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ENDEMIC EQUILIBRIUM POINT OF A MATHEMATICAL MODEL FOR DENGUE CHIKUNGUNYA VIRUS

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Abstract

The global stability analysis of endemic equilibria, for non-linear higher-dimensional problems are generally difficult. This paper attempts to determine the endemic equilibrium of the Mathematical model for Dengue virus and its co-existence with Chikungunya virus. The unique positive endemic equilibrium of the model is globally asymptotically stable when $R_0 > 1$.

Keywords: *Basic reproduction number, disease-free equilibrium, epidemic, dengue disease, infective, co-circulating, cross-immunity (CI), antibody-dependent enhancement (ADE)*

1.0 Introduction

Dengue virus is distributed by several species of mosquito of the Aedes Aegypti type which is the first. The second potential vector is Aedes Albopictus, third is Aedes Polynesiensis and the fourth is Aedes Scutellaris [1]. The urban-adapted, day-biting Aedes aegypti is the predominant mosquito vector of dengue although transmission may also occur through a secondary vector, Aedes albopictus [2]. Aedes aegypti is a cosmotropical species distributed worldwide. Dengue fever is an international health problem in recent years [3], the number of cases of Dengue have increased sharply in the tropical and sub-tropical regions around the world [4, 3]. Chikungunya (CHIKV) is a genus of single-stranded virus that infect humans directly from bites of an Aedes spp. mosquitoes [5]. The manifestation of Chikungunya illness are fever without signs are discomfort and pain, skin rash, joint pain, headache, abdominal pain, nausea and vomiting, positive tourniguet test and leukopenia. The symptoms of Chikungunya are similar to those of Dengue diseases because they are spread by the same mosquitoes. Thus, there are no specific antiviral drugs to treat Chikungunya, so patient are advised to get enough rest, drink fluids and take drugs such as paracetamol to reduce fever and pain [6].

Mathematical model has been developed in [7], it was shown to exhibit the phenomenon of backward bifurcation at $R_{DC} = 1$, which was caused by the induced death for humans for both Dengue and Chikungunya [7]. The occurrence of backward bifurcation make effective disease control difficult, hence the need for the global asymptotic stability in the absence of induced death for humans for both Dengue and Chikungunya be shown in other to ascertain the successful eradication of the disease from the population.

2.0 Model Formation

Consider the following model for the transmission dynamics of Dengue Chikungunya model [8] which consist of seventeen nonlinear ordinary differential equations given by,

$$\frac{dS_H}{dt} = \Lambda_H - (\lambda_{DH} + \lambda_{CH} + \mu_H)S_H,$$
$$\frac{dE_D}{dt} = \lambda_{DH} S_H - (\gamma_D + \mu_H)E_D,$$
$$\frac{dI_{D1}}{dt} = \gamma_D E_D - (\delta_D + \mu_H + \theta_D)I_{D1},$$
$$\frac{dI_{D2}}{dt} = \theta_D(1-P_D)I_{D1} - (\alpha_D\delta_D + \tau_D + \mu_H)I_{D2} - \phi_D I_{WD},$$
$$\frac{dI_{WD}}{dt} = \phi_D P_D I_{D1} - (\mu_H + \delta_D + \phi_D)I_{WD},$$
$$\frac{dR_D}{dt} = \tau_D I_{D2} - \mu_H R_D,$$
$$\frac{dE_C}{dt} = \lambda_{CH} S_H - (\gamma_C + \mu_H)E_C,$$
$$\frac{dI_{C1}}{dt} = \gamma_C E_C - (\delta_C + \mu_H + \theta_C)I_{C1},$$
$$\frac{dI_{C2}}{dt} = \theta_C(1-P_C)I_{C1} - (\alpha_C\delta_C + \tau_C + \mu_H)I_{C2} - \phi_C I_{WC},$$
$$\frac{dI_{WC}}{dt} = \phi_C P_C I_{C1} - (\mu_H + \delta_C + \phi_C)I_{WC},$$
$$\frac{dR_C}{dt} = \tau_C I_{C2} - \mu_H R_C,$$
$$\frac{dS_{MD}}{dt} = \Lambda_{VD} - \lambda_{VD} S_{MD} - \mu_V S_{MD},$$
$$\frac{dE_{MD}}{dt} = \lambda_{VD} S_{MD} - (\gamma_{MD} + \mu_V)E_{MD},$$
$$\frac{dI_{MD}}{dt} = \gamma_{MD} E_{MD} - \mu_V I_{MD},$$
$$\frac{dS_{MC}}{dt} = \Lambda_{VC} - \lambda_{VC} S_{MC} - \mu_V S_{MC},$$
$$\frac{dE_{MC}}{dt} = \lambda_{VC} S_{MC} - (\gamma_{MC} + \mu_V)E_{MC},$$
$$\frac{dI_{MC}}{dt} = \gamma_{MC} E_{MC} - \mu_V I_{MC},$$

(1)

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Where the associated variable and parameters are described in Table 1.

