Journal of AppliedMath 2024, 2(3), 160.
https://doi.org/10.59400/jam.v2i3.160

Article

Mathematical modelling of transmission dynamics of Dengue Fever in the presence of infective immigrants

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CITATION

Donkoh EK, Otoo D, Osman S, et al. Mathematical modelling of transmission dynamics of Dengue Fever in the presence of infective immigrants. Journal of AppliedMath. 2024; 2(3): 160. https://doi.org/10.59400/jam.v2i3.160

ARTICLE INFO

Received: 8 August 2023
Accepted: 23 February 2024
Available online: 8 May 2024

Abstract: Dengue fever is one of the neglected tropical diseases around the globe and its ravaging effect over the period has been enormous in the affected areas. Globalisation, immigration and urbanization and poor urban planning have become the contributory factors in the spread of infectious diseases. In this paper, a model describing the dynamics of dengue fever incorporated with infection immigrants is formulated and analysed using ordinary differential equations with a constant immigration recruitment rate. The model was qualitatively and quantitatively analysed for its local stability, basic reproductive number and sensitivity of the model parameters values to the basic reproductive number to understand the impact of the parameters on the disease spread. In the analysis, it was found that in the presence of infectious immigrants, there cannot be a disease free state demonstrated by $\emptyset \geq 0$ where the model demonstrates a unique endemic equilibrium state if the fraction of infectious immigrants $\emptyset$ is positive. The unique endemic equilibrium for which there is a fraction of infectious immigrants is globally asymptotically stable. Numerical simulation was performed and the results displayed graphically and discussed. It was revealed that immigration of infected immigrants contributes significantly in the spread of dengue fever and that it can be controlled by preventing the influx of infected immigrants and reducing the mosquitoes and human contact rate.

Keywords: Dengue Model; endemic equilibrium; infectious immigrants; reproduction number

1. Introduction

Dengue is a vector-borne infection transmitted by the principal vector Aedes aegypti a mosquito specie. A person infected with one serotype of the viruses has partial immunity against the other strains. Dengue infection can only be managed since there is no yet a specific medication and that awareness is very important in controlling the infection and staying uninfected. Due to the complex nature of the viruses, it is said to be the most challenging arboviruses infection to deal with [1].

Dengue is regarded as a re-emerging deadly infectious disease and the most threatening health problem around the world in recent times [2–4]. Global accounts on dengue shows that some 2.5 billion people in the world today are susceptible to dengue infection and about 100 million infections of dengue fever of which over 500000 dengue incidence are dengue hemorrhagic fever occur yearly and close to 25000 die from dengue [5].

Dengue disease is prevalence in the tropical and subtropical regions such as Africa, Asia the Americans, Eastern Mediterranean and the Caribbean [6]. Dengue infection has astronomically increased across the nations with an estimation of almost 390 million infections yearly [7].

Dengue is increasingly becoming a worrying health issue to humanity especially to people living in these regions. Some 3.9 billion people around the globe are estimate to interact with dengue virus infection [7]. Individuals bitten by an infected mosquito starts to manifest symptoms of dengue fever for the period of 2 to 7 days. The virus goes through the period of 3 to 14 days to be able to invade the host body [1].

Mathematical models provide an effective and efficient tool to unravel the transmission dynamics and better understanding to the spread of infections in epidemiology [8–11]. Different models over the years have been proposed and analysed to study the dynamics of infectious diseases [12–19].

Karanja et al. [20] formulated SIR/SI mathematical model incorporated with mobility or movement of people from one area to another area to investigate the dynamics of dengue. Basically the model was to investigate the nature of spread among people when they move from one place to another. Onsongo et al. [21] constructed a mathematical model incorporated with Wolbachia-carrying mosquitoes as an intervention or effective tool to reduce dengue fever.

Nuraini et al. [1] proposed a two strain SIR epidemic model to investigate the dynamic nature of dengue fever. Their model assumed that infection with one strain brings permanent immunity against that strain but severe complications are brought about by an infection with a second strain which leads to DHF. Researchers in [21] developed a model incorporated with loss of immunity to examine the dynamism of dengue fever in terms of its transmission process. The work showed that immunity and loss of immunity are very crucial in dengue epidemic control.

Figure 1 shows the situational report on countries affected with dengue fever.

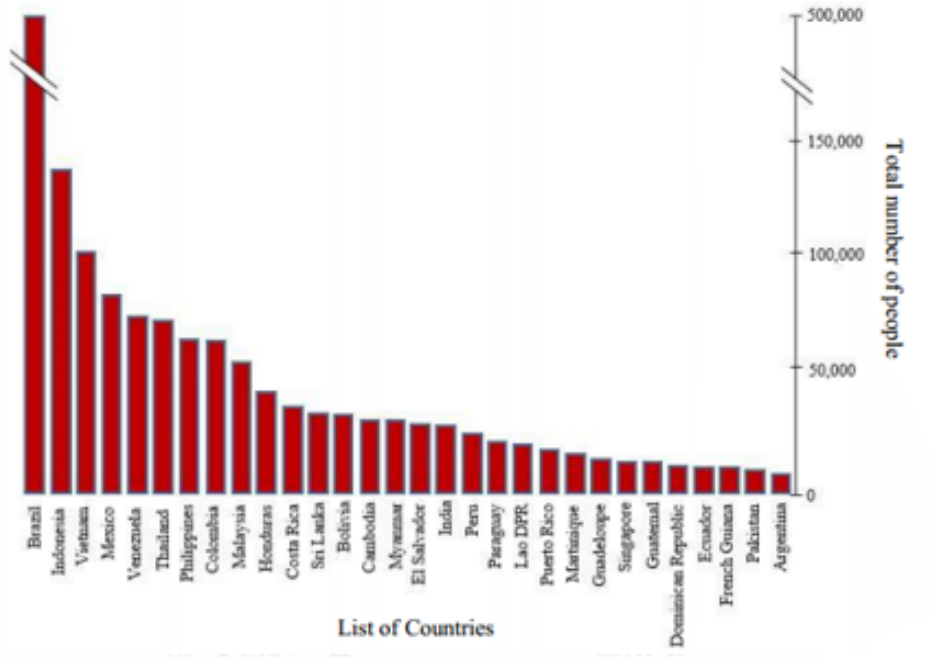

Figure 1. Dengue endemic countries, Source: World Health Organisation (2004).

2. Dengue model description and formulation

The Dengue model is divided into two groups, human and vector populations as shown in **Figure 2**. The populations at any time t are also divided into five subcompartments with respect to their status of the disease in the system. Human population denoted by (N_h), is divided into subpopulations such as Susceptible humans(S_h), Infected humans (i_h), and Recovered humans (R_h).

Table 1. Dengue model variables and their interpretations.

Variable	Interpretations
$S_h\,(t)$	Individuals who are at risk of contracting Dengue infection
$I_h\,(t)$	Individuals who are showing symptoms of Dengue infections
$R_h\,(t)$	Individuals who have recovered from Dengue infections
$S_v\,(t)$	Mosquitoes that are at risk of contracting Dengue infections
$I_v\,(t)$	Mosquitoes that are showing symptoms of Dengue infections

Tables 1 and **2** shows the Dengue fever model variables, parameters and their interpretations respectively.

Table 2. Dengue model parameters and their interpretations.

