



Backward Bifurcation Analysis of a Dengue-Chikungunya Model

Akhaze R.U. and Ako I.I.

Department of Mathematics, University of Benin, Benin City, Nigeria
 Email: rosemary.akhaze@uniben.edu, Tel: 07012183667

Article Info

Received 03 Dec. 2021
 Revised 07 January 2022
 Accepted 17 January 2022
 Available online 05 March 2022

Keywords: Backward bifurcation, basic reproduction number, Chikungunya, co-endemicity, Dengue, disease-free equilibrium, epidemic, endemic equilibrium point and misdiagnosis.



<https://doi.org/10.37933/nipes/4.1.2022.1>

<https://nipesjournals.org.ng>
 © 2022 NIPES Pub. All rights reserved.

Abstract

A new deterministic model for the transmission dynamics of Dengue and its co-endemicity with Chikungunya virus is designed and theoretically used to assess the misdiagnoses due to the co-endemicity of the two viruses in the human population. The phenomenon of backward bifurcation is characterized by the co-existence of a stable disease-free equilibrium (DFE) and a stable endemic equilibrium point (EEP). When the associated reproduction number of the model is less than unity in a population where there is co-endemicity of Dengue and Chikungunya, the classical requirement of having the reproduction number less than unity, while necessary is no longer sufficient for the effective control. The model shows that backward bifurcation does not occur if and only if the disease induced death for humans for both Dengue and Chikungunya are absent.

1. Introduction

In the study of the transmission dynamics of diseases with two viruses co-existing is one of the important problems in mathematical epidemiology. Consequently, the mathematical modeling of diseases with multiple pathogen strains, such as Dengue fever, HIV/AIDS, influenza, malaria and West Nile Virus, has been considered as a global concern [1, 5]. These studies have, in general, focused in the determination of threshold conditions for the co-existence of the strains, as well as the evaluation of the role co-endemicity (a disease persisting in the population or region, generally having settled to a relatively constant rate) in the transmission dynamics of disease strains.

The threshold quantity R_0 , called the basic reproduction number, measures the average number of new cases generated by a typical infected individual introduced into a completely susceptible population [1-3]. Typically, when R_0 less than unity, a small influx of infected individual will not generate large outbreaks, and the disease dies out in time (in this case, the disease free equilibrium DFE is asymptotically stable). On other hand, the disease will persist if R_0 exceeds unity, where a stable endemic equilibrium exists. This phenomenon, where the disease-free equilibrium loses its stability and a stable endemic equilibrium appears as R_0 increases through one, is known as not

comparable bifurcation [4, 5, 6, 7, 8, 9]. Other model for disease transmission undergo another type of bifurcation, known as backward bifurcation where a stable endemic equilibrium co-exists with DFE when $R_0 < 1$.

The epidemiological implication of backward bifurcation is that the requirement $R_0 < 1$, while necessary, is not sufficient for effective disease control. In a backward bifurcation setting, once R_0 crosses unity, the diseases can be invaded to a relatively high endemic level [10]. In this case, decreasing R_0 to its former level will not necessarily make the disease disappear [6]. The aim of this study is to know the effect of previous Dengue infection on the dynamics of Chikungunya, taking into consideration the effect of misdiagnosis of Dengue infection due to its co-endemicity with the Chikungunya virus in a given human population. The paper contains rigorous analysis on the threshold for previously published results on models that shows the reproduction number and some new results.

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
ϕ_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

2.0 Model Formulation

Consider the following model for the transmission dynamics of Dengue Chikungunya model (see [11])

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

where the associated variables and parameters are described in Table (1).

