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Modelling Zika Virus, Dengue Fever and Chikungunya Virus: Gaining Insights into the Co-Dynamics of the Three Diseases

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Abstract The recent spike in the concurrent circulation of Zika, Dengue fever, and the Chikungunya virus poses a severe threat to public health, both at home and in the diaspora. This study dives into the interplay of these three diseases, applying mathematical analysis to explain their co-dynamics within a population where they coexist. A comprehensive investigation of the model indicates that the sub-models experience backward bifurcation when the relevant reproduction numbers for each disease fall below unity. To gain insights, real-life data from Espirito Sant o State in Brazil, where both diseases are co-circulating and endemic, was gathered and incorporated into our model. This allowed us to estimate important parameter values that were embedded in the model. Through uncertainty and sensitivity analysis, we identified the top-ranked parameters that drive the spread of these three diseases, which are, effective contact rate of infected mosquitoes with susceptible humans, infected humans interacting with susceptible mosquitoes, and sexual transmission (specifically for the Zika virus). Simulations of the comprehensive Zika-Dengue-Chikungunya model revealed that minimizing the biting and contact rates of mosquitoes with humans decreases the disease load. Conversely, the absence of pesticide spraying and failure to utilize treated nets, together with unprotected sexual intercourse with sick individuals, result in the co-circulation of the three diseases, considerably aggravating the overall disease burden.

Keywords Modeling, Zika virus, Dengue fever, Chikungunya, co-infection, stability analysis

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1. Introduction

Zika virus was first found in Africa [1] and subsequently migrated to Yap [2] and French Polynesia, where it caused outbreaks in 2007 and 2013–2014 [3], respectively.

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It also spread to neighboring Pacific countries and later to South American countries, including Brazil and Colombia [4,5]. In 2015, the virus was commonly transmitted via mosquitoes, but it was discovered that it may also be transferred through sexual contact with an infected individual and also through blood transfusions [4]. The principal way in which the Zika virus is transmitted is by the Aedes species mosquito [9]. Furthermore, it serves as a vector for the dengue virus. Research has suggested that the Zika virus can remain in tropical places outside of Africa and South America, continuing its transmission [10]. The indications of a Zika virus infection consist of fever, skin rashes, and neurological abnormalities, such as microcephaly, in babies born to moms who have been infected [11–13]. The World Health Organization declared a public health emergency of international concern because of the higher prevalence of microcephaly and other neurological abnormalities during the current Zika virus outbreaks in Brazil and French Polynesia [14]. However, the outbreak in French Polynesia witnessed 42 instances of Guillain-Barré syndrome [11, 15]. A previous investigation identified ten occurrences of microcephaly, each linked to severe brain malformations [12]. Given its global potential for dispersion, it is crucial to understand the disease's transmission patterns. On the other hand, dengue fever is an infection transmitted by vectors and largely caused by the dengue virus. This virus comprises multiple serotypes, notably DENV 1 to DENV 4, which are members of the Flavivirus family. This illness poses a severe threat to many countries globally, with the most heavily hit regions being the Americas, subtropical climates, the Eastern Mediterranean, Africa, and particularly the Western Pacific region and Southeast Asia. [16–18]. After malaria, dengue fever emerges as one of the most lethal diseases carried by mosquitoes or other vectors, resulting in thousands of fatalities and impacting over 390 million individuals globally [16,17]. A 2012 analysis underlines that more than 100 countries globally face the risk of dengue fever infection [19]. This illness is spread by numerous mosquito species, with Aedes, notably Aedes aegypti, functioning as the predominant carriers. Classical dengue fever, commonly known as "break bone fever," typically leads to both modest morbidity and mortality, with patients usually recuperating within one to two weeks from the onset of fever [20]. However, certain individuals may develop severe illnesses such as dengue shock syndrome (DSS) or hemorrhagic fever (DHF) [21]. Every year, the World Health Organization (WHO) registers a substantial number of cases of dengue hemorrhagic fever (DHF) internationally [22]. The principal mechanism of transmission to humans is through bites from mosquitoes infected with the dengue virus [23]. These mosquitoes acquire the virus by feeding on an infected person and subsequently transferring it to others. It is important to emphasize that recovery from one specific DENV serotype gives only partial or transitory immunity against other serotypes [21]. Presently, there is no effective treatment available for dengue virus infection other than fluid replacement therapy, which is most beneficial when begun early. Some traditional medicines are also in existence [24]. Furthermore, there is currently no effective vaccine on the market for preventing dengue virus infection in vulnerable individuals. Although the World Health Organization (WHO) has advocated the development of a dengue vaccine, none has thus far proven effective and accessible on the market. A 2015 report mentioned the creation of the first dengue vaccine in Mexico [25].

Chikungunya, a viral disease carried by mosquitoes, was originally detected in Tanzania in 1952 [26]. In 1964, an epidemic of Chikungunya raged in the Vellore, Calcutta, and Maharashtra regions of India [27]. Another outbreak occurred in 1969

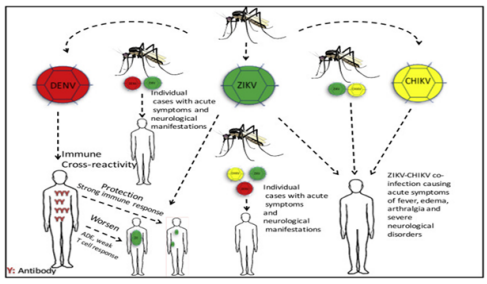


Figure 1. Zika co-circulation and co-infection with Dengue and Chikungunya, Rothan et. al [52]

in Ibadan, South Western Nigeria, where the virus was isolated from 49 patients [28]. This ailment has been recorded in more than 60 nations spanning Asia, Africa, Europe, and the Americas, and its name is derived from the unique bent posture of the people affected [29]. Chikungunya is caused by an RNA virus belonging to the arbovirus family [30]. The signs of the condition include a rapid onset of fever, joint pain, muscular aches, headaches, nausea, and rashes [31]. Chikungunya infections can occasionally go unreported or be misdiagnosed, appearing as acute, sub-acute, or chronic illnesses. In recent years, the virus has moved from relative obscurity to a substantial worldwide public health concern, impacting millions of individuals in tropical and subtropical locations around the world. Consequently, it has become a common cause of travel-related fever diseases [32].

Chikungunya virus primarily spreads through the bites of female Aedes aegypti and Aedes albopictus mosquitoes. Aedes aegypti often breeds in tiny water pools in and around human settlements [33]. In contrast, Aedes albopictus can live not only in tropical and subtropical regions but also in temperate places, potentially spreading Chikungunya to new biological settings [34]. These mosquito species are active biters during daylight hours. Additionally, there have been recorded incidences of Chikungunya transmission from mother to child. Diagnosing the condition includes establishing the existence of anti-Chikungunya antibodies in the patient's blood. Currently, there is no vaccine or particular therapy for Chikungunya. Protective measures include wearing long pants and long-sleeved shirts to cover exposed skin, using insect repellents, applying pesticides, and utilizing treated mosquito nets. In recent years, mathematical modeling has become a vital component in the study of disease dynamics and the development of successful techniques for disease control and intervention.

While different mathematical models have been constructed to study the simultaneous incidence of Zika and Dengue, Zika and Chikungunya, and Dengue and Chikungunya co-infections, there is currently a shortage of research exploring the concurrent presence of all three diseases within a single individual. Garba et al. [35] established a model for investigating the dissemination of dengue disease. Their research demonstrated that the velocity of disease transmission depended on the interaction between vulnerable humans and infected mosquitoes. Gao et al. [36] investigated the propagation of Zika and determined that both mosquito and sexual transmission must be taken into account to successfully curb the spread of the disease.

Tang et al. [37] created a mathematical model to investigate the transmission dynamics of Dengue and Zika co-infection, with a specific focus on how vaccina-

tion against Dengue in human hosts can influence Zika epidemics. Their findings demonstrated that the dengue vaccine could either decrease or raise the frequency of Zika-infected people, depending on the model's parameters. This highlights the multifaceted nature of co-infections and the importance of incorporating numerous aspects into the creation of public health interventions. In a similar vein, Ebonyah et al. [38] explored the stability of disease-free equilibrium in the context of Zika and dengue co-infection when the reproduction numbers of both diseases were less than one. Bifurcation research found that the endemic disease equilibrium displayed a backward bifurcation. Subsequently, the authors applied Pontryagin's maximal principle to identify the most efficient techniques for controlling both disorders. A numerical examination of optimal management strategies revealed that the prevention and treatment of each disease were crucial to controlling and finally eliminating both ailments. Furthermore, Aldila & Augustin [39] provided a mathematical model defining the spread of Dengue-Chikungunya co-infection inside a closed population. They carried out a numerical and analytical investigation of equilibrium points and their local stability and determined that the maximum of three unique basic reproduction numbers inside a comprehensive system is the basic reproduction number, which works as an endemic indicator. It was also determined that the basic reproduction number for the co-infection sub-system takes precedence over other basic reproduction numbers if it exceeds unity. Additionally, numerical simulations were done to validate these analytical conclusions by applying optimal control procedures.

Abboubakar et al. [40] created a mathematical model to project the spread of vector-borne diseases using recent data from a Chikungunya virus outbreak in Chad. They extended prior models by Ai et al. and Traoré et al., integrating density-dependent rates to lower the disease burden in the population. Their approach provided four control functions, including larvicides, insecticides, measures to protect humans from mosquito bites, and effective therapies. They employed the center-manifold principle to illustrate the presence of bifurcation analysis and did global sensitivity analysis to understand the impact of critical factors on mosquito populations, mosquito-human contact rates, and the number of affected humans. Their findings revealed that the use of larvicides, insecticides, bed nets, repellent items, and effective therapies could lead to a reduction in these disease-related parameters. Pontryagin's maximal principle was applied to characterize the optimal control schemes. Isea & Karl [41] focused on a co-infection model incorporating Zika virus, Chikungunya virus, and dengue fever (DF), investigating the dynamics of all three diseases concurrently. They divided the population into 24 compartments, considering diverse ways of transmission among the three viruses while omitting human-to-human and sexual transmission of the Zika virus to uninfected individuals. Their investigation investigated the potential for co-infections based on existing data.

Jose et al. [42] proposed a deterministic mathematical model for co-infection between dengue fever (DF) and Zika virus (ZIKV). Sub-model analysis revealed that both ZIKV-only and DF-only submodels displayed backward bifurcation when their respective reproduction numbers (R+0z and R0d) were less than one. The model's numerical analysis of the model examined the modes of transmission when crucial parameters changed between compartments to understand the dynamics of both single and co-infection.

Omame et al. [43] created an optimal control mathematical model to examine

the co-dynamics of COVID-19, Zika, Chikungunya, and Dengue, exploring the impact of COVID-19 on the other diseases and vice versa. They conducted local and global stability evaluations and identified backward bifurcation under certain conditions. To regulate the co-circulation of these illnesses in an endemic situation, they introduced time-dependent control mechanisms for COVID-19, Zika, Dengue, and Chikungunya prevention. Their calculations suggested that COVID-19 prophylaxis alone could greatly lower the burden of COVID-19 and associated co-infections with other arboviruses. They suggested that focusing simply on COVID-19 prevention without efforts to reduce arboviruses like Zika, Dengue, and Chikungunya could have limited or detrimental impacts, and that the most successful approach was shown to be a combined intervention strategy against all four diseases.

Mathematics has found use in human day-to-day efforts. In this regard, studies by [44] and [45] are relevant. It is also crucial to highlight that researchers in the field of mathematical epidemiology continue to produce cutting-edge research to help individuals in the healthcare sector comprehend the transmission dynamics of infectious illnesses and effective techniques for reducing their disease burden. Many works have been done in this area in the recent past by researchers such as [46–59]. However, because there has been no research effort to model the transmission dynamics of the three diseases, Zika, Dengue, and Chikungunya, this current study intends to address the gap in the literature on the transmission and co-circulation of these three diseases. The remaining parts of the paper are structured as follows: Section 2 outlines the model formulation, whereas Section 3 deals with the Zika-only sub-model. Section 4 digs into the examination of dengue fever and Chikungunya virus sub-models, respectively. On the other hand, in Section 5, we study the co-infection dynamics of Zika, Dengue, and Chikungunya viruses in relation to the overall model analysis. Section 6 presents an in-depth discussion of data fitting and sensitivity analysis of the sub-models. Following this, Section 7 presents numerical simulations, ending with final remarks in Section 8.

