_H}, 0, 0, \frac{\Pi_V}{\mu_V + \nu_V}, 0, 0
\end{array} \right]
\]

Following Vanden [31], the linear stability of \( E_0 \) can be established using the next generation operator method on system. The matrices, \( F_1 \) (for the new infection terms) and \( V_1 \) (of the transition terms) are given, respectively, by
\[ F_1 = \begin{bmatrix} 0 & 0 & C_{AB} \mu_h & C_{HV} \\ \frac{\mu_h e^{-\lambda_s} S}{T_1} & \frac{\mu_h e^{-\lambda_s} S}{T_1} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \]

\[ V_1 = \begin{bmatrix} T_1 & 0 & 0 & 0 \\ -\sigma_h & \mu_h & 0 & 0 \\ 0 & 0 & T_2 & 0 \\ 0 & 0 & -\sigma_v & T_3 \end{bmatrix} \]

where,

\[ T_1 = \sigma_h + \mu_h, \quad T_2 = \sigma_v + \mu_v + \nu_v \]

and \[ T_3 = \mu_v + \nu_v + \delta_v. \]

It then follows that the basic reproduction number, denoted by \( R_0 \), is given by

\[ R_0 = \rho(F_1 V_1^{-1}) = \sqrt{\frac{C_{AB} \Pi_h (\eta_h \mu_h + \sigma_h) \eta_v T_3 + \sigma_v}{\Pi_h (\mu_v + \nu_v) T_1 T_2 T_3}}, \]

where \( \rho \) is the spectral radius (dominant eigenvalue in magnitude) of the next generation matrix \( F_1 V_1^{-1} \). Hence, using Theorem 2 of Vanden [31], we have established the following result:

**Lemma 2** The disease free equilibrium, \( E_0 \), of the model (5), is locally asymptotically stable (LAS) if \( R_0 < 1 \), and unstable if \( R_0 > 1 \).

The threshold quantity \( R_0 \) is the basic reproduction number of the disease (Anderson [1, 2] and Hethcote [21]). It represents the average number of secondary cases that one infected case can generate if introduced into a completely susceptible population. It can be interpreted as follows. Susceptible mosquitoes can acquire infection following effective contact with either an asymptotically infected human (\( I_h \)) or symptomatically infected humans (\( I_v \)). The number of vector infections generated by an asymptotically infectious human (near the DFE) is given by the product of the infection rate \( C_{i-C} \eta_h \mu_h / \Pi_h \) and the average duration in the \( A_H \) class \( 1/T_1 \). Furthermore, the number of vector infections generated by an infectious human (near the DFE) is given by the product of the infection rate of infectious humans \( C_{i-C} \eta_h \mu_h / \Pi_h \), the probability that an asymptotically infectious human survives the asymptomatic stage and move to the symptomatic infectious stage \( \sigma_h / T_1 \) and the average duration in the infectious stage \( (1/\nu_v) \). Thus, the average number of new mosquito infections generated by infected humans (asymptomatically or symptomatically) is given by (noting that \( S_0 = \Pi_h / (\mu_h + \nu_v) \))

\[ C_{HV} \left( \frac{\eta_h \mu_h + \sigma_h}{} \Pi_h \right) \]

Similarly, susceptible humans acquire infection following effective contact with either an exposed (\( E_v \)) or infectious mosquito (\( I_v \)). The number of human infections generated by an exposed mosquito is the product of the infection rate of exposed mosquito \( C_{i-C} \eta_v \mu_h / \Pi_h \) and the average duration in the exposed class \( 1/T_v \). The number of human infections generated by an infectious mosquito is the product of the infection rate of infectious mosquitoes \( C_{i-C} \mu_h / \Pi_h \), the probability that an exposed mosquito survives the exposed class and move to the infectious stage \( \sigma_v / T_3 \) and the average duration in the infectious stage \( (1/T_v) \). Thus, the average number of new human infections generated by an infected mosquito (exposed or infectious) is given by (noting that \( S_0 = \Pi_i / \mu_i \))

\[ C_{HV} \left( \frac{\eta_v T_3 + \sigma_v}{} \Pi_v \right) \]

The geometric mean of (6) and (7) gives the basic reproduction number, \( R_0 \) (interpretation for \( R_0 \) for dengue disease is also given in Chowell [8], Esteva [11]).

The epidemiological implication of Lemma 2 is that, in general, when \( R_0 \) is less than unity, a small influx of infected mosquitoes into the community would not generate large outbreaks, and the disease dies out in time (since the DFE is LAS).