Table 1: Description of state variables of the model (1)

State Variables	Description
$S_H(t)$	Population of susceptible individuals
$E_D(t)$	Population of humans exposed to dengue
$I_{D1}(t)$	Population of infectious humans with dengue
$I_{D2}(t)$	Population of infectious humans with dengue correctly diagnosed
$I_{DW}(t)$	Population of wrongly diagnosed dengue cases
$R_D(t)$	Population of humans who recovered from dengue
$E_C(t)$	Population of humans exposed to chikungunya
$I_{C1}(t)$	Population of infectious humans with chikungunya
$I_{C2}(t)$	Population of infectious humans with chikungunya correctly diagnosed
$I_{CW}(t)$	Population of wrongly diagnosed chikungunya cases
$R_C(t)$	Population of humans who recovered from chikungunya
$S_{MD}(t)$	Population of susceptible dengue vectors
$E_{MD}(t)$	Population of exposed dengue vectors
$I_{MD}(t)$	Population of infectious vectors with dengue
$S_{MC}(t)$	Population of susceptible chikungunya vectors
$E_{MC}(t)$	Population of exposed chikungunya vectors
$I_{MC}(t)$	Population of infectious vectors with chikungunya

Table 2: Description of parameters of model (1)

Parameter	Description
$\Lambda_H(t)$	Recruitment rate for humans.
$\mu_H(t)$	Natural mortality rate for humans.
β_{DV}	Probability of transmission of dengue from humans to vectors
β_{DH}	Probability of transmission of dengue from vectors to humans
b_{DV}	Biting rate of vectors that transmit dengue
η_{D1}	Modification parameter for reduced infectiousness of humans exposed to dengue
η_{D2}	Modification parameter for reduced infectiousness of humans rightly diagnosed for dengue
η_{D3}	Modification parameter for increased infectiousness of humans wrongly diagnosed for dengue
γ_D	Progression rate of humans exposed to dengue
δ_D	Human disease induced death for dengue
θ_D	Rate of diagnoses for dengue
P_D	Fraction of humans wrongly diagnosed for dengue
α_D	Modification parameter for reduced mortality of humans rightly diagnosed for dengue
τ_D	Recovery rate of humans from dengue
θ_D	Rate of re-diagnoses for dengue
Λ_V	Recruitment rate of vectors that transmit dengue
μ_V	Natural mortality rate for vector
γ_{MD}	Progression rate of vectors exposed to dengue
β_{CV}	Probability of transmission of chikungunya from humans to Vectors
β_{CH}	Probability of transmission of chikungunya from vectors to humans

b_{CV}	Biting rate of vectors that transmit chikungunya
η_{C1}	Modification parameter for reduced infectiousness of humans exposed to chikungunya
η_{C2}	Modification parameter for reduced infectiousness of human rightly diagnosed for Chikungunya
η_{C3}	Modification parameter for increased infectiousness of humans wrongly diagnosed for chikungunya
γ_C	Progression rate of humans exposed to chikungunya
δ_C	Human disease induced death for chikungunya
θ_C	Rate of diagnoses for chikungunya
P_C	Fraction of humans wrongly diagnosed for chikungunya
α_C	Modification parameter for reduced mortality of humans rightly diagnosed for chikungunya
τ_C	Recovery rate of humans from chikungunya
ϕ_C	Rate of re-diagnoses for chikungunya
Λ_{VC}	Recruitment rate of vectors that transmit chikungunya
γ_{MC}	Progression rate of vectors exposed to chikungunya

If in model (1) $\delta_D = \delta_C = 0$, special case is attained in which the disease induced death for humans for both dengue and chikungunya i.e., removing the parameters that cause the backward bifurcation. The resulting sub-model is given by