2. Model formulation and descriptions

The model subdivides the total human population $N_H(t)$ at time $t$into sixteen mutually exclusive compartments, namely, susceptible human $S_H(t)$, exposed human to ZIKV only $E_Z(t)$, exposed human to DENV only $E_D(t)$, exposed human to CHIKV only $E_C(t)$, exposed human to both ZIKV and DENV only $E_{ZD}(t)$, exposed human to both DENV and CHIKV only $E_{DC}(t)$, exposed human to both ZIKV and CHIKV only $E_{ZC}(t)$, exposed human to ZIKV, DENV and CHIKV $E_{ZDC}(t)$, infectious human with ZIKV only $I_Z(t)$, infectious human with DENV only $I_D(t)$, infectious human with CHIKV only $I_C(t)$, infectious human with both ZIKV and DENV only $I_{ZD}(t)$, infectious human with both DENV and CHIKV only $I_{DC}(t)$, infectious human with both ZIKV and CHIKV only $I_{ZC}(t)$, infectious human with the three diseases (ZIKV, DENV and CHIKV) $\Im_{ZDC}(t)$, recovered human from the three diseases (ZIKV, DENV and CHIKV) R(t), so that: $N_H = S_H + E_Z + E_D + E_C + E_{ZD} + E_{DC} + E_{ZC} + E_{ZDC} + I_Z + I_D + I_C + I_{ZD} + I_{DC} + I_{ZD} + \Im_{ZDC} + R$. The total vector (mosquito) population at time t, denoted by $N_M(t)$ is subdivided into susceptible mosquitoes $S_M(t)$, exposed mosquitoes to ZIKV only $E_{MZ}(t)$, exposed mosquitoes to DENV only $E_{MD}(t)$, exposed mosquitoes to CHIKV only $E_{MC}(t)$, exposed mosquitoes to both ZIKV and DENV only $E_{MZD}(t)$, exposed mosquitoes to both DENV and CHIKV only $E_{MDC}(t)$, exposed mosquitoes to both

ZIKV and CHIKV only $E_{MZC}(t)$, exposed mosquitoes to three diseases (ZIKV, DENV and CHIKV) $E_{MZDC}(t)$, infected mosquitoes with ZIKV only $I_{MZ}(t)$, infected mosquitoes with DENV only $I_{MD}(t)$, infected mosquitoes with CHIKV only $I_{MC}(t)$, infected mosquitoes with both ZIKV and DENV only $I_{MZD}(t)$, infected mosquitoes with both DENV and CHIKV only $I_{MDC}(t)$ and infected mosquitoes with both ZIKV and CHIKV only I_{mzc} (t), so that: $N_M = S_M + E_{MZ} + E_{MD} + E_{MC} + E_{MZD} + E_{MDC} + E_{MZC} + I_{MZ} + I_{MD} + I_{MC} + I_{MZD} + I_{MDC} + I_{MZD}$. We assume that susceptible humans are recruited into the human population at this rate. Humans are susceptible to ZIKV infections through sexual contact with infected humans and effective contact with infected mosquitoes at the rate given by: $\lambda_Z = \frac{m_i \beta_{MZ} I_{MZ}}{N_H} + \frac{\beta_Z (I_Z + I_{ZD} + I_{ZC} + \Im_{ZCD})}{N_H}$, where m is the mosquito biting rate, β_{mz} is the transmission probability from $I_{MZ}(t)$ to $S_H(t)$, β_Z is the transmission probability from $I_Z(t)$,$I_{ZD}(t)$, $I_{ZC}(t)$ and $\Im_{ZDC}(t)$ to $S_H(t)$. Similarly, susceptible human acquire Dengue fever through effective contact with infected mosquitoes at the rate: $\lambda_D = \frac{m\beta_{MD} I_{MD}}{N_H}$, where β_{MD} is the transmission probability from $I_{MD}(t)$ to $S_H(t)$ and m is the mosquito biting rate. Moreover, susceptible humans acquire Chikungunya virus through effective contact with the infected mosquitoes at the rate: $\lambda_C = \frac{m\beta_{MC} I_{MC}}{N_H}$, where, β_{MC} is the transmission probability from $I_{MC}(t)$ to $S_H(t)$ and m is the mosquito biting rate. The population of the susceptible mosquitoes is generated by the recruitment rate Λ_M, susceptible mosquitoes acquired ZIKV through effective contact with infected humans with ZIKV at the rate: $\lambda_{MZ} = \frac{m\beta_{MZ} I_Z}{N_H}$, acquired DENV at the rate $\lambda_{MD} = \frac{m\beta_{MD} I_D}{N_H}$, CHIKV at the rate of $\lambda_{MC} = \frac{m\beta_{MC} I_C}{N_H}$, and also acquire both ZIKV and DENV at the rate: $\lambda_{MZC} = \frac{m\beta_{MZC}(I_{ZC} + \Im_{ZCD})}{N_H}$, DENV and CHIKV at the rate $\lambda_{MDC} = \frac{m\beta_{MDC}(I_{DC} + \Im_{ZDC})}{N_H}$ and ZIKV and CHIKV at the rate: $\lambda_{MZD} = \frac{m\beta_{MZD}(I_{ZD} + \Im_{ZCD})}{N_H}$. All humans suffer from natural death at a constant rate μ_H. Susceptible humans infected with ZIKV only move to the exposed class $E_Z(t)$ at the rate $\lambda_Z$then progress to the infectious class at the rate: σ_1; susceptible humans infected with DENV only move to the exposed class$E_D(t)$ and then progress to the infectious class at the rate $I_D(t)$; likewise, infected humans with CHIKV only move to the exposed class at the rate$E_C(t)$, then move to the infectious class $I_C(t)$. Humans exposed to ZIKV only move to both exposed classes with ZIKV and DENV $E_{ZD}(t)$ and ZIKV & CHIKV $E_{ZC}(t)$ at the rate $\lambda_D E_Z$ and $\lambda_C E_Z$ respectively.

Similarly, human exposed to DENV only $E_D(t)$ moves to exposed class of both ZIKV & DENV only $E_{ZD}(t)$ and class exposed to both DENV & CHIKV at the rate $\lambda_Z E_D$ and $\lambda_C E_D$ respectively.

Moreover, human exposed to CHIKV only $E_C(t)$ moves to class exposed to both ZIKV & CHIKV and class exposed to both DENV & CHIKV at the rate $\lambda_Z E_C$ and $\lambda_D E_C$ respectively.

Humans exposed to $E_{ZD}(t)$,$E_{ZC}(t)$ and $E_{DC}(t)$ progress to $E_{ZDC}(t)$ at the rates $\lambda_C E_{ZD}$, $\lambda_D E_{ZC}$ and $\lambda_Z E_{DC}$ respectively. Infectious humans with ZIKV only $I_Z(t)$ move to class infected with both ZIKV & DENV only $I_{ZD}(t)$ and ZIKV & CHIKV only $I_{ZC}(t)$ at the rates η_1 and η_2, $I_{ZD}(t)$ and $I_{ZC}(t)$ classes progress to $\Im_{ZDC}(t)$ at the rates δ_1 and δ_2, respectively. Infectious humans with DENV only $I_D(t)$ move to both classes infected with ZIKV & DENV only $I_{ZD}(t)$ and DENV & CHIKV only $I_{DC}(t)$ at the rates ϕ_1 and ϕ_2, I_{DC} class progresses to $\Im_{ZDC}(t)$ at the rate δ_3. Infectious humans with ZIKV I_Z, DENV I_D and CHIKV I_C only recover at the rates α_1, α_2 and α_3 respectively. Similarly, infectious humans with ZIKV

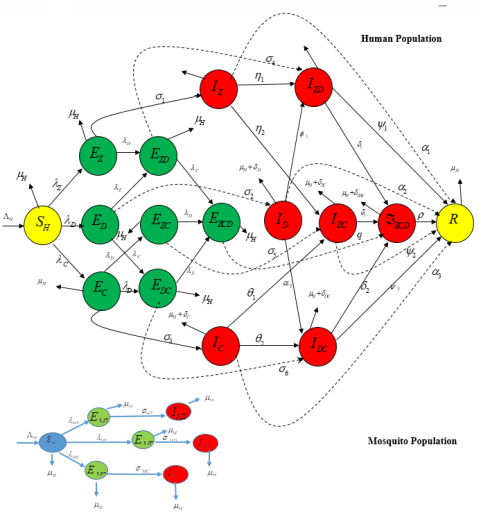


Figure 2. Model flow diagram

& DENV I_{zd}, ZIKV & CHIKV I_{zd} and DENV CHIKV I_{DC} recover at the rates ψ_1, ψ_2 and ψ_3 respectively. Infectious humans infected with three diseases $\Im_{ZDC}$ recover at the rate ρ and $\delta_H(\delta_Z, \delta_D, \delta_C)$ are the disease induced death rates.

2.1. Model assumptions

1. There is homogeneous mixing of the individuals in the population, which suggests that all susceptible individuals are equally at risk of being infected upon contact with infectious humans.
2. Individuals can either get Zika virus, dengue fever, or Chikungunya virus, but not more than one of these diseases at a time [38].
3. Once patients recover from Zika virus, dengue fever, and Chikungunya sickness, they become permanently immune to these diseases and cannot become sensitive to them again [38].
4. Each of the diseases is spread by mosquitoes [40].
5. There is continual disease-induced mortality that occurs solely in the infected compartments [39].
6. The natural death rate is the same in all the divisions of the model [38].

In accordance with the assumptions and the descriptions of the model formulations, the Zika, Dengue and Chikungunya virus co-infection model is given by the following system of non-linear differential equations:

Variables	Description
N_H	Total human population
$S_H(S_M)$	Susceptible humans (Mosquitoes)
$E_Z(E_D, E_C)$	Exposed Humans to ZIKV, DF and CHIKV
$E_{ZD}(E_{DC}, E_{ZC})$	Exposed humans to both ZIKV and DF, DF and CHIKV and ZIKV and CHIKV respectively
E_{ZDC}	Exposed humans to ZIKV, DF and CHIKV
$I_Z(I_D, I_C)$	Infected humans with ZIKV, DF and CHIKV
$I_{ZD}(I_{ZC}, I_{DC})$	Infectious humans with ZIKV and DF, ZIKV and CHIKV and DF and CHIKV respectively
I_{ZDC}	Infected humans with ZIKV, DF and CHIKV
R_H	Recovered humans
$E_{MZ}(E_{MD}, E_{MC})$	Exposed mosquitoes to ZIKV, DF and CHIKV
$E_{MZD}(E_{MDC}, E_{MZC})$	Exposed Mosquitoes to both ZIKV and DF, DF and CHIKV and ZIKV and CHIKV respectively
$I_{MZ}(I_{MC}, I_{MD})$	Infected mosquitoes with ZIKV, DF and CHIKV respectively

Table 1. Model variables

Parameters	**Interpretation**
$\Lambda_H(\Lambda_M)$	Recruitment rate for humans (mosquitoes) population
m_r	Mosquito biting rate
$\beta_{MZ}(\beta_{MD}, \beta_{MC})$	Transmission probability from I_{MZ}, I_{MD} and I_{MC} to S_H respectively
$\beta_{MZD}(\beta_{MZC}, \beta_{MDC})$	Transmission probability from I_{MZD}, I_{MZC} and I_{MDC} to S_H respectively
$\mu_H(\mu_M)$	Natural death rate of humans (Mosquitoes)
$\sigma_{MZ}(\sigma_{MD}, \sigma_{MC})$	Progression rate from E_{MZ}, E_{MD} and E_{MC} class to I_{MZ}, I_{MD} and I_{MC} respectively
$\sigma_1(\sigma_2, \sigma_3)$	Progression rate from exposed human with ZIKV, DF and CHIKV to infected humans with ZIKV, DF and CHIKV respectively
η_1	Progression rate from infected humans with ZIKV to Infected humans with both ZIKV and DF
η_2	Progression rate from infected humans with ZIKV to infected humans with both ZIKV and DF
θ_1	Progression rate from infected humans with CHIKV to infected humans with both ZIKV and CHIKV
θ_2	Progression rate from infected humans with CHIKV to infected humans with both DF and CHIKV
ϕ_1	Progression rate from infected humans with CHIKV to infected humans with both ZIKV and CHIKV
ϕ_2	Progression rate from infected humans with DF to infected humans with both DF and CHIKV
$\delta_H(\delta_Z, \delta_D, \delta_C)$	Disease induced death rate for humans with ZIKV (DF and CHIKV)
$\delta_{ZD}, \delta_{DC}, \delta_{ZC}$	Disease induced death rate for humans with ZIKV and DF, DF and CHIKV and ZIKV and CHIKV
$\psi_1(\psi_2, \psi_3)$	Recovery rate of infectious Human with I_{zd}, I_{dc} and I_{zc}

Table 2. Model Parameters

Parameters	Interpretation
$\alpha_1(\alpha_2, \alpha_3)$	Recovery rate of infected humans with ZIKV, DF and CHIKV respectively
σ_4	Transmission rate from exposed humans with both ZIKV and DF to infected humans with both ZIKV and DF
σ_5	Transmission rate from exposed humans with both ZIKV and CHIKV to infected humans with both ZIKV and CHIKV
σ_6	Transmission rate from exposed humans with both DF and CHIKV to an infected humans with DF and CHIKV
ρ	Recovery rate of infected human with ZIKV, DF and CHIKV

