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A Mathematical Model On Dengue Fever Transmission And Control

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Abstract: ***We investigated the transmission of Dengue disease and the different ways they can be controlled. We analyzed the dynamics of Dengue using a system of eight differential equations where the first five compartments are for human population and the last three compartments for mosquitoes with reduction of breeding sites, use of ITN's, vaccines and treatment as control strategies in limiting the disease. We obtained the equilibrium points of the model and investigated their stabilities. Our analysis shows that if the basic reproduction number*** R_0 ***< 1, the disease free equilibrium point is stable, but if*** R_0 ***> 1, then the disease free equilibrium is unstable, In such case the endemic state has a unique equilibrium. This means that re-invasion of the disease is possible, and the Dengue disease persists in the human population. The result of our work showed that reduction of mosquito breeding sites, spraying of insecticide, treatment in form of vaccines, treating early infected humans, sleeping under treated nets are best practices that aids dengue prevention and control.***

Keywords: basic reproduction number, compartments, control, dengue, model.

I. INTRODUCTION

Dengue fever is a mosquito-borne tropical disease caused by the dengue virus. Dengue virus is transmitted by female mosquitoes mainly of the species Aedes aegypti and to a lesser extent, Aedes albopictus [1]. These mosquitoes have adjusted to human neighborhood with larval habitats and oviposition in natural and artificial (e.g., rock pools, tree holes, blocked drains, pot plants and food and beverage containers, and leaf axis) collections in the urban and sub-urban environment [2]. Dengue is caused by a virus of the flaviviridae family and there are five distinct, but closely related, serotypes of the virus that cause dengue (DENV-1, DENV-2, DENV-3, DENV-4 and DENV-5). Recovery from infection with one serotype provides lifelong immunity to that serotype, but only short-term immunity to the others. Subsequent infection with a different type increases the risk of severe complications.[9]

Dengue can be brought on by any of four viral serotypes (Dengue Virus (DENV) 1-5), and is transmitted by day-biting urban-adapted Aedes mosquito species [3]. After an incubation period ranging from 4 to 14 days, patients normally can encounter a range of symptoms, from a sub-clinical disease to debilitating but transient Dengue Fever (DF) to life-threatening Dengue Hemorrhagic Fever (DHF) or Dengue Shock Syndrome (DSS) [4,5]. The most severe forms of dengue disease are DHF and DSS. They are life debilitating, and youngsters with DENV disease are especially at danger of advancing to severe DHF/DSS [6]. Until now there is no specific treatment or vaccine for dengue.

DF is a major public health concern and also re-emerging infectious disease that affects millions of people worldwide. It

is also a major public health concern for over half of the world's population and is a main source of hospitalization and death especially for youngsters in endemic nations. The majority of the poor nations are particularly vulnerable to the transmission of dengue infection [6]. This vector borne disease always can be found in urban and suburban areas of regions such as Africa, South-East Asia, Americas, Eastern Mediterranean and Western Pacific [7]. It is assessed that consistently, there are 70 million dengue infections, 36 million cases of DF and 21 million cases of DHF and DSS, with more than 20000 deaths per year [7].

II. MODEL FORMULATION

We assume that the disease can only be transmitted by the primary vector(Aedes aegypti), and that those recovered can still go back to being susceptible. We also assumed that those undergoing treatment can also die of the disease. Furthermore, individuals can recover from the infection even without being treated. The study was carried out in the tropical region. We have our Classes as; $S_h, E_h, I_h, I_{h_T}, S_v, E_v, and\ I_v$. Let $\alpha_h = \frac{\theta_{mh}\,\phi I_V}{N_h}$ be rate of progression from susceptible humans to exposed humans. And let $\tau_v = \frac{\theta_{hm}\,\phi I_h}{N_h}$ be rate of progression from susceptible mosquitoes to exposed mosquitoes.

