The Existence and Stability Analysis of the Equilibria in Dengue Disease Infection Model

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Abstract.
In this paper we formulate an SIR (Susceptible - Infective - Recovered) model of Dengue fever transmission with constant recruitment. We found a threshold parameter $R_0$, known as the Basic Reproduction Number (BRN). This model has two equilibria, disease-free equilibrium and endemic equilibrium. By constructing suitable Lyapunov function, we show that the disease-free equilibrium is globally asymptotic stable whenever BRN is less than one and when it is greater than one, the endemic equilibrium is globally asymptotic stable. Numerical result shows the dynamic of each compartment together with effect of multiple bio-agent intervention as a control to the dengue transmission.

1. Introduction
Dengue Haemorrhagic Fever (DHF) is caused by four serotype of viruses. It may result in various clinical manifestations, from an asymptomatic to a fatal one. T Dengue virus infection can be devided into two groups: the asymptomatic manifestation (without symptoms) and the symptomatic manifestation (with symptoms). The latter usually appears in common fever (virus syndrome), dengue fever, or dengue hemorrhagic fever (DHF) which includes the dengue shock syndrome (DSS). Common fever occurs in infants, young children, and adults that have been infected by the dengue virus for the first time (primary dengue infection). Common fever cannot be distinguished from the fever caused by infection from other viruses. Basically dengue fever is an acute biphasic fever with symptoms such as headaches and cutaneous rashes. Although dengue fever is not fatal, it may reduce bodily functions. This includes, for instance, aches in joint muscles. DHF and DSS symptoms include fever and signs of blood circulation failure [16]. Preliminary researches on the mathematical model for one-strain DHF epidemiology have been conducted by using DHF models and constant population [6], inconstant population [7], and deterministic models that include vaccination [5],[8],[9]. When ones recover from dengue infection, sometimes later they can be re-infected by the Dengue virus. The reason is due to the reduction of immunity or wanning immunity, as it affects the immunity previously acquired. These patients are categorized under healthy humans who have been infected. Infected humans are divided into two compartments: those who are infected without symptoms and...
those who are infected with symptoms. This phenomenon has been modeled in [1] but there is no thorough analysis theorem. The global dynamics of the seventh-dimensional model of dengue disease transmission model in [1] is analyzed using Lyapunov function. In particular, we follow closely the ideas used recently in [13], [14], [15] to establish the global stability of the endemic equilibrium. The organization of this paper is as the following: in section 2, we present the mathematical model describing the transmission of dengue fever with asymptomatic and symptomatic classes [1]. A Mathematical analysis of this model is done in section 3 and section 4. Section 3 discusses the BRN of the model. It also discusses the Local Stability analysis for the endemic equilibrium point, while its global stability analysis is discussed in section 4. The last section shows the numerical analysis of dynamics of each compartment, including the effects of multi agent bio-control. Finally, some conclusions are presented in Section 6.

2. Model formulation

In order to derive the equations of the mathematical model, we assumed that host and vector populations have a constant size with birth and death rates for human and vector are constant equal to $\mu_h$ and $\mu_v$ respectively. In the Esteva - Vargas model [6], the majority of the host population eventually becomes permanently immune and the host have long-term immunity. In reality, human usually have one or more than one infection. In our model, individuals in host population become immune or loose immunity.

We assume that the susceptible host is divided into two compartments, $S_0$ (susceptible virgin host) and $Z_0$ (susceptible previously infected host). We consider $S_0$ as a susceptible class with virgin population comes from newborn, while $Z_0$ is a class coming from recovered human with no immunity. The infected class is divided into two classes namely $I$, the asymptomatic of infected human class, and $Y$, the symptomatic of infected human class (DF, DHF, DSS). There is no transmission from $I$ to $Y$ because we assume that the class $Y$ is detectable, hence individuals in $Y$ can be isolated. $Z$ is the class of removed human population. The vector population, due to short life period, is divided into the susceptible $V_0$ and the infective $V_1$. The model is represented by the diagram in Figure 1, with the description of the parameters shown in Table 1. The dynamics equation for host and vector are[1]:

\[
\frac{dS_0}{dt} = \mu_h N_h - \frac{b_r \alpha_1}{N_h} S_0 V_1 - \mu_h S_0,
\]

\[
\frac{dZ_0}{dt} = \xi Z - \frac{b_r \alpha_2}{N_h} Z_0 V_1 - \mu_h Z_0.
\]
\[
\begin{align*}
\frac{dI}{dt} &= \frac{b_r \alpha_1}{N_h} S_0 V_1 - (\gamma + \mu_h) I, \\
\frac{dY}{dt} &= \frac{b_r \alpha_2}{N_h} Z_0 V_1 - (\gamma + \mu_h) Y, \\
\frac{dZ}{dt} &= \gamma (Y + I) - (\xi + \mu_h) I, \\
\frac{dV_0}{dt} &= \mu_v N_v - \frac{b_r \alpha_v}{N_h} V_0 I - \mu_v V_0, \\
\frac{dV_1}{dt} &= \frac{b_r \alpha_v}{N_h} V_0 I - \mu_v V_1,
\end{align*}
\]

where: \( N_h = S_0 + Z_0 + I + Y + Z \) is the total population of host, and \( N_v = V_0 + V_1 \) is the total population of vectors.

Note that all trajectories in the first quadrant enter or stay inside the region

\[
\Omega = \{(S_0, Z_0, I, Z, V_0, V_1) \in [0,1]^6 \mid 0 \leq V_0 + V_1 \leq N_v, 0 \leq S_0 + Z_0 + I + Z \leq N_h\}. \quad (2)
\]

| Parameter | Description |
|-----------|-------------|
| \( \mu_h \) | Host death rate |
| \( \mu_v \) | Vector death rate |
| \( \alpha_i \) | Probability of successful transmission from host to vector |
| \( \alpha_v \) | Probability of successful transmission from vector to host |
| \( \xi \) | Wanning immunity |
| \( b_r \) | Biting rate per population human |
| \( \gamma \) | Recovery rate |
| \( N_h \) | Total population of host |
| \( N_v \) | Total population of host |

Table 1. Definition of parameter

3. ANALYSIS OF THE MODEL

3.1. Basic Reproduction Number

As shown in [1] the BRN of the model without protection is:

\[
R_0 = \sqrt{\frac{b_r^2 \alpha_1 \alpha_v N_v}{\mu_v (\mu_h + \gamma) N_h}}. \quad (3)
\]

The value of the basic reproduction number depends on the value of the biting rate per person. This is the reason that if we want to control dengue disease, we can reduce the biting rate per person, for example by applying insect repellent. We can also control the disease by reducing the life time of mosquitoes.

3.2. Stability of the endemic equilibrium

Before proving the local stability of the disease equilibrium, we present some result concerning the existence of equilibrium points of system (1).
Proposition 3.1 The model 1 has two equilibrium points, the disease free equilibrium $E_0 = (S_0^*, Z_0^*, I_0^*, Y_0^*, V_0^*, V_1^*) = (N_h, 0, 0, 0, N_e, 0)$, and the endemic equilibrium $E_e = (S_e^*, Z_e^*, I^*, Y^*, Z^*, V_0^*, V_1^*)$, where:

\[
S_0^* = \frac{N_h(A_1 + \mathbb{R}_0^2 K)}{\mathbb{R}_0^2 (A_1 + K)}, \quad (4)
\]

\[
Z_0^* = \frac{A_1 C (\mathbb{R}_0^2 - 1) (A_1 + K \mathbb{R}_0^2) \xi}{M (A_1 + K) \mathbb{R}_0^2}, \quad (5)
\]

\[
I^* = \frac{A_1 (\mathbb{R}_0^2 - 1) K}{\mathbb{R}_0^2 (A_1 + K) C}, \quad (6)
\]

\[
Y^* = \frac{A_1 A_2 K (\mathbb{R}_0^2 - 1)^2 \xi \gamma}{\mathbb{R}_0^2 (A_1 + K) CM}, \quad (7)
\]

