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Bifurcation and Global Stability Analysis of a Zika Virus Model

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Abstract
In this paper, global stability of disease free equilibrium and endemic equilibrium point of a Zika virus model was considered with backward bifurcation analysis. It was found that the disease free equilibrium and endemic equilibrium points were globally asymptotically stable if the effective reproduction number is less than unity and greater than unity respectively. It was also discovered that the situation where a stable disease free equilibrium coexist with a stable endemic equilibrium does not occur if the effective reproduction number is less than unity, as such backward bifurcation does not exist. Numerical simulations confirmed the global stability of both the disease-free and the endemic equilibrium state.

Keywords: Zika Virus, Backward Bifurcation, Global Stability.

INTRODUCTION
Zika virus (ZIKV) is a Flavivirus belonging to the family of Flaviviridae. Specifically, ZIKV transmission is basically vector-borne, however, in some circumstances it can also be transmitted through sexual contact and blood transfusions process. The virus was subsequently isolated from Aedes mosquitoes and humans in 1948 and 1954, respectively. The virus is closely related to many other well-known notorious pathogen causing encephalitis viruses such as Dengue, Japanese encephalitis and West Nile virus. Two species of mosquitoes, namely, Aedes aegypti and Aedes albopictus, were identified as the main vectors for ZIKV transmission. ZIKV was first discovered from a Rhesus monkey during a research study on Yellow fever in Zika Forest, Uganda in 1947 (Suparit *et al.*, 2018). Epidemiologically, ZIKV cases were only sporadically recorded in some African and

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Southeast Asian countries until the late 2000s. Over 19,000 suspected cases were estimated during this epidemic. Since then, the expansion of the outbreaks seems unstoppable. The situation was worse when the virus reached and became well-established in Latin America; Brazil is one of the most affected countries. The number of suspected cases in Brazil was estimated at 440,000 to 1,300,000 in 2015 (Nugent *et al.,* 2017).

Even though, human infections were demonstrated by serology to have occurred previously in East Africa, the virus was demonstrated in the first human case(s) in Nigeria in 1954 and subsequently in different settings. Further studies have demonstrated transmission in East Africa, West Africa, Asia, and the Pacific Islands. Previous evidence of detection of Zika virus in man, and antibodies to Zika virus in Nigerian populations, together with the presence of the vectors indicate that the virus is widely circulated in Nigeria. Thus, in the absence of continued surveillance or periodic national surveys, the epidemiology of the Zika virus in Nigeria remains poorly understood. Majority of those infected with Zika remain asymptomatic. For those who develop symptoms, fever, rash, conjunctivitis, headaches, muscle and joint pains typically start three to six days after infection. The virus may however stay in the body for weeks following infection (Kindhauser *et al.*, 2016; Karwowski *et al.,* 2016; NCDC, 2016).

Although the limited number of published studies on the short- and long-term impacts of ZIKV restricts us from highlighting its social impact, the studies are considered to be of substantial value. ZIKV has been affecting tourism and hampering commercial turnover. Disability due to the ZIKV is associated with lower education levels, higher unemployment status, and additional financial costs for families. The growing demand for proper health care and support services for users with neurological sequelae perpetuates the rooted poverty cycle and contributes to the strain put on the different levels of health care. Globally ZIKV has the potential to spread across all continents, therefore, it is critical to characterize the transmission dynamics of the disease (Dias *et al.*, 2018; Bonyah and Okosun, 2016).

Mathematical models have been recognized as essential tools for investigating the dynamics of the spread of infectious diseases. Application of mathematical models to study mosquito related diseases have been studied by several researchers. The present work therefore seeks to analyse the global properties and investigate the existence of backward bifurcation of the Zika virus model which was not proved in Eguda *et al.* (2019).

MATERIALS AND METHODS

In this work, we consider the model in Eguda *et al.* (2019) in which global stability of disease free equilibrium and endemic equilibrium states were not proved. The total population of human and vectors was divided into the following mutually exclusive epidemiological classes, namely, susceptible humans ($S_h(t)$), Infectious humans with Zika Virus ($I_h(t)$), Recovered humans ($R_h(t)$), Susceptible mosquitoes ($S_m(t)$) and Infectious mosquitoes ($I_m(t)$).