**Global stability of disease-free equilibrium**

**Theorem 1**

The disease-free equilibrium \( E_0 \) of the treatment-free model is globally asymptotically stable (GAS) if \( R_0 < 1 \).

**Proof:** the proof is based on using the following Lyapunov function.
\[ f = g_1 A_H + g_2 I_H + g_3 E_V + g_4 I_V \]

Where,
\[ g_1 = C_{mv} \Pi_H T_3 (\eta_H T_3 + \sigma_{HV})(\eta_H \mu_H + \sigma_H), \]
\[ g_2 = C_{mv} \Pi_H T_3 (\eta_H T_3 + \sigma_{HV}), \]
\[ g_3 = \Pi_H \mu_V T_3 R_0 (\eta_V T_3 + \sigma_V), \]
\[ g_4 = \Pi_H \mu_H T_3 T_2 R_0. \]

The Lyapunov derivatives is given by (where a dot represent differentiation with respect to \( t \))
\[ \dot{f} = g_1 \dot{A}_H + g_2 \dot{I}_H + g_3 \dot{E}_V + g_4 \dot{I}_V. \]

Thus \( \dot{f} \leq 0 \) if \( \mathcal{R}_0 \leq 1 \) with \( \dot{f} = 0 \) if and only if \( A_H = I_H = E_V = I_V = 0 \). Further, the largest compact invariant set in \( \{(S_H, A_H, I_H, E_V, I_V) \in \Gamma : \dot{f} = 0\} \) is the singleton \( \{E_0\} \). It follows from LaSalle Invariance Principle that every solution to equation (5) with initial condition in \( \Gamma \) converges to DFE \( E_0 \) as \( t \to \infty \). That is, \( (A_H(t), I_H(t), E_V(t), I_V(t), T(t)) \to (0, 0, 0, 0, 0) \) as \( t \to \infty \). Substituting \( A_H = I_H = E_V = I_V = 0 \) into the first and the fourth equations of the treatment-free model (5) gives \( S_H(t) \to S_H^0 \) and \( S_V(t) \to S_V^0 \) as \( t \to \infty \). Thus:
\[ (S_H(t), A_H(t), I_H(t), E_V(t), I_V(t), T(t)) \to (S_H^0, 0, S_V^0, 0, 0) \]

as \( t \to \infty \) for \( \mathcal{R}_0 < 1 \), so that \( E_0 \) is GAS in \( \Gamma \) if \( \mathcal{R}_0 \leq 1 \).

The above result show that, for the model, dengue disease can be eliminated from the community if the associated threshold quantity, \( \mathcal{R}_0 \), can be brought to a value less than unity. It also shows that, for the dengue treatment-free model, the classical epidemiological requirement of \( \mathcal{R}_0 < 1 \) is both necessary and sufficient for dengue elimination from the community.

**Endemic equilibrium**

The non-trivial equilibria of the model, where at least one of the infected variables is non-zero, can be obtained by solving the equations at steady state. Let \( E''_0 = (S''_H, A''_H, I''_H, S''_V, E''_V, I''_V) \) represents any arbitrary endemic equilibrium of the model. Further, let
\[ \lambda''_H = C_{mv} \mu_H \eta_H E''_H / \Pi_H \]
\[ \lambda''_V = C_{mv} \mu_H \eta_H E''_V / \Pi_H \]
be the forces of infection in humans and vectors at steady state, respectively. Solving the equations of the model at steady state gives
\[ S''_H = \frac{\Pi_H}{\lambda''_H + \mu_H}, \quad A''_H = \frac{\lambda''_H \Pi_H}{\lambda''_H + \mu_H}, \]
\[ I''_H = \frac{\mu_H \Pi_L}{\lambda''_H + \mu_H}, \quad S''_V = \frac{\Pi_L}{\sigma_{HV}(\lambda''_H + \mu_H)}, \]
\[ E''_V = \frac{\sigma_{HV} \lambda''_H \Pi_L}{\lambda''_H + \mu_H + \nu_V} \]

Non-existence of endemic equilibria for \( \mathcal{R}_0 \leq 1 \)

In this section, the non-existence of endemic equilibria of the model when \( \mathcal{R}_0 \leq 1 \), will be explored. We claim the following:

**Theorem 2** The dengue treatment-free model, given by (5), has no endemic equilibrium when \( \mathcal{R}_0 \leq 1 \)

Proof Using (9) in the expression for \( \lambda''_H \) and \( \lambda''_V \) in (8) and simplifying shows that the non zero (endemic) equilibria of the model satisfy the following linear equation
\[ a_1 \lambda''_H + b_1 = 0, \]
where
\[ a_1 = \Pi_H \mu_H T_2 T_3 \left(C_{mv} + \mu_H + \sigma_H \right), \]
and \[ b_1 = \Pi_H \mu_H \sigma_{HV} T_2 T_3 (1 - \mathcal{R}_0^2) \]

It is clear that \( a_1 > 0, \) and \( b_1 < 0 \) whenever \( \mathcal{R}_0 > 1 \). Thus, the basic linear system has a unique positive solution, given by \( \lambda''_H = b_1 / a_1 \) whenever \( \mathcal{R}_0 > 1 \). Therefore the treatment-free model, has a unique positive endemic equilibrium whenever \( \mathcal{R}_0 > 1 \), and no positive endemic equilibrium whenever \( \mathcal{R}_0 \leq 1 \).

**Analysis of the treatment model**

Consider, now, the full treatment model, given by with similar assumption of dengue-induced mortality rate negligible (\( \delta = 0 \)). Setting \( \mathcal{R}_m = \Pi_H / \mu_H \) and \( \delta = 0 \) in model (4) gives the following reduced model:
\[ \frac{dS_H}{dt} = \Pi_H - \lambda_H S_H - \mu_H S_H, \]
\[ \frac{dA_H}{dt} = \lambda_H S_H - (\sigma_H + \mu_H) A_H, \]
\[ \frac{dI_H}{dt} = \sigma_H A_H - (\tau_H + \mu_H + \delta_H) I_H, \]
\[ \frac{dT_H}{dt} = \tau_H S_H - (\gamma_H + \mu_H + \delta_H) T_H, \]
\[ \frac{dF_H}{dt} = \gamma_H T_H - (\mu_H + \delta_H) F_H, \]
\[ \frac{dS_V}{dt} = \Pi_V - \lambda_V S_V - (\mu_V + \nu_V) S_V, \]
\[ \frac{dE_V}{dt} = \lambda_V S_V - (\sigma_V + \mu_V + \nu_V) E_V, \]
\[ \frac{dI_V}{dt} = \sigma_V E_V - (\mu_V + \nu_V + \delta_V) I_V. \]

(10)

Hence, using Theorem 2 of Vanden [31], we have established the following result:

**Lemma 3** The disease free equilibrium, \( E_r \), of the model is locally asymptotically stable (LAS) if \( R_r < 1 \), and unstable if \( R_r > 1 \).

**Global Stability of disease-free equilibrium**

The disease-free equilibrium, \( E_r \), of the treatment model, is globally asymptotically stable (GAS) in \( D \) if \( R_r \leq 1 \).

The proof is based on using a comparison theorem. Notice, first of all, that the equations for the infected components in \( \beta \) can be written in terms of \( \beta V \) matrix.

**Endemic equilibrium**

In order to find endemic equilibria of the treatment model (that is, equilibria where at least one of the infected components of the model is non-zero), the following steps are taken. Let

\[ E^* = \left( S_H^*, A_H^*, I_H^*, T_H^*, F_H^*, S_V^*, E_V^*, I_V^* \right) \]

represents any arbitrary endemic equilibrium of the model. Further, let

\[ \lambda^*_H = C_{ir} \frac{\eta_H E^*_H + I^*_H}{\Pi_H} \]
and

\[ \lambda^*_V = C_{ir} \frac{\eta_V A^*_V + I^*_V + \nu_V F^*_V}{\Pi_V} \]

(11)

be the forces of infection of humans and vectors at steady state, respectively. Solving the equations in (10) at steady state gives

\[ S_H^* = \frac{\Pi_H}{\lambda^*_H + \mu_H}, \quad A_H^* = \frac{\lambda^*_H \Pi_H}{P \lambda^*_H + \mu_H}, \]
\[ I_H^* = \frac{\sigma_H \lambda^*_H \Pi_H}{P \lambda^*_H + \mu_H}, \quad T_H^* = \frac{\tau_H \sigma_H \lambda^*_H \Pi_H}{P \lambda^*_H + \mu_H}, \]
\[ F_H^* = \frac{\tau_H \lambda^*_H \Pi_H}{P \lambda^*_H + \mu_H}, \quad S_V^* = \frac{\Pi_V}{\lambda^*_V + \mu_V + \nu_V}, \]
\[ I_V^* = \frac{\sigma_V \lambda^*_V \Pi_V}{\lambda^*_V + \mu_V + \nu_V}. \]

(12)