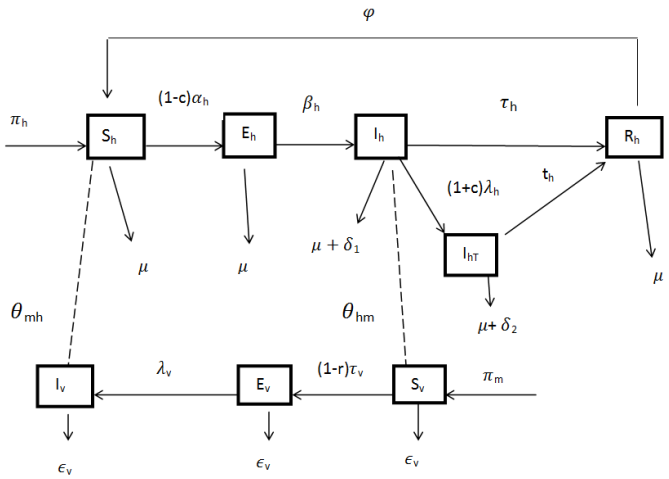

Figure 1: flow diagram for the model

MODEL EQUATION

$$\left.\begin{aligned}
\frac{dS_h}{dt} &= \pi_h + \varphi R_h - (1-c)\alpha_h S_h - \mu S_h \\
\frac{dE_h}{dt} &= (1-c)\alpha_h S_h - \beta_h E_h - \mu E_h \\
\frac{dI_h}{dt} &= \beta_h E_h - \tau_h I_h - (1+c)\lambda_h I_h - (\mu + \delta_1) I_h \\
\frac{dI_{hT}}{dt} &= (1+c)\,\lambda_h I_h - t_h I_{hT} - (\mu + \delta_2) I_{hT} \\
\frac{dR_h}{dt} &= \tau_h I_h + t_h I_{hT} - \varphi R_h - \mu R_h \\
\frac{dS_v}{dt} &= \pi_m - (1-r)\,\tau_v S_v - \epsilon_v S_v \\
\frac{dE_v}{dt} &= (1-r)\,\tau_v S_v - \lambda_v E_v - \epsilon_v E_v \\
\frac{dI_v}{dt} &= \lambda_v E_v - \epsilon_v I_v
\end{aligned}\right\} \quad (1)$$

INVARIANT REGION

We start by determining the invariant region to check if the model is biologically meaningful and that all solutions of (1) are positive for all t $\geq$ 0 and

are attracted in that region.

This region can be obtained by this theorem.

Theorem 1

The solutions of the system (1) are feasible for all t > 0 if they enter the invariant region

$$\Omega = \Omega_h \, x \, \Omega_m$$

Let $\Omega_h = (S_h, E_h, I_h, I_{hT}, R_h)$ and $\Omega_m = (S_v, E_v, I_v)$. Then since $\Omega = \Omega_h \, x \, \Omega_m$

we have:

$\Omega = (S_h, E_h, I_h, I_{hT}, R_h, S_v, E_v, I_v) \in R_+^{\,8}$ be any solution of the system (1) with non

negative initial conditions, ie at t=0, $S_h>0$, $E_h\geq 0$, $I_h\geq 0$, $I_{hT}\geq 0$, $R_h\geq 0$, $S_v\geq 0$, $E_v\geq 0$, $I_v\geq 0$.

In the absence of disease (dengue) that is $E_h, I_h, I_{hT} = 0$, equation 4.2.3 becomes

$$\frac{dN_h}{dt} \leq \pi_h - \mu N_h$$

$$\frac{dN_h}{dt} + \mu N_h \leq \pi_h \quad (2)$$

The integrating factor for (2) is (IF) $= e^{\int \mu dt} = e^{\mu t}$

Multiplying both sides of (2) by $e^{\mu t}$ and solving we have;

All the feasible solution set of the human population of the model (4.2.1) enters the region. $\Omega_h = \{ (S_h, E_h, I_h, I_{hT}, R_h) \in R_+^{\,5} : S_h > 0, E_h \geq 0, I_h \geq 0, I_{hT} \geq 0, R_h \geq 0, N_h \leq \frac{\pi_h}{\mu}$

Similarly the feasible solution set of the mosquito population enters the region

$$\Omega_m = \left\{ (S_v, E_v, I_v) \in R_3^{+} : S_v > 0, E_v \geq 0, I_v \geq 0, N_m \leq \frac{\pi_m}{\epsilon_v} \right\}$$

III. LOCAL STABILITY OF THE DISEASE-FREE EQUILIBRIUM

At DFE;