Let $N_h(t)$ and $N_m(t)$ denote the total number of humans and vectors at time t, respectively. Hence, we have that,

$$N_h(t) = S_h(t) + I_h(t) + R_h(t)$$

and

$$N_m(t) = S_m(t) + I_m(t)$$

The model equations are given by

$$\begin{aligned}
\dot{S}_h &= \Lambda_h - \frac{\alpha_{mh} b_V S_h I_m}{N_h} - (\mu_h + v_h) S_h \\
\dot{I}_h &= \frac{\alpha_{mh} b_V S_h I_m}{N_h} - (\gamma + \delta_h + \mu_h) I_h \\
\dot{R}_h &= \gamma I_h + v_h S_h - \mu_h R_h \\
\dot{S}_m &= \Lambda_m - \frac{\alpha_{hm} b_V S_m I_h}{N_h} - (\mu_m + \delta_m) S_m \\
\dot{I}_m &= \frac{\alpha_{hm} b_V S_m I_h}{N_h} - (\mu_m + \delta_m) I_m
\end{aligned} \tag{1}$$

In the above let,

$$k_1 = \mu_h + v_h, \quad k_2 = \gamma + \delta_h + \mu_h, \quad k_3 = \mu_m + \delta_m$$

expressing (1) in terms of forces of infection gives

$$\begin{aligned}
\dot{S}_h &= \Lambda_h - \lambda_h S_h - k_1 S_h \\
\dot{I}_h &= \lambda_h S_h - k_2 I_h \\
\dot{R}_h &= \gamma I_h + v_h S_h - \mu_h R_h \\
\dot{S}_m &= \Lambda_m - \lambda_m S_m - k_3 S_m \\
\dot{I}_m &= \lambda_m S_m - k_3 I_m
\end{aligned} \tag{2}$$

where,

$$\lambda_h = \frac{\alpha_{mh} b_V I_m}{N_h}, \quad \lambda_m = \frac{\alpha_{hm} b_V I_h}{N_h} \tag{3}$$

Parameters	Description
α_{mh}	Effective virus transmission rate from mosquito to human
α_{hm}	Effective transmission rate from human to mosquito
δ_m	Death rate of mosquito from insecticide
Λ_h	Human recruitment rate
Λ_m	Mosquito recruitment rate
γ	Recovery rate of human from infection
μ_m	Natural death rate of mosquito
μ_h	Natural death rate of human
δ_h	Death rate of human from infection
v_h	Vaccination rate of human
b_V	Mosquito biting rate

Disease- Free Equilibrium (DFE) of Zika Virus Model

It was shown in Eguda *et al.*, 2019 that the region

$D_1 = \left\{ (S_h, I_h, R_h, S_m, I_m) \in \mathbb{R}^5_+ : N_h \le \frac{\Lambda_h}{\mu_h},\ N_m \le \frac{\Lambda_m}{\mu_m} \right\}$ is positively invariant and attracts all positive solutions of the model (1).

The system (1) has a disease-free equilibrium obtained by setting the right hand side to zero and the disease classes to zero to give

$$\xi^* = (S_h^*, I_h^*, R_h^*, S_m^*, I_m^*) = \left(\frac{\Lambda_h}{\mu_h + v_h}, 0, \frac{v_h \Lambda_h}{\mu_h(\mu_h + v_h)}, \frac{\Lambda_m}{\mu_m + \delta_m}, 0 \right) \tag{4}$$

It follows that the effective reproduction number (Eguda *et al.*, 2019) is

$$R_E = \sqrt{R_h . R_m} \tag{5}$$

$$R_h = \frac{\alpha_{mh} b_V S_h^*}{N_h^*(\gamma + \delta_h + \mu_h)} \text{ and } R_m = \frac{\alpha_{hm} b_V S_m^*}{N_h^*(\mu_m + \delta_m)} \tag{6}$$

Bifurcation Analysis of the Zika Virus Model

We employ the phenomenon of bifurcations to investigate whether the disease can be eradicated if the reproduction number is less than one. To investigate the possibility of the existence of a backward bifurcation at $R_E < 1$ we use the centre manifold theorem as presented by Chavez & Song (2004); Agusto *et al*. (2017).