$$\frac{dS_H}{dt} = \Lambda_H - (\lambda_{DH} + \lambda_{CH} + \mu_H)S_H,$$
$$\frac{dE_D}{dt} = \lambda_{DH}S_H - (\gamma_D + \mu_H)E_D,$$
$$\frac{dI_{D1}}{dt} = \gamma_D E_D - (\mu_H + \theta_D)I_{D1},$$
$$\frac{dI_{D2}}{dt} = \theta_D(1-P_D)I_{D1} - (\tau_D + \mu_H)I_{D2} - \phi_D I_{WD},$$
$$\frac{dI_{WD}}{dt} = \phi_D P_D I_{D1} - (\mu_H + \phi_D)I_{WD},$$
$$\frac{dR_D}{dt} = \tau_D I_{D2} - \mu_H R_D,$$
$$\frac{dE_C}{dt} = \lambda_{CH}S_H - (\gamma_C + \mu_H)E_C,$$
$$\frac{dI_{C1}}{dt} = \gamma_C E_C - (\mu_H + \theta_C)I_{C1},$$
$$\frac{dI_{C2}}{dt} = \theta_C(1-P_C)I_{C1} - (\tau_C + \mu_H)I_{C2} - \phi_C I_{WC},$$
$$\frac{dI_{WC}}{dt} = \phi_C P_C I_{C1} - (\mu_H + \phi_C)I_{WC},$$
$$\frac{dR_C}{dt} = \tau_C I_{C2} - \mu_H R_C,$$
$$\frac{dS_{MD}}{dt} = \Lambda_{VD} - \lambda_{VD}S_{MD} - \mu_V S_{MD},$$
$$\frac{dE_{MD}}{dt} = \lambda_{VD}S_{MD} - (\gamma_{MD} + \mu_V)E_{MD},$$
$$\frac{dI_{MD}}{dt} = \gamma_{MD}E_{MD} - \mu_V I_{MD},$$
$$\frac{dS_{MC}}{dt} = \Lambda_{VC} - \lambda_{VC}S_{MC} - \mu_V S_{MC},$$
$$\frac{dE_{MC}}{dt} = \lambda_{VC}S_{MC} - (\gamma_{MC} + \mu_V)E_{MC},$$
$$\frac{dI_{MC}}{dt} = \gamma_{MC}E_{MC} - \mu_V I_{MC},$$

(2)

The effective reproduction number corresponding to the mass action model (2) is obtain using the method of next generation matrix operator in [17] this is given by

$$\Re_T^m = \max[\Re_{TD}^m, \Re_{TC}^m], \qquad (3)$$

where

$$\Re_{TD}^m = \sqrt{\frac{\beta_{DH}\beta_{DV}b_{DV}^2 S_{MD}^* S_H^* \gamma_{MD}(g_2 g_3 g_4 \eta_{D1} + g_3 g_4 \gamma_D + g_4 \gamma_D \eta_{D2}\theta_D(1-P_D) + P_D\gamma_D\theta_D g_3\eta_{D3} + P_D\gamma_D\theta_D\phi_D\eta_{D3})}{g_1 g_2 g_3 g_4 g_9 \mu_V}},$$

$$\Re_{TC}^m = \sqrt{\frac{\beta_{CH}\beta_{CV}b_{CV}^2 S_{MC}^* S_H^* \gamma_{MC}(g_5 g_6 g_8 \eta_{C1} + g_7 g_8 \gamma_C + g_8 \gamma_C \eta_{C2}\theta_C(1-P_C) + P_C\gamma_C\theta_C g_3\eta_{C3} + P_C\gamma_C\theta_C\phi_C\eta_{C3})}{g_5 g_6 g_7 g_8 g_{10} \mu_V}}, \qquad (4)$$

and $g_1 = \gamma_D + \mu_H$, $g_2 = \mu_H + \theta_D$, $g_3 = \tau_D + \mu_H$, $g_4 = \phi_C + \mu_H$, $g_5 = \gamma_{MC} + \mu_H$, $g_6 = \mu_H + \theta_C$, $g_7 = \tau_C + \mu_H$, $g_8 = \phi_C + \mu_H$, $g_9 = \gamma_{MD} + \mu_V$, $g_{10} = \gamma_{MC} + \mu_V$

The global stability analysis of endemic equilibria, for non-linear higher-dimensional problems, such as the one in (2), is generally difficult to obtain [9]. For some special differential equation systems, one can be able to find a suitable Lyapunov function [10, 11], to prove the global stability. Unfortunately, there is no systemic way to construct or find Lyapunov functions, which hinders the application of this approach to more general model systems [9].

Theorem

The disease free equilibrium (DFE) of the mass action of the model (2), in the absence of disease-induced death for human (δ_D *and* δ_C) is globally asymptotically stable (GAS) in D if $R_T^m \le 1$ and unstable if $R_T^m \ge 1$.

Proof:

Consider the following Lyapunov function

$$\begin{aligned} K = {} & (K_1 E_D + K_2 I_{D1} + K_3 I_{D2} + K_4 I_{WD} + k_5 E_C + K_6 I_{C1} + K_7 I_{C2} + K_8 I_{WC} \\ & + K_9 E_{MD} + K_{10} I_{MD} + K_{11} E_{MC} + K_{12} I_{MC} \end{aligned} \qquad (5)$$

where

$$K_1 = \frac{\beta_{DV} b_{DV} S_{MD}^* \gamma_{MD}}{g_1 g_2 g_3 g_4 g_9 \mu_V}(g_2 g_3 g_4 \eta_{D1} + g_3 g_4 \gamma_D + \gamma_D \theta_D \eta_{D2}(g_4(1-P_D)P_D\phi_D) + P_D\gamma_D\theta_D\eta_{D3}g_3)$$