\[
Z^* = \frac{A_1 (\mathbb{R}_0^2 - 1) (A_1 + A_1 (\mathbb{R}_0^2 - 1) + K \mathbb{R}_0^2)}{M (A_1 + K) \mathbb{R}_0^2}, \quad (8)
\]

\[
V_0^* = \frac{N_e (A_1 + K)}{A_1 + K \mathbb{R}_0^2}, \quad (9)
\]

\[
V_1^* = \frac{K (\mathbb{R}_0^2 - 1) N_v}{A_1 + K \mathbb{R}_0^2}, \quad (10)
\]

\[
A_i = b \alpha_i N_i; \quad i = 1, 2, v, \quad K = N_h N_e,
\]

\[
C = \gamma + \mu_h, \quad D = \xi + \mu_h
\]

\[
M = K \mathbb{R}_0^2 DC + \mu_h [A_1 + A_2 (\mathbb{R}_0^2 - 1)] D + A_2 (\mathbb{R}_0^2 - 1) \gamma \mu_h + A_1 D
\]

It can be verified that if $\mathbb{R}_0 > 1$, then there exists an endemic equilibrium point, and if $\mathbb{R}_0 < 1$ then the endemic equilibrium disappears. It indicates that to reduce the outbreak of DHF, we should make the value of $\mathbb{R}_0$ lower.

The next proposition gives a condition for the local stability of the endemic equilibrium state $E_0$, the local stability of the disease free equilibrium proven in [1].

Proposition 3.2 If $\mathbb{R}_0 > 1$, then the endemic equilibrium $E_e$ is locally asymptotically stable if the inequality

\[
C (A_1 + K) N_h (A_1 + K \mathbb{R}_0^2) < A_1 K (\mathbb{R}_0^2 - 1)^2
\]

is also satisfied, otherwise $E_e$ is unstable.

Proof. Let the equilibrium $E_e = (S_e^*, Z_e^*, I^*, Y^*, Z^*, V_0^*, V_1^*)$, exists, that is when $\mathbb{R}_0 > 1$. By using the coordinate system $E_e$, of model (1) at point $E_e$ gives the Jacobian matrix $J(E_e)$:

\[
J(E_e) = \begin{bmatrix}
J_1 & J_2 \\
J_3 & J_4
\end{bmatrix}
\]

where

\[
J_1 = \begin{bmatrix}
-\frac{(b \alpha_i N_i + K)}{N_h} & 0 & 0 \\
0 & -\frac{(b \alpha_i N_i + K)}{N_h} & 0 \\
\frac{(b \alpha_i N_i)}{N_h} & 0 & -\gamma - \mu_h
\end{bmatrix}; \quad J_2 = \begin{bmatrix}
0 & 0 & 0 & \frac{(b \alpha_i N_i)}{N_h} \\
0 & \xi & 0 & \frac{(b \alpha_i N_i)}{N_h} \\
0 & 0 & 0 & \frac{(b \alpha_i N_i)}{N_h}
\end{bmatrix}
\]
The values of $C$ and $K$ are in the equation (11). Note that the coefficient $a_2, b_2, c_2 > 0$ if $\Re_0 > 1$, hence all the roots of polynomial $p_2(x)$ have negative real part when $\Re_0 > 1$. If $\Re_0 > 1$, then coefficient $a_3, b_3, c_3 > 0$, for the coefficient $c_3, d_3$ will be greater than zero with the condition $G_{cd} > 0$, then $Q < 0$. Then the condition $C(A_1 + K)N_h(A_1 + K\Re_0^2) < A_1 K(\Re_0^2 - 1)^2$ will be satisfied.

Applying Routh - Hurwitz criteria to the polynomial with third degree will ensure that be stability is acquired if the condition $a_3d_3 < b_3c_3$ is satisfied. From equation (11), it can be seen that

$$a_3d_3 = \frac{1}{2} a_3(2b_{3A}C\mu_v + 2b_{3B}(\mu_v^2 + \gamma \mu_v) + b_{3C} \mu_v \mu_h + 2G_{cd} + 2d_{3A})$$
$$a_3d_3 < \frac{1}{2}(b_{3A} + b_{3B} + b_{3C} + a_3 \mu_v)(2b_{3A}(C + \mu_v) + 2b_{3B}C + b_{3C}(2\gamma + \mu_h + \mu_v) + 2G_{cd})$$
$$< b_3c_3$$

this means that $E_c$ is a locally asymptotically stable when $\Re_0 > 1$, and a saddle point where $\Re_0 < 1$. This proves the proposition.