For system (2), let $x_1 = S_h$, $x_2 = I_h$, $x_3 = R_h$, $x_4 = S_m$, $x_5 = I_m$

The model equation can be rewritten as

$$\begin{aligned}
\dot{x}_1 &= \Lambda_h - \frac{\alpha_{mh} b_V x_1 x_5}{N_h} - k_1 x_1 \\
\dot{x}_2 &= \frac{\alpha_{mh} b_V x_1 x_5}{N_h} - k_2 x_2 \\
\dot{x}_3 &= \gamma x_2 + v_h x_1 - \mu_h x_3 \\
\dot{x}_4 &= \Lambda_m - \frac{\alpha_{hm} b_V x_4 x_2}{N_h} - k_3 x_4 \\
\dot{x}_5 &= \frac{\alpha_{hm} b_V x_4 x_2}{N_h} - k_3 x_5
\end{aligned} \tag{7}$$

The Jacobian of the transformed system (1) evaluated at the DFE is given by

$$J(\xi^*) = \begin{pmatrix}
-k_1 & 0 & 0 & 0 & \frac{-\alpha_{mh}^* b_V x_1^*}{N_h^*} \\
0 & -k_2 & 0 & 0 & \frac{\alpha_{mh}^* b_V x_1^*}{N_h^*} \\
v_h & \gamma & -\mu_h & 0 & 0 \\
0 & \frac{-\alpha_{hm} b_V x_4^*}{N_h^*} & 0 & -k_3 & 0 \\
0 & \frac{\alpha_{hm} b_V x_4^*}{N_h^*} & 0 & 0 & -k_3
\end{pmatrix} \tag{8}$$

Consider the case when $\alpha_{mh} = \alpha_{mh}^*$ is chosen as the bifurcation parameter at $R_E = 1$, we have that

$$\alpha_{mh}^* = \alpha_{mh} = \frac{N_h^{*2} k_2 k_3}{b_V S_h^* \alpha_{hm} b_V S_m^*} \tag{9}$$

The right eigenvector of $J(\xi^*)_{\alpha_{mh}=\alpha_{mh}^*}$ is given by

$$\mathrm{w} = (w_1, w_2, w_3, w_4, w_5)$$

where

$$w_1 = \frac{-\alpha_{mh}^* b_V x_1^* w_5}{N_h^* k_1} < 0 \quad , \quad w_2 = \frac{\alpha_{mh}^* b_V x_1^* w_5}{N_h^* k_2} \tag{10}$$

$$w_3 = \frac{\alpha_{mh}^* b_V x_1^* (\gamma k_1 - v_h k_2) w_5}{N_h^* k_1 k_2 \mu_h} \quad , \quad w_4 = \frac{-\alpha_{hm} b_V x_4^* \alpha_{mh}^* b_V x_1^* w_5}{N_h^{*2} k_2 k_3} < 0$$

$$w_5 = w_5 > 0$$

The above right eigenvectors were obtained by solving the equations below

$$-k_1 w_1 - \frac{\alpha_{mh}^* b_V x_1^* w_5}{N_h^*} = 0$$

$$-k_2 w_2 + \frac{\alpha_{mh}^* b_V x_1^* w_5}{N_h^*} = 0 \tag{11}$$

$$v_h w_1 + \gamma w_2 - \mu_h w_3 = 0$$

$$-\frac{\alpha_{hm} b_V x_4^* w_2}{N_h^*} - k_3 w_4 = 0$$

$$\frac{\alpha_{hm} b_V x_4^* w_2}{N_h^*} - k_3 w_5 = 0$$

Similarly, $J(\xi^*)_{\alpha_{mh}=\alpha_{mh}^*}$ has a left eigenvector given by