The model has a disease-free equilibrium (DFE) given by

$$\begin{aligned} \xi_0 &= (S_H^0, E_D^0, I_{D1}^0, I_{D2}^0, I_{WD}^0, R_D^0, E_C^0, I_{C1}^0, I_{WC}^0, R_C^0, S_{MD}^0, E_{MD}^0, I_{MD}^0, S_{MC}^0, E_{MC}^0, I_{MC}^0) \\ &= \left(\frac{\Lambda_H}{\mu_H}, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{\Lambda_{VD}}{\mu_V}, 0, 0, \frac{\Lambda_{VC}}{\mu_V}, 0, 0 \right). \end{aligned} \quad (2)$$

Furthermore, the associated reproduction number [11] of the model (1) is $\mathfrak{R}_0 = \rho(ST^{-1}) = \max[\mathfrak{R}_{0D}, \mathfrak{R}_{0C}]$,

With ρ being the spectral radius of ST^{-1} , is given by

$$\begin{aligned} \mathfrak{R}_{0D} &= \sqrt{\frac{\beta_{DH}\beta_{DV}b_{DV}^2\Lambda_{VD}\mu_H\gamma_{MD}(g_3g_4(\gamma_D + g_2\eta_{D1}) + g_4\gamma_D\eta_{D2}\theta_D(1-P_D) + P_D\gamma_D\theta_D(g_3\eta_{D3} + \eta_{D2}\phi_D))}{\Lambda_H\mu_V^2g_1g_2g_3g_4g_9}}, \\ \mathfrak{R}_{0C} &= \sqrt{\frac{\beta_{CH}\beta_{CV}b_{CV}^2\Lambda_{VC}\mu_H\gamma_{MC}(g_7g_9(\gamma_C + g_6\eta_{C1}) + g_8\gamma_C\eta_{C2}\theta_C(1-P_C) + P_C\gamma_C\theta_C(g_7\eta_{C3} + \eta_{C2}\phi_C))}{\Lambda_H\mu_V^2g_5g_6g_7g_8g_{10}}}, \end{aligned} \quad (3)$$

3.0 Backward Bifurcation Analysis

Theorem 1: The model (1) exhibits backward bifurcation phenomenon at $\mathfrak{R}_{0D} = 1$ whenever a bifurcation coefficient, denoted by a is positive.

Proof:

The existence of backward bifurcation is explored using the Center manifold Theory [12]

Let

$$S_H = x_1, E_D = x_2, I_{D1} = x_3, I_{D2} = x_4, I_{WD} = x_5, R_D = x_6, E_C = x_7, I_{C1} = x_8, I_{C2} = x_9, I_{WC} = x_{10}, R_C = x_{11}, S_{MD} = x_{12}, E_{MD} = x_{13}, I_{MD} = x_{14}, S_{MC} = x_{15}, E_{MC} = x_{16}, I_{MC} = x_{17}$$

$$\text{So that } N_H = \sum_{i=1}^{11} x_i$$

The forces of infection can be written as

$$\begin{aligned} \lambda_{DV} &= \frac{\beta_{DV}b_{DV}(\eta_{D1}x_2 + x_3 + \eta_{D2}x_4 + \eta_{D3}x_5)}{N_H} \\ \lambda_{CV} &= \frac{\beta_{CV}b_{CV}(\eta_{C1}x_7 + x_8 + \eta_{C2}x_9 + \eta_{C3}x_{10})}{N_H} \\ \lambda_{DV} &= \frac{\beta_{DH}b_{DV}x_{14}}{N_H}, \quad \text{and} \quad \lambda_{CV} = \frac{\beta_{CH}b_{CV}x_{17}}{N_H} \end{aligned}$$