Table 3. Model Parameters (continued)

$$
\begin{aligned}
\frac{dS_H}{dt} &= \Lambda_H - \lambda_Z S_H - \lambda_D S_H - \lambda_C S_H - \mu_H S_H,\\
\frac{dE_Z}{dt} &= \lambda_Z S_H - \lambda_D E_Z - \lambda_C E_Z - (\sigma_1 + \mu_H) E_Z,\\
\frac{dI_Z}{dt} &= \sigma_1 E_Z - (\eta_1 + \eta_2 + \alpha_1 + \delta_H + \mu_H) I_Z,\\
\frac{dE_D}{dt} &= \lambda_D S_H - \lambda_Z E_D - \lambda_C E_D - (\sigma_2 + \mu_H) E_D,\\
\frac{dI_D}{dt} &= \sigma_2 E_D - (\phi_1 + \phi_2 + \alpha_2 + \delta_H + \mu_H) I_D,\\
\frac{dE_C}{dt} &= \lambda_C S_H - \lambda_Z E_C - \lambda_D E_C - (\sigma_3 + \mu_H) E_C,\\
\frac{dI_C}{dt} &= \sigma_3 E_C - (\theta_1 + \theta_2 + \alpha_3 + \delta_H + \mu_H) I_C,\\
\frac{dE_{ZD}}{dt} &= \lambda_D E_Z + \lambda_Z E_D - \lambda_C E_{ZD} - (\sigma_4 + \mu_H) E_{ZD},\\
\frac{dE_{ZC}}{dt} &= \lambda_C E_Z + \lambda_Z E_C - \lambda_D E_{ZD} - (\sigma_5 + \mu_H) E_{ZC},\\
\frac{dE_{DC}}{dt} &= \lambda_C E_D + \lambda_D E_C - \lambda_Z E_{DC} - (\sigma_6 + \mu_H) E_{DC},\\
\frac{dE_{ZDC}}{dt} &= \lambda_C E_{ZD} + \lambda_D E_{ZC} + \lambda_Z E_{DC} - (q + \mu_h) E_{ZDC},\\
\frac{dI_{ZD}}{dt} &= \delta_4 E_{ZD} + \eta_1 I_Z + \phi_1 I_D - (\delta_1 + \psi_1 + \delta_{ZD} + \mu_H) I_{ZD},\\
\frac{dI_{ZC}}{dt} &= \delta_5 E_{ZC} + \eta_2 I_Z + \theta_1 I_C - (\delta_2 + \psi_2 + \delta_{ZC} + \mu_H) I_{ZC},\\
\frac{dI_{DC}}{dt} &= \delta_6 E_{DC} + \theta_2 I_C + \phi_2 I_D - (\delta_3 + \psi_3 + \delta_{DC} + \mu_H) I_{DC},\\
\frac{d\Im_{ZCD}}{dt} &= \varepsilon_1 I_{ZD} + \delta_2 I_{ZC} + \delta_3 I_{DC} - (\rho + \delta_{ZCD} + \mu_H) \Im_{ZCD},\\
\frac{dR}{dt} &= \alpha_1 I_Z + \alpha_2 I_D + \alpha_3 I_C + \psi_1 I_{ZD} + \psi_2 I_{ZC} + \psi_3 I_{DC} + \rho \Im_{ZCD} - \mu R,\\
\frac{dS_M}{dt} &= \Lambda_M - (\lambda_{MZ} + \lambda_{MD} + \lambda_{MC} + \lambda_{MZC} + \lambda_{MZD} + \lambda_{MCD} + \mu_M) S_M.
\end{aligned}
\tag{2.1}
$$

$$\begin{aligned}
\frac{dE_{MZ}}{dt} &= (\lambda_{MZ} + \varepsilon_1\lambda_{MZC} + \varepsilon_2\lambda_{MZD})S_M - (\sigma_{MZ} + \mu_M)E_{MZ},\\
\frac{dE_{MD}}{dt} &= (\lambda_{MD} + (1-\varepsilon_2)\lambda_{MZD} + x_1\lambda_{MCD})S_M - (\sigma_{MD} + \mu_M)E_{MD},\\
\frac{dE_{MC}}{dt} &= (\lambda_{MC} + (1-\varepsilon_1)\lambda_{MZC} + (1-x_1)\lambda_{MCD})S_M - (\sigma_{MC} + \mu_M)E_{MC},\\
\frac{dI_{MZ}}{dt} &= \sigma_{MZ}E_{MZ} - \mu_M I_{MZ},\\
\frac{dI_{MD}}{dt} &= \sigma_{MD}E_{MD} - \mu_M I_{MD},\\
\frac{dI_{MC}}{dt} &= \sigma_{MC}E_{MC} - \mu_M I_{MC},
\end{aligned}$$

where:

$$\begin{aligned}
\lambda_Z &= \frac{m\beta_{MZ}I_{MZ}}{N_H} + \frac{\beta_Z(I_Z + I_{ZD} + I_{ZC} + \Im_{ZDC})}{N_H},\\
\lambda_C &= \frac{m\beta_C I_{MC}}{N_H},\\
\lambda_D &= \frac{m\beta_D I_{MD}}{N_H},\\
\lambda_{MZ} &= \frac{m\beta_{MZ}I_Z}{N_H},\\
\lambda_{MD} &= \frac{m\beta_{MD}I_D}{N_H},\\
\lambda_{MC} &= \frac{m\beta_{MC}I_C}{N_H},\\
\lambda_{MZC} &= \frac{m\beta_{MZC}(I_{ZC} + \Im_{ZCD})}{N_H},\\
\lambda_{MDC} &= \frac{m\beta_{MDC}(I_{DC} + \Im_{ZCD})}{N_H},\\
\lambda_{MZD} &= \frac{m\beta_{MZD}(I_{ZD} + \Im_{ZCD})}{N_H}.
\end{aligned}$$

3. Model analysis

In order to delve into the analysis of the complete co-infection model, the study will scrutinize the qualitative properties of the individual sub-models.

3.1. Zika virus sub-model

The model focusing solely on the Zika virus is derived from the co-infection model (2.1) by excluding the other two diseases, Dengue fever and Chikungunya. This involves setting all variables and parameters associated with Dengue fever and Chikungunya to zero, denoted as follows:

$E_D = E_C = I_D = I_C = I_{ZD} = I_{ZC} = I_{DC} = \xi_{ZDC} = E_{MC} = E_{MD} = I_{DC} = I_{ZDC} = I_{MD} = 0$.

We have:

$$\begin{aligned}
\frac{dS_H}{dt} &= \Lambda_H - \lambda_Z S_H - \mu_H S_H, \\
\frac{dE_Z}{dt} &= \lambda_Z S_M - (\sigma_1 + \mu_H) E_Z, \\
\frac{dI_Z}{dt} &= \sigma_1 E_Z - (\alpha_1 + \delta_Z + \mu_H) I_Z, \\
\frac{dR_Z}{dt} &= \alpha_1 I_Z - \mu_H R_Z, \\
\frac{dS_M}{dt} &= \Lambda_M - \lambda_{MZ} S_M - \mu_M S_M, \\
\frac{dE_{MZ}}{dt} &= \lambda_{MZ} S_M - (\sigma_{MZ} + \mu_M) E_{MZ}, \\
\frac{dI_{MZ}}{dt} &= \sigma_{MZ} E_{MZ} - \mu_M I_M,
\end{aligned} \tag{3.1}$$

with

$\lambda_Z = \frac{m\beta_{HZ} I_{MZ}}{N_H} + \frac{\beta_Z I_Z}{N_H}$,

$\lambda_{MZ} = \frac{m\beta_{MZ} I_Z}{N_H}$.

3.2. Invariant region

In order to establish the invariant region, it is essential to demonstrate that the model's solution remains within bounds. The collective human populations considered in the model are:

$$N_H = S_H + E_Z + I_Z + R_Z.$$

Taking the derivative of both sides and substituting the corresponding expressions, we obtain $\frac{dS_H}{dt}, \frac{dE_Z}{dt}, \frac{dI_Z}{dt}$ and $\frac{dR_Z}{dt}$. From (3.1), we get:

$$\frac{dN_H}{dt} = \Lambda_H - N_H \mu_H - \delta_Z I_Z.$$

That is,

$$\frac{dN_H}{dt} \leq \Lambda_H - N_H \mu_H. \tag{3.2}$$

Solving (3.2), we get:

$\Omega_Z = \left\{ (S_H, E_Z, I_Z, R) \in R_+^4 : 0 \leq N_H \leq \frac{\Lambda_H}{\mu_H} \right\}$.

Similarly, for the vector population $N_M = S_M + E_{MZ} + I_{MZ}$, we have:

$\Omega_M = \left\{ (S_M, E_{MZ}, I_{MZ}) \in R_+^3 : 0 \leq N_M \leq \frac{\Lambda_M}{\mu_M} \right\}$.

Hence, the solution set of equation (3.1) is confined within the specified region: $\Omega = \Omega_Z \times \Omega_M$.

3.3. Positivity of solutions

Theorem 3.1. *If the initial value $S_H \geq 0$, $E_Z \geq 0$, $I_Z \geq 0$, $R_Z \geq 0$, $S_{MZ} \geq 0$, $E_{MZ} \geq 0$, $I_{MZ} \geq 0$, then the solution of ZIKV-only model are non-negative.*

Proof.

$$N(t) = S_H(t) + E_Z(t) + I_Z(t) + R_Z(t). \tag{3.3}$$

Thus, at any time t, $S_H(t) \leq N(t)$, $E_Z(t) \leq N(t)$, $I_Z(t) \leq N(t)$, $R_Z(t) \leq N(t)$, $S_H(t) \leq N(t)$, $E_{MZ}(t) \leq N(t)$ and $I_{MZ}(t) \leq N(t)$.

Hence, the susceptible class in system (3.1) becomes:

$$\frac{dS_H}{dt} = \Lambda_H - \lambda_Z S_H - \mu_H S_H. \tag{3.4}$$

Solving (3.3), we get:

$$S_H(t) \geq S_H(0)e^{-\mu_H t}.$$

Similarly, from other state variables, we have
$E_Z(t) > 0$,$I_Z(t) > 0$,$R_Z(t) > 0$,$S_M(t) > 0$,$E_{MZ}(t) > 0$,$I_{MZ}(t) > 0$.
Therefore, all the solution sets are positive at $t \geq 0$. □

3.4. ZIKAV-disease free equilibrium point

The disease-free equilibrium point for ZIKAV is the state where no disease is present in the population. For system (3.1), this occurs when all differential equations in (3.1) are set to zero. Thus, the disease-free equilibrium point (ZDFEP) is obtained as follows:

$_Z = (S_H, E_Z, I_Z, R_Z, S_M, E_{MZ}, I_{MZ}) = \left(\frac{\Lambda_H}{\mu_H}, 0, 0, 0, \frac{\Lambda_M}{\mu_M}, 0, 0\right)$.

3.5. Basic reproduction number for ZIKV

It is essential to understand the significance of the Basic Reproduction Number (ZBRN) in model (3.1). The ZBRN (R_{0Z}) represents the count of secondary infections in an entirely susceptible population resulting from the introduction of ZIKV by a single infectious individual into that susceptible population. Evaluating the infected compartments (E_Z, I_Z, E_{MZ}, I_{MZ}) at Zika Disease-Free Equilibrium Point (ZDFEP), the basic reproduction number R_{0Z} is determined utilizing the Next Generation Matrix method (NGM), as proposed by [40, 41 and 46]. The R_{0Z} is obtained as follows:

$$F = \begin{pmatrix} 0 & \beta_Z & 0 & m\beta_{HZ} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{m\beta_{MZ}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \text{ and } V = \begin{bmatrix} D_1 & 0 & 0 & 0 \\ -\sigma_1 & D_2 & 0 & 0 \\ 0 & 0 & D_3 & 0 \\ 0 & 0 & -\sigma_{MZ} & \mu_M \end{bmatrix},$$

where $D_1 = \sigma_1 + \mu_H$, $D_2 = \alpha_1 + \delta_Z + \mu_H$ and $D_3 = \sigma_{MZ} + \mu_M$.

Hence, it follows from [46] that,$R_{0Z} = \rho\left(\frac{F}{V}\right)$, where $\rho$is the spectral radius or the maximum eigenvalues of matrix $\left(F.V^{-1}\right)$ given by:

$$R_{0Z} = \frac{\beta_Z\sigma_1}{D_1D_2} + \frac{m^2\beta_{MZ}\Lambda_M\mu_H\sigma_1\beta_{HZ}\sigma_{MZ}}{\Lambda_H{\mu_M}^2D_1D_2D_3}, \tag{3.5}$$

$R_{MZ} = \frac{m^2\beta_{MZ}\Lambda_M\mu_H\sigma_1 m\beta_{HZ}\sigma_{MZ}}{\Lambda_H{\mu_M}^2D_1D_2D_3}$ and $R_{HZ} = \frac{\beta_Z\sigma_1}{D_1D_2}$.

3.6. Local stability of ZDFEP

Theorem 3.2. *The equilibrium point $\Im_Z$ of the system (3.1) is asymptotically stable (LAS) if $R_{0Z}^{+} < 1$ and unstable if $R_{0Z}^{+} > 1$. The ZIKA disease free equilibrium (ZDFE) is locally stable if $R_{0Z} < 1$.*

Proof. To analyze the stability of the disease free equilibrium of Zika sub-model, we consider the Jacobian of transformation of system (3.1).

Thus, we acquire the following matrix

$$\Im(Z) = \begin{pmatrix} -\mu_H & 0 & -\beta_Z & 0 & 0 & 0 & -m\beta_{HZ} \\ 0 & -D_1 & \beta_Z & 0 & 0 & 0 & m\beta_{HZ} \\ 0 & \sigma_1 & -D_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -\mu_H & 0 & 0 & 0 \\ 0 & 0 & -\frac{m\beta_{MZ}\Lambda_M\mu_H}{\mu_M\Lambda_H} & 0 & -\mu_M & 0 & 0 \\ 0 & 0 & \frac{m\beta_{MZ}\Lambda_M\mu_H}{\mu_M\Lambda_H} & 0 & 0 & -D_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_{MZ} & -\mu_M \end{pmatrix},$$

where

$a_{53} = -\frac{m\beta_{MZ}\Lambda_M\mu_H}{\mu_M\Lambda_H}$, $a_{63} = \frac{m\beta_{MZ}\Lambda_M\mu_H}{\mu_M\Lambda_H}$.