$$v = (v_1, v_2, v_3, v_4, v_5)$$

where

$$-v_1 k_1 + v_3 v_h = 0$$

$$-v_2 k_2 + v_3 \gamma - \frac{v_4 \alpha_{hm} b_V x_4^*}{N_h^*} + \frac{v_5 \alpha_{hm} b_V x_4^*}{N_h^*} = 0 \tag{12}$$

$$-v_3 \mu_h = 0$$

$$-v_4 k_3 = 0$$

$$-\frac{v_1 \alpha_{mh}^* b_V x_1^*}{N_h^*} + \frac{v_2 \alpha_{mh}^* b_V x_1^*}{N_h^*} - v_5 k_3 = 0.$$

Solving gives

$$v_1 = v_3 = v_4 = 0 \quad , \quad v_2 = \frac{\alpha_{hm} b_V x_4^* v_5}{N_h^* k_2}, \quad v_5 = v_5 > 0$$

Formulation of a and b

The associated non-zero partial derivatives at DFE were computed and the bifurcation parameters are presented as follows

$$a = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0) \tag{13}$$

which gives

$$a = 2v_2 w_1 w_5 \frac{\alpha_{mh}^* b_V}{N_h^*} + 2v_5 w_2 w_4 \frac{\alpha_{hm}^* b_V}{N_h^*} \tag{14}$$

$$a = \frac{-2\alpha_{hm} b_v^3 \alpha_{mh}^2 x_4^* v_5 x_1^* w_5}{N_h^{*3} k_1 k_2} - \frac{2\alpha_{hm}^2 b_v^4 \alpha_{mh}^2 x_4^* v_5 x_1^{*2} w_5}{N_h^{*4} k_2^2 k_3} < 0$$

Computing for b

$$b = \sum_{k,i=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \alpha_{mh}^*}(0,0) = \frac{\alpha_{hm} b_v^2 x_4^* v_5 x_1}{N_h^{*2} k_2} > 0 \tag{15}$$

Thus $a < 0$ *and* $b > 0$. Since the bifurcation coefficient a is negative and b is positive, thus from Castillo-Chavez and Song (2004), the model equation (1) does not undergo backward bifurcation at $R_E = 1$

Global Stability Analysis of Disease Free Equilibrium

We can use the Lyapunov function approach to determine the global stability of the DFE of model (1) when $R_E \le 1$

Lemma: The disease free equilibrium of (1) is globally asymptotically stable (GAS) in D_1 if $R_E < 1$

Proof:

Consider the Lyapunov function

$$V = N_h^* I_h + N_h^* I_m \tag{16}$$

Its derivative along the solution of the model is

$$\dot{V} = N_h^* \dot{I}_h + N_h^* \dot{I}_m$$

$$\dot{V} = N_h^* \left(\frac{\alpha_{mh} b_V S_h I_m}{N_h^*} - k_2 I_h \right) + N_h^* \left(\frac{\alpha_{hm} b_V S_m I_h}{N_h^*} - k_3 I_m \right)$$

$$\dot{V} = N_h^* \left(\frac{\alpha_{mh} b_V S_h I_m}{N_h^*} - k_2 I_h \right) + N_h^* \left(\frac{\alpha_{hm} b_V S_m I_h}{N_h^*} - k_3 I_m \right) \tag{17}$$

$$\dot{V} = N_h^* k_3 I_m \left(\frac{\alpha_{mh} b_V S_h^*}{N_h^* k_3} - 1 \right) + N_h^* k_2 I_h \left(\frac{\alpha_{hm} b_V S_m}{N_h^* k_2} - 1 \right)$$

$$\dot{V} \le N_h^* k_3 I_m \left(R_h - 1 \right) + N_h^* k_2 I_h \left(R_m - 1 \right)$$

Clearly on D_1, $S_h \le N_h \le \frac{\Lambda_h}{\mu_h}$ and $S_m \le N_m \le \frac{\Lambda_m}{\mu_m}$ for all time $t > 0$. Hence, $\dot{V} \le 0$ if $R_h \le 1 \, and \, R_m \le 1$ with $\dot{V} = 0$ if and only if $I_m = I_h = 0$. Therefore V is a lyapunov function

in D_1, and it follows from LaSalle's invariance principle that every solution to the equation (1) with initial conditions in D_1 converges to the DFE as $t \to \infty$. So the DFE is globally asymptotically stable in D_1.