Parameter	Interpretation
$\wedge$	Constant recruitment rate by birth and immigration
$(1-\emptyset)$	A fraction of humans susceptible to dengue infection
$\emptyset$	A fraction of the infective human immigrants
β_h	Human contact rate
α_h	Natural death rate for humans
ρ_h	Diseased-induced death rate for humans
$\wedge_v$	Recruitment rate for mosquitoes
β_v	Mosquito contact rate
α_v	Natural death rate for mosquitoes
θ_h	Recovery rate for humans
π_h	Rate of rejoining the susceptible class

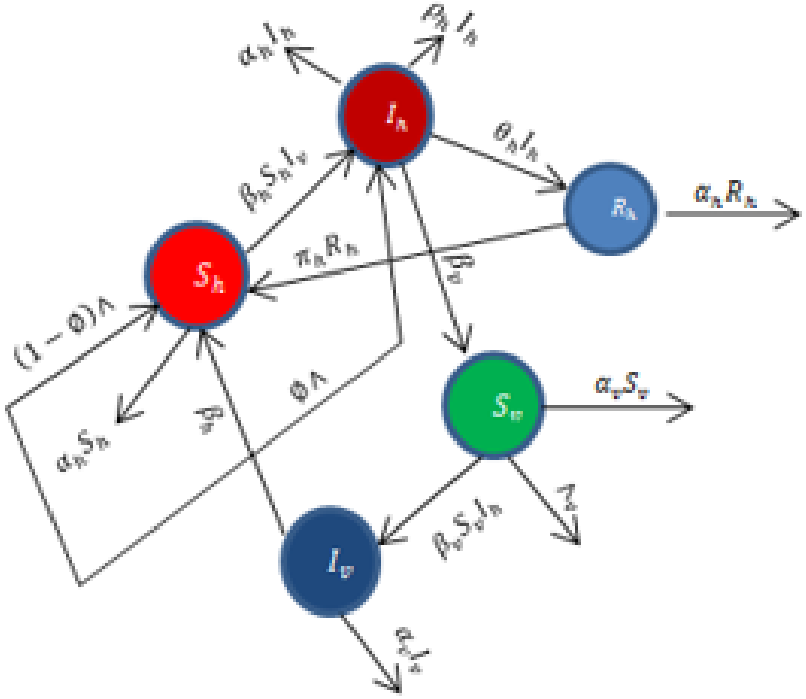

Figure 2. Flow diagram of Dengue model.

Figure 2 shows the Flow diagram of Dengue model. Both humans and mosquitoes become infected with dengue at a rate $\beta_h S_h I_v$ and $\beta_v S_v I_h$ respectively.

The total human population is given by:

$$N_h(t) = S_h(t) + I_h(t) + R_h(t) \tag{1}$$

The vector population represented by N_v is divided into subpopulations of susceptible vector(S_v), and Infectious vector (I_v). The total vector population is given by:

$$N_v(t) = S_v(t) + I_v(t). \tag{2}$$

The following system of ordinary differential equations is obtained from the model:

$$\begin{cases} \frac{dS_h}{dt} = (1-\emptyset)\wedge + \pi_h R_h - \alpha_h S_h - \beta_h S_h I_v \\ \frac{dI_h}{dt} = \emptyset\wedge + \beta_h S_h I_v - \theta_h I_h - \alpha_h I_h - \rho_h I_h \\ \frac{dR_h}{dt} = \theta_h I_h - \pi_h R_h - \alpha_h R_h \\ \frac{dS_v}{dt} = \wedge_v - \alpha_v S_v - \beta_v S_v I_h \\ \frac{dI_v}{dt} = \beta_v S_v I_h - \alpha_v I_v \end{cases} \tag{3}$$

3. Dengue model analysis

3.1. Positivity and boundedness of solutions

Positivity and boundedness of the solutions to the system of differential equations 3 of the dengue model prove for the biological validity of the model if all the solutions with non-negative initial conditions maintain non-negative with time. A negative population is not biologically feasible.

Theorem 1. *Let* $\sigma = (S_h(t), I_h(t), R_h(t), S_v(t), I_v(t)) \in \mathbb{R}^5_+ : (S_h(0), I_h(0),$ $r\ R_h(0),\ S_v(0), I_v(0)) > 0$ *then the solution region* $\sigma = S_h(t),\ I_h(t),\ R_h(t),$ $S_v(t),\ I_v(t)$ *is always non-negative at all time* $t \geq 0$. *and will remain positive in* $\mathbb{R}^5_+$.

This implies that, if $S_h(0),\ I_h(0),\ R_h(0),\ S_v(0),\ I_v(0)$ are non-negative, then $S_h(t), I_h(t), R_h(t), S_v(t), I_v(t)$ are also non-negative for all time $t > 0$.

From system (3) human population at any time, *t* is given by:

$$N_h(t) = S_h(t) + I_h(t) + R_h(t) \tag{4}$$

$$\frac{dN_h}{dt} = (1-\emptyset)\wedge + \emptyset\wedge - \alpha_h(R_h + S_h + I_h) - \rho_h I_h \tag{5}$$

In the absence of mortality due to dengue infections:
$\frac{dN_h}{dt} \leq (1-\emptyset)\wedge - \alpha_h N_h$.

$$N_h \leq \frac{(1-\emptyset)\wedge}{\alpha_h} + \left[N_h(0) - \frac{(1-\emptyset)\wedge}{\alpha_h}\right] e^{-\alpha_h t} \tag{6}$$

At $t \to \infty$, the population size, $N_h \to \frac{(1-\emptyset)\wedge}{\alpha_h}$.
$0 \leq N_h \leq \frac{(1-\emptyset)\wedge}{\alpha_h}$ and $N_h(t) \leq \frac{(1-\emptyset)\wedge}{\alpha_h}$.
Also, if $N_h(0) \leq \frac{(1-\emptyset)\wedge}{\alpha_h}$, then $N_h(t) \leq \frac{(1-\emptyset)\wedge}{\alpha_h}$

$$\sigma_h = \left\{(S_h, I_h, R_h) \in \mathbb{R}^3_+ : S_h + I_h + R_h \leq \frac{(1-\emptyset)\wedge}{\alpha_h}\right\} \tag{7}$$

From system (3) mosquito population at any time t is given by:

$$N_v(t) = S_v(t) + I_v(t) \tag{8}$$

$$\frac{dN_v}{dt} = \wedge_v - (S_v + I_v)\alpha_v \tag{9}$$

$\frac{dN_v}{dt} \leq \wedge_v - N_v\alpha_v$.

$$N_v = N_v(0)\, e^{-\alpha_v t} + \frac{\wedge_v}{\alpha_v}\left[1 - e^{-\alpha_v t}\right] \tag{10}$$

At $t \to \infty$, the population size, $N_v \to \frac{\wedge_v}{\alpha_v}$
$0 \leq N_v \leq \frac{\wedge_v}{\alpha_v}$ and $N_v(t) \leq \frac{\wedge_v}{\alpha_v}$
Also, if $N_v(0) \leq \frac{\wedge_v}{\alpha_v}$, then $N_v(t) \leq \frac{\wedge_v}{\alpha_v}$
Therefore,

$$\sigma_v = \left\{(S_v, I_v) \in \mathbb{R}^3_+ : S_v + I_v \leq \frac{\wedge_v}{\alpha_v}\right\} \tag{11}$$

Feasible region is given by:

$$\sigma = \sigma_h \times \sigma_v \subset R^3_+ \times R^2_+ \tag{12}$$

where,

$$\sigma_h = \left\{(S_h, I_h, R_h) \in R^3_+ : S_h + I_h + R_h \leq \frac{(1-\emptyset)\wedge}{\alpha_h}\right\} \tag{13}$$

and

$$\sigma_v = \left\{(S_v, I_v) \in R^3_v : S_v + I_v \leq \frac{\wedge_v}{\alpha_v}\right\} \tag{14}$$

where, σ is positively invariant set of the system 3.