Our objective is to demonstrate that all eigenvalues of the Jacobian matrix at the Disease-Free Equilibrium Point (ZDFEP) are evident. Clearly, this is apparent from the matrix. $\Im(Z)$. The negative eigenvalues$-\mu_H$,$-\mu_H$ and $-\mu_M$ and the roots of the characteristics polynomials (3.6) is shown below:

$$(\lambda^{**})^4 + A_1(\lambda^{**})^3 + A_2(\lambda^{**})^2 + A_3(\lambda^{**}) + A_4 = 0, \tag{3.6}$$

where

$A_1 = D_1 + D_2 + D_3 + \mu_M$,
$A_2 = D_1D_2 + D_1D_3 + D_1\mu_M + D_2D_3 + D_2\mu_M + D_3\mu_M - \beta_Z\sigma_1$,
$A_3 = D_1D_2D_3 + D_1D_2\mu_M + D_1D_3\mu_M + D_2D_3\mu_M - \beta_Z\sigma_1(D_3 + \mu_M)$.
$A_4 = D_1D_2D_3\mu_M(1 - R_{0Z})$.

Applying the Routh-Hurwitz criterion in [44], which states that all roots of the polynomials (3.6) have negative real part if and only if the co-efficient$A_i > 0$, for $i = 1, 2, 3, 4$ Therefore, by Routh-Hurwitz criterion, the ZDFEP of model (3.1) is locally asymptotically stable.

□

3.7. Existence of ZIKV endemic equilibrium point (ZEEP)

In this sub-section, we explore the existence of ZEEP which occurs when the infected variables are nonzero. To obtain the necessary condition for the existence of ZEEP, the Zika virus sub-model is solved in terms of force of infections λ_Z and λ_{MZ} which gives:

$$
\begin{aligned}
S_H^{**} &= \frac{\Lambda_H}{\lambda_Z^{**} + \mu_H}, \\
E_Z^{**} &= \frac{\lambda_Z^{**}\Lambda_H}{D_1\left(\lambda_Z^{**} + \mu_H\right)}, \\
I_Z^{**} &= \frac{\lambda_Z^{**}\Lambda_H\sigma_1}{D_1D_2\left(\lambda_Z^{**} + \mu_H\right)}, \\
R_Z^{**} &= \frac{\lambda_Z^{**}\Lambda_H\sigma_1\alpha_1}{\mu_HD_1D_2\left(\lambda_Z^{**} + \mu_H\right)}, \\
S_M^{**} &= \frac{\Lambda_M}{\lambda_{MZ}^{**} + \mu_M}, \\
E_{MZ}^{**} &= \frac{\lambda_{MZ}^{**}\Lambda_M}{D_3\left(\lambda_{MZ}^{**} + \mu_M\right)}, \\
I_Z^{**} &= \frac{\lambda_{MZ}^{**}\Lambda_M\sigma_{MZ}}{\mu D_3\left(\lambda_{MZ}^{**} + \mu_M\right)}.
\end{aligned} \tag{3.7}
$$

$N_H^{**} = S_H^{**} + E_Z^{**} + I_Z^{**} + R_Z^{**}$,
where

$$\lambda_{MZ} = \frac{m\beta_{MZ}I_Z}{N_H}. \tag{3.8}$$

Substituting equation (3.7) into equation (3.8) and simplifying, we obtain

$$\lambda_{MZ} = \frac{m\beta_{MZ}\Lambda_H\sigma_1\lambda_Z^{**}}{\Lambda_HD_1D_2\mu_H + \lambda_Z^{**}\Lambda_HD_2\mu_H + \lambda_Z^{**}\Lambda_H\sigma_1\mu_H + \lambda_Z^{**}\Lambda_H\sigma_1\alpha_1}. \tag{3.9}$$

More so,

$$\lambda_Z = \frac{m\beta_ZI_{MZ}}{N_H}. \tag{3.10}$$

Similarly, we derive the characteristic polynomial below by substituting the expression in equation (3.9) into equation (3.10) to get

$$\lambda_Z^{**}f(\lambda_Z^{**}) = \lambda_Z^{**}\left(A\lambda_Z^{**2} + B\lambda_Z^{**2} + C\right) = 0, \tag{3.11}$$

where

$$
\begin{aligned}
A =& \Lambda_H^2D_1D_2D_3\mu_M\left(m\beta_{MD}\sigma_2\mu_H + \mu_MD_1D_2\right), \\
B =& \Lambda_H^2D_1D_2D_3\mu_H\mu_M\left(m\beta_{MD}\sigma_2\mu_H + 2\mu_MD_1D_2\right) \\
&- m^2\beta_D\beta_{MD}\Lambda_H\Lambda_M\sigma_2\sigma_{MD}D_1D_2\mu_H^2, \\
C =& \Lambda_H^2D_1^2D_2^2D_3\mu_H^2\mu_M^2\left(1 - R_{0Z}\right).
\end{aligned}
$$

The solution to equation (3.12), $\lambda_Z^{**} = 0$ corresponds to the Zika virus disease-free equilibrium point (ZDFEP), whose stability has been previously investigated. Then $f\left(\lambda_Z^{**}\right) = 0$ corresponds to the endemic equilibrium. The occurrence of backward bifurcation is described by the coexistence of a stable disease-free equilibrium point

(ZDFEP) and a stable endemic equilibrium, particularly when the associated reproduction number of the Zika-only model is smaller than unity. From a biological standpoint, the meaning of backward bifurcation is that the essential condition for efficiently managing the Zika virus in the population, when the reproduction number is below unity, is no longer appropriate. In circumstances of backward bifurcation, numerous endemic equilibria are required to exist. Thus, this indicates that there are three possibilities for $(f(\lambda_Z^{**}) = 0)$ that are to be addressed in (3.12), depending on the sign of B and C, since A is always positive. That is:

- If $A < 0$ and $C = 0$ or $B^2 - 4AC = 0$, then equation (3.12) has a unique endemic equilibrium point (one positive root) and no possibility of backward bifurcation.
- If $B < 0$, $C > 0$ and $B^2 - 4AC > 0$, then equation (3.12) has two endemic equilibria (two possible roots), and therefore it is possible for backward bifurcation to occur.
- Otherwise, there is none.

However, it is important to note that C is always positive if $R_{0Z}^{+} < 1$ and negative if $R_{0Z}^{+} > 1$. Hence, the above observation leads to the following theorem.

Theorem 3.3. *The ZIKV-only model (3.1) has:*

(a) Precisely one unique endemic equilibrium if $C < 0$ (i.e., $R_{0Z}^{+} > 1$);

(b) Precisely one unique endemic equilibrium if $B < 0$ and $C = 0$ or $B^2 - 4AC = 0$;

(c) Precisely two endemic equilibra if $C > 0$ (i.e., $R_{0Z}^{+} < 1$), $B < 0$ and $B^2 - 4AC > 0$.

Hence, (from case c) the Zika virus sub-model (3.1) exhibits a backward bifurcation which occur when the ZEEP exist if only if $R_{0Z}^{+} < 1$.

We explored the occurrence of backward bifurcation in model (3.1) by applying the Center Manifold theory as given by Castillo-Chaves and Song [44]). This investigation attempted to determine whether backward bifurcation is present in the model (3.1).

Theorem 3.4. *The model of system (3.1) exhibits backward bifurcation if the condition below holds:*

$$
\begin{aligned}
a = &- \frac{2v_2w_2\mu_H\left(D_1D_2 - \beta_Z\sigma_1\right)\left(w_2\left(\alpha_1\sigma_1 + D_1\left(\sigma_1 + D_1\right)\right)\right)}{\Lambda_H D_1 D_2^2 \mu_M} \\
&- \frac{2\beta_Z\sigma_1 w_2^2 v_2\mu_H\left(D_1\mu_M + \alpha_1\sigma_1\right)}{\Lambda_H D_1 D_2 \mu_M} - \frac{2m\beta_{MZ}\beta_{HZ}\sigma_{MC}\sigma_1\Lambda_M v_2 w_2 \mu_H^2}{\Lambda_H^2 D_2 D_3 \mu_M^2} \\
&\left(\frac{m^2\beta_{MZ}\sigma_1 w_2^2}{D_2D_3} + \sigma_1 w_2 \frac{\left(D_1\mu_M + D_2\alpha_1\right)}{D_1 D_2 \mu_M} + \frac{w_2\left(\mu_M - D_1\right)}{\mu_H}\right) > 0.
\end{aligned}
$$

Proof. Let $\vartheta^Z = (S_H^{**}, E_Z^{**}, I_Z^{**}, R_Z^{**}, S_M^{**}, E_M^{**}, I_M^{**})$ represent any endemic equilibrium system of (3.1). By changing the variables as follows:

$x_1 = S_H$, $x_2 = E_Z$, $x_3 = I_Z$, $x_4 = R_H$, $x_5 = S_M$, $x_6 = E_{MZ}$, and $x_7 = I_{MZ}$.

Then model (3.1) above can be transformed into the following:

$$\begin{aligned}
\frac{dx_1}{dt} &= \Lambda_H - \lambda_Z x_1 - \mu_H x_1 : f_1,\\
\frac{dx_2}{dt} &= \lambda_Z x_1 - D_1 x_2 : f_2,\\
\frac{dx_3}{dt} &= \sigma_1 x_2 - D_2 x_3 : f_3,\\
\frac{dx_4}{dt} &= \alpha_1 x_3 - \mu_H x_4 : f_4,\\
\frac{dx_5}{dt} &= \Lambda_M - \lambda_{MZ} x_5 - \mu_H x_5 : f_5,\\
\frac{dx_6}{dt} &= \lambda_{MZ} x_5 - D_3 x_6 : f_6,\\
\frac{dx_7}{dt} &= \sigma_{MZ} x_6 - \mu_M x_7 : f_7,
\end{aligned} \tag{3.12}$$

where

$\lambda_Z = \frac{m\beta_{HZ}x_7+\beta_Z x_3}{x_1+x_2+x_3+x_4+x_5}$, $\lambda_{MZ} = \frac{m\beta_{MZ}x_3}{x_1+x_2+x_3+x_4+x_5}$.

Take $\beta_Z^* = \beta_Z^*$ as the bifurcation parameter. Solving for $\beta_Z^* = \beta_Z^*$ from $R_{0Z}^+ = 1$,

$$\beta_Z^* = \frac{\Lambda_H D_1 D_2 D_3 \mu_M^2}{\sigma_1 \left(\Lambda_H D_4 \mu_M^2 + m^2 \beta_{MZ}\sigma_{MZ}\Lambda_M \mu_H\right)}.$$

Therefore the Jacobian matrix ($\Im(\zeta_Z)$) of system (3.12), evaluated at $\Im_Z$ with $\beta_Z^* = \beta_Z^*$ is given by:

$$\Im(\zeta_Z) = \begin{pmatrix}
-\mu_H & 0 & -\beta_Z & 0 & 0 & 0 & -m\beta_{HZ}\\
0 & -D_1 & \beta_Z & 0 & 0 & 0 & m\beta_{HZ}\\
0 & \sigma_1 & -D_2 & 0 & 0 & 0 & 0\\
0 & 0 & \alpha_1 & -\mu_H & 0 & 0 & 0\\
0 & 0 & a_{53} & 0 & -\mu_M & 0 & 0\\
0 & 0 & a_{63} & 0 & 0 & -D_3 & 0\\
0 & 0 & 0 & 0 & 0 & \sigma_{MZ} & -\mu_M
\end{pmatrix},$$

where $a_{53} = -\frac{m\beta_{MZ}\Lambda_M\mu_H}{\mu_M\Lambda_H}$, $a_{63} = \frac{m\beta_{MZ}\Lambda_M\mu_H}{\mu_M\Lambda_H}$. The matrix $\Im(\zeta_Z)$ at $\beta_Z^* = \beta_Z^*$ has a single zero eigenvalue, and all other eigenvalues possess a negative real part, indicating that the center manifold theorem can be applied [44]. It can be demonstrated that at $\beta_Z^* = \beta_Z^*$. The right eigenvalues are given by $\omega_i = (w_1, w_2, w_3, w_4, w_5, w_6, w_7)^T$,
where $a_{53} = -\frac{m\beta_{MZ}\Lambda_M\mu_H}{\Lambda_H\mu_M}$ and $a_{63} = \frac{m\beta_{MZ}\Lambda_M\mu_H}{\Lambda_H\mu_M}$.