$S_h = \frac{\pi h}{\mu}$, $E_h = 0$, $I_h = 0$, $R_h = 0$, $S_v = \frac{\pi_m}{\epsilon_v}$, $E_v = 0$, $I_v = 0$,

Also

$$\frac{dS_h}{dt} = \frac{dE_v}{dt} = \frac{dI_h}{dt} = \frac{dI_{hT}}{dt} = \frac{dR_h}{dt} = \frac{dS_v}{dt} = \frac{dE_v}{dt} = \frac{dI_v}{dt} = 0$$

The Jacobian matrix is given as

$$J = \begin{bmatrix}
-(1-C)\alpha_h - \mu & 0 & 0 & 0 & \varphi & 0 & 0 & \frac{-(1-c)\theta_{mh}\phi S_h}{N_h} \\
(1-C)\alpha_h & -\beta_h - \mu & 0 & 0 & 0 & 0 & 0 & \frac{(1-c)\theta_{mh}\phi S_h}{N_h} \\
0 & \beta_h & -\tau_h - (1+c)\lambda_h - (\mu+\delta_1) & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & (1+c)\lambda_h & -t_h - (\mu+\delta_2) & 0 & 0 & 0 & 0 \\
0 & 0 & \tau_h & t_h & -\varphi - \mu & 0 & 0 & 0 \\
0 & 0 & \frac{-(1-r)\theta_{hm}\phi S_v}{N_h} & 0 & 0 & -(1-r)\tau_v - \epsilon_v & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & (1-r)\tau_v & -\lambda_v - \epsilon_v & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \lambda_v & -\epsilon_v
\end{bmatrix}$$

Evaluating at DFE we have;

$$J = \begin{bmatrix} -\mu & 0 & 0 & 0 & \varphi & 0 & 0 & -(1-c)\theta_{mh}\phi \\ 0 & -\beta_h-\mu & 0 & 0 & 0 & 0 & 0 & (1-c)\theta_{mh}\phi \\ 0 & \beta_h & -\tau_h-(1+c)\lambda_h-(\mu+\delta_1) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & (1+c)\lambda_h & -\tau_h-(\mu+\delta_2) & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_h & t_h & -\varphi-\mu & 0 & 0 & 0 \\ 0 & 0 & (1-r)\theta_{hm}\phi & 0 & 0 & -\epsilon_v & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\lambda_v-\epsilon_v & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \lambda_v & -\epsilon_v \end{bmatrix}$$

Evaluating |A – λI|, we have

$\lambda_1 = -\mu$, $\lambda_2 = -\epsilon_v$, $\lambda_3 = (-\varphi-\mu)$, $\lambda_4 = -\tau_h-(1+c)\lambda_h-(\mu+\delta_1)$, $\lambda_5 = -t_h-(\mu+\delta_2)$, $\lambda_6 = -\lambda_v-\epsilon_v$

$\lambda_7 = -\epsilon_v$ $\lambda_8 = -\beta_h-\mu$

Here, the system is asymptotically stable since all its eigen values are negative.

IV. BASIC REPRODUCTION NUMBER R_0

The basic reproduction number (reproduction ratio) $R_0$is given by

$R_0 = \gamma(FV^1)$

Where γ(A) denotes the spectral radius of a matrix A and the spectral radius, $\gamma(FV^1)$, is the biggest nonnegative eigen value of the next generation matrix.

From the system (1), F_i *and* $V_i$are defined as

$$F_i = \begin{bmatrix} \frac{(1-c)\theta_{mh}\phi I_v S_h}{N_h} \\ 0 \\ 0 \\ \frac{(1-r)\theta_{hm}\phi I_h S_v}{N_h} \\ 0 \end{bmatrix} \quad (3)$$

$$V_i = \begin{bmatrix} \beta_h E_h + \mu E_h \\ -\beta_h E_h + \tau_h I_h + (1+c)\lambda_h I_h + (\mu+\delta_1)I_h \\ -(1+c)\lambda_h I_h + t_h I_{hT} + (\mu+\delta_2)I_{hT} \\ \lambda_v E_v + \epsilon_v E_v \\ \epsilon_v I_v - \lambda_v E_v \end{bmatrix} \quad (4)$$