Global Stability of Endemic Equilibrium Point (EEP)

Lemma: The unique endemic equilibrium of (1) is globally asymptotically stable(GAS) in D_1 whenever $R_E > 1$

Proof:

To prove the global asymptotic stability of EEP we use a previously described approach (Andrawus and Eguda 2017; Iboi and Okuonghae 2016).

Consider the model (1) with $\delta_h = 0$ and the Lyapunov function (of the Goh-Volterra type)

$$V = S_h - S_h^{**} - S_h^{**} \ln \frac{S_h}{S_h^{**}} + I_h - I_h^{**} - I_h^{**} \ln \frac{I_h}{I_h^{**}} + S_m - S_m^{**} - S_m^{**} \ln \frac{S_m}{S_m^{**}} + I_m - I_m^{**} - I_m^{**} \ln \frac{I_m}{I_m^{**}} \quad (18)$$

Its derivative along the solution of the model is

$$\dot{V} = \dot{S}_h - \frac{S_h^{**}}{S_h}\dot{S}_h + \dot{I}_h - \frac{I_h^{**}}{I_h}\dot{I}_h + \dot{S}_m - \frac{S_m^{**}}{S_m}\dot{S}_m + \dot{I}_m - \frac{I_m^{**}}{I_m}\dot{I}_m \quad (19)$$

with $N_h = \frac{\Lambda_h}{\mu_h}$, $N_m = \frac{\Lambda_m}{\mu_m}$ and $\lambda_h = \frac{\alpha_{mh} b_V I_m}{N_h} = \beta_1 I_m$, $\lambda_m = \frac{\alpha_{hm} b_V I_h}{N_h} = \beta_2 I_h$ where

$\beta_1 = \frac{\alpha_{mh} b_V \mu_h}{\Lambda_h}$, $\beta_2 = \frac{\alpha_{hm} b_V \mu_h}{\Lambda_h}$

$$\dot{V} = \Lambda_h - \beta_1 S_h I_m - (\mu_h + v_h) S_h - \frac{S_h^{**}}{S_h}\left(\Lambda_h - \beta_1 S_h I_m - (\mu_h + v_h) S_h\right) + \beta_1 S_h I_m - (\gamma + \mu_h) I_h$$

$$- \frac{I_h^{**}}{I_h}\left(\beta_1 S_h I_m - (\gamma + \mu_h) I_h\right) + \Lambda_m - \beta_2 S_m I_h - (\mu_m + \delta_m) S_m - \frac{S_m^{**}}{S_m}\left(\Lambda_m - \beta_2 S_m I_h - (\mu_m + \delta_m) S_m\right)$$

$$+ \beta_2 S_m I_h - (\mu_m + \delta_m) I_m - \frac{I_m^{**}}{I_m}\left(\beta_2 S_m I_h - (\mu_m + \delta_m) I_m\right) \quad (20)$$

It can be shown from (1) that at steady state

$\Lambda_h = \beta_1 S_h^{**} I_m^{**} + (\mu_h + v_h) S_h^{**}$, $\Lambda_m = \beta_2 S_m^{**} I_h^{**} + (\mu_m + \delta_m) S_m^{**}$, $\beta_1 S_h^{**} I_m^{**} = (\gamma + \mu_h) I_h^{**}$