And the right eigenvalues of $\Im(\zeta_Z)$ are as given below:

$w_1 = \frac{-D_1}{\mu_H} w_2^* < 0, w_2 = w_2^* > 0,$

$w_3 = \frac{\sigma_1}{D_2} w_2 > 0, w_4 = \frac{\alpha_1 \sigma_1}{D_1 \mu_M} w_2 > 0,$

$w_5 = -\left(\frac{m\beta_{MZ}\Lambda_M \sigma_1 \mu_H}{D_2 D_3 \Lambda_H \mu_M}\right) w_2^* < 0,$

$w_6 = \frac{m\beta_{MZ}\Lambda_M \sigma_1 \mu_H}{D_2 D_3 \Lambda_H \mu_M} w_2^* > 0,\ w_7 = \left(\frac{D_1 D_2 - \beta_Z \sigma_1}{m D_2 \beta_{HZ}}\right) w_2 > 0.$

Similarly, we calculate the left eigenvector of $\Im(\zeta_Z)$ at $\beta_Z^* = \beta_Z^*$ given by:

$v_i = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)$ and satisfies $v.\omega = 1$

$v_1 = v_4 = v_5 = 0,\ v_3 = \frac{D_1}{\sigma_1} v_2 > 0,\ v_6 = \frac{m\sigma_{MZ}\beta_{HZ}}{D_3 \mu_M} v_2 > 0,$

$v_7 = \frac{m\beta_{HZ}}{\mu_M} v_2 > 0.$

By employing Theorem 4.1 in [44] nonzero partial derivatives of f_1, f_2, f_3, f_4, f_5, f_6 and f_7 at Zika disease free equilibrium point $\Im(\zeta_Z)$, the associated bifurcation coefficients are as given below:

$a = \sum_{k,i,j=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial w_i \partial w_j}(\zeta_Z)$ and

$b = \sum_{k,i,=1}^{7} v_k w_i \frac{\partial^2 f_k}{\partial w_i \partial \beta_Z}(\zeta_Z),$

where

$$a = -\frac{2v_2 w_2 \mu_H (D_1 D_2 - \beta_Z \sigma_1)(w_2(\alpha_1\sigma_1 + D_1(\sigma_1 + D_1)))}{\Lambda_H D_1 D_2^2 \mu_M} - \frac{2\beta_Z \sigma_1 w_2^2 v_2 \mu_H (D_1\mu_M + \alpha_1\sigma_1)}{\Lambda_H D_1 D_2 \mu_M} - \frac{2m\beta_{MZ}\beta_{HZ}\sigma_{MC}\sigma_1 \Lambda_M v_2 w_2 \mu_H^2}{\Lambda_H^2 D_2 D_3 \mu_M^2} \left(\frac{m^2 \beta_{MZ}\sigma_1 w_2^2}{D_2 D_3} + \sigma_1 w_2 \frac{(D_1\mu_M + D_2\alpha_1)}{D_1 D_2 \mu_M} + \frac{w_2(\mu_M - D_1)}{\mu_H}\right) > 0.$$

$$b = \left(\frac{D_1 D_2 - \beta_Z \sigma_1}{D_2 \beta_{HZ}}\right) w_2^{**} > 0. \tag{3.13}$$

According to Theorem 4.1 in [44], the system described in equation (3.1) will exhibit a subcritical (backward) bifurcation if the condition $a > 0$ is met. This implies that since the bifurcation coefficient b is positive, it follows that, the Zika virus sub-model (3.1) undergoes backward bifurcation at $R_{0Z}^+ = 1$ whenever $a > 0$. The bifurcation diagram is presented below.

□

3.8. Dengue fever-only sub-model

The dengue fever sub-model is obtained from the complete system (2.1) by neglecting the other two diseases, Zika virus and Chikungunya, with their associated state variables and parameters to get.

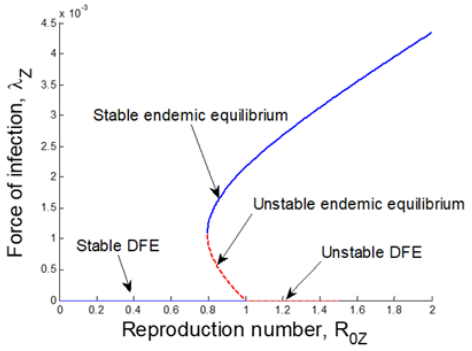


Figure 3. Bifurcation diagram for Zika virus (with parameter values the same as given in the table of parameter values)

$$\begin{aligned}
\frac{dS_H}{dt} &= \Lambda_H - \lambda_D S_H - \mu_H S_H,\\
\frac{dE_{HD}}{dt} &= \lambda_D S_H - (\sigma_2 + \mu_H) E_{HD},\\
\frac{dI_{HD}}{dt} &= \sigma_2 E_{HD} - (\alpha_2 + \delta_D + \mu_H) I_{HD},\\
\frac{dS_M}{dt} &= \Lambda_M - \lambda_{MD} S_M - \mu_M S_M,\\
\frac{dE_{MD}}{dt} &= \lambda_{MD} S_H - (\sigma_{MD} + \mu_M) E_{MD},\\
\frac{dI_{MD}}{dt} &= \sigma_{MD} E_{MD} - (\alpha_{MD} + \mu_M) I_{MD}.
\end{aligned} \tag{3.14}$$

where

$\lambda_D = \frac{m\beta_D I_{MD}}{N_H}$ and $\lambda_D = \frac{m\beta_{MD} I_D}{N_H}$ are the associated forces of infections for system (3.14) above.

3.9. Stability of Dengue fever-disease-free equilibrium point (DDFEP)

The Dengue Disease Free Equilibrium Point (DDFEP) is given as:

$$\zeta_D = (S_H, E_D, I_D, R_D, S_M, E_{MD}, I_{MD}) = \left(\frac{\Lambda_H}{\mu_H}, 0, 0, 0, \frac{\Lambda_M}{\mu_M}, 0, 0\right).$$

3.10. Basic reproduction number for Dengue fever (BRNDF)

It's pertinent to note that R_{0D} represents the BRNDF of the model (3.14). The BRNDF (R_{0D}) is the number of secondary infection in a completely susceptible population due to the infection from one introduced infectious individual with DF. Taking the infected compartment $(E_D, I_D, E_{MD}, I_{MD})$ at the DBRN, the R_{0D} is obtained using the next generation matrix method adopted in [45] at the DDFEP. Given that, $S_H = N_H$ and $S_M = \frac{\Lambda_M}{\mu_M}$ we get:

$$F = \begin{pmatrix} 0 & 0 & 0 & m\beta_D \\ 0 & 0 & 0 & 0 \\ 0 & \frac{m\beta_{MD}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} q_1 & 0 & 0 & 0 \\ & q_2 & 0 & 0 \\ 0 & 0 & q_3 & 0 \\ 0 & 0 & -\sigma_{MD} & \mu_M \end{pmatrix},$$

where

$q_1 = \sigma_2 + \mu_H$,$q_2 = \alpha_2 + \delta_D + \mu_H$, $q_3 = \sigma_{MD} + \mu_M$, $q_4 = \alpha_{MD} + \mu_M$,

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{m\beta_D\sigma_{MD}}{q_3\mu_M} & \frac{m\beta_D}{\mu_M} \\ 0 & 0 & 0 & 0 \\ \frac{m\beta_{MD}\Lambda_M\sigma_2\mu_H}{\Lambda_H\mu_M q_1 q_2} & \frac{m\beta_{MD}\Lambda_M\mu_H}{\Lambda_H\mu_M q_2} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

It follows that R_{0D} is the spectral radius of the matrixFV^{-1}, hence, the reproduction number of Dengue fever is given by:

$$R_{0D} = \sqrt{\frac{m^2\beta_D\beta_{MD}\Lambda_M\sigma_2\sigma_{MD}\mu_H}{\Lambda_H q_1 q_2 q_3 \mu_M^2}}. \tag{3.15}$$

3.11. Local stability of DDFEP

Theorem 3.5. *The equilibrium point of the system (3.14) is Locally Asymptotically Stable (LAS) if $R_{0D} < 1$ and unstable if $R_{0D} > 1$.*

Proof. The Jacobian matrix of the system (3.14) evaluated at Dengue fever Disease free equilibrium point (ζ_D) is given by:

$$\Im(_D) = \begin{pmatrix} -\mu_H & 0 & 0 & 0 & 0 & 0 & -m\beta_D \\ 0 & -q_1 & 0 & 0 & 0 & 0 & m\beta_D \\ 0 & & -q_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_2 & -\mu_H & 0 & 0 & 0 \\ 0 & 0 & -\frac{m\beta_{MD}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & \mu_M & 0 & 0 \\ 0 & 0 & \frac{m\beta_{MD}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & 0 & -q_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_{MD} & -\mu_m \end{pmatrix},$$

where $b_{53} = -\frac{m\beta_{MD}\Lambda_M\mu_H}{\Lambda_H\mu_M}$,$b_{63} = \frac{m\beta_{MD}\Lambda_M\mu_H}{\Lambda_H\mu_M}$.

Clearly, from Jacobian matrix $\Im(_D)$, the negative eigenvalues are $-\mu_H$,$-\mu_H$,$-\mu_M$.

The roots of polynomial (3.16) are presented below:

$$\lambda^4 + R\lambda^3 + S\lambda^2 + T\lambda + U = 0, \tag{3.16}$$

where

$$R = q_1 + q_2 + q_3 + \mu_M,\ S = q_1q_2 + q_1q_3 + q_2q_3 + q_1\mu_M + q_2\mu_M + q_3\mu_M,$$

$$T = q_1q_2q_3 + q_1q_2\mu_M + q_1q_3\mu_M + q_2q_3\mu_M \text{ and } U = q_1q_2q_3\mu_M\left(1 - R_{0D}^2\right).$$

By applying the Routh-Hurwitz criterion [44, 45], which asserts that all roots of the polynomial (3.16) have negative real parts if and only if the coefficient $R, S, T, U > 0$ and positive, we can conclude that the equilibrium point of the system in equation (3.14) is locally asymptotically stable whenever $R_{0D} < 1$.

3.12. Existence of DF-endemic equilibrium point (DEEP)

In this part, we explore the existence of DEEP which occurs when the infected variables in the model are nonzero. To obtain the condition necessary for the existence of DEEP, the DF sub-model is solved in terms of the forces of infection (λ_D and λ_{MD}) to obtain the following:

$$\begin{aligned} S_H^{**} =& \frac{\Lambda_H}{\lambda_D + \mu_H}, \\ E_D^{**} =& \frac{\Lambda_H\lambda_D}{(\lambda_D + \mu_H)\, q_1}, \\ I_D^{**} =& \frac{\alpha_2\Lambda_H\lambda_D}{(\lambda_D + \mu_H)\, q_1q_2}, \\ R_D =& \frac{\alpha_2\sigma_2\Lambda_H\lambda_D}{(\lambda_D + \mu_H)\, \mu_H q_1q_2}, \end{aligned} \tag{3.17}$$

$$\begin{aligned} S_M^{**} =& \frac{\Lambda_M}{\lambda_{MD} + \mu_M}, \\ E_{MD}^{**} =& \frac{\Lambda_M\lambda_{MD}}{(\lambda_{MD} + \mu_M)\, q_3}, \\ I_{MD}^{**} =& \frac{\sigma_{MD}\Lambda_M\lambda_{MD}}{(\lambda_{MD} + \mu_M)\, q_3\mu_M}, \end{aligned} \tag{3.18}$$

$$N_H = \frac{\Lambda_H q_2\mu_H(q_1+\lambda_D)+\Lambda_H\sigma_2\lambda_D(\alpha_2+\mu_H)}{q_1q_2(\lambda_D+\mu_H)\mu_H},$$

$$\lambda_{MD} = \frac{m\beta_{MD}\Lambda_H\sigma_2\mu_H\lambda_D}{\Lambda_H\left(q_2\mu_H\left(q_1 + \lambda_D\right) + \sigma_2\lambda_D\left(\alpha_2 + \mu_H\right)\right)}, \tag{3.19}$$

$$\lambda_D = \frac{m\beta_D I_{MD}}{N_H}. \tag{3.20}$$

By substituting equationS (3.17), (3.18) and (3.19) into (3.20) we obtain the characteristic polynomial:

$$\lambda_D^{**}\left(A\lambda_D^{**2} + B\lambda_D^{**2} + C\right) = 0. \tag{3.21}$$

where

$$\begin{aligned} A =& m\beta_{MD}\Lambda_H^2 q_3\sigma_2\mu_M\mu_H\left(\mu_H\left(q_2 + \sigma_2\right) + \alpha_2\sigma_2\right) + \Lambda_H^2 q_3\mu_M^2(\mu_H\left(q_2 + \sigma_2\right) + \alpha_2\sigma_2)^2, \\ B =& m\beta_{MD}\beta_D\Lambda_M\Lambda_H^2 q_1q_2\sigma_2\mu_M\mu_H^2 + 2\Lambda_H^2 q_1q_2q_3\mu_M^2\mu_H\left(\mu_H\left(q_2 + \sigma_2\right) + \alpha_2\sigma_2\right) \end{aligned}$$

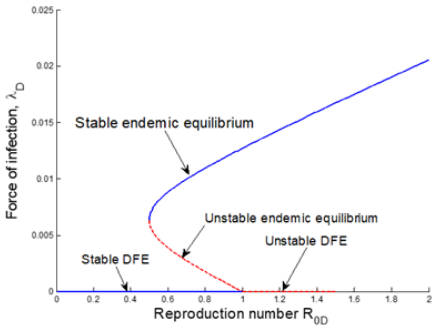


Figure 4. Bifurcation diagram for Dengue Fever (with parameter values the same as given in the table of parameter values)

$$+ m^2\beta_{MD}\beta_D\Lambda_M\Lambda_H q_1 q_2\sigma_2\sigma_{MD}\mu_H^2,$$
$$C = \Lambda_H^2 q_1^2 q_2^2 q_3 \mu_M^2\mu_H^2\left(1 - R_{0D}^2\right).$$

From the polynomial in (3.21), it could be observed that the coefficient A is always positive and C is positive if $R_{0D} < 1$ and negative if $R_{0D} > 1$. The structure of the polynomial in (3.21) is suggestive of the phenomenon of backward bifurcation.