The partial derivatives of (3) with respect to *(E_h, I_h, I_{hT} , E_v ,I_v)*and the Jacobian matrix of F_i at the disease-free equilibrium point is:

$$F = \begin{bmatrix} 0 & 0 & 0 & 0 & (1-C)\theta_{mh}\phi \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{(1-r)\theta_{hm}\phi\pi_m\mu}{\epsilon_v\pi_h} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad (5)$$

Similarly, the partial derivatives of (4) with respect to *(E_h, I_h, I_{hT} , E_v , I_v)*and the Jacobian matrix of V_i is:

$$V = \begin{bmatrix} (\beta_h+\mu) & 0 & 0 & 0 & 0 \\ -\beta_h & \tau_h+(1+c)\lambda_h+(\mu+\delta_1) & 0 & 0 & 0 \\ 0 & -(1+c)\lambda_h & t_h+\mu+\delta_2 & 0 & 0 \\ 0 & \frac{(1-r)\theta_{hm}\phi\pi_m\mu}{\epsilon_v\pi_h} & 0 & \lambda_v+\epsilon_v & 0 \\ 0 & 0 & 0 & -\lambda_v & \epsilon_v \end{bmatrix} \quad 4.5.5$$

The inverse of matrix V is given as:

$$V^1 = \begin{bmatrix} \frac{1}{(\beta_h+\mu)} & 0 & 0 & 0 & 0 \\ \frac{\beta_h}{(\beta_h+\mu)(\tau_h+(1+c)\lambda_h+\mu+\delta_1)} & \frac{1}{\tau_h+(1+c)\lambda_h+(\mu+\delta_1)} & 0 & 0 & 0 \\ \frac{(-\beta_h)(1+c)}{(\beta_h+\mu)(\tau_h+(1+c)\lambda_h+\mu+\delta_1)+(t_h+\mu+\delta_2)} & \frac{-(1+c)(\lambda_v+\epsilon_v)}{\tau_h+(1+c)\lambda_h+(\mu+\delta_1)(t_h+\mu+\delta_2)} & \frac{1}{t_h+\mu+\delta_2} & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{(t_h+\mu+\delta_2)} & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\lambda_v+\epsilon_v} \end{bmatrix}$$

4.5.6

To compute FV^1

$FV^1 = [F] \times [V^1]$

Let: a = $\beta_h+\mu$ b = $-\beta_h$ c = $\tau_h+(1+c)\lambda_h+\mu+\delta_1$ e = $-(1+c)\lambda_h$ f = $t_h+\mu+\delta_2$ g = $\lambda_v+\epsilon_v$ h = $-\lambda_v$ i = ϵ_v k = $(1-c)\theta_{mh}\phi$ l = $\frac{(1-r)\theta_{hm}\phi\pi_m\mu}{\epsilon_v x\ \pi_h}$

$$FV^1 = \begin{bmatrix} 0 & 0 & 0 & \frac{ihk}{g} & -ik \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ \frac{-bl}{ac} & \frac{l}{c} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad 4.5.7.$$

From (4.5.7), the eigen values can be calculated as to determine the basic reproduction number

R_0 by taking the spectral radius (dominant eigen value) of the matrix FV^1.

It is thus computed by|A – λI| = 0, we have

$$FV^{-1} = \begin{bmatrix} -\lambda & 0 & \frac{ihk}{g} & 0 & -ik \\ 0 & -\lambda & 0 & 0 & 0 \\ 0 & 0 & -\lambda & 0 & 0 \\ \frac{-bl}{ac} & \frac{l}{c} & 0 & -\lambda & 0 \\ 0 & 0 & 0 & 0 & -\lambda \end{bmatrix} = 0$$