3.2. Existence of the equilibria

In this section, we examine the existence of the equilibrium points. It can be noticed that the region σ is positively invariant with respect to the system 3. To compute the steady states of system 3, we set the derivatives with respect to time in system 3 equal to zero, and then on simplification, the following algebraic expressions are obtained:

$$S^*_h = \frac{\left[(1-\emptyset)\wedge(\pi_h+\alpha_h)+\pi_h\theta_h I^*_h\right]\left[\alpha_v\left(\alpha_v+\beta_v I^*_h\right)\right]}{\left(\pi_h+\alpha_h\left[\beta_h\beta_v\wedge_v I^*_h+\alpha_v\alpha_h\left(\alpha_v+\beta_v I^*_h\right)\right]\right)}, I^*_v = \frac{\beta_v\wedge_v I^*_h}{\alpha_v\left(\alpha_v+\beta_v I^*_h\right)}$$

We put the two expressions into second equation in system (3) to give the quadratic expression:

$$\begin{aligned}\left(\frac{\beta_h\beta_v\wedge_v\pi_h\theta_h}{(\pi_h+\alpha_h)\,\alpha_v^2\alpha_h\,(\alpha_h+\rho_h+\theta_h)} - \frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} - \frac{\beta_v}{\alpha_v}\right) I_h^2 + \\ \left(\frac{\emptyset\wedge\beta_v}{\alpha_v\,(\alpha_h+\rho_h+\theta_h)} + (R_0^2-1)\right) I_h + \\ \left(\frac{\emptyset\wedge\beta_v\beta_h}{\alpha_v^2\alpha_h\,(\alpha_h+\rho_h+\theta_h)} + \frac{\emptyset\wedge}{(\alpha_h+\rho_h+\theta_h)}\right) = 0\end{aligned} \tag{15}$$

We consider the following cases:
For the case $\emptyset = 0$, equation (15) reduces to

$$\left(\frac{\beta_h\beta_v\wedge_v\pi_h\theta_h}{(\pi_h+\alpha_h)\,\alpha_v^2\alpha_h\,(\alpha_h+\rho_h+\theta_h)} - \frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} - \frac{\beta_v}{\alpha_v}\right) I_h^2 + \left(R_0^2-1\right) I_h = 0 \tag{16}$$

Equation (16) produces two roots, it has one root $I_h = 0$, which demonstrates absence of dengue infection in the population at $\emptyset = 0$ and a second root;

$$I_h = \frac{\left(R_0^2 - 1\right)\left[\left(\pi_h + \alpha_h\right)\alpha_v^2\alpha_h\left(\alpha_h + \rho_h + \theta_h\right)\alpha_v^2\alpha_h\alpha_v\right]}{\left(\ \beta_v\beta_h \wedge_v + \beta_v - \beta_h\beta_v \wedge_v \pi_h\theta_h\right)}, \tag{17}$$

Which shows the presence and persistence of dengue infection in the population. Equation (19) is positive provided,

$$\left(R_0^2 - 1\right)\left[\left(\pi_h + \alpha_h\right)\alpha_v^2\alpha_h\left(\alpha_h + \rho_h + \theta_h\right)\alpha_v^2\alpha_h\alpha_v\right] > 0 \tag{18}$$

It is therefore showed that if $\emptyset = 0$, the model demonstrates a disease-free and endemic equilibrium points. We then interrogate the disease-free and endemic equilibrium points.

4. Disease free equilibrium

For disease free we assumed that all the immigrants enter into the population as susceptible thus,$\emptyset = 0$, hence; $I_h = 0, I_v = 0, R_h = 0$. we set the derivatives of system equations in 3 to zero, and then on simplification, the disease free equilibrium point E_0 is obtained as;

$$E_0 = \left\{\frac{(1 - \emptyset)\wedge}{\alpha_h},\ 0,\ 0,\ \ \frac{\wedge_v}{\alpha_v},\ 0\right\} \tag{19}$$

5. Dengue reproductive number

We adopt the "Next Generation Matrix" technique to determine R_0. Dengue reproductive number depicts the number of secondary cases produced on the average by one infected mosquito or person in a completely susceptible population. The spread of the disease is determined by the threshold parameter.

Considering only the infection states in the system in 3:

$$\frac{dI_h}{dt} = \emptyset \wedge + \beta_h S_h I_v - \alpha_h I_h - \rho_h I_h - \theta_h I_h \tag{20}$$

$$\frac{dI_v}{dt} = \beta_v S_v I_h - \alpha_v I_v \tag{21}$$

Let F be the number of new infections coming into the system and V be the number of infections that are leaving the system.

$$F = \begin{bmatrix}\beta_h S_h I_v \\ \beta_v S_v I_v\end{bmatrix}, V = \begin{bmatrix}(\theta_h + \alpha_h + \rho_h)I_h \\ \alpha_v I_v\end{bmatrix}$$

The Jacobian matrix of F and V at disease free equilibrium is obtained as:

$$F = \begin{bmatrix}0 & \beta_h S_h \\ \beta_v S_v & 0\end{bmatrix} = \begin{bmatrix}0 & \frac{\beta_h(1-\emptyset)\wedge}{\alpha_h} \\ \frac{\beta_v \wedge_v}{\alpha_v} & 0\end{bmatrix} \tag{22}$$

$$V = \begin{bmatrix}\theta_h + \alpha_h + \rho_h & 0 \\ 0 & \alpha_v\end{bmatrix} \tag{23}$$

$$FV^{-1}\left(E_0\right)=\begin{bmatrix}0 & \beta_h\frac{(1-\emptyset)\wedge}{\alpha_h\alpha_v}\\ \frac{\beta_v\wedge_v}{\alpha_v(\theta_h+\alpha_h+\rho_h)} & 0\end{bmatrix} \tag{24}$$

Computing the eigenvalues ofFV^{-1} . Let λ represent the eigenvalue to determine the basic reproduction number R_0 by computing $\left|FV^{-1}(E_0)-\lambda I\right|=0$ and select the dominant eigenvalue.

$$\begin{vmatrix}0-\lambda & \beta_h(1-\theta)\wedge/\alpha_h\alpha_v\\ \beta_v\wedge_v/\alpha_v(\theta_h+\alpha_h+\rho_h) & 0-\lambda\end{vmatrix}=0 \tag{25}$$

$$\lambda^2-\left[\left(\frac{\beta_h\left(1-\emptyset\right)\wedge}{\alpha_h\alpha_v}\right)\left(\frac{\beta_v\wedge_v}{\alpha_v\left(\theta_h+\alpha_h+\rho_h\right)}\right)\right]=0 \tag{26}$$

$$\lambda=\pm\sqrt{\left(\frac{\beta_h\left(1-\emptyset\right)\wedge}{\alpha_h\alpha_v}\right)\left(\frac{\beta_v\wedge_v}{\alpha_v\left(\theta_h+\alpha_h+\rho_h\right)}\right)} \tag{27}$$

The basic reproduction number is determined as the dominant eigenvalue of the matrix FV^{-1}. Therefore

$$\lambda=+\sqrt{\left(\frac{\beta_h\left(1-\emptyset\right)\wedge}{\alpha_h\alpha_v}\right)\left(\frac{\beta_v\wedge_v}{\alpha_v\left(\theta_h+\alpha_h+\rho_h\right)}\right)}$$

$$R_0=\sqrt{\left(\frac{\beta_h\left(1-\emptyset\right)\wedge}{\alpha_h\alpha_v}\right)\left(\frac{\beta_v\wedge_v}{\alpha_v\left(\theta_h+\alpha_h+\rho_h\right)}\right)} \tag{28}$$

It can be deduced from equation (28) that higher values of $\beta_h,\beta_v,\wedge,\wedge_v$ Can lead to a surge and outbreak of the Dengue infection in the population and that the infection may persist and become endemic in the population. And lower values of the parameters can also lead to a reduction in the infection leading to the extinction of the infection from the population. So that if $\beta_h\left(1-\emptyset\right)\wedge\beta_v\wedge_v>\alpha_v\left(\theta_h+\alpha_h+\rho_h\right)\alpha_h\alpha_v$ the disease will persist in the population and that $R_0^2>1$ and if $\beta_h\left(1-\emptyset\right)\wedge\beta_v\wedge_v<\alpha_v\left(\theta_h+\alpha_h+\rho_h\right)\alpha_h\alpha_v$then it is obvious to show that $R_0^2<1$, and the disease dies out.