It follows, that the model (1) can be re-written as

$$\begin{aligned}
 \frac{dx_1}{dt} &= F_1 \equiv \Lambda_H - \lambda_{DH}x_1 - \lambda_{CH}x_1 - \mu_Vx_1, \\
 \frac{dx_2}{dt} &= F_2 \equiv \lambda_{DH}x_1 - (\gamma_D + \mu_H)x_2, \\
 \frac{dx_3}{dt} &= F_3 \equiv \gamma_Dx_2 - (\mu_H + \delta_D + \theta_D)x_3, \\
 \frac{dx_4}{dt} &= F_4 \equiv \theta_D(1 - p_D)x_3 - (\alpha_D\delta_D + \mu_H + \tau_D)x_4 + \phi_Dx_5, \\
 \frac{dx_5}{dt} &= F_5 \equiv \theta_Dp_Dx_3 - (\delta_D + \mu_H + \phi_D)x_5, \\
 \frac{dx_6}{dt} &= F_6 \equiv \tau_Dx_6 - \mu_Hx_6, \\
 \frac{dx_7}{dt} &= F_7 \equiv \lambda_{CH}x_1 - (\gamma_C + \mu_H)x_7, \\
 \frac{dx_8}{dt} &= F_8 \equiv \gamma_Cx_7 - (\mu_H + \delta_C + \theta_C)x_8, \\
 \frac{dx_9}{dt} &= F_9 \equiv \theta_C(1 - p_C)x_8 - (\alpha_C\delta_C + \mu_H + \tau_C)x_9 + \phi_Cx_{10}, \\
 \frac{dx_{10}}{dt} &= F_{10} \equiv \theta_Cp_Cx_8 - (\delta_C + \mu_H + \phi_C)x_{10}, \\
 \frac{dx_{11}}{dt} &= F_{11} \equiv \tau_Cx_9 - \mu_Hx_{11}, \\
 \frac{dx_{12}}{dt} &= F_{12} \equiv \Lambda_{VD} - \lambda_{VD}x_{12} - \mu_Vx_{12}, \\
 \frac{dx_{13}}{dt} &= F_{13} \equiv \lambda_{VD}x_{12} - (\gamma_{MD} + \mu_V)x_{13}, \\
 \frac{dx_{14}}{dt} &= F_{14} \equiv \gamma_{MD}x_{13} - \mu_Vx_{14}, \\
 \frac{dx_{15}}{dt} &= F_{15} \equiv \Lambda_{VC} - \lambda_{VC}x_{15} - \mu_Vx_{15}, \\
 \frac{dx_{16}}{dt} &= F_{16} \equiv \lambda_{VC}x_{15} - (\gamma_{MC} + \mu_V)x_{16}, \\
 \frac{dx_{17}}{dt} &= F_{18} \equiv \gamma_{MC}x_{16} - \mu_Vx_{17},
 \end{aligned} \tag{4}$$

Consider the case with $\beta_{DH} = \beta_{DH}^*$, is a bifurcation parameter. Solving for $\beta_{DH} = \beta_{DH}^*$
From $\Re_{0D} = 1$ yields

$$\beta_{DH} = \beta_{DH}^* = \frac{\Lambda_H g_1 g_2 g_3 g_4 g_9 \mu_V^2}{\beta_{DV} b_{DV}^2 \gamma_{MD} \mu_H \Lambda_{VD} (g_3 g_4 (\gamma_D + g_2 \eta_{D1}) + g_4 \gamma_D \eta_{D2} \theta_D (1 - p_D) + p_D \gamma_D \theta_D (g_3 \eta_{D3} + \phi_D \eta_{D2}))} \tag{5}$$

The Jacobian of the system (4) at the DFE with $\beta_{DH} = \beta_{DH}^*$, is given by:

$$J_{\beta_{DH}^*} = J(\mathcal{E}_0) |_{\beta_{DH}^*} = (J_{1(17 \times 15)} \quad J_{2(17 \times 5)} \quad J_{3(17 \times 7)}) \quad (6)$$

The matrix $J_{\beta_{DH}^*}$ has a simple zero eigenvalue and all other eigenvalues have negative real part