$\beta_2 S_m^{**} I_h^{**} = (\mu_m + \delta_m) I_m^{**}$

Substituting gives

$$\dot{V} = \beta_1 S_h^{**} I_m^{**} + (\mu_h + v_h) S_h^{**} - (\mu_h + v_h) S_h - \frac{S_h^{**2} \beta_1 I_m^{**}}{S_h} - \frac{S_h^{**2} (\mu_h + v_h)}{S_h} + \beta_1 S_h^{**} I_m$$

$$+ (\mu_h + v_h) S_h^{**} - \frac{\beta_1 S_h^{**} I_m^{**} I_h}{I_h^{**}} - \frac{I_h^{**} \beta_1 S_h I_m}{I_h} + \beta_1 S_h^{**} I_m^{**} + \beta_2 S_m^{**} I_h^{**} + (\mu_m + \delta_m) S_m^{**}$$

$$- (\mu_m + \delta_m) S_m - \frac{S_m^{**2} \beta_2 I_h^{**}}{S_m} - \frac{S_m^{**2} (\mu_m + \delta_m)}{S_m} + \beta_2 S_m^{**} I_h + (\mu_m + \delta_m) S_m^{**} - \frac{\beta_2 S_m^{**} I_h^{**} I_m}{I_m^{**}} \quad (21)$$

$$- \frac{I_m^{**} \beta_2 S_m I_h}{I_m} + \beta_2 S_m^{**} I_h^{**}$$

$$\dot{V} = 2(\mu_h + v_h)S_h^{**} - (\mu_h + v_h)S_h - \frac{S_h^{**2}(\mu_h + v_h)}{S_h} + \beta_1 S_h^{**} I_m - \frac{\beta_1 S_h I_h^{**} I_m}{I_h} + 2\beta_1 S_h^{**} I_m^{**}$$
$$- \frac{S_h^{**2}\beta_1 I_m^{**}}{S_h} - \frac{\beta_1 S_h^{**} I_m^{**} I_h}{I_h^{**}} + 2(\mu_m + \delta_m)S_m^{**} - (\mu_m + \delta_m)S_m - \frac{S_m^{**2}(\mu_m + \delta_m)}{S_m} + \beta_2 S_m^{**} I_h \quad (22)$$
$$- \frac{\beta_2 I_m^{**} S_m I_h}{I_m} + 2\beta_2 S_m^{**} I_h^{**} - \frac{\beta_2 S_m^{**2} I_h^{**}}{S_m} - \frac{\beta_2 S_m^{**} I_h^{**} I_m}{I_m^{**}}$$

which simplifies to

$$\dot{V} = (\mu_h + v_h)S_h^{**}\left(2 - \frac{S_h}{S_h^{**}} - \frac{S_h^{**}}{S_h}\right) + \beta_1 S_h^{**} I_m\left(1 - \frac{S_h}{S_h^{**}}\frac{I_h^{**}}{I_h}\right) + \beta_1 S_h^{**} I_m^{**}\left(2 - \frac{S_h^{**}}{S_h} - \frac{I_h}{I_h^{**}}\right)$$
$$+(\mu_m + \delta_m)S_m^{**}\left(2 - \frac{S_m}{S_m^{**}} - \frac{S_m^{**}}{S_m}\right) + \beta_2 S_m^{**} I_h\left(1 - \frac{I_m^{**}}{I_m}\frac{S_m}{S_m^{**}}\right) + \beta_2 S_m^{**} I_h^{**}\left(2 - \frac{S_m^{**}}{S_m} - \frac{I_m}{I_m^{**}}\right) \quad (23)$$

Since the arithmetic mean exceeds the geometric mean, the following inequalities hold

$$2 - \frac{S_h}{S_h^{**}} - \frac{S_h^{**}}{S_h} \le 0\ ,\quad 1 - \frac{S_h}{S_h^{**}}\frac{I_h^{**}}{I_h} \le 0\ ,\quad 2 - \frac{S_h^{**}}{S_h} - \frac{I_h}{I_h^{**}} \le 0\ ,\quad 2 - \frac{S_m}{S_m^{**}} - \frac{S_m^{**}}{S_m} \le 0$$
$$1 - \frac{I_m^{**}}{I_m}\frac{S_m}{S_m^{**}} \le 0\ ,\quad 2 - \frac{S_m^{**}}{S_m} - \frac{I_m}{I_m^{**}} \le 0$$

Thus, $\dot{V} \le 0$ for $R_E > 1$. Hence V is a lyapunov function in D_1

Numerical Results and Discussions

Our numerical simulations examine the dynamics of the Zika virus model in order to confirm the global stability of both the disease-free and the endemic equilibrium state using Maple Software. It was discovered that the model equation (1) will not undergo backward bifurcation at $R_E = 1$ because the bifurcation parameter a is negative.