6. Endemic equilibrium

In this section we consider the state of the model where dengue infection persists in the population. Thus, the case $\emptyset>0$, and that $I_h\neq0,\ R_h\neq0\ and I_v\neq0$. Then Equation (17) is written as

$$\begin{aligned}\left(-\frac{\beta_h\beta_v\wedge_v\pi_h\theta_h}{\left(\pi_h+\alpha_h\right)\alpha_v^2\alpha_h\left(\alpha_h+\rho_h+\theta_h\right)}+\frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h}+\frac{\beta_v}{\alpha_v}\right)I_h^2-\\ \left(\frac{\emptyset\wedge\beta_v}{\alpha_v\left(\alpha_h+\rho_h+\theta_h\right)}+\left(R_0^2-1\right)\right)I_h-\\ \left(\frac{\emptyset\wedge\beta_v\beta_h}{\alpha_v^2\alpha_h\left(\alpha_h+\rho_h+\theta_h\right)}+\frac{\emptyset\wedge}{\left(\alpha_h+\rho_h+\theta_h\right)}\right)=0\end{aligned} \tag{29}$$

From Equation (29), two roots can be obtained, one positive and one negative-

biologically meaningless. Therefore the positive root is given by:

$$I_h^* = \frac{\left(\frac{\emptyset \wedge \beta_v}{\alpha_v(\alpha_h+\rho_h+\theta_h)} + R_0^2 - 1\right) + \sqrt{F_a + F_b}}{2\left(\frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} + \frac{\beta_v}{\alpha_v} - \frac{\beta_h\beta_v\wedge_v\pi_h\theta_h}{\alpha_v^2\alpha_h(\pi_h+\alpha_h)(\alpha_h+\rho_h+\theta_h)}\right)}$$

where

$$F_a = \left(\frac{\emptyset \wedge \beta_v}{\alpha_v\left(\alpha_h+\rho_h+\theta_h\right)} + R_0^2 - 1\right)^2$$

$$F_b = 4\left(\frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} + \frac{\beta_v}{\alpha_v} - \frac{\beta_h\beta_v\wedge_v\pi_h\theta_h}{\alpha_v^2\alpha_h(\pi_h+\alpha_h)(\alpha_h+\rho_h+\theta_h)}\right)\left(\frac{\emptyset\wedge\beta_v\beta_h}{\alpha_v^2\alpha_h(\alpha_h+\rho_h+\theta_h)} + \frac{\emptyset\wedge}{(\alpha_h+\rho_h\theta_h)}\right)$$

So the unique endemic equilibrium is given by

$E^* = \{S_h^*,\ I_h^*,\ \ R_h^*,\ \ S_v^*,\ \ I_v^*\}$ where $S_h^*,\ I_h^*,\ \ R_h^*,\ \ S_v^*,\ \ I_v^*$ are determined from the system equation in 3 as:

$$S_h^* = \frac{\left[(1-\emptyset)\wedge(\pi_h+\alpha_h)+\pi_h\theta_h I_h^*\right]\left[\alpha_v\left(\alpha_v+\beta_v I_h^*\right)\right]}{\left(\pi_h+\alpha_h\left[\beta_h\beta_v\wedge_v I_h^*+\alpha_v\alpha_h\left(\alpha_v+\beta_v I_h^*\right)\right]\right)}$$

$$I_h^* = \frac{\left(\frac{\emptyset \wedge \beta_v}{\alpha_v(\alpha_h+\rho_h+\theta_h)} + R_0^2 - 1\right) + \sqrt{F_a + F_b}}{2\left(\frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} + \frac{\beta_v}{\alpha_v} - \frac{\beta_h\beta_v\wedge_v\pi_h\theta_h}{\alpha_v^2\alpha_h(\pi_h+\alpha_h)(\alpha_h+\rho_h+\theta_h)}\right)}$$

$$I_v^* = \frac{\beta_v\wedge_v I_h^*}{\alpha_v\left(\alpha_v+\beta_v I_h^*\right)}$$

$$R_h^* = \frac{\theta_h I_h^*}{\alpha_h+\pi_h}$$

$$S_v^* = \frac{\wedge_v}{\alpha_v+\beta_v I_h^*} \tag{30}$$

For $\emptyset > 0$, system 3 has an endemic equilibrium point for all parameter values for which the disease will persist in the population. if $R_0 < 1$, then endemic equilibrium approaches disease-free equilibrium point as $\emptyset$ goes to zero, and if $R_0 > 1$, then for $\emptyset \geq 0$ the model has a unique endemic equilibrium.

7. Stability of the equilibrium points

In this section, we analyzed the stability of the disease-free equilibrium E_0 when $\emptyset = 0$, and the endemic equilibrium E^* when $\emptyset = 0$ and $R_0 > 1$.

7.1. Local stability of the disease free equilibrium point E_0

Theorem The disease free equilibrium point is locally asymptotically stable if $\emptyset = 0$ and $R_0 < 1$ and unstable if $R_0 > 1$. The DFE was obtained as; $\left\{\frac{(1-\emptyset)\wedge}{\alpha_h},\ 0,\ 0,\ \ \frac{\wedge_v}{\alpha_v},\ 0\right\}$

The Jacobian matrix of the system is given by:

$$\begin{bmatrix} -\beta_h l_v - \alpha_h & 0 & \pi_h & 0 & -\beta_h s_h \\ \beta_h l_v & -\theta_h - \alpha_h - \rho_h & 0 & 0 & \beta_h s_h \\ 0 & \theta_h & -\pi - \alpha_h & 0 & 0 \\ 0 & -\beta_v S_v & 0 & -\beta_v I_h - \alpha_v & 0 \\ 0 & \beta_v S_v & 0 & \beta_v l_h & -\alpha_v \end{bmatrix} \tag{31}$$

The Jacobian matrix at disease free equilibrium:

DFE $= E_0 = \left(\frac{(1-\emptyset)\wedge}{\alpha_h},\ 0, 0, \frac{\wedge_v}{\alpha_v}, 0\right)$ is given by

$$J(E_0) = \begin{bmatrix} -\alpha_h & 0 & \pi_h & 0 & -\beta_h(1-\theta)\wedge/\alpha_h \\ 0 & (-\theta_h - \alpha_h - \rho_h) & 0 & 0 & \beta_h(1-\theta)\wedge/\alpha_h \\ 0 & \theta_h & -\pi - \alpha_h & 0 & 0 \\ 0 & -\beta_v \wedge_v /\alpha_v & 0 & -\alpha_v & 0 \\ 0 & \beta_v \wedge_v /\alpha_v & 0 & 0 & -\alpha_v \end{bmatrix} \quad (32)$$

The expression $|J(E_O) - \lambda I| = 0$ is then used to calculate the eigenvalues λ.

$$\begin{bmatrix} -\alpha_h - \lambda & 0 & \pi_h & 0 & -\beta_h(1-\theta)\wedge/\alpha_h \\ 0 & (-\theta_h - \alpha_h - \rho_h) - \lambda & 0 & 0 & \beta_h(1-\theta)\wedge/\alpha_h \\ 0 & \theta_h & (-\pi - \alpha_h) - \lambda & 0 & 0 \\ 0 & -\beta_v \wedge_v /\alpha_v & 0 & -\alpha_v - \lambda & 0 \\ 0 & \beta_v \wedge_v /\alpha_v & 0 & 0 & -\alpha_v - \lambda \end{bmatrix} = 0 \quad (33)$$