$$J_1 = \begin{bmatrix} \mu_H & 0 & 0 & 0 & 0 \\ 0 & -g_1 & 0 & 0 & 0 \\ 0 & \gamma_D & -g_2 & 0 & 0 \\ 0 & 0 & \theta_D(1-p_D) & -g_3 & \phi_D \\ 0 & 0 & \theta_D p_D & 0 & -g_4 \\ 0 & 0 & 0 & \tau_D & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & -\beta_{DV} b_{DV} \eta_{D1} \frac{S_{MD}}{N_H} & -\beta_{DV} b_{DV} \frac{S_{MD}}{N_H} & -\beta_{DV} b_{DV} \eta_{D2} \frac{S_{MD}}{N_H} & -\beta_{DV} b_{DV} \eta_{D3} \frac{S_{MD}}{N_H} \\ 0 & \beta_{DV} b_{DV} \eta_{D1} \frac{S_{MD}}{N_H} & \beta_{DV} b_{DV} \frac{S_{MD}}{N_H} & \beta_{DV} b_{DV} \eta_{D2} \frac{S_{MD}}{N_H} & \beta_{DV} b_{DV} \eta_{D3} \frac{S_{MD}}{N_H} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$J_2 = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ -\mu_H & 0 & 0 & 0 & 0 \\ 0 & -g_5 & 0 & 0 & 0 \\ 0 & \gamma_C & -g_6 & 0 & 0 \\ 0 & 0 & \theta_C(1-p_C) & -g_7 & \phi_C \\ 0 & 0 & \theta_C p_C & 0 & -g_8 \\ 0 & 0 & 0 & \tau_C & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & -\beta_{CV} b_{CV} \eta_{C1} \frac{S_{MC}}{N_H} & -\beta_{CV} b_{CV} \frac{S_{MC}}{N_H} & -\beta_{CV} b_{CV} \eta_{C2} \frac{S_{MC}}{N_H} & -\beta_{CV} b_{CV} \eta_{C3} \frac{S_{MC}}{N_H} \\ 0 & \beta_{CV} b_{CV} \eta_{C1} \frac{S_{MC}}{N_H} & \beta_{CV} b_{CV} \frac{S_{MC}}{N_H} & \beta_{CV} b_{CV} \eta_{C2} \frac{S_{MC}}{N_H} & \beta_{CV} b_{CV} \eta_{C3} \frac{S_{MC}}{N_H} \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$J_3 = \begin{bmatrix} 0 & 0 & 0 & -\beta_{DH}^* b_{DV} & 0 & 0 & -\beta_{CH} b_{CV} \\ 0 & 0 & 0 & \beta_{DH}^* b_{DV} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_{CH} b_{CV} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \mu_H & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\mu_V & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -g_9 & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_{MD} & -\mu_V & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_V & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -g_{10} & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma_{MC} & -\mu_V \end{bmatrix}$$

The Jacobian $J_{\beta_{DH}^*}$ has a right eigenvector given by $W=(w_1, w_2, w_3, \dots, w_{17})^T$

Where

$$\begin{aligned} w_1 &= -\frac{\beta_{DH}^* b_{DV} \gamma_{MD} w_{13}}{\mu_H \mu_V} - \frac{\beta_{CH} b_{CV} \gamma_{MC} w_{16}}{\mu_H \mu_V}, \quad w_2 = \frac{\beta_{DH}^* b_{DV} \gamma_{MD} w_{13}}{g_1 \mu_V}, \quad w_3 = \frac{\beta_{DH}^* b_{DV} \gamma_{MD} w_{13}}{g_1 \mu_V}, \\ w_4 &= \frac{\beta_{DH}^* b_{DV} \gamma_{MD} \gamma_D \theta_D w_{13} (g_4 (1 - p_D) + \phi_D p_D)}{g_1 g_2 g_3 g_4 \mu_V}, \quad w_5 = \frac{\beta_{DH}^* b_{DV} \gamma_{MD} \gamma_D \theta_D p_D w_{13}}{g_1 g_2 g_4 \mu_V}, \\ w_6 &= \frac{\beta_{DH}^* b_{DV} \gamma_{MD} \gamma_D \theta_D \tau_D w_{13} ((g_4 (1 - p_D) + \phi_D p_D))}{g_1 g_2 g_3 g_4 \mu_V \mu_H}, \quad w_7 = \frac{\beta_{CH} b_{DV} \gamma_{MC} w_{16}}{g_5 \mu_V}, \\ w_8 &= \frac{\beta_{CH} b_{DV} \gamma_{MC} \gamma_C w_{16}}{g_5 \mu_V}, \quad w_9 = \frac{\beta_{CH} b_{DV} \gamma_{MC} \gamma_C \theta_C w_{16} (g_8 (1 - p_C) + \phi_C p_C)}{g_5 g_6 g_7 g_8 \mu_V}, \\ w_{10} &= \frac{\beta_{CH} b_{CV} \gamma_{MC} \gamma_C \theta_C p_C w_{16}}{g_5 g_6 g_8 \mu_V}, \quad w_{11} = \frac{\beta_{CH} b_{CV} \gamma_{MC} \gamma_C \theta_C \tau_C w_{16} ((g_8 (1 - p_C) + \phi_C p_C))}{g_5 g_6 g_7 g_8 \mu_V \mu_H}, \\ w_{12} &= -\frac{\beta_{DV} b_{DV}^2 x_{12}^* w_{13} \beta_{DH}^* \gamma_{MD}}{N_H^* g_1 g_2 g_3 g_4 \mu_V^2} \times (\eta_{D1} g_2 g_3 g_4 + \gamma_D g_3 g_4 + \eta_{D2} \gamma_D \theta_D p_D g_3 + \eta_{D3} \gamma_D \theta_D p_D (g_4 (1 - p_D) + \phi_D p_D)) \\ , \quad w_{13} &= w_{13} > 0, \quad w_{14} = \frac{\gamma_{MD} w_{13}}{\mu_V}, \\ w_{15} &= -\frac{\beta_{CV} b_{CV}^2 x_{15}^* w_{16} \beta_{CH} \gamma_{MC}}{N_H^* g_5 g_6 g_7 g_8 \mu_V^2} \times (\eta_{C1} g_6 g_7 g_8 + \gamma_C g_7 g_8 + \eta_{C2} \gamma_C \theta_C p_C g_7 + \eta_{C3} \gamma_C \theta_C (g_8 (1 - p_C) + \phi_C p_C)) \\ w_{16} &= w_{16} > 0, \quad w_{17} = \frac{\gamma_{MC} w_{16}}{\mu_V} \end{aligned} \tag{7}$$