$\lambda_1 = 0, \lambda_2 = 0, \lambda_3 = 0$

$$\begin{bmatrix} \lambda & \frac{-ihk}{g} \\ \frac{-bl}{ac} & \lambda \end{bmatrix} \Rightarrow \lambda^2 = \frac{ihk}{g} \times \frac{bl}{ac}$$

$$\lambda = \sqrt{\frac{ihk}{g} \times \frac{bl}{ac}}$$

$$\lambda = \sqrt{\frac{\epsilon_v x - \lambda_v x (1-c)\theta_{mh}\phi}{(\lambda_v+\epsilon_v)} \times \frac{-\beta_h x (1-r)\theta_{hm}\phi\pi_m\mu}{\epsilon_v x \pi_h x (\beta_h+\mu) x \tau_h+(1+c)\lambda_h+(\mu+\delta_1)}} \quad 4.5.8$$

$$R_0 = \sqrt{\frac{(1-c)\theta_{mh}\phi\beta_h(1-r)\theta_{hm}\phi\mu}{\pi_h\, x\, (\beta_h+\mu)\, x\, (\tau_h+(1+c)\lambda_h+\mu+\delta_1)}}\; x\; \frac{\epsilon_v\, x\, \lambda_v\, x\, \pi_m}{\epsilon_v(\lambda_v+\epsilon_v)} \quad 4.5.9$$

$$R_0 = \sqrt{R_h\, x\, R_m}$$

$$R_{0h} = \frac{(1-c)\theta_{mh}\phi\beta_h(1-r)\theta_{hm}\phi\mu}{\pi_h\, x\, (\beta_h+\mu)\, x\, (\tau_h+(1+c)\lambda_h+\mu+\delta_1)} \quad 4.5.10$$

$$R_{0m} = \frac{\epsilon_v\, x\, \lambda_v\, x\, \pi_m}{\epsilon_v(\lambda_v+\epsilon_v)} \quad 4.5.11$$

V. NUMERICAL SIMULATION

ESTIMATION OF PARAMETERS

Estimated parameter values and their sources for model (1)

PARAMETER	VALUE	SOURCE
π_h	700,025	[14]
φ	1.460×10^{-2}	[14]
μ	0.004	[12]
β_h	0.08333	[12]
t_h	0.1429	[12]
τ_h	0.00019	[14]
C	0.75	[14]
α_h	0.85	Estimated
λ_h	0.0723	Estimated
δ_2	0.533	Estimated
δ_1	0.333	[16]
π_m	23350	[14]
τ_v	0.09091	[14]
λ_v	0.75	[12]
ϵ_v	0.86	Estimated
R	0.59	Estimated
θ_{hm}	0.86	[12]
θ_{mh}	0.083	[16]
ϕ	0.029	[14]

Table 1

The initial conditions are:

S_h	406,250	Estimated
E_h	369,150	Estimated
I_h	156,170	Estimated
I_{hT}	104,114	Estimated
R_h	72,056	Estimated
S_v	40,200	Estimated
E_v	32,000	Estimated
I_v	21,200	Estimated

Table 2

The simulation was run in days.

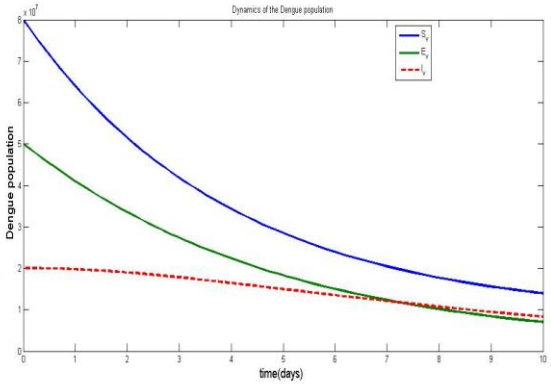

Figure 4.1: Graph of the mosquito population in the presence of control measures. Since this is a disease free state, the number of infected humans is very small, thus the number of the mosquitoes that are infected is in the decline and the control measures adopted by the humans helped to ensure that the whole mosquito population continues to reduce