The eigenvalues to analysed the stability of the DFE are given by:

$\lambda_1 = -\alpha_h \lambda_2 = -\alpha_v,\ \lambda_3 = -(\pi_h + \alpha_h)$ and the quadratic equation;

$$\left\{[(-\theta_h - \alpha_h - \rho_h) - \lambda](-\alpha_v - \lambda) - \left(\frac{\beta_h(1-\emptyset)\wedge}{\alpha_h}\right)\left(\frac{\beta_v \wedge_v}{\alpha_v}\right)\right\} = 0$$

$$\lambda^2 + (\theta_h + \alpha_h + \rho_h + \alpha_v)\lambda + (\theta_h + \alpha_h + \rho_h)\alpha_v - \left(\frac{\beta_h(1-\emptyset)\wedge}{\alpha_h}\right)\left(\frac{\beta_v \wedge_v}{\alpha_v}\right) = 0$$

The roots of the quadratic equation have negative real parts if and only if

$$(\theta_h + \alpha_h + \rho_h)\alpha_v - \left(\frac{\beta_h(1-\emptyset)\wedge}{\alpha_h}\right)\left(\frac{\beta_v \wedge_v}{\alpha_v}\right) > 0$$

$$\frac{(\theta_h + \alpha_h + \rho_h)\alpha_v}{(\theta_h + \alpha_h + \rho_h)\alpha_v} - \frac{\left(\frac{\beta_h(1-\emptyset)\wedge}{\alpha_h}\right)\left(\frac{\beta_v \wedge_v}{\alpha_v}\right)}{(\theta_h + \alpha_h + \rho_h)\alpha_v} > 0$$

$$1 - R_0^2 > 0.$$

Therefore,

$$R_0^2 < 1$$

Therefore E_0 the disease free equilibrium point of system (3) is locally asymptotically stable if $R_0^2 < 1$ and unstable if $R_0^2 > 1$.

7.2. Global stability of the disease-free equilibrium point E_0

The following assumptions are used to examine the global stability of the disease-free equilibrium point E_0.

We assume that all the immigrants that enter into the population are susceptible, that is $\emptyset = 0$. Then,

(1) the disease-free equilibrium $E_0 = \left\{\frac{(1-\emptyset)\wedge}{\alpha_h},\ 0,\ 0,\ \frac{\wedge_v}{\alpha_v},\ 0\right\} \in \sigma$, exists for all non-negative values of its parameters and it is globally asymptotically stable when $R_0 \leq 1$ and it is unstable when $R_0 > 1$.

(2) if $R_0 > 1$, solutions to system 3 starting close to E_0 in σ move away from E_0 except those close to the invariant S_h-axis which approachE_0 along this axis,

(3) if $R_0 > 1$, system 3 has a unique endemic equilibrium $E^* = (S_h,\ I_h, I_v)$.

Proof. Consider the Lyapunov function $P(t) = \beta_v S_v I_h + (\theta_h + \alpha_h + \rho_h) I_v$

The time derivative of P along the solutions of the system in 3;

$$\frac{dp(t)}{dt} = (\beta_v S_v)\frac{dI_h}{dt} + (\theta_h + \alpha_h + \rho_h)\frac{dI_v}{dt} = (\beta_v S_v)$$
$$[\beta_h S_h I_v - (\theta_h + \alpha_h + \rho_h) I_h] + (\theta_h + \alpha_h + \rho_h)[\beta_v S_v I_h - \alpha_v I_v]$$
$$\leq \beta_v S_v \beta_h S_h I_v - (\theta_h + \alpha_h + \rho_h)\alpha_v I_v$$
$$\left(\frac{\beta_h(1-\emptyset)\wedge}{\alpha_h}\right)\left(\frac{\beta_v \wedge_v}{\alpha_v}\right) I_v - (\theta_h + \alpha_h + \rho_h)\alpha_v I_v$$
$$= \alpha_v(\theta_h + \alpha_h + \rho_h) I_v\left[R_0^2 - 1\right] \leq 0, if R_0 \leq 1.$$

The time derivative of P along the solutions of the system of differential equations in 3:

$\left(\frac{dp(t)}{dt}\right) \leq 0$, if and only if $R_0 \leq 1$ and $\left(\frac{dp(t)}{dt}\right) = 0$ only if $I_v = I_h = 0$.

The maximum invariant set in $\left\{(S_h,\ I_h,\ \ R_h,\ S_v,\ I_v) \in \sigma,\ \frac{dp(t)}{dt} = 0\right\}$, is the singleton $E_{0.}$ Where E_0 is the DFE. □

7.3. Local stability of the endemic equilibrium points

In this section, we analysed the local stability of the endemic equilibrium point E^* of the system in 3.

Theorem 2. *If $\emptyset = 0$ and $R_0 > 1$, the unique endemic equilibrium of system (3) is locally asymptotically stable.*

The EE can only exist if and only if $R_0 > 1$ and $\emptyset = 0$. By implication the EE exists. We consider the quadratic expression given by;

$$\left(\frac{\beta_h\beta_v \wedge_v \pi_h\theta_h}{(\pi_h + \alpha_h)\alpha_v^2\alpha_h(\alpha_h + \rho_h + \theta_h)} - \frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} - \frac{\beta_v}{\alpha_v}\right) I_h^2 +$$
$$\left(\frac{\emptyset \wedge \beta_v}{\alpha_v(\alpha_h + \rho_h + \theta_h)} + (R_0^2 - 1)\right) I_h + \tag{34}$$
$$\left(\frac{\emptyset \wedge \beta_v\beta_h}{\alpha_v^2\alpha_h(\alpha_h + \rho_h + \theta_h)} + \frac{\emptyset\wedge}{(\alpha_h + \rho_h + \theta_h)}\right) = 0$$

If $\emptyset = 0$, then equation (36) reduces to:

$$\left(\frac{\beta_h\beta_v \wedge_v \pi_h\theta_h}{(\pi_h + \alpha_h)\alpha_v^2\alpha_h(\alpha_h + \rho_h + \theta_h)} - \frac{\beta_v\beta_h\wedge_v}{\alpha_v^2\alpha_h} - \frac{\beta_v}{\alpha_v}\right) I_h^2 + \left(R_0^2 - 1\right) I_h = 0 \tag{35}$$

By simplification, gives the root:

$$I_h^* = \frac{\left(R_0^2 - 1\right)\left[(\pi_h + \alpha_h)\alpha_v^2\alpha_h(\alpha_h + \rho_h + \theta_h)\alpha_v^2\alpha_h\alpha_v\right]}{(\ \beta_v\beta_h \wedge_v + \beta_v - \beta_h\beta_v \wedge_v \pi_h\theta_h)}. \tag{36}$$

Equation (38) is a positive root and demonstrates the presence and persistence of dengue infection in the susceptible population at $\emptyset = 0$. Provided, $\left(R_0^2 - 1\right)[(\pi_h + \alpha_h)$ $\alpha_v^2\alpha_h(\alpha_h + \rho_h + \theta_h)\alpha_v^2\alpha_h\alpha_v] > 0$.

This implies that $\left(R_0^2 - 1\right) > 0$.

Therefore $R_0^2 > 1$.

Hence the unique endemic equilibrium E^* for $\emptyset = 0.$ and $R_0 > 1$ for system 3 are locally asymptotically stable.

7.4. Global stability of the endemic equilibrium points E^*

We investigate the global stability of the endemic equilibrium points E^* of system 3 using the approach.