3.13. Possibility of the existence of backward bifurcation

By applying Theorem 3.4 in section 3.7 above, the model equations in (3.14) undergo a backward bifurcation at $R_{0D} = 1$, hence the values of a and b after some algebraic manipulation (using non-zero partial derivatives of (3.14) in computing the value of a and $b$respectively) are given as:

$$a = \sum_{i,j,k=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial w_i \partial w_j}(0,0) = -\frac{2m\sigma_{MD}\sigma_2 v_2^{**} w_2^{**2}}{\Lambda_H q_2}\left(\frac{\beta_{MD}q_2 + \sigma_2\mu_H + \sigma_2}{q_2\mu_H}\right.$$
$$\left. + \frac{\beta_{MD}\beta_D\Lambda_M}{\Lambda_H q_3\mu_M}\left(\frac{m\beta_{MD}\sigma_2\mu_H + \mu_M^2\sigma_2\left(\alpha_2 + \mu_H\right) + q_2\mu_M^2\left(q_1 + \mu_H\right)}{q_2\mu_M^2}\right)\right),$$

and

$$b = \sum_{k=1}^{7} v_k w_j \frac{\partial^2 f_k}{\partial w_j \partial\beta_D}(0,0) = \frac{m\sigma_{MD}\sigma_3}{q_2\mu_H} v_2^{**} w_2^{**} > 0.$$

It then follows from Theorem 3.4 that, the Dengue-only model undergoes backward bifurcation since the value of $b < 0$.

□

3.14. Sub-model for Chikungunya-only disease

The Chikungunya-only sub-model is obtained from co-infection system (2.1) by neglecting the other two diseases, Dengue fever and Zika virus, together with their associated state variables and parameters, to obtain:

$$\begin{aligned}
\frac{dS_H}{dt} &= \Lambda_H - \lambda_C S_H - \mu_H S_H,\\
\frac{dE_C}{dt} &= \lambda_C S_H - (\sigma_3 + \mu_H)\, E_C,\\
\frac{dI_C}{dt} &= \sigma_3 E_C - (\alpha_3 + \delta_C + \mu_H)\, I_C,\\
\frac{dR_C}{dt} &= \alpha_3 I_C - \mu_H R_C,\\
\frac{dS_M}{dt} &= \Lambda_M - \lambda_{MC} S_M - \mu_M S_M,\\
\frac{dE_{MC}}{dt} &= \lambda_{MC} S_M - (\sigma_{MC} + \mu_M)\, E_{MC},\\
\frac{dI_{MC}}{dt} &= \sigma_{MC} E_{MC} - \mu_M I_{MC},
\end{aligned} \tag{3.22}$$

where $\lambda_C = \frac{m\beta_C I_{MC}}{N_H}$ and $\lambda_{MC} = \frac{m\beta_{MC} I_C}{N_H}$ are the associated Chikungunya forces of infection.

3.15. Stability of Chikungunya disease free equilibrium point

The Chikungunya only sub-model (3.22), has a disease free equilibrium by equating the right hand of model (3.22) to zero, given by:

$$\zeta_C = (S_H, E_C, I_C, R_C, S_M, E_{MC}, I_{MC}) = \left(\tfrac{\Lambda_H}{\mu_H}, 0, 0, 0, \tfrac{\Lambda_M}{\mu_M}, 0, 0\right).$$

The linear stability ζ_C of CDFEP can be determined using the Next Generation Operator method, as outlined in [46]. Therefore, when applied to the Chikungunya model (3.22), consequently, the Chikungunya reproduction number is denoted by R_{0C} and it is calculated as:

$$F = \begin{pmatrix} 0 & 0 & 0 & m\beta_C \\ 0 & 0 & 0 & 0 \\ 0 & \frac{m\beta_{MC}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} q_4 & 0 & 0 & 0 \\ 0 & q_5 & 0 & 0 \\ 0 & 0 & q_6 & 0 \\ 0 & 0 & -\sigma_{MC} & \mu_H \end{pmatrix},$$

$$F.V^{-1} = \begin{pmatrix} 0 & 0 & \frac{m\beta_C\sigma_{MC}}{q_6\mu_H} & \frac{m\beta_C}{\mu_H} \\ 0 & 0 & 0 & 0 \\ \frac{m\beta_{MC}\Lambda_M\sigma_3}{\Lambda_H q_4 q_5} & \frac{m\beta_{MC}\Lambda_M}{\Lambda_H q_5} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

The Chikungunya reproduction number R_{0C}, is defined as the spectral radius of the matrix $\rho\left(F.V^{-1}\right)$. Hence, it can be expressed as:

$$R_{0C} = \sqrt{\frac{m^2\Lambda_M\beta_{MC}\beta_C\sigma_{MC}\sigma_3\mu_H}{\Lambda_H q_4 q_5 q_6 \mu_M^2}}. \tag{3.23}$$

The disease free equilibrium point for Chikungunya-only sub-model (3.22) is locally asymptotically stable if $R_{0C} < 1$ and unstable if $R_{0C} > 1$. The proof is as follows:

$$\Im_C(\zeta_C) = \begin{pmatrix} -\mu_H & 0 & 0 & 0 & 0 & 0 & -m\beta_C \\ 0 & -q_4 & 0 & 0 & 0 & 0 & m\beta_C \\ 0 & \sigma_3 & -q_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_3 & -\mu_H & 0 & 0 & 0 \\ 0 & 0 & -\frac{m\beta_{MC}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & -\mu_M & 0 & 0 \\ 0 & 0 & \frac{m\beta_{MC}\Lambda_M\mu_H}{\Lambda_H\mu_M} & 0 & 0 & -q_6 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_{MC} & -\mu_H \end{pmatrix}.$$

The eigenvalues of the above Jacobian matrix are $-\mu_H$, $-\mu_H$, $-\mu_M$ and the roots of the characteristic polynomials:

$$\lambda^4 + A_1\lambda^3 + A_2\lambda^2 + A_3\lambda + A_4 = 0, \tag{3.24}$$

where

$$\begin{aligned} A_1 &= q_4 + q_5 + q_6 + \mu_H, \\ A_2 &= q_4q_5 + q_4q_6 + q_5q_6 + q_4\mu_H + q_5\mu_H + q_6\mu_H, \\ A_3 &= q_4q_5q_6 + q_4q_5\mu_H + q_4q_6\mu_H + q_5q_6\mu_H, \\ A_4 &= q_4q_5q_6\mu_H\left(1 - R_{0C}^2\right). \end{aligned}$$

By Routh-Hurtwitz criterion [44,45] all the roots of the polynomial (3.24) have negative real parts if and only if the coefficient $A_1, A_2, A_3 < 0$ and $A_4 < 0$ if $R_{OC} < 1$.

3.16. Endemic equilibrium for Chikungunya virus

$$\begin{aligned} S_H^{**} &= \frac{\Lambda_H}{\lambda_C + \mu_H}, \\ E_C^{**} &= \frac{\Lambda_H\lambda_C}{D_7(\lambda_C + \mu_H)}, \\ I_C^{**} &= \frac{\Lambda_H\lambda_C}{D_7D_8(\lambda_C + \mu_H)}, \\ R_C^{**} &= \frac{\Lambda_H\alpha_3\sigma_3\lambda_C}{D_7D_8\mu_H(\lambda_C + \mu_H)}, \\ S_M^{**} &= \frac{\Lambda_M}{\lambda_{MC} + \mu_M}, \\ E_{MC}^{**} &= \frac{\Lambda_M\lambda_{MC}}{D_9(\lambda_{MC} + \mu_M)}, \\ I_{MC}^{**} &= \frac{\Lambda_M\sigma_{MC}\lambda_{MC}}{D_9\mu_M(\lambda_{MC} + \mu_M)}, \end{aligned} \tag{3.25}$$

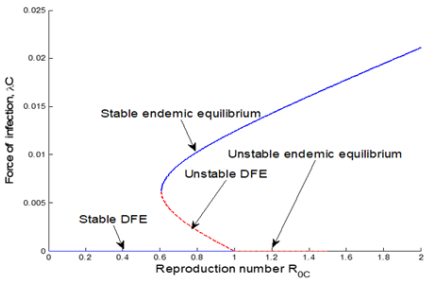


Figure 5. Bifurcation diagram for Chikungunya virus (with parameter values the same as given in the table of parameter values)

where $N_H = S_H + E_C + I_C + R$,

$$N_H = \frac{\Lambda_H D_7 D_8 \mu_H + \Lambda_H \lambda_C \left(\left(D_8 + \sigma_3\right)\mu_H + \sigma_3\alpha_3\right)}{D_7 D_8 \mu_H \left(\lambda_C + \mu_M\right)}, \tag{3.26}$$

$$\lambda_{MC} = \frac{m\beta_{MC}\Lambda_H\sigma_3\mu_H\lambda_C^{**}}{\Lambda_H q_4 q_5 \mu_H + \Lambda_H\left(\mu_H\left(q_5+\sigma_3\right)+\alpha_3\sigma_3\right)\lambda_C^{**}}, \tag{3.27}$$

$$\lambda_C = \frac{m\beta_C I_{MC}}{N_H}. \tag{3.28}$$

By substituting (3.25),(3.26) and (3.27) into (3.28), we have the characteristic polynomials:

$$\lambda_C^{**}\left(Y_1{\lambda_C^{**}}^2 + Y_2\lambda_C^{**} + Y_3\right) = 0, \tag{3.29}$$

where

$$\begin{aligned}
Y_1 =& m\beta_{MC}\Lambda_H^2 q_6\sigma_3\mu_M\mu_H\left(\mu_H\left(q_5+\sigma_3\right)+\alpha_3\sigma_3\right) + \Lambda_H^2 q_6\mu_M^2\left(\mu_H\left(q_5+\sigma_3\right)+\alpha_3\sigma_3\right)^2,\\
Y_2 =& m\beta_{MC}\beta_C\Lambda_M\Lambda_H^2 q_4 q_5\sigma_3\mu_M\mu_H^2 + 2\Lambda_H^2 q_4 q_5 q_6\mu_M^2\mu_H\left(\mu_H\left(q_5+\sigma_3\right)+\alpha_3\sigma_3\right)\\
&+ m^2\beta_{MC}\beta_C\Lambda_M\Lambda_H q_4 q_5\sigma_3\sigma_{MC}\mu_H^2,\\
Y_3 =& \Lambda_H^2 q_4^2 q_5^2 q_6\mu_M^2\mu_H^2\left(1-{R_{0C}}^2\right).
\end{aligned}$$

The root $\lambda_C^{**} = 0$, as obtained from equation (3.29), corresponds to the Chikungunya free equilibrium (ζ_C), the stability of which has already been established. For backward bifurcation to occur, it is necessary for multiple non-zero equilibria to exist. It can be deduced from equation (3.29) that the non-zero equilibria of model (3.22) satisfy the following conditions:

Theorem 3.6. *The Chikungunya-only model (3.22) has:*

1. *Precisely one unique endemic equilibrium if* $Y_3 < 0$ *(i.e.,* $R_{0C} > 1$ *).*
2. *Precisely one unique endemic equilibrium if* $Y_2 < 0$*, and* $Y_3 = 0$ *or* $B^2 - 4AC = 0$*.*
3. *Precisely two endemic equilibria if* $Y_3 > 0$ *(i.e.*$R_{0C} < 1$*),* $Y_2 < 0$ *and* $B^2 - 4Y_1Y_2 > 0$*.*

4. No endemic equilibrium otherwise. The possible presence of two endemic equilibria

(Case (3) above indicates the possibility of backward bifurcation in the model (3.22).

3.17. Existence of backward bifurcation

The Chikungunya sub-model above can be reformulated into the following set of equations:

Let $S_H = N_1$,$E_C = N_2$,$I_C = N_3$, $R_C = N_4$,$S_M = N_5$,$E_{MC} = N_6$ and $I_{MC} = N_7$.