Substituting the expressions in (12) into (11), and simplifying, it follows that the non-zero equilibria
of the treatment model satisfy the quadratic
\[ \lambda_H^w (a_{22} \lambda_H^w + b_{22}) = 0, \]
where,
\[ a_{22} = \prod_{j} P_1 P_2 P_3 \left[ \frac{C_{	ext{inj}} P_1 P_2 (\eta + \sigma_H) + C_{	ext{inf}} \eta P_1 P_2 \sigma_H}{P_1 P_2 P_3 (\mu_H + \nu)} \right] \]
and
\[ b_{22} = \prod_{j} P_1 P_2 P_3 \left[ \mu_H + \nu \right] (1 - \Re_T^2). \]

The positive endemic equilibrium of the model can be obtained by solving for \( \lambda_H^w \) in (13) and substituting the result into (12). Clearly, \( \lambda_H^w = 0 \) is a fixed point of (13) which corresponds to the DFE, \( E_T \). For \( \lambda_H^w \neq 0 \) equation can be reduced to
\[ a_{22} \lambda_H^w + b_{22} = 0. \]
Since all the model parameters are assumed to be non-negative, it follows that \( a_{22} > 0 \) and \( b_{22} < 0 \) whenever \( \Re_T > 1 \). Thus, the linear equation has a unique positive solution, given by \( \lambda_H^w = b_{22} / a_{22} \), whenever \( \Re_T > 1 \), and no positive solution when \( \Re_T < 1 \). This solution is summarized below.

**Lemma 4** The model has a unique positive endemic equilibrium whenever \( \Re_T > 1 \).

It can be shown, using the same approach as in the proof of Theorem 3, that the unique endemic equilibrium, \( E_T \), is LAS whenever \( \Re_T > 1 \).

In summary, it is clear that the treatment model has the same dynamical features as the treatment-free model (i.e., both models have globally-asymptotically stable DFE whenever the associated reproduction number is less than unity; and unique locally-asymptotically stable endemic equilibrium whenever the reproduction number exceeds unity). Thus, adding treatment to the model does not alter its dynamical features.

**Numerical simulations**

Since both models have been shown to exhibit similar qualitative dynamical features. Consequently, numerical simulations will be carried out on the treatment model. With the set of parameters in Table 2, the basic reproduction numbers \( \Re_T = 0.0547 \) so that \( \Re_T < 1 \). Thus by Theorem 5, the DFE is GAS Figure 2 depicts simulation of this model when \( \Re_T < 1 \). This result also holds for \( \Re_T = 1 \), confirming the global asymptotic stability property of the DFE whenever \( \Re_T \leq 1 \).

It is also shown that, with the set of parameters in Table 2, and \( \tau_H = 0.1 \), the prevalence of the infected individual is lower when an effective treatment strategy is applied (i.e., \( \tau_H = 0.99 \)), compared with less effective treatment method (i.e., \( \tau_H = 0.1 \)) as depicted in Figure 3A. Similarly, the number of treated individual is higher when \( \tau_H = 0.99 \) and lower when \( \tau_H = 0.1 \), as shown in Figure 3B, confirming the positive epidemiological impact of dengue treatment in the community (by reducing disease burden). Using the set of parameter in Table 2 and different values of \( (\nu) \), it is shown that with a higher and effective mosquito control strategy, the population of susceptible and exposed mosquitoes is lower \( (\nu = 5) \), compared with less effective mosquito control strategy \( (\nu = 0.5) \) as shown in Figure 4A-B.

**Conclusions**

This paper presents a deterministic model for the transmission dynamics of a single strain of dengue disease. The model, which allows dengue transmission by exposed vectors, was extended to include treatment for dengue. The two models were rigorously analysed to gain insights into their qualitative dynamics. The following results were obtained:

1. The basic (treatment-free) model has a locally stable disease-free equilibrium whenever the associated reproduction number is less than unity.
2. The treatment model, like the treatment-free model, has a globally-stable DFE whenever their associated reproduction number is less than unity.
3. Each of the models has a unique endemic equilibrium whenever their associated reproduction number exceeds unity.
4. Dengue treatment would always have positive epidemiological impact in the community (by reducing disease burden), or even disease elimination in the community.
5. Simulation of the treatment model shows that the use of vector control strategies can result in the effective control of dengue in a community by reducing the population.
of susceptible and exposed mosquitoes.