Theorem 3. *If $\emptyset = 0$ and $R_0 > 1$, then E_0 becomes unstable and E^* is the unique endemic equilibrium of system 3, and it is globally asymptotically stable.*

It has been established that a model in which a fraction of the new members are infective demonstrates no disease-free equilibrium only when this fraction gradually goes to zero. This implies that the disease always exist for $R_0 > 1$, thus the disease will persist at an equilibrium level if it initially exists. We now establish for the global stability of our system using a defined Lyapunov function. Consider the Lyapunov function defined by:

$$\begin{aligned} L\left(S_h,\ I_h,\ \ R_h,\ S_v,\ I_v\right) = \left(S_h - S_h^* - S_h^* \ln \frac{S_h^*}{S_h}\right) \\ + \left(I_h - I_h^* - I_h^* \ln \frac{I_h^*}{I_h}\right) + \left(R_h - R_h^* - R_h^* \ln \frac{R_h^*}{R_h}\right) \\ + \left(S_v - S_v^* - S_v^* \ln \frac{S_v^*}{S_v}\right) + \left(I_v - I_v^* - I_v^* \ln \frac{I_v^*}{I_v}\right) \end{aligned} \tag{37}$$

Computing the derivative of L along the solution of the system in [3] directly;

$$\begin{aligned} \frac{dL}{dt} = \left(\frac{S_h - S_h^*}{S_h}\right)\frac{dS_h}{dt} + \left(\frac{I_h - I_h^*}{dt}\right)\frac{dI_h}{dt} + \left(\frac{R_h - R_h^*}{R_h}\right)\frac{dR_h}{dt} + \\ \left(\frac{S_v - S_v^*}{S_v}\right)\frac{dS_v}{dt} + \left(\frac{I_v - I_v^*}{I_v}\right)\frac{dI_v}{dt} \end{aligned} \tag{38}$$

Hence

$$\begin{aligned} \frac{dL}{dt} = \left(\frac{S_h - S_h^*}{S_h}\right)\left[(1-\emptyset) \wedge + \pi_h R_h - \alpha_h S_h - \beta_h S_h I_v\ \right] + \\ \left(\frac{I_h - I_h^*}{dt}\right)\left[\emptyset \wedge + \beta_h S_h I_v - \theta_h I_h - \alpha_h I_h - \rho_h I_h\right] \\ + \left(\frac{R_h - R_h^*}{R_h}\right)\left[\theta_h I_h - \pi_h R_h - \alpha_h R_h\ \right] + \\ \left(\frac{S_v - S_v^*}{S_v}\right)\left[\wedge_v - \alpha_v S_v - \beta_v S_v I_h\right] + \left(\frac{I_v - I_v^*}{I_v}\right)\left[\beta_v S_v I_h - \alpha_v I_v\ \right] \end{aligned} \tag{39}$$

This can also be written as:

$$\frac{dL}{dt} = (1-\emptyset) \wedge + \pi_h R_h - \alpha_h S_h - \beta_h S_h I_v \ - \frac{(1-\emptyset) \wedge S_h^*}{S_h} +$$
$$\alpha_h S_h^* - \frac{\pi_h R_h S_h^*}{S_h} + \beta_h S_h^* I_v + \emptyset \wedge + \beta_h S_h I_v -$$
$$(\theta_h + \alpha_h + \rho_h h) I_h - \frac{\emptyset \wedge I_h^*}{I_h} + \theta_h I_h^* + \alpha_h I_h^* + \rho_h I_h^* - \frac{\beta_h I_v S_h I_h^*}{I_h} + \quad (40)$$
$$\theta_h I_h - \pi_h R_h - \alpha_h R_h - \frac{\theta_h I_h R_h^*}{R_h} + \pi_h R_h^* + \alpha_h R_h^* + \wedge_v - \alpha_v S_v - \beta_v S_v I_h$$
$$-\frac{\wedge_v S_v^*}{S_v} + \alpha_v S_v^* + \beta_v I_h S_v^* + \beta_v S_v I_h - \alpha_v I_v - \frac{\beta_v S_v I_h I_v^*}{I_v} + \alpha_v I_v^*$$

Given:

$\frac{dL}{dt} = M - N$ Where M and N are positive and negative respectively. Therefore:

$$M = (1-\emptyset) \wedge + \pi_h R_h + \alpha_h S_h^* + \beta_h S_h^* I_v + \emptyset \wedge + \beta_h S_h I_v + \theta_h I_h^*$$
$$+ \alpha_h I_h^* + \rho_h I_h^* + \theta_h I_h + \pi_h R_h^* + \alpha_h R_h^* + \wedge_v + \alpha_v S_v^* + \beta_v I_h S_v^* \quad (41)$$

$$+\beta_v S_v I_h + \alpha_v I_v^* N = \alpha_h S_h + \beta_h S_h I_v \ + \frac{(1-\emptyset) \wedge S_h^*}{S_h} + \frac{\pi_h R_h S_h^*}{S_h} + (\theta_h + \alpha_h + \rho_h h) I_h$$

$$+ \frac{\emptyset \wedge I_h^*}{I_h} + \frac{\beta_h I_v S_h I_h^*}{I_h} + \pi_h R_h + \alpha_h R_h + \frac{\theta_h I_h R_h^*}{R_h} + \alpha_v S_v + \beta_v S_v I_h \quad (42)$$

$$+\frac{\wedge_v S_v^*}{S_v} \alpha_v I_v - \frac{\beta_v S_v I_h I_v^*}{I_v}$$

If $M < N$, then the derivative of the Lyapunov function with respect to time is less than or equal to zero. If M<N, then $\frac{dL}{dt} \leq 0$.

But $\frac{dL}{dt} = 0$, if and only if:

$S_h = S_h^*, I_h = I_h^*, R_h = R_h^*, S_v = S_v^*, I_v = I_v^*$ The largest invariant set in:

$$\left\{ (S_h^*, I_h^*, R_h^*, S_v^*, I_v^*) \in \sigma : \frac{dL}{dt} = 0 \right\} \quad (43)$$

Is singleton E^*, where E^* is the EE.

Since all the model parameters are assumed to be non-negative, then the derivative of the Lyapunov function is less than or equal one, if R_0 of the system in 3 is greater than one, $(R_0 > 1)$. Hence by LaSalle's Invariant Principle, as t approaches infinity, all the solution of the system in 3 approaches the EE point if $R_0 > 1$. Hence, EE is globally asymptotically stable in the invariant set if $M < N$.

Numerical Simulations

Numerical simulation was done by solving the state equations of the model in **Figure 2** using Range-Kutta fourth order scheme.

Table 3 shows values of parameters and variables used in the simulation of the model in **Figure 2**.

Table 3. Variables and parameter values of Dengue model.

Parameter	Values	Reference
θ_h	0.9	[18]
$\wedge$	1.2	[19]
$\wedge_v$	300	Assumed
β_v	0.09	Assumed
β_h	0.01	[18]
α_h	0.05	Assumed
α_v	2	[18]
ρ_h	0.01	[18]
π_h	0.5	Assumed
θ	0.32	[19]

8. Sensitivity analysis of the basic reproductive number, R_0

In Biological modelling, the basic reproduction number is important in the study of infectious diseases and it determines the threshold of infection for the spread of the infection and determines whether an epidemic will occur in a population. Hence the effectiveness of the parameters on the basic reproductive number is carried out. Sensitivity analysis demonstrates the importance of each parameter in the transmission of the infection. Sensitivity analysis provides for the robustness of the model to the parameter values, and helps to identify the most effective parameter with respect to the basic reproductive number and inform policy direction in the quest to eradicate or eliminate the infection from the population, so as to adopt optimal control strategies.

8.1. Disease free equilibrium

(1) If the values of β_h and β_v are decreased to 0.001 and 0.04 respectively or more and the values of the other parameters remain same then $R_0 < 1$. That is dengue fever dies out.

(2) If the values of $\wedge_v$ and $\wedge$ are decreased to 125 and 1.0 respectively or more and the values of the other parameters remain same then $R_0 < 1$. That is the disease dies out.