$$K_2 = \frac{\beta_{DV} b_{DV} S_{MD} \gamma_{MD}}{g_2 g_3 g g_4 g_9 \mu_V}(g_3 g_4 + \theta_D \eta_{D2}(g_4(1-P_D) + P_D\phi_D) + P_D\theta_D\eta_{D3}g_3)$$

$$K_3 = \frac{\beta_{DV} b_{DV} S_{MD}^* \gamma_{MD} \eta_{D2}}{g_3 g_4 \mu_V}, \qquad K_4 = \frac{\beta_{DV} b_{DV} S_{MD}^* \gamma_{MD}}{g_3 g_4 g_9 \mu_V}(\phi_D \eta_{D2} + g_3 \eta_{D3})$$

$$K_5 = \frac{\beta_{CV} b_{CV} S_{MC}^* \gamma_{MC}}{g_1 g_2 g_3 g_4 g_9 \mu_V}(g_6 g_7 g_8 \eta_{C1} + g_7 g_8 \gamma_C + \gamma_C \theta_C \eta_{C2}(g_8(1-P_C)P_C\phi_{\mathrm{D}}) + P_D\gamma_D\theta_D\eta_{D3}g_3),$$

$$K_6 = \frac{\beta_{CV} b_{CV} S_{MC} \gamma_{MC}}{g_6 g_7 g_8 g_{10} \mu_V}(g_7 g_8 + \theta_C \eta_{C2}(g_8(1-P_C) + P_C\phi_C) + P_C\theta_C\eta_{C3}g_7),$$

$$K_7 = \frac{\beta_{CV} b_{CV} S_{MC}^* \gamma_{MC} \eta_{D2}}{g_7 g_8 \mu_V}, \qquad K_8 = \frac{\beta_{CV} b_{CV} S_{MC}^* \gamma_{MC}}{g_7 g_8 g_{10} \mu_V}(\phi_C \eta_{C2} + g_7 \eta_{C3}),$$

$$K_9 = \frac{R_{DT}^m \gamma_{MD}}{g_9 \mu_V}, \quad K_{10} = \frac{R_{DT}^m}{\mu_V}, \quad K_{11} = \frac{R_{CT}^m \gamma_{MC}}{g_{10} \mu_V}, \quad K_{12} = \frac{R_{CT}^m}{\mu_V}$$

With Lyapunov derivative (where a dot represents a time derivative)

$$\begin{aligned} \dot{K} = {} & (K_1 \dot{E}_D + K_2 \dot{I}_{D1} + K_3 \dot{I}_{D2} + K_4 \dot{I}_{WD} + k_5 \dot{E}_C + K_6 \dot{I}_{C1} + K_7 \dot{I}_{C2} + K_8 \dot{I}_{WC} \\ & + K_9 \dot{E}_{MD} + K_{10} \dot{I}_{MD} + K_{11} \dot{E}_{MC} + K_{12} \dot{I}_{MC} \end{aligned} \qquad (6)$$

Substituting the right hand side of mass action version of the model (2) into (6) yields the following.

$$\begin{aligned} \dot{K} = {} & K_1(\lambda_{DH} S_H - g_1 E_D) + K_2(\gamma_D E_D - g_2 I_{D1}) + K_3(\theta_D(1-P_D)I_{D1} - \phi_D I_{WD} - g_3 I_{D2}) \\ & + K_4(\phi_D P_D I_{D1} - g_4 I_{WD}) + k_5(\lambda_{CH} S_H - g_5 E_C) + K_6(\gamma_C E_C - g_6 I_{C1}) \\ & + K_7(\theta_C(1-P_C)I_{C1} - \phi_C I_{WC} - g_7 I_{C2}) + K_8(\theta_C P_C I_{C1} + g_8 I_{WC}) + K_9(\lambda_{VD} S_{MD} - g_9 E_{MD}) \\ & + K_{10}(\gamma_{DM} E_{MD} - \mu_V I_{MD}) + K_{11}(\lambda_{VC} S_{MC} - g_{10} E_{MC}) + K_{12}(\gamma_{DM} E_{MD} - \mu_V I_{MC}) \end{aligned} \qquad (7)$$

Substituting values of $K_1 - K_{12}$ into (7) and after some algebraic simplifications, we have the following:

$$\dot{K} = \Re_{DT}^{m} I_{MD}\left[\frac{S_H}{S_H^*}\Re_{DT}^{m} - 1\right] + \aleph_{CT}^{m} I_{MC}\left[\frac{S_H}{S_H^*}\Re_{CT}^{m} - 1\right] + \left[\frac{\beta_{DV} b_{DV} \gamma_{MD} S_{MD}^*}{g_9 \mu_V}\right]\left(\eta_{D1}E_D + I_{D1} + \eta_{D2}I_{D2} + \eta_{D3}I_{WD}\right)\left[\frac{S_H}{S_H^*}\Re_{DT}^{m} - 1\right]$$

$$+ \left[\frac{\beta_{CV} b_{CV} \gamma_{MC} S_{MC}^*}{g_{10}\mu_V}\right]\left(\eta_{C1}E_C + I_{C1} + \eta_{C2}I_{C2} + \eta_{C3}I_{WC}\right)\left[\frac{S_H}{S_H^*}\Re_{CT}^{m} - 1\right] \quad (8)$$