Moreover,

$f_1 = S_H^I$,$f_2 = E_C^I$,$f_3 = I_C^I$,$f_4 = R_C^I$,$f_5 = S_M^I$,$f_6 = E_{MC}^I$ and $f_7 = I_{MC}^I$.

$$\begin{aligned}
\frac{dN_1}{dt} &= \Lambda_H - \frac{m\beta_C N_7 N_1}{N_1+N_2+N_3+N_4} - \mu_H N_1 : f_1,\\
\frac{dN_2}{dt} &= \frac{m\beta_C N_7 N_1}{N_1+N_2+N_3+N_4} - q_4 N_2 : f_2,\\
\frac{dN_3}{dt} &= \sigma_3 N_3 - q_5 N_3 : f_3,\\
\frac{dN_4}{dt} &= \alpha_3 q_5 - \mu_H N_4 : f_4,\\
\frac{dN_5}{dt} &= \Lambda_M - \frac{m\beta_{MC} N_3 N_5}{N_1+N_2+N_3+N_4} - \mu_M N_5 : f_5,\\
\frac{dN_6}{dt} &= \frac{m\beta_{MC} N_3 N_5}{N_1+N_2+N_3+N_4} - q_6 N_6 : f_6,
\end{aligned} \tag{3.30}$$

where $\lambda_C = \frac{m\beta_C N_7}{N_1+N_2+N_3+N_4}$,$\lambda_{MC} = \frac{m\beta_{MC} N_3}{N_1+N_2+N_3+N_4}$ with the Jacobian matrix of system (3.30) at disease free equilibrium point given by:

$$\begin{pmatrix}
-\mu_H & 0 & 0 & 0 & 0 & 0 & -m\beta_C\\
0 & -q_4 & 0 & 0 & 0 & 0 & m\beta_C\\
0 & \sigma_3 & -q_5 & 0 & 0 & 0 & 0\\
0 & 0 & \alpha_3 & -\mu_H & 0 & 0 & 0\\
0 & 0 & b_{53} & 0 & -\mu_M & 0 & 0\\
0 & 0 & b_{63} & 0 & 0 & -q_6 & 0\\
0 & 0 & 0 & 0 & 0 & \sigma_{MC} & -\mu_H
\end{pmatrix} = 0,$$

where

$b_{53} = -\frac{m\beta_{MC}\Lambda_M\mu_H}{\Lambda_H\mu_M}$and

$b_{63} = \frac{m\beta_{MC}\Lambda_M\mu_H}{\Lambda_H\mu_M}$.

The Jacobian of system (3.30), evaluated at disease free equilibrium point for Dengue-only model has a left eigenvectors (associated with zero eigenvalues) as given below:

$$v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)^T,$$

where $v_1 = v_4 = v_5 = 0$, $v_2 = v_2^{**}$,

$v_3 = \frac{q_4}{\sigma_3} v_2^{**}$,

$v_6 = \frac{m\beta_C \sigma_{MC}}{q_6 \mu_H} v_2^{**}$,

$v_7 = \frac{m\beta_C}{\mu_H} v_2^{**}$.

The Jacobian of system (3.30), evaluated at disease free equilibrium point for Chikungunya-only model has a right eigenvectors (associated with zero eigenvalues) as given below:

$w = (w_1, w_2, w_3, w_4, w_5, w_6, w_7)^T$,

$w_1 = \frac{q_4}{\mu_H} w_2^{**}$,$w_2 = w_2^{**}$,

$w_3 = \frac{\sigma_3}{q_5} w_2^{**}$,

$w_4 = \frac{\alpha_3 \sigma_3}{q_5 \mu_H} w_2^{**}$, $w_5 = -\frac{m\beta_{MC}\Lambda_M \sigma_3 \mu_H}{q_6 \Lambda_H \mu_M^2} w_2^{**}$, $w_6 = \frac{m\beta_{MC}\Lambda_M \sigma_3 \mu_H}{q_6 \Lambda_H \mu_M^2} w_2^{**}$ and $w_7 = \frac{\sigma_{MC}\sigma_3}{q_5 \mu_H} w_2^{**}$.

Non-zero partial derivatives are given by:

$\frac{\partial^2 f_1}{\partial N_2 \partial N_7} = \frac{\partial^2 f_1}{\partial N_7 \partial N_2} = \frac{\partial^2 f_1}{\partial N_3 \partial N_7} = \frac{\partial^2 f_1}{\partial N_7 \partial N_3} = \frac{\partial^2 f_1}{\partial N_4 \partial N_7} = \frac{\partial^2 f_1}{\partial N_7 \partial N_4} = \frac{2m\beta_C \mu_H}{\Lambda_H}$,

$\frac{\partial^2 f_2}{\partial N_2 \partial N_7} = \frac{\partial^2 f_2}{\partial N_7 \partial N_2} = \frac{\partial^2 f_2}{\partial N_3 \partial N_7} = \frac{\partial^2 f_2}{\partial N_7 \partial N_3} = \frac{\partial^2 f_2}{\partial N_4 \partial N_7} = \frac{\partial^2 f_2}{\partial N_7 \partial N_4} = -\frac{2m\beta_C \mu_H}{\Lambda_H}$,

$\frac{\partial^2 f_5}{\partial N_3^2} = \frac{\partial^2 f_5}{\partial N_1 \partial N_3} = \frac{\partial^2 f_5}{\partial N_3 \partial N_1} = \frac{\partial^2 f_5}{\partial N_2 \partial N_3} = \frac{\partial^2 f_5}{\partial N_3 \partial N_2} = \frac{\partial^2 f_5}{\partial N_4 \partial N_3} = \frac{\partial^2 f_5}{\partial N_3 \partial N_4} = \frac{2m\beta_{MC}\Lambda_M \mu_H^2}{\Lambda_H^2 \mu_M}$,

$\frac{\partial^2 f_6}{\partial N_3^2} = \frac{\partial^2 f_6}{\partial N_1 \partial N_3} = \frac{\partial^2 f_6}{\partial N_3 \partial N_1} = \frac{\partial^2 f_6}{\partial N_2 \partial N_3} = \frac{\partial^2 f_6}{\partial N_3 \partial N_2} = \frac{\partial^2 f_6}{\partial N_4 \partial N_3} = \frac{\partial^2 f_6}{\partial N_3 \partial N_4} = -\frac{2m\beta_{MC}\Lambda_M \mu_H^2}{\Lambda_H^2 \mu_M}$,

$\frac{\partial^2 f_5}{\partial N_3 \partial N_5} = \frac{\partial^2 f_5}{\partial N_5 \partial N_3} = -\frac{2m\beta_{MC}\mu_H}{\Lambda_H}, \frac{\partial^2 f_6}{\partial N_3 \partial N_5} = \frac{\partial^2 f_6}{\partial N_5 \partial N_3} = \frac{2m\beta_{MC}\mu_H}{\Lambda_H \mu_M}$,

$\frac{\partial^2 f_1}{\partial N_7 \partial \beta_C} = -m, \frac{\partial^2 f_2}{\partial N_7 \partial \beta_C} = m.$

Arising from the above, we compute a as follows:

$$a = \sum_{i,j,k=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial w_i \partial w_j}(0,0) = -\frac{2m\sigma_{MC}\sigma_3 v_2^{**} w_2^{**2}}{\Lambda_H q_5}\left(\frac{\beta_{MC}q_5 + \sigma_3\mu_H + \sigma_3}{q_5\mu_H} + \frac{\beta_{MC}\beta_C\Lambda_M}{\Lambda_H q_6 \mu_M}\left(\frac{m\beta_{MC}\sigma_3\mu_H + \mu_M^2\sigma_3(\alpha_3+\mu_H) + q_5\mu_M^2(q_4+\mu_H)}{q_5\mu_M^2}\right)\right).$$

And for the coefficient b we have:

$$\frac{\partial^2 f_1}{\partial N_7 \partial \beta_C} = -m,$$

where $w_7 = \frac{\sigma_{MC}\sigma_3}{q_5\mu_H} w_2^{**} > 0$, $v_1 = 0$, $v_2 = v_2^{**}$, $w_7 = \frac{\sigma_{MC}\sigma_3}{q_5\mu_H} w_2^{**} > 0$.

Hence, $b = \sum_{k=1}^{7} v_k w_j \frac{\partial^2 f_k}{\partial w_j \partial \beta_C}(0,0) = \frac{m\sigma_{MC}\sigma_3}{q_5\mu_H} v_2^{**} w_2^{**} > 0$.

It then follows from Theorem 3.4 that Chikungunya-only model (3.21) undergoes a backward bifurcation if $R_{0C} < 1$ whenever

$$a = -\frac{2m\sigma_{MC}\sigma_3 v_2^{**} w_2^{**2}}{\Lambda_H q_5}\left(\frac{\beta_{MC}q_5 + \sigma_3\mu_H + \sigma_3}{q_5\mu_H} + \frac{\beta_{MC}\beta_C\Lambda_M}{\Lambda_H q_6 \mu_M}\left(\frac{m\beta_{MC}\sigma_3\mu_H + \mu_M^2\sigma_3(\alpha_3+\mu_H) + q_5\mu_M^2(q_4+\mu_H)}{q_5\mu_M^2}\right)\right) > 0. \tag{3.31}$$

Theorem 3.7. *The Chikungunya-only model (3.21) undergoes backward bifurcation at $R_{0C} < 1$ whenever the inequality in (3.31) holds.*

4. Dengue − Chikungunya co-infection model

The Dengue-Chikungunya co-infection model is obtained from system (2.1) by neglecting the Zika virus disease and its associated parameters, to obtain:

$$
\begin{aligned}
\frac{dS_H}{dt} &= \Lambda_H - (\lambda_D + \lambda_C) S_H - \mu_H S_H, \\
\frac{dE_D}{dt} &= \lambda_D S_H - \lambda_C E_D - (\sigma_2 + \mu_H) E_D, \\
\frac{dI_D}{dt} &= \sigma_2 E_D - (\phi_2 + \alpha_2 + \delta_D + \mu_H) I_D, \\
\frac{dE_C}{dt} &= \lambda_C S_H - \lambda_D E_C - (\sigma_3 + \mu_H) E_C, \\
\frac{dI_C}{dt} &= \sigma_3 E_C - (\theta_2 + \alpha_3 + \delta_C + \mu_H) I_C, \\
\frac{dI_{DC}}{dt} &= \sigma_6 E_{DC} + \phi_2 I_D + \theta_2 I_C - (\delta_3 + \psi_3 + \delta_{DC} + \mu_H) I_{DC}, \\
\frac{dR}{dt} &= \alpha_2 I_D + \alpha_3 I_C + \psi_3 I_{DC} - \mu_H R, \\
\frac{dS_M}{dt} &= \Lambda_M - (\lambda_{MD} + \lambda_{MC} + \lambda_{MCD}) S_M - \mu_M S_M, \\
\frac{dE_{MD}}{dt} &= (\lambda_{MD} + y_1 \lambda_{MCD}) S_M - (\sigma_{MD} + \mu_M) E_{MD}, \\
\frac{dE_{MC}}{dt} &= (\lambda_{MC} + (1 - y_1) \lambda_{MCD}) S_M - (\sigma_{MC} + \mu_M) E_{MC}, \\
\frac{dI_{MD}}{dt} &= \sigma_{MD} E_{MD} - \mu_M I_{MD}, \\
\frac{dI_{MC}}{dt} &= \sigma_{MC} E_{MC} - \mu_M I_{MC}.
\end{aligned}
\tag{4.1}
$$

4.1. Local stability of disease free equilibrium.

The disease free equilibrium of Dengue-Chikungunya co-infection model (4.1) is given by:

$$
\zeta_{DC} = \left({}^{\Lambda_H}/_{\mu_H}, 0, 0, 0, 0, 0, 0, 0, {}^{\Lambda_M}/_{\mu_M}, 0, 0, 0, 0 \right). \tag{4.2}
$$

It's easier to show, the next generation operator matrix (subsection 3.9 and 3.15) that the associated reproduction number for the Dengue-Chikungunya co-infection model is given by:

$$
R_{DC} = max \left(R_{0D}, R_{0C} \right). \tag{4.3}
$$

Hence, the following results hold from Theorem 2 of [45].

Theorem 4.1. *The disease free equilibrium of the Dengue-Chikungunya model (4.1) given by (4.2), is locally asymptotically stable if $R_{DC} < 1$ and unstable if $R_{DC} > 1$.*

Given that the Dengue-only and Chikungunya-only sub-models exhibit backward bifurcation, it follows that the Dengue-Chikungunya co-infection model (4.1) will also undergo backward bifurcation. Similarly, other co-infection models, such as Zika-Dengue and Zika-Chikungunya co-infections, will experience the same phenomenon.

Theorem 4.2. *Dengue-Chikungunya model (4.1) undergoes backward bifurcation at $R_{DC} = 1$whenever inequality (4.6) is satisfied.*

4.2. Existence of a backward bifurcation.

The model equations (4.1) above can be transformed by letting:
$\frac{dS_H}{dt} = h_1, \frac{dE_D}{dt} = h_2, \frac{dI_D}{dt} = h_3, \frac{dE_C}{dt} = h_4, \frac{dI_C}{dt} = h_5, \frac{dE_{DC}}{dt} = h_6, \frac{dI_{DC}}{dt} = h_7, \frac{dR}{dt} = h_8, \frac{dS_M}{dt} = x_9, \frac{dE_{MD}}{dt} = h_{10}, \frac{dE_{MC}}{dt} = h_{11}, \frac{dI_{MD}}{dt} = h_{12}, \frac{dI_{MC}}{dt} = h_{13}, S_H = x_1, E_D = x_2, I_D = x_3, E_C = x_4, I_C = x_5, E_{DC} = x_6, I_{DC} = x_7, R = x_8, S_M = x_9, E_{MD} = x_{10}, E_{MC} = x_{11}, I_{MD} = x_{12}$and $I_{MC} = x_{13}$.