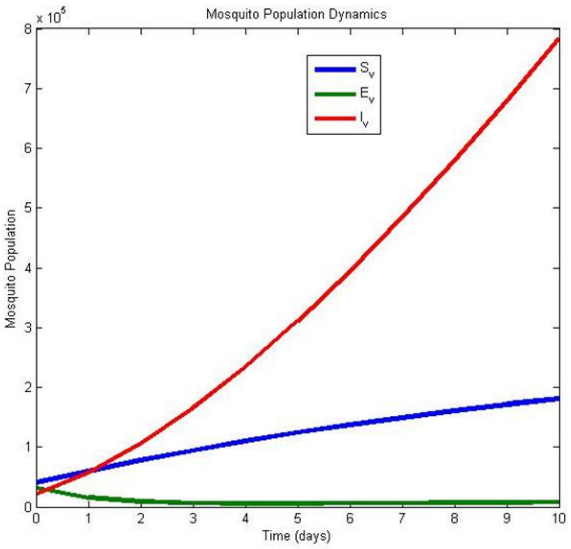

Figure 4.2: Transmission dynamics in an endemic situation on mosquito population

The figure above is a simulation of the transmission dynamics in an endemic situation. As shown on the graph, though the infection keeps increasing massively, the control measures adopted are keeping the mosquito population under check.

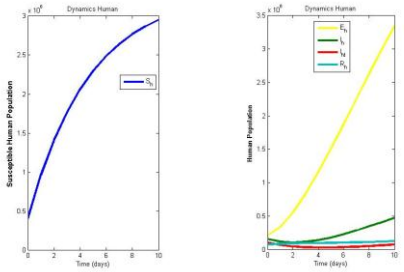

Figure 4.3: Transmission dynamics in an endemic situation on human population

The figure above is a simulation of the transmission dynamics in an endemic situation. As shown on the graph, though the exposed human population keeps increasing

massively, the control measures adopted are keeping the disease under check.

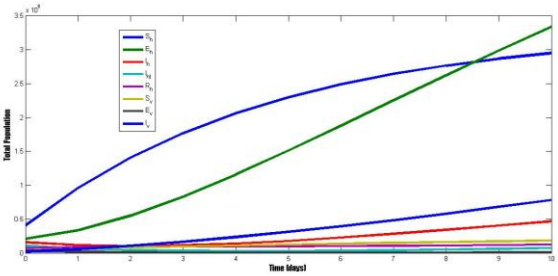

Figure 4.4: Transmission dynamics in an endemic situation of the whole population

The figure above is a simulation of the transmission dynamics in an endemic situation. As shown on the graph, though the exposed human population keeps increasing massively, the control measures adopted are reducing the mosquito population and also the disease.

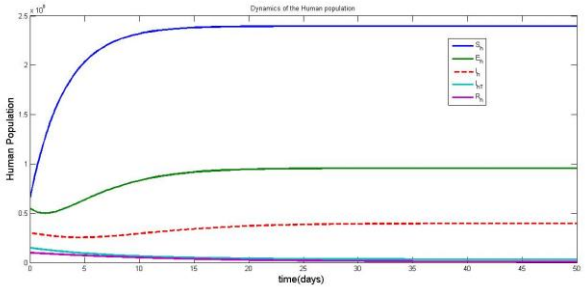

Figure 4.5: graph of the human population only

Here, we considered what happens in the human population alone. The susceptible humans are increasing and with time it didn't decrease. Meanwhile, the exposed and infected classes are kept under check as a result of control measures being adopted.

VI. CONCLUSION

We derived and analyzed a mathematical model to better understand the transmission and control of dengue in the population. The model considered a varying total human population that Incorporated recruitment of new individuals into the susceptible class through either birth or Immigration.

Mathematically, we modeled dengue as an 8-dimensional system of ordinary differential Equations. We first showed that there exists a domain where the model is epidemiologically and mathematically well-posed. We defined the basic reproduction number, R_0, which provides the expected number of new infections (in mosquitoes or humans) from one infectious individual (human or mosquito) over the duration of the infectious period given that all other members of the population are susceptible. We proved if R_0<1, the disease cannot persist in the country and when R_0>1the disease can persist. We perform stability analysis of the model. We have Proved that the disease-free equilibrium is locally asymptotically stable if R_0<1and unstable when R_0>1.

In chapter four, the analysis for dengue showed that the disease-free and Endemic equilibrium points are asymptotically stable. The numerical analysis of the model Suggested that the most effective strategies for controlling or eradicating dengue are the use of Insecticide-treated bed nets and indoor residual spraying and prompt and effective diagnosis and treatment of infected individuals. The effect of reducing mosquito bites has great impact in the reduction of the spreading of the disease (dengue), but the combination of two interventions can play a bigger role in reducing or eradicating the transmission of the disease and dengue related deaths in the population.

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