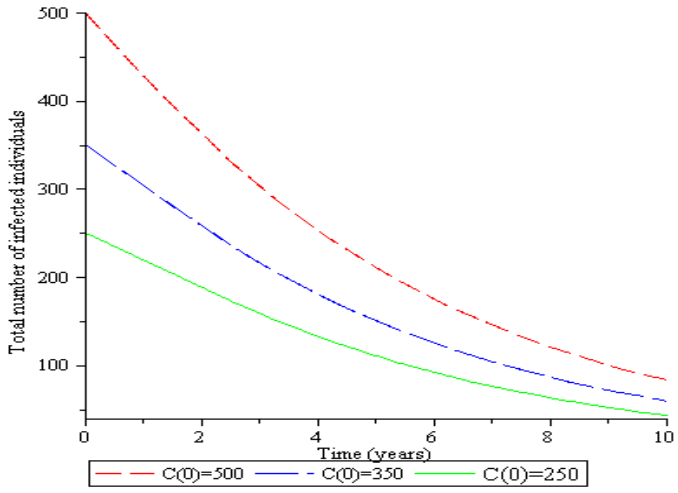

Figure 1: Population of individuals infected with Zika virus for different initial population

of $C(0) = 250$, $C(0) = 350$ and $C(0) = 500$. Parameter values used are in Table 1 of Eguda *et al*. (2019), with $\gamma = 0.118$, $\delta_h = 0.05$ $\mu_m = 0.0714$, so that $R_E = 0.36$. This confirms both the local and global asymptotic stability of the disease-free equilibrium of Zika Virus model

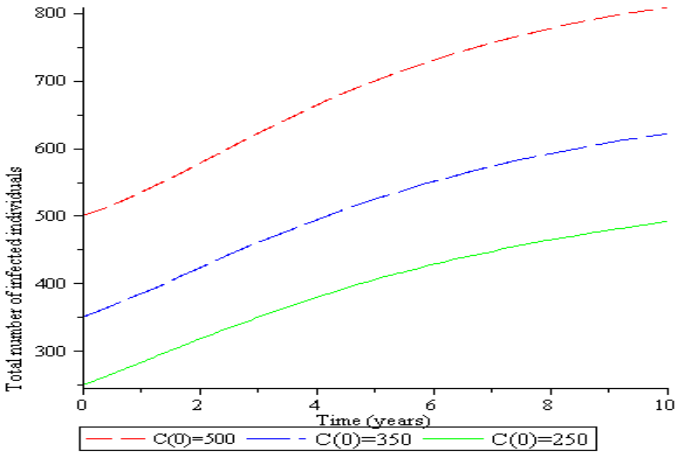

Figure 2: Population of individuals infected with Zika virus for different initial population of $C(0) = 250$, $C(0) = 350$ and $C(0) = 500$. Parameter values used are in Table 1 of Eguda *et al*. (2019), with $\gamma = 0$, $\delta_h = 0.005$ $\mu_m = 0.0714$, $\delta_m = 0.001$, so that $R_E = 5.97$. This confirms both the local and global asymptotic stability of the disease-free equilibrium of Zika Virus model

CONCLUSION

In this paper, a mathematical model for Zika virus was analyzed for global stability in order to gain a better understanding of its transmission pattern in the population. It was proved that the disease free equilibrium point is globally asymptotically stable using the Lyapunov function approach if the control reproduction number is less than unity. The Lyapunov function (of the Goh-Volterra type) was constructed and used to show that the endemic equilibrium point is globally asymptotically stable if the control reproduction number is greater than unity. Also, it has been shown that the model does not undergo backward bifurcation if $R_E = 1$. Numerical simulations were presented to confirm the global stability of both the disease-free and the endemic equilibrium state.

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