Acknowledgement

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References


Table 1: Description of variables and parameters of the models

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Interpretation</th>
<th>Nominal value</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_{H}$</td>
<td>Susceptible humans</td>
<td>variable</td>
</tr>
<tr>
<td>$A_{H}$</td>
<td>Asymptomatically infected humans</td>
<td>variable</td>
</tr>
<tr>
<td>$I_{H}$</td>
<td>Symptomatically infected humans</td>
<td>variable</td>
</tr>
<tr>
<td>$T_{H}$</td>
<td>Individuals in treatment class</td>
<td>variable</td>
</tr>
<tr>
<td>$F_{H}$</td>
<td>Individuals in whom treatment fails</td>
<td>variable</td>
</tr>
<tr>
<td>$S_{V}$</td>
<td>Susceptible mosquitoes</td>
<td>variable</td>
</tr>
<tr>
<td>$E_{V}$</td>
<td>Exposed mosquitoes</td>
<td>variable</td>
</tr>
<tr>
<td>$A_{V}$</td>
<td>Infectious mosquitoes</td>
<td>variable</td>
</tr>
<tr>
<td>$b_{I}$</td>
<td>Biting rate of infectious mosquitoes</td>
<td>5 /day</td>
</tr>
<tr>
<td>$b_{S}$</td>
<td>Biting rate of susceptible mosquitoes</td>
<td>5/day</td>
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<tr>
<td>$\rho_{VH}$</td>
<td>Transmission probability from mosquitoes to humans</td>
<td>0.5</td>
</tr>
<tr>
<td>$\rho_{HV}$</td>
<td>Transmission probability from humans to mosquitoes</td>
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<tr>
<td>$c_{VH}$</td>
<td>Infection rate of humans</td>
<td>3.6/day</td>
</tr>
<tr>
<td>$c_{HV}$</td>
<td>Infection rate of mosquitoes</td>
<td>3.6 /day</td>
</tr>
<tr>
<td>$\Pi_{H}$</td>
<td>Recruitment rate of humans</td>
<td>50000/day</td>
</tr>
<tr>
<td>$\Pi_{V}$</td>
<td>Recruitment rate of mosquitoes</td>
<td>4000000/day</td>
</tr>
<tr>
<td>$\frac{1}{\tau_{H}}$</td>
<td>Average lifespan of humans</td>
<td>67 years</td>
</tr>
<tr>
<td>$\frac{1}{\tau_{V}}$</td>
<td>Average lifespan of mosquitoes</td>
<td>14 days</td>
</tr>
<tr>
<td>$\sigma_{H}$</td>
<td>Progression rate from $A_{H}$ to $I_{H}$ class</td>
<td>0.0548 /day</td>
</tr>
<tr>
<td>$\sigma_{V}$</td>
<td>Progression rate from $E_{V}$ to $I_{V}$ class</td>
<td>0.0384 /day</td>
</tr>
<tr>
<td>$\delta_{H}$</td>
<td>Disease-induced death rate for humans</td>
<td>0.0005 /day</td>
</tr>
<tr>
<td>$\delta_{V}$</td>
<td>Disease-induced death rate for mosquitoes</td>
<td>0.6 /day</td>
</tr>
<tr>
<td>$\tau_{H}$</td>
<td>Treatment rate for humans</td>
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<td>$\tau_{V}$</td>
<td>Failed treatment rate for humans</td>
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<tr>
<td>$\nu_{V}$</td>
<td>Vector control induced death for mosquitoes</td>
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</tr>
<tr>
<td>$\eta_{H}, \eta_{V}$</td>
<td>Modification parameters</td>
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<tr>
<td>$\eta_{F}$</td>
<td>Relative risk of infectiousness of individuals in whom treatment fails</td>
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</tr>
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</table>
Figure 1: Schematic diagram of the model
Figure 2: Time series plots for the model (16). (A) Asymptotically infected individuals ($A_H$); (B) Symptomatically infected individuals ($I_H$); (C) Treated individuals ($T_H$); and (D) Individuals in whom treatment fails ($F_H$). Parameter values used are as in Table 2 with $\sigma_z = 0.09$ (so that $R_f = 0.0547 < 1$).

Figure 3: Prevalence as a function of time for the treatment model (16). (A) Symptomatically infected individuals ($I_H$); (B) Treated individuals ($T_H$); using various values of treatment rate ($\tau_H = 0.10$ (dotted line) and $\tau_H = 0.99$ (solid line)). Other parameter values used are as in Table 2.
Figure 4: Graph that show the dynamics of (A) Susceptible mosquitoes (B) exposed mosquitoes using different mosquitoes control strategies for the treatment model (16). $\nu_H = 0.5$ (solid line). Other parameter values used are as in Table 2.