Since $S_H < S_H^*$, $S_{MD} < S_{MD}^*$, $S_{MC} < S_{MC}^*$, we have that

$$\dot{K} \le \Re_{DT}^{m} I_{MD}\left[\Re_{DT}^{m} - 1\right] + \aleph_{CT}^{m} I_{MC}\left[\Re_{CT}^{m} - 1\right] + \left[\frac{\beta_{DV} b_{DV} \gamma_{MD} S_{MD}^*}{g_9 \mu_V}\right]\left(\eta_{D1}E_D + I_{D1} + \eta_{D2}I_{D2} + \eta_{D3}I_{WD}\right)\left[\Re_{DT}^{m} - 1\right]$$

$$+ \left[\frac{\beta_{CV} b_{CV} \gamma_{MC} S_{MC}^*}{g_{10}\mu_V}\right]\left(\eta_{C1}E_C + I_{C1} + \eta_{C2}I_{C2} + \eta_{C3}I_{WC}\right)\left[\Re_{CT}^{m} - 1\right] \quad (9)$$

Hence, $\dot{K} \le 0$, whenever $\Re_T^m \le 1$, with $\dot{K} = 0$ if and only if

$$\left(E_D = I_{D1} = I_{D2} = I_{WD} = E_C = I_{C1} = I_{C2} = I_{WC} = E_{MD} = I_{MD} = E_{MC} = I_{MC} = 0\right) \quad (10)$$

Hence, $\dot{K} \le 0$, is a Lyapunvo functional defined in the domain D. Thus, it follows from *Lasalle's Invariance principle* [12] that:

$$\begin{pmatrix} E_D(t), I_{D1}(t), I_{D2}(t), I_{WD}(t), E_C(t), I_{C1}(t), I_{C2}(t), I_{WC}(t), E_{MD}(t), \\ I_{MD}(t), E_{MC}(t), I_{MC}(t) \end{pmatrix} \to (0,0,0,0,0,0,0,0,0,0,0,0) \quad (11)$$

as $t \to \infty$.

Hence, every orbit of the equations of the mass action version of model (2) with $\delta_D = \delta_C = 0$, approaches the DFE, as $t \to \infty$ for $R_T^m \le 1$.

This result shows that in a population where there are incidences of misdiagnosis of either disease with negligible disease induced mortality for humans, i.e., $\delta_D = \delta_C = 0$, the DFE will be GAS whenever $R_T^m \le 1$.

3.0 Numerical Simulations

In this section, we investigate the sensitivity of the parameters of the system (1) with respect to the reproduction number, the numerical simulation results is also shown to illustrates the impact of varying certain key parameter on the total disease incidence in a population. The work done in this section is based on parameter values in the table below.

Table 3: Baseline values and ranges of the parameters of our model (1)

Parameters	Baseline values	Ranges	References
ΛVC	5000 day^{-1}	(3000, 50000)	[13]
βCH	0.60 day^{-1}	(0.43, 0.79)	[14]
βCV	0.53 day^{-1}	(0.60, 0.75)	[13]
bCV	0.53 day^{-1}	(0.002, 0.54)	Assumed
$\eta C1$	0.5 day^{-1}	(0, 1)	Assumed
$\eta C2$	0.8 day^{-1}	(0, 1)	Assumed
$\eta C3$	1.2 day^{-1}	(0, 1)	Assumed
γC	0.071 day^{-1}	(0, 1)	Assumed
δC	0.001day^{-1}	(0, 1)	[13]
θC	0.099 day^{-1}	(0.3, 1.0)	Assumed
αC	0.4 day^{-1}	(0.005, 0.14284)	Assumed
PC	0.5 day^{-1}	(0.002, 0.051)	Assumed
τC	0.15 day^{-1}	(0.11, 0.17)	[15]
φC	0.5 day^{-1}	(0.002, 0.051)	Assumed
γMC	0.3333 day^{-1}	(0.02, 0.533)	Assumed

Table 4: Baseline values and ranges of the parameters of our model (1)

Parameters	Baseline values	Ranges	References
Λ_H	18250 day^{-1}	$(\frac{1}{18300}, \frac{1}{18200})$	[16]
μ_H	20075 day^{-1}	$(\frac{1}{26,280}, \frac{1}{12775})$	[14]
ΛV	5000 day^{-1}	(3000,	50000)