(3) If $\emptyset = 0$ and other parameters maintain same values, then $R_0 < 1$ that is the disease dies out.

8.2. Endemic equilibrium

Substituting the parameter values in Table 3 into the R_0 formula, since it corresponds to the endemic equilibrium and it is stable, this implies that the dengue fever will persist, with $R_0 > 1$.

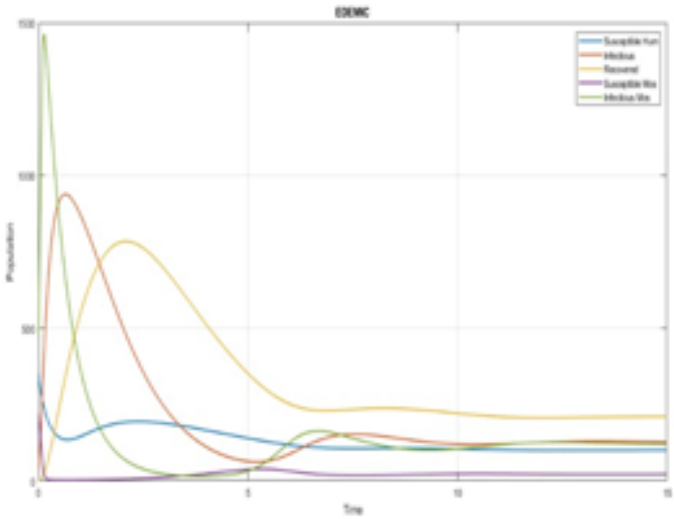

Figure 3. Time responses of the state variables S_h, I_h, S_v, I_v.

The parameter values in **Table 3** were used to perform the simulations of the model. **Figure 3** above describes the simulation of the population sizes S_h, I_h, R_h, S_v, I_v plotted against time. From **Figure 3** above it can be observe that; all the five populations co-exist and approaches endemic equilibrium, which indicate clearly that dengue infections will persist in the populations. **Figure 2** again demonstrates that the basic reproductive number $R_0 > 1$ with the endemic equilibrium points; $E_0{}^* = (S_h{}^*, I_h{}^*, R_h{}^*, S_v{}^*, I_v{}^*)$ being locally asymptotically stable. **Figure 3** shows that susceptible population initially decreases at low level and then kept constant to its carrying capacity. The infectious human population initially increase which lead to many susceptible individuals get infection due to the influx of infected immigrants but decreases with time to become stable due to more individuals recovering from the infection. It again shows that the recovery population decreases with time which means the natural resistance to the second strain of infection is impossible.

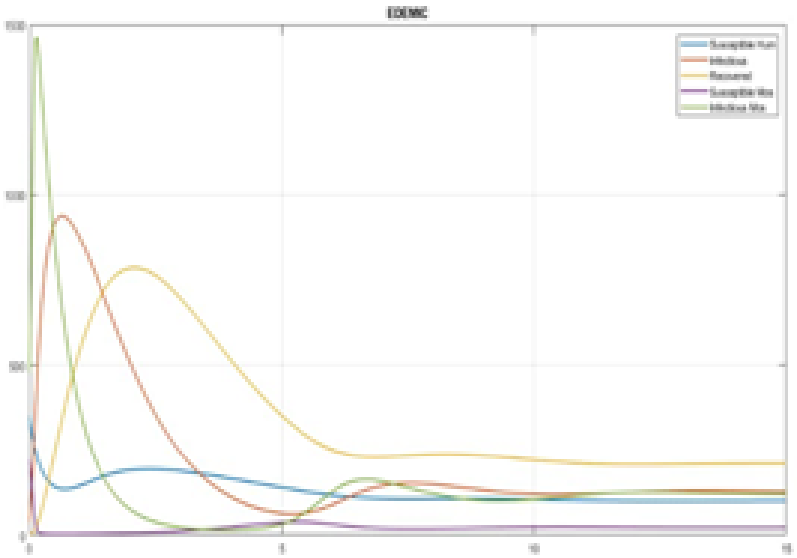

Figure 4. Time responses of the state variables S_h, I_h, S_v, I_v.

Figure 4 shows the simulation of parameter values in **Table 3**. But we put $\emptyset = 0$ to analysed the sensitive nature of the model at $\emptyset = 0$. Here we observed from the simulation that if infective immigrant is zero, the model still approaches endemic equilibrium, where all the populations in terms of the disease statutes coexist. It therefore indicates that $\emptyset = 0$, does not depict absence of infection in the population rather, the model is depicting that in the presence of infective immigrants there cannot be a disease free population. Thus, a small number of infectious immigrants can cause infection. This affirms Equation (19).

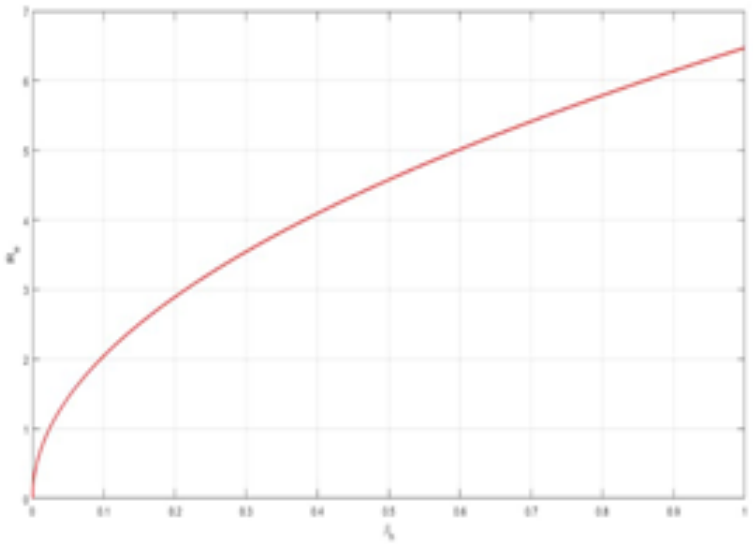

Figure 5. Relationship between R_0, and β_h.

Figure 5 shows the simulation of the R_0 as against the human transmission or contact rate β_h. From **Figure 5** we noticed that the basic reproduction number increases exponentially as the human contact with the infected mosquitoes increase with time.

The basic reproduction number shows a significant trend of dengue infection in the human population with respect to contact; people become infected when their contact with the mosquitoes increases. We notice that a small contact has the potential to cause infection as shown by the basic reproduction number.

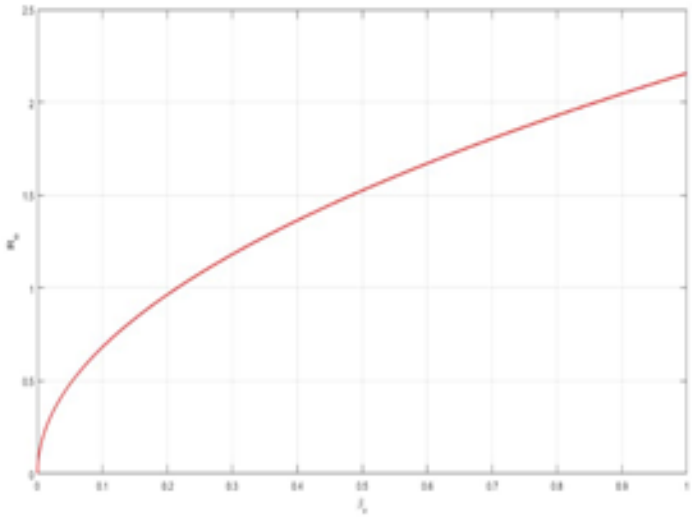

Figure 6. Relationship between R_0, and β_v.