Similarly $J_{\beta_{DH}^*}$ has a left eigenvector given by $v = (v_1, v_2, v_3, \dots, v_{17})$, satisfying $v \cdot w = 1$, with

$$v_1 = v_6 = v_{11} = v_{15} = 0, \quad v_{13} = v_{13} > 0, \quad v_{16} = v_{16} > 0,$$

$$\begin{aligned}
 v_2 &= \frac{\beta_{DV} b_{DV} x_{12}^* v_{13}}{N_H^* g_1 g_2 g_3 g_4} \times (\gamma_D (\theta_D (1 - p_D) \eta_{D2} g_4 + \theta_D p_D (\eta_{D2} \phi_D + g_3 \eta_{D3}) + g_3 g_4) + g_2 g_3 g_4 \eta_{D1}), \\
 v_3 &= \frac{\beta_{DV} b_{DV} x_{12}^* v_{13}}{N_H^* g_2 g_3 g_4} (\theta_D (1 - p_D) \eta_{D2} g_4 + \theta_D p_D (\eta_{D2} \phi_D + g_3 \eta_{D3}) + g_3 g_4), \\
 v_4 &= \frac{\beta_{DV} b_{DV} \eta_{D2} x_{12}^* v_{13}}{N_H^* g_3}, \quad v_5 = \frac{\beta_{DV} b_{DV} x_{12}^* v_{13}}{N_H^* g_3} (\eta_{D2} \phi_D + g_3 \eta_{D3}), \\
 v_7 &= \frac{\beta_{DV} b_{DV} x_{12}^* v_{13}}{N_H^* g_5 g_6 g_7 g_8} \times (\gamma_C (\theta_C (1 - p_C) \eta_{C2} g_8 + \theta_C p_C (\eta_{C2} \phi_C + g_7 \eta_{C3}) + g_7 g_8) + g_6 g_7 g_8 \eta_{C1}), \\
 v_8 &= \frac{\beta_{CV} b_{CV} x_{15}^* v_{16}}{N_H^* g_6 g_7 g_8} (\theta_C (1 - p_C) \eta_{C2} g_8 + \theta_C p_C (\eta_{C2} \phi_C + g_7 \eta_{C3}) + g_7 g_8), \\
 v_9 &= \frac{\beta_{CV} b_{CV} \eta_{C2} x_{15}^* v_{16}}{N_H^* g_7}, \quad v_{10} = \frac{\beta_{CV} b_{CV} x_{15}^* v_{16}}{N_H^* g_3} (\eta_{C2} \phi_C + g_7 \eta_{C3}), \\
 v_{14} &= \frac{\beta_{DH} b_{VD} v_2}{\mu_V}, \\
 v_{17} &= \frac{\beta_{CH} b_{VC} v_7}{\mu_V}
 \end{aligned} \tag{8}$$