β_{DH}	0.60 day^{-1}	(0.43, 0.79)	[14]
β_{DV}	0.43 day^{-1}	(0.60, 0.75)	[13]
b_{DV}	0.53 day^{-1}	(0.002, 0.54)	Assumed
η_{D1}	0.5 day^{-1}	(0, 1)	Assumed
η_{D2}	0.8 day^{-1}	(0, 1)	Assumed
η_{D3}	1.2 day^{-1}	(0, 1)	Assumed
γ_D	0.071 day^{-1}	(0, 1)	Assumed
δ_D	0.001day^{-1}	(0, 1)	[13]
θ_D	0.099 day^{-1}	(0.3, 1.0)	Assumed
α_D	0.4 day^{-1}	(0.005, 0.14284)	Assumed
P_D	0.5 day^{-1}	(0.002, 0.051)	Assumed
τ_D	0.11 day^{-1}	(0.11, 0.15)	[13]
φ_D	0.5 day^{-1}	(0.002, 0.051)	Assumed
γ_{MD}	0.3333 day^{-1}		Assumed

Table 5: Provides the elasticity indices of $R0D$ and $R0C$ to the 36 parameter values for the parameters of the model (1) using the reproduction number

Parameters	$R0D$	Parameters	$R0D$
βDH	**0.5**	θD	-0.238239
βDV	**0.5**	$\eta D1$	0.1065
b_{DV}	**1.00**	$\eta D2$	0.0972003
ΛH	**-0.5**	$\eta D3$	0.159365
ΛVD	**0.5**		
μH	0.499364		
μV	-1.21983		
γMD	-0.110927		
γD	-0.110927		
φD	-0.155139		
αD	-0.0000336831		
δD	-0.00902911		
τD	-0.00926286		
P_D	-0.238239		

Parameters	$R0C$	Parameters	$R0C$
βCH	**0.5**	θC	-0.238239
βCV	**0.5**	$\eta C1$	0.1065
b_{CV}	**1.00**	$\eta C2$	0.0972003
ΛH	**-0.5**	$\eta C3$	0.159365
ΛVC	**0.5**		
μH	0.499364		
μV	-1.21983		
γMC	-0.110927		
γC	-0.110927		
φC	-0.155139		
αC	-0.0000336831		
δC	-0.00902911		
τC	-0.00926286		
P_C	-0.238239		

The system (1) is numerically simulated so as to investigate the impact of certain important parameters which relates to the effective reproduction number. The value of the parameters in Table 3 and 4 are used for simulation. The contour plot of figure 1 shows that with increased infectiousness of humans wrongly diagnosed for dengue (η_{D3}) is at 55 percent, the rate of diagnosed for Dengue (θ_D) must be 60 percent and above for the disease to be eradicated from the population. The contour plot of figure 2 shows that with increased infectiousness of humans wrongly diagnosed for dengue (η_{D3}), it will require a very high rate of re-diagnosis for Dengue (ϕ_D) for proper eradication of the disease. This implies that high percentage of infectiousness require a higher percentage of proper re-diagnosis for eradication of Dengue disease from the population.

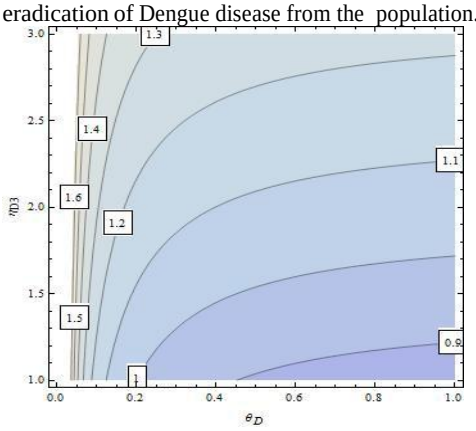


Figure 1: Contour plot of R_{0D} as a function of η_{D3} and θ_D, other parameters are at baseline.

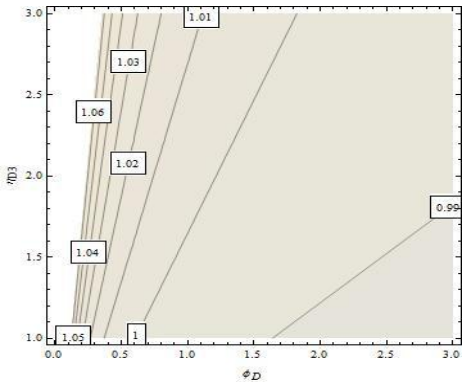


Figure 2: Contour plot of R_{0D} as a function of η_{D3} and ϕ_D, other parameters are at baseline.

The contour plot of figure 3 shows that with increased infectiousness of humans wrongly diagnosed for chikungunya η_{C3} is at 63 percent, the rate of diagnosed for chikungunya ϕ_C must be 80 percent and above for the disease to be eradicated from the population. The contour plot of figure 4 shows that with increased infectiousness of humans wrongly diagnosed for chikungunya (η_{C3}), the disease can be eradicated from the population in the presence of re-diagnoses for chikungunya (ϕ_C).