Figure 6 shows the simulation of the R_0 as against the vector transmission or contact rate β_v. From **Figure 5** we noticed that the basic reproduction number increases asymptotically as the mosquito contact with the infected humans increase with time. The basic reproduction number shows a significant number of mosquitoes infected with dengue infection when their contact increases with time. This explains that as more mosquitoes become infected, the ripple effect is more people will then become infected and also shows the relationship of the basic reproductive number in terms of mosquito contact.

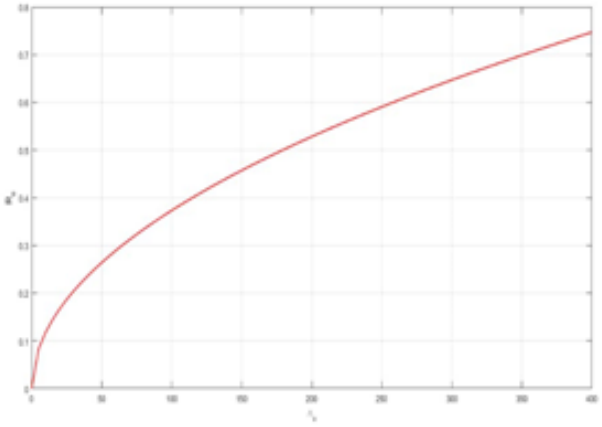

Figure 7. Relationship between R_0 and $\wedge_v$.

Figure 7 show that as more mosquitoes are borne into the system, more susceptible individuals become infected, thus their number go up causing dengue infection in the

system to go up.

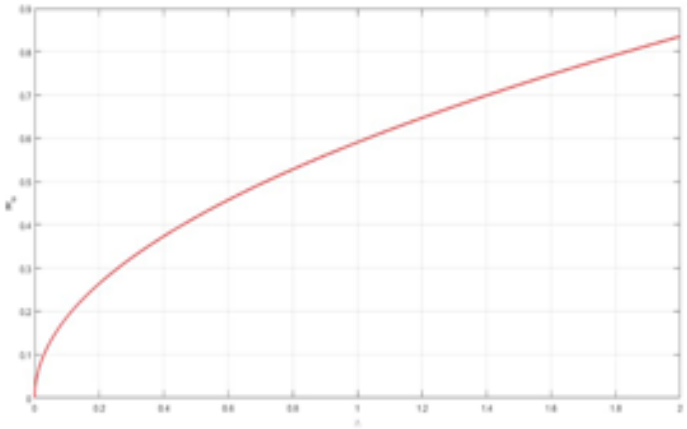

Figure 8. Relationship between R_0 and $\wedge$.

It can be observed from **Figure 8** that, as more humans are both borne and migrated into the the system the basic reproduction number also increase asymptotically, indicating increase in dengue infection.

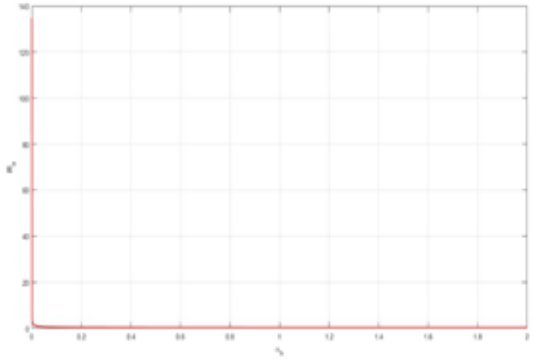

Figure 9. Relationship between R_0 and α_h.

Figure 9 shows that the basic reproduction number decreases with increase in the remove rate of humans. Thus as more humans are removed either by death or migration, the reproduction number decrease approaching zero.

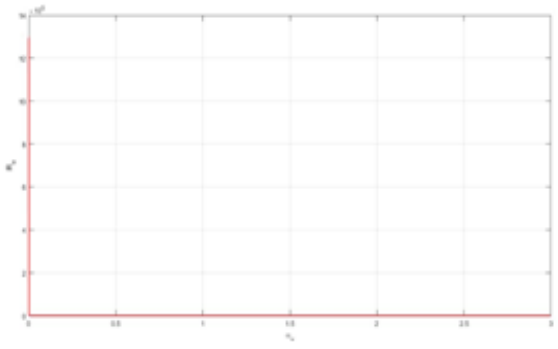

Figure 10. Relationship between R_0 and α_v.

Figure 10 shows that the rate the basic reproduction number decreases with increase in the remove rate of mosquitoes.Thus as more mosquitoes are removed either by death or migration, the reproduction number decreases approaching zero.

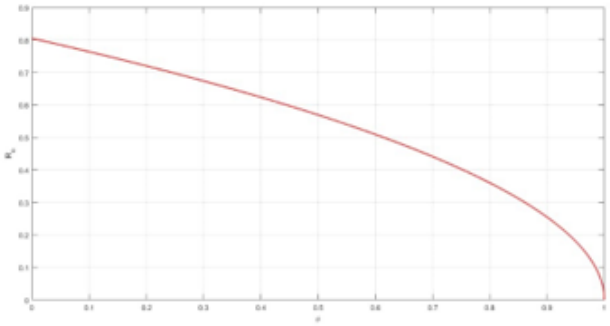

Figure 11. Relationship between R_0 and $\emptyset$.

The simulation shows that the reproduction number increases asymptotically as the number of infective immigrants increases. This depicts the already established that, at $\emptyset \geq 0, R_0 > 1$. Significantly, it also shows that a small influx of infectious immigrants can cause infection as shown in **Figure 11**.

9. Discussion and conclusion

In this paper, we propose a mathematical model that analysed the dynamics of host-vector disease such as dengue fever. Our propose dengue model incorporated with immigration of infective humans. The theorems of the existence of disease-free and diseas-endemic equilibrium points were analysed by the model. The model demonstrated clearly that in the presence of infective immigrants, the model cannot exhibit a disease free state and that a steady state with a positive fraction of infective immigrants always exist, whereby the disease persist in the population for a very long time and this can be verify by **Figure 3** where $\emptyset = 0$ and the $R_0 > 1$ and **Figure 2**. The basic reproduction number in this case can only show some significance in the eradication of the infection only when the fraction of the infective immigrants approaches zero that the frequent influx of the infective immigrants will always make the basic reproductive number a little effective in the disease control. Our analysis showed that if the reproduction number is less than one then the (DFE) is locally asymptotically stable. Moreover, if the reproduction number is greater than one the (EE) is stable and the model approaches endemic equilibrium. Where the disease persist in the population. This has been verified numerically by simulations in **Figures 2** and **3**. **Figures 4-9** shows the graphs of the reproduction number in terms of the parameters $\beta_h, \beta_v, \wedge_v, \wedge, \alpha_h, \alpha_v$

Our sensitivity analysis shows that the most effective parameters are infection rate of humans β_h, infection rate of mosquitoes β_v, which are verified numerically by simulations in **Figures 4** and **5**. These results are useful in predicting dengue transmission and provides the clue to an effective methodology to adopt in preventing dengue fever.

This work has demonstrated that human migration features prominently in the

transmission and spread of dengue virus infection. Small migratory influx of infected individuals plays essential role in the transmission of dengue fever. For $\emptyset = 0$ and $R_0 > 1$, the unique endemic equilibrium point is globally asymptotically stable and dengue disease will persist in the population.

Author contributions: Conceptualization, EKD and SO; methodology, SO and OD; validation, OD and MB; formal analysis, MA and SO; supervision, EKD and OD; writing original draft preparation, EYB and MA; writing review and editing, MB and EYB. All authors have read and agreed to the published version of the manuscript.

Acknowledgments: Authors profoundly acknowledged the encouragement and support from members of department. Our appreciation goes to the numerous review comments and suggestions. Authors have expressed their gratitude for such a wonderful support and comments.

Data availability statement: The data supporting this model analysis are taken from published articles and are cited at relevant places within the text as references. Some of the parameter values are assumed.

Conflict of interest: The authors declare no conflict of interest.

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