3.1 Computation of bifurcation coefficients a and b

Applying the Center Manifold Theory as stated in [12], we compute the associated non-zero partial derivatives of the right hand sides of the transformed system (4), (evaluated at the DFE with $\beta = \beta^*$) the associated bifurcation coefficients, a and b, are given by

$$a = \sum_{k,i,j=1}^n v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} (0,0), \quad b = \sum_{k,i,j=1}^n v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta^*} (0,0), \tag{9}$$

Substituting (7) and (8) in (9), (having computed the associated non-zero partial derivatives for a and b), after several algebraic calculations, we obtain

$$\begin{aligned}
 a = & -\frac{2v_2\beta_{DH}b_{DV}w_{14}}{N_H^*}(w_2 + w_3 + w_4 + w_5 + w_6 + w_7 + w_8 + w_9 + w_{10} + w_{11}) \\
 & -\frac{2v_2\beta_{CH}b_{CV}w_{17}}{N_H^*}(w_2 + w_3 + w_4 + w_5 + w_6 + w_7 + w_8 + w_9 + w_{10} + w_{11}) \\
 & -\frac{2v_{13}\beta_{DV}b_{DV}w_{12}}{N_H^*}(\eta_{D1}w_2 + w_3 + \eta_{D2}w_4 + \eta_{D3}w_5) \\
 & -\frac{2v_{16}\beta_{CV}b_{CV}w_{15}}{N_H^*}(\eta_{C1}w_7 + w_8 + \eta_{C2}w_9 + \eta_{C3}w_{10}) \\
 & +\left(\frac{2v_{13}\beta_{DV}b_{DV}x_{12}^*}{N_H^{*2}}(\eta_{D1}w_2 + w_3 + \eta_{D2}w_4 + \eta_{D3}w_5)\right. \\
 & \left. +\frac{2v_{16}\beta_{CV}b_{CV}x_{15}^*}{N_H^{*2}}(\eta_{C1}w_7 + w_8 + \eta_{C2}w_9 + \eta_{C3}w_{10})\right) \times \\
 & (\delta_D\gamma_D(\theta_D\alpha_D\delta_D + \theta_D P_D\tau_D + \theta_D\mu_H P_D + \theta_D\phi_D\alpha_D + g_3g_4) \\
 & +\delta_C\gamma_C(\theta_C\alpha_C\delta_C + \theta_C P_C\tau_C + \theta_C\mu_H P_C + \theta_C\phi_C\alpha_C + g_7g_8))
 \end{aligned} \tag{10}$$

and

$$b = \frac{v_{13}\beta_{DV}b_{DV}^2x_{12}^*\gamma_{MD}}{g_1g_2g_3g_4\mu_v N_H^*}(\gamma_D(\theta_D(1-p_D)\eta_{D2}g_4 + \theta_D P_D(\eta_{D2}\phi_D + g_3\eta_{D3}) + g_3g_4) + g_2g_3g_4\eta_{D1}) > 0$$

Obviously, $b > 0$ for all biologically feasible values. However, it is required that $a < 0$ and $b > 0$ for the backward bifurcation phenomenon to occur. The bifurcation coefficient a can only be negative when the disease-induced deaths for the human population for both Dengue and Chikungunya, δ_D and δ_C , respectively have been eliminated from the model system i.e. after substituting $\delta_D = \delta_C = 0$, into the expression for a , a can be now be written as