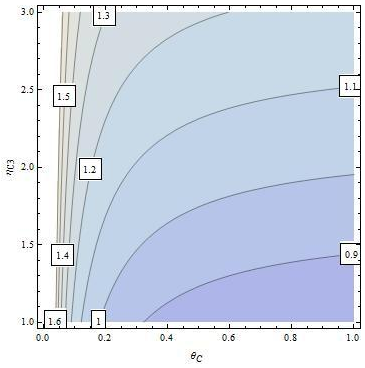


Figure 3: Contour plot of R_{0C} as a function of η_{C3} and θ_C, other parameters are at baseline.

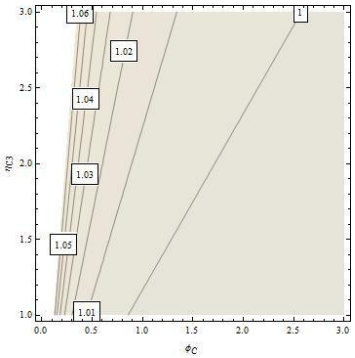


Figure 4: Contour plot of R_{0C} as a function of η_{C3} and ϕ_C, other parameters are at baseline..

Figure 5 depicts the cumulative incidence of Dengue and Chikungunya as the rate of increased infectiousness of wrongly diagnosed for Chik η_{C3} was varied from 0 to 1. The result indicate that the burden of Chik disease will be higher with more than 20 new cases due to the presence of increased infectiousness of wrongly diagnosed for Chik. Figure 6 depicts the cumulative incidence of Dengue and Chikungunya as the rate of increased infectiousness of wrongly diagnosed for Dengue η_{C3} was varied from 0 to 1. The result shows that the burden of Dengue disease increased with 30,000 new cases in 2,000 days due to the presence of wrong diagnosis.

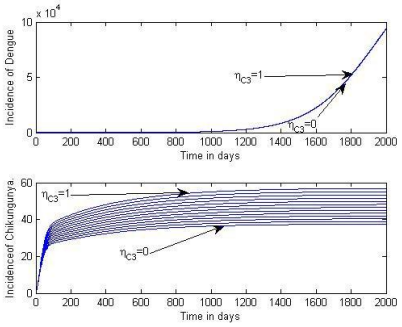


Figure 5 (a) Incidence Dengue in variation in increased infectiousness of human wrongly diagnosed of Chikungunya (b) Incidence Chikungunya with variation in increased infectiousness of human wrongly diagnosed of Chikungunya.

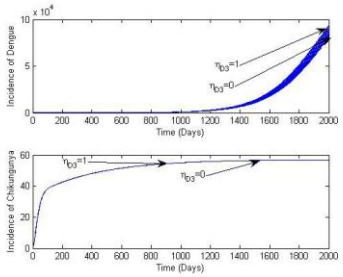


Figure 6: (a) Incidence Dengue with variation in increased infectiousness of human wrongly diagnosed of Dengue (b) Incidence Chikungunya with variation in increased infectiousness of human wrongly diagnosed of Dengue

Figure 7 depicts the cumulative incidence of Dengue and Chikungunya as the fraction of humans wrongly diagnosed for Chikungunya (p_C) was varied from 0 to1. The result shows that 1,750 new cases was detected which is great significance of the disease burden on the human population. Figure 8 depicts the cumulative incidence of Dengue and Chikungunya as the fraction of humans wrongly diagnosed for Dengue (P_D) was varied from 0 to 1. The result shows that 110 new cases was detected which is also a great significance of the disease burden on the human population.

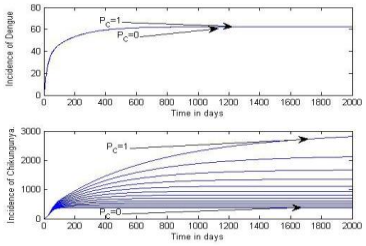


Figure 7: (a) Incidence Dengue with variation in Fraction of humans wrongly diagnosed for Chikungunya (b) incidence Chikungunya with variation in Fraction of humans wrongly diagnosed for Chikungunya

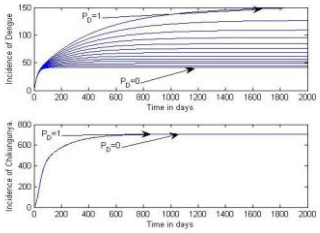


Figure 8: (a) Incidence Dengue with variation in Fraction of humans wrongly diagnosed for Dengue (b) Incidence Chikungunya with variation in Fraction of humans wrongly diagnosed for Dengue

Figure (9) depicts the cumulative incidence of Dengue with the rate of re-diagnosis for Chikungunya (ϕ_C) was varied from 0 to 1. The incidence increase as (ϕ_C) tend to 1, this implies that there is a great significance in the number of persons that will recover due to re-diagnosis of Chikungunya. Figure (10) depicts the cumulative incidence of Dengue and Chikungunya with the rate of re-diagnosis for Dengue (ϕ_D) was varied from 0 to 1. The incidence increase as (ϕ_D) tend to 1, this implies that there is a great significance in the number of persons that will recover due to re-diagnosis of Dengue.