### 4. GLOBAL STABILITY ANALYSIS

#### 4.1. Disease-free equilibrium

We now study the global behavior of disease - free equilibrium for system (1).
Proposition 4.1 If $R_0 \leq 1$, then the disease - free equilibrium $E_0$ model (1) is globally asymptotically stable.

Proof.
We follow closely the ideas used recently in [13, 14, 15] to establish the global stability of the non endemic equilibrium. In proving the global asymptotical stability of $E_0$ in $\Omega$ for $R_0 \leq 1$, we construct a Lyapunov function $V : \Omega \rightarrow R$, where

$$V(t) = S_0^0 \left( \frac{S_0}{S_0^0} - S_0^0 \ln S_0 / S_0^0 \right) + \frac{N_h(\gamma + \mu_h)}{N_e b r \alpha_v} V_1 + I + \frac{N_h(\gamma + \mu_h)}{N_e b r \alpha_v} V_0 \left( \frac{V_0}{V_0^0} - \frac{V_0^0 \ln V_0}{V_0^0} \right). \quad (14)$$

Differentiating with respect to time yields and from model (1) we have

$$\dot{V}(t) = \mu_h N_h \left( 2 - \frac{S_0}{S_0^0} - \frac{S_0^0}{S_0^0} \right) + \frac{N_h(\gamma + \mu_h)}{N_e b r \alpha_v} \mu_v N_e \left( 2 - \frac{V_0}{V_0^0} - \frac{V_0^0}{V_0^0} \right) + V_1 (\sqrt{h_0} - 1) \left( \frac{N_h(\gamma + \mu_h)}{N_e b r \alpha_v} \right)$$

$$\leq 0$$

From the inspection of model (1), it can be seen that $E_0$ is the largest invariant set under the flow generated by the vector field of model (1) for which $S_0 = S_0^0, Y = Z = 0, V_0 = V_0^0$. Therefore, by [12] the equilibrium $E_0$ is globally asymptotically stable in $\Omega$ for $R_0 \leq 1$. This concludes the proof.  

4.2. Endemic equilibrium

Proposition 4.2 Assume that

$$N_h = S_0^*, N_v = V_0^*, b_r = \frac{\mu_v (\gamma + \mu_h)}{\alpha_1 p_i V_0^*} \quad (16)$$

If $R_0 > 1$, then the disease equilibrium $E_v^*$ is globally asymptotically stable.

Proof. The same approach to proposition 4.1 is applied. In proving the global asymptotical stability of $E_v^*$ in $\Omega$ for $R_0 > 1$, we construct a Lyapunov function $L : \Omega \rightarrow R$, where

$$L(t) = (S_0 - S_0^0 \ln S_0) + \frac{(\gamma + \mu_h)}{p_e V_0^*} (V_0 - V_0^0 \ln V_0) + I + \frac{(\gamma + \mu_h)}{p_i V_0^*} V_1. \quad (17)$$

with : $p_i = \frac{b_r \alpha_1}{N_h}$, $i = 1, v$. Differentiating with respect to time yields

$$\dot{L}(t) = \mu_h N_h \left( 1 - \frac{S_0}{S_0^0} \right) + \mu_h S_0^0 \left( 1 - \frac{S_0}{S_0^0} \right) + \frac{(\gamma + \mu_h)}{p_e V_0^*} (p_e V_0^* I) - (\gamma + \mu_h) I$$

$$+ \frac{(\gamma + \mu_h)}{p_e V_0^*} \left[ \mu_v N_v \left( 1 - \frac{V_0}{V_0^0} \right) + \mu_v V_0^* \left( 1 - \frac{V_0^0}{V_0^0} \right) \right]$$