$$\begin{aligned}
 a = & -\frac{2v_2\beta_{DH}b_{DV}w_{14}}{N_H^*}(w_2 + w_3 + w_4 + w_5 + w_6 + w_7 + w_8 + w_9 + w_{10} + w_{11}) \\
 & -\frac{2v_2\beta_{CH}b_{CV}w_{17}}{N_H^*}(w_2 + w_3 + w_4 + w_5 + w_6 + w_7 + w_8 + w_9 + w_{10} + w_{11}) \\
 & -\frac{2v_{13}\beta_{DV}b_{DV}w_{12}}{N_H^*}(\eta_{D1}w_2 + w_3 + \eta_{D2}w_4 + \eta_{D3}w_5) \\
 & -\frac{2v_{16}\beta_{CV}b_{CV}w_{15}}{N_H^*}(\eta_{C1}w_7 + w_8 + \eta_{C2}w_9 + \eta_{C3}w_{10}).
 \end{aligned} \tag{11}$$

Clearly, $a < 0$.

Hence, backward bifurcation phenomenon does not occur if and only if the disease-induced deaths for humans for both Dengue and Chikungunya, δ_D and δ_C , respectively, are absent.

Thus, the analysis in this section has confirmed that the backward bifurcation phenomenon can be induced by disease-induced deaths for humans for both Dengue and Chikungunya. Furthermore, the DFE of system (4) can be shown to be globally asymptotically stable (GAS) after the cause of the backward bifurcation is removed from the model (1)

4.0 Conclusion

The phenomenon of backward bifurcation Is characterized by the co-existence of a stable DFE and a stable EEP when the associated reproduction number of the model is less than unity.

In a population where there is co-endemicity of Dengue and Chikungunya, the classical requirement of having the reproduction number less than unity, while necessary, is no longer sufficient for effective control, in this case. Effective control policies will now be highly dependent on the initial sizes of the sub-population of the model.

References

- [1] R.M. Anderson, R.M. May (Eds.), *Infectious Diseases of Humans: Dynamics and Control*, Oxford Univ. Press, London/New York, 1991.
- [2] K. Dietz, Transmission and control of arbovirus disease, in: k. L. Cooke (Ed.), *Epidemiology*, SIAM, Philadelphia, 1975, pp. 104-121
- [3] H.W. Hethcote, The Mathematics of infectious diseases, *SIAM Rev.*42 (4) (2000) 599-653
- [4] C. Castillo-Chavez, K. Cooke, W. Huang, S.A. Levin, Results on the dynamics for models for the sexual transmission of the human immunodeficiency virus, *Appl. Math. Lett.* 2 (1989) 327-331.
- [5] C. Castillo-Chavez, K. Cooke, W. Huang, S.A. Levin, The role of long incubation periods the dynamics of HIV/AIDS. Part 2: multiple group models, in: Carlos Castillo-Chavez (Ed.), *Mathematical and Statistical Approaches to AIDS Epidemiology*, in: *Lecture Notes in Biomathematics*, vol. 83, Springer-Verlag, 1989, pp. 200-217.
- [6] J. Dushoff, H. Wenzhang, C. Castillo-Chavez, Backwards bifurcations and catastrophe in simple models of fatal diseases, *J. Math. Biol.* 36 (1998) 227-248.
- [7] W.O. Kermack, A.G. Mckendrick, A contribution to the mathematical theory of epidemics, *Proc. Roy. Soc. A.* 115 (1927) 700-721.
- [8] S. M. Garba and A. B. Gumel, (2010). Effect of cross-immunity on the transmission dynamics of two strains of dengue, *International Journal of Computer Mathematics*, 87:10.
- [9] Van den Driessche and watmough, J. (2002). 'Reproduction numbers and sub- threshold endemic equilibria for compartmental models of disease transmission *mathematical Biosciences* vol.180.
- [10] A. B. Gumel, (2012). Causes of backward bifurcations in some epidemiological models, *Journal of Mathematical Analysis and Applications* Vol. 395, pp. 355-365.
- [11] R. U. and O. O. Olowu (2021). Theoretical Study of a Model for Dengue and Its Co-Endemicity with Chikungunya Virus, *Journal of Science and Technology Research* 3(4), pp.1-15.
- [12] Carlos Castillo-Chavez and Baojun Song (2004). Dynamical models of Tuberculosis and their Applications based on center manifold theory. *Mathematical Biosciences and Engineering.* MBE 1(2):361-404.