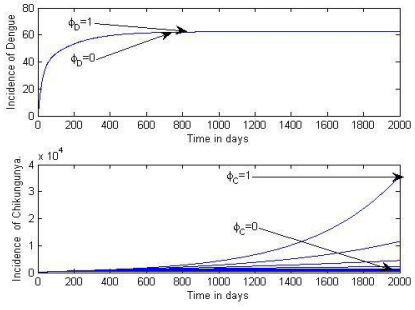
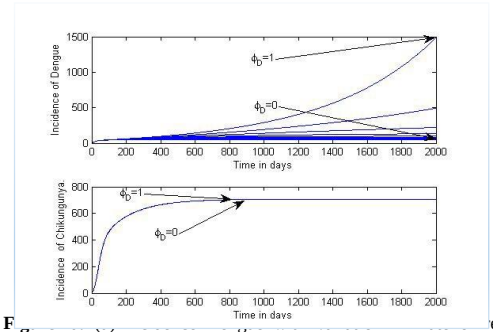


Figure 9: (a) Incidence Dengue with variation in Rate of re-diagnoses for Chikungunya (b) Incidence chikungunya with variation in Rate of re-diagnoses for Chikungunya



F e-diagnoses for Dengue (b)Incidence Chikungunya with variation in Rate of re-diagnoses for Dengue

Figure (11) depicts the cumulative incidence of Dengue and Chikungunya with the rate of diagnosis for Dengue (θ_D) varied from 0 to 1. The incidence increase as (ϕ_D) tend to 1, this implies that there is a great significance in the number of persons that will

recover due to proper diagnosis for Dengue. Figure (12) depicts the cumulative incidence of Dengue and Chikungunya with the rate of diagnosis for Dengue (θ_D) varied from 0 to 1. The incidence increase as (ϕ_C) tend to 1, this implies that there is a great significance in the number of persons that will recover due to proper diagnosis for Chikungunya. This result means that both disease can be eradicated from the population if there is a proper diagnose.

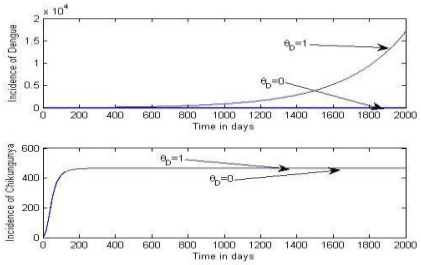


Figure 11: (a) Incidence Dengue with variation in Rate of diagnoses for dengue (b) Incidence Chikungunya with variation in Rate of diagnoses for dengue

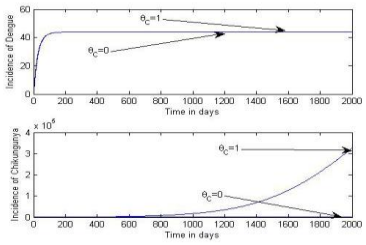


Figure 12: (a) Incidence of Dengue with variation in Rate of diagnoses for Chikungunya (b) Incidence of Chikungunya with variation in Rate of diagnoses for Chikungunya

4.0 CONCLUSION

A special case of the model system (2) was shown to be globally asymptotically stable (GAS), when the associated effective reproduction number was below unity. This result shows that in a population where there are incidences of misdiagnosis of either disease with negligible disease induced mortality for humans $(\delta_D = \delta_C = 0)$, the DFE will be GAS whenever $(R_T^m \leq 1)$.

Numerical study of the effective reproduction number showed that, the rate of diagnosed for Dengue must be 60 percent above and the rate of diagnosed for chikungunya (θ_C) must be 80 percent and above for the disease to be eradicated from the population.

It also shows that with increased infectiousness of humans wrongly diagnosed for dengue and Chikungunya, it will require a very high rate of re-diagnosis for proper eradication of both disease. This implies that high percentage of infectiousness require a higher percentage of proper re-diagnosis for eradication of Dengue and Chikungunya disease from the population.

Local sensitivity analysis was carried out on key parameter using the effective repro -duction number as a response function. Ten parameters that had the highest index were: the transmission probability from humans to vectors with Dengue and Chikungunya $(\beta_{DV} \text{ and } \beta_{CV})$, the transmission probability from vectors to humans with Dengue and Chikungunya $(\beta_{DH} \text{ and } \beta_{CH})$ death rate for the vectors μ_V, the biting rate of vector with with Chikungunya and Dengue $(b_{DV} \text{ and } b_{CV})$, human recruitment rate and vectors recruitment rate $(\Lambda_H, \Lambda_{VD} \text{ and } \beta_{VC})$.

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