$$+ \frac{(\mu_v (\gamma + \mu_h)}{\alpha_1 p_i V_0^*} \frac{\alpha_1}{N_h} N_h V_1 - \frac{(\gamma + \mu_h)}{p_i V_0^*} \mu_v V_1 \quad (18)$$
From model (1) and condition (16) we have 
\[ S_*^0 = N_h \quad \text{and} \quad V_*^0 = N_v, \]
then equation (19) becomes:
\[ \dot{L}(t) = \mu_h N_h (2 - \frac{S_*^0}{S_0} - \frac{S_0}{S_*^0}) + \mu_v N_v (2 - \frac{V_*^0}{V_0} - \frac{V_0}{V_*^0}) \]
\[ = -\mu_h N_h \left( \frac{S_0 - S_*^0}{S_0 S_*^0} \right) - \mu_v N_v \left( \frac{V_0 - V_*^0}{V_0 V_*^0} \right)^2 \]
\[ \leq 0 \quad (19) \]

From inspection of system (1), it can be proved readily, that \( E_e \) is the only positively invariant subset of the set where \( \dot{L}(t) = 0 \). Therefore, by [12] the equilibrium \( E_e \) is globally asymptotically stable in \( \Omega \). This proves the theorem. ■

5. Numerical Examples and Remarks

Numerical examples are shown in this section. The parameters are determined by real life observation as follows. The life expectancy of human is 60 years. The life time of vector is 30 days. The bitting rate of vector is 1/3 or 1/5 per day. The time for each person can recover is 7 days. The total human population is 100,000 person. Finally, the total vector population is 10,000. The transmission probability are arbitrarily chosen. Figure (2, left) is a dynamic projection model (1) in \( IY \) field with fixed values of \( b_r \). There is indication of oscillations at \( b_r \) greater than 3. Figure (2, right) shows the dynamics of a subpopulation of healthy humans but has the possibility of infection. The figure includes the projected dynamics model (1) into the phase plane of \( Z_0 - S_0 \). For this numerical example we used a set of values of the parameters with the same initial conditions and the average value of unity mosquitoes at different times. The integration time used was 100 days. In this case both population approaching certain positive numbers, or in other word, \( S_0 \) and \( Z_0 \) are co - exist. The increased of \( b_r \) causes the increase of \( Z_0 \) and decrease \( S_0 \). We can explore the effect of bio-control in a multi-agents intervention by substituting \( N_v \) with \( u_1, N_v \) and \( \mu_v \) by \( u_2 \mu_v \). Here \( u_1 \leq 1 \) indicates the effect of bio control, such as predatory in larvae stage of the mosquitoes. For \( u_2 \leq 1 \) indicates the effect of wolbachia infection in reducing life span of mosquitoes.

![Figure 2](image-url)

**Figure 2.** Left figure represent the numerical simulation of system (1) on the phase of \( I - Y \) and right figure the phase of \( S_0 - Z_0 \) with parameter values \( \gamma = 0.071, \beta_1 = 0.1, \beta_2 = 0.1, \alpha_1 = 0.2, \alpha_2 = 0.2, b = 3, \) and different values of \( b_r \).
Figure 3. The dynamics of Compartment I dan Y with wolbachia control for fixed value of $u_1$.
Figure 4. Dynamical Compartment I and Y with wolbachia control for fixed value of $u_2$

6. Conclusion
In this paper we construct and analyze a model of the spread of Dengue Hemorrhagic Fever, with and without symptoms, regardless the infecting virus serotype. We found a threshold for the model, $R_0$. The threshold associated with the BRN and it determined the existence and the stability of the equilibrium point. The model has two equilibrium points. The first, the disease-free equilibrium that always exists and globally asymptotically stable, if $R_0 < 1$. The second, the endemic equilibrium which its existence is guaranteed when the threshold $R_0 > 1$. In other words, if the threshold value or $R_0$ is less than or equal to one, then the dengue disease will...
disappear from the population. This shows the relationship between the existence or stability of the endemic point and the value of Basic Reproduction Number. Numerical examples show that the implementation of multiple bio-agent is prospective in reducing dengue transmission. Further analysis is being undertaken.

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