We have:

$$
\begin{aligned}
\frac{dx_1}{dt} &= \Lambda_H - (\lambda_D + \lambda_C)\, x_1 - \mu_H x_1 : h_1,\\
\frac{dx_2}{dt} &= \lambda_D x_1 - \lambda_C x_2 - l_1 x_2 : h_2,\\
\frac{dx_3}{dt} &= \sigma_2 x_2 - l_2 x_3 : h_3,\\
\frac{dx_4}{dt} &= \lambda_C x_1 - \lambda_D x_4 - l_3 x_4 : h_4,\\
\frac{dx_5}{dt} &= \sigma_3 x_4 - l_4 x_5 : h_5,\\
\frac{dx_6}{dt} &= \lambda_C x_2 + \lambda_D x_4 - l_5 x_6 : h_6,\\
\frac{dx_7}{dt} &= \sigma_6 x_6 + \phi_2 x_3 + \theta_2 x_5 - l_6 x_7 : h_7,\\
\frac{dx_8}{dt} &= \alpha_2 x_3 + \alpha_3 x_5 + \psi_3 x_7 - \mu_H x_8 : h_8,\\
\frac{dx_9}{dt} &= \Lambda_M - (\lambda_{MD} + \lambda_{MC} + \lambda_{MCD})\, x_9 - \mu_M x_9 : h_9,\\
\frac{dx_{10}}{dt} &= (\lambda_{MD} + y_1 \lambda_{MCD})\, S_M - l_7 x_{10} : h_{10},\\
\frac{dx_{11}}{dt} &= (\lambda_{MC} + (1 - y_1)\, \lambda_{MCD})\, x_{19} - l_8 x_{11} : h_{11},\\
\frac{dx_{12}}{dt} &= \sigma_{MD} x_{10} - \mu_M x_{12} : h_{12},\\
\frac{dx_{13}}{dt} &= \sigma_{MC} x_{11} - \mu_M x_{13} : h_{13}.
\end{aligned}
\tag{4.4}
$$

With the associated force of infections given as:

$\lambda_D = \frac{m\beta_D x_{12}}{\sum_{i=1}^{8} x_i}, \lambda_C = \frac{m\beta_C x_{13}}{\sum_{i=1}^{8} x_i}, \lambda_{MD} = \frac{m\beta_{MD} x_3}{\sum_{i=1}^{8} x_i}, \lambda_{MD} = \frac{m\beta_D x_5}{\sum_{i=1}^{8} x_i}$and $\lambda_{MCD} = \frac{m\beta_{MCD} x_7}{\sum_{i=1}^{8} x_i}$,

where

$l_1 = \sigma_2 + \mu_H, l_2 = \phi_2 + \alpha_2 + \delta_D + \mu_H, l_3 = \sigma_3 + \mu_H, l_4 = \theta_2 + \alpha_3 + \delta_C + \mu_H, l_5 = \sigma_6 + \mu_H, l_6 = \delta_3 + \psi_3 + \delta_{DC} + \mu_H, l_7 = \sigma_{MD} + \mu_M, l_8 = \sigma_{MC} + \mu_M$.

Supposing that β_D^* and β_C^* are chosen as bifurcation parameters hence solving (3.15) and (3.23) at $R_{0D} = 1$ and $R_{0C} = 1$, we have:

$$\begin{aligned} \beta_D &= \frac{(\sigma_2+\mu_H)(\alpha_2+\delta_D+\mu_H)(\sigma_{MD}+\mu_M)\Lambda_H{\mu_M}^2}{m^2\sigma_{MD}\Lambda_M\sigma_2\beta_{MD}\mu_H}, \\ \beta_C &= \frac{(\sigma_3+\mu_H)(\alpha_2+\delta_C+\mu_H)(\sigma_{MC}+\mu_M)\Lambda_H{\mu_M}^2}{m^2\sigma_{MC}\Lambda_M\sigma_3\beta_{MC}\mu_H}. \end{aligned} \tag{4.5}$$

The Jacobian of system (4.4), evaluated at disease free equilibrium point for Dengue-Chikungunya co-infection has a left eigenvectors (associated with zero eigenvalues) as given by:

$$v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9, v_{10}, v_{11,}v_{12}, v_{13})^T,$$

where $v_1 = v_8 = v_9 = 0$, $v_2 = -\frac{k_1}{m\beta_{MD}}$, $v_3 = \frac{v_2 l_1}{\sigma_2}$, $v_4 = -\frac{k_8}{m\beta_{MC}}$, $v_5 = \frac{l_3 v_4}{\sigma_3}$, $v_6 = v_6^{**}$, $v_7 = \frac{l_5 v_6}{\sigma_6}$,$v_{10} = -\frac{\Lambda_H\mu_M k_9}{m\beta_{MD}\Lambda_M\mu_H}$,$v_{11} = \frac{-k_2\Lambda_H}{m\beta_{MC}\Lambda_M\mu_H}$,$v_{12} = \frac{l_7 v_{10}}{\sigma_{MD}}$,$v_{13} = \frac{l_8 v_{11}}{\sigma_{MC}}$.

Similarly, the Jacobian matrix of system (4.4) has a right eigenvectors (associated with zero eigenvalues) as given by:

$$w = (w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8, w_9, w_{10}, w_{11,}w_{12}, w_{13})^T,$$

where

$\omega_1 = -\frac{mk_1}{\mu_H}$, $\omega_2 = \frac{mk_1}{l_1}$, $\omega_3 = \frac{\sigma_2\omega_2}{l_2}$, $\omega_4 = \frac{mk_1}{l_3}$, $\omega_6 = 0$, $w_7 = \frac{k_5}{l_6}$, $w_8 = \frac{k_4}{\mu_H}$, $\omega_9 = -\frac{m\Lambda_M\mu_H k_6}{\Lambda_H\mu_M^2}$, $\omega_{10} = \frac{m\Lambda_M\mu_H(\beta_{MCD}\omega_7 y_1 - \beta_{MD}\omega_3)}{\Lambda_H\mu_M^2}$, $\omega_{11} = \frac{m\Lambda_M\mu_H(\beta_{MCD}\omega_7(1-y_1) - \beta_{MC}\omega_5)}{\Lambda_H l_8\mu_M^2}$, $\omega_{12} = \frac{\sigma_{MC}\omega_{10}}{\mu_M}$, $\omega_{13} = \frac{\sigma_{MC}\omega_{13}}{\mu_M}$.

And

$k_1 = \beta_{MC}\omega_{13} + \beta_{MD}\omega_{12}$, $k_2 = \theta_2 v_7 - l_4 v_5$, $k_3 = \beta_{MC}\omega_{13} + \beta_{MD}\omega_2$,

$k_4 = \psi_3\omega_7 + \alpha_2\omega_3 + \alpha_3\omega_5$, $k_5 = \phi_2\omega_3 + \theta_2\omega_5$, $k_6 = \beta_{MC}\omega_5 + \beta_{MCD}\omega_7 + \beta_{MD}\omega_3$,

$k_7 = m\beta_{MD}v_4 + \mu_M v_{12}$, $k_8 = m\beta_{MD}v_2 + \mu_M v_{13}$, $k_9 = \phi_2 v_7 - l_2 v_3$.

By applying the Center Manifold Theory adopted in [45], we calculate the relevant non-zero partial derivatives of the right-hand sides of the transformed system (4.4). These are evaluated at the disease-free equilibrium point (refer to the appendix for the associated non-zero partial derivatives of the transformed model) (4.4). The corresponding bifurcation coefficients a and b are expressed as follows:

$a_i = \sum_{k,i,j=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial w_i \partial w_j}(0,0)$ and $b = \sum_{k,i,=1}^{7} v_k w_i \frac{\partial^2 f_k}{\partial w_i \partial \beta_Z}(0,0)$.

From the transformed system (4.4), the associated non-zero partial derivatives used in computing the value of a are in appendices, hence the value of a given by:

$$
\begin{aligned}
a = & -2m\sigma_{MC}\mu_H\hat{X}_1\hat{X}_2 \\
& - \frac{2m\beta_D\mu_H\sigma_{MC}(\beta_{MC}w_{13}+\beta_{MD}w_{12})^2\left(l_1B_{MC}w_{12}+l_3\beta_{MD}w_{11}\right)}{\beta_{MC}\beta_{MD}\Lambda_H\mu_M} \\
& - \frac{2m\beta_D\mu_H\sigma_{MC}w_{10}\left(m\beta_{MD}v_2+\mu_Mv_{13}\right)\left(B_{MC}w_{13}+\beta_{MD}w_{12}\right)}{\beta_{MC}\Lambda_Hl_3} \\
& + \frac{2v_6m^2\sigma_{MC}\mu_H\left(B_{MC}w_{13}+\beta_{MD}w_{12}\right)}{\Lambda_H\mu_M}\hat{X}_3 \\
& + \frac{2m\beta_{MCD}y_1\mu_H\left(\phi_2V_7-l_2v_3\right)\left(\beta_{MC}w_5+\beta_{MCD}w_7+\beta_{MD}w_3\right)\left(\phi_2w_3+\theta_2w_5\right)}{\beta_{MD}\Lambda_H\mu_Ml_6} \\
& + 2\mu_H\left(\phi_2V_7-l_2v_3\right)\left(\hat{X}_4+\hat{X}_5\right) \\
& \times\left(\frac{y_1\beta_{MCD}\left(\phi_2w_3+\theta_2w_5\right)}{\beta_{MD}\Lambda_Hl_6}+\frac{\sigma_2w_2}{\Lambda_Hl_2}\right) \\
& + 2\mu_H\left(\phi_2V_7-l_2v_3\right) \\
& \times\left(\frac{y_1\beta_{MCD}\left(\phi_2w_3+\theta_2w_5\right)}{\beta_{MD}\Lambda_Hl_6}+\frac{\sigma_2w_2}{\Lambda_Hl_2}\right)\hat{X}_6 \\
& + \frac{2\sigma_2w_2\left(\phi_2V_7-l_2v_3\right)}{\beta_{MD}l_2}\hat{X}_7 \\
& + \frac{2\mu_Hm\left(\phi_2V_7-l_4v_5\right)\left(\beta_{MC}w_{13}+\beta_{MD}w_{12}\pi\right)}{\Lambda_H\mu_M}\hat{X}_8\hat{X}_8 \\
& + \frac{2\left(1-y_1\right)\beta_{MCD}\mu_H\left(\phi_2V_7-l_4v_5\right)\left(\phi_2w_3+\theta_2w_5\right)^2}{\beta_{MC}\Lambda_Hl_6^2\mu_M} \\
& + \frac{2\sigma_3^2w_4^2\left(\phi_2V_7-l_4v_5\right)}{\Lambda_Hl_4^2\mu_M} \\
& + \frac{2m\sigma_3\mu_Hw_4\left(\theta_2V_7-l_4v_5\right)\left(\beta_{MC}w_5+\beta_{MCD}w_7+\beta_{MD}w_3\right)}{\Lambda_H\mu_M^2l_4} \\
& + 2\left(\theta_2V_7-l_4v_5\right)\left(\phi_2w_3+\theta_2w_5\right) \\
& \times\left(\begin{array}{l}\dfrac{\sigma_3\mu_Hw_4\left(1-y_1\right)\beta_{MCD}+\beta_{MC}}{\Lambda_H\mu_Ml_4} \\ +\dfrac{m\left(1-y_1\right)\beta_{MCD}\mu_H\left(\beta_{MC}w_5+\beta_{MCD}w_7+\beta_{MD}w_3\right)}{\Lambda_H\mu_M^2}\end{array}\right)>0.
\end{aligned}
\tag{4.6}
$$

Similarly, it also follows that the value of b is given by:

$$b = \frac{\sigma_{MC}k_7\omega_{10}}{\mu_M} > 0,$$

where

$$\hat{X}_1 = \frac{\beta_D(\beta_{MC}w_{13}+\beta_{MD}w_{12})w_{10}}{m\beta_{MD}\Lambda_H\mu_M} + \frac{\beta_C(m\beta_{MD}v_2+\mu_Mv_{13})w_{11}}{m\beta_{MC}\Lambda_H\mu_Ml_1},$$

$$\hat{X}_2 = \frac{m(\beta_{MC}w_{13}+\beta_{MD}w_{12})}{l_1} + \frac{\sigma_2l_4w_2+\sigma_3l_2w_4}{l_2l_4} + \frac{(\alpha_2+\phi_2)w_3+(\alpha_3+\theta_2)w_5+\psi_3w_7}{l_6},$$

$$\hat{X}_3 = \frac{\beta_Cl_3w_{11}+\beta_Dl_1w_{10}}{l_1l_3},\ \hat{X}_4 = \frac{m(\beta_{MC}w_{13}+\beta_{MD}w_{12})(l_3\mu_H+\mu_Hl_1-l_1l_3)}{\mu_Hl_1l_3},$$

$$\hat{X}_5 = \frac{l_6\sigma_3w_4+(\psi_3w_7+\alpha_2w_3+\alpha_3w_5)l_4}{l_4l_6},\hat{X}_6 = \frac{\sigma_2w_2}{l_2} + \frac{\phi_2w_3+\theta_2w_5}{l_6},$$

$$\hat{X}_7 = \frac{m\beta_{MD}\mu_H(\beta_{MC}w_5+\beta_{MCD}w_7+\beta_{MD}w_3)}{\Lambda_H\mu_M} + \frac{\mu_H(y_1\beta_{MCD}+\beta_{MD})(\phi_2w_3+\theta_2w_5)}{\Lambda_H l_6},$$

$$\hat{X}_8 = \frac{\mu_H(l_1+l_3)+l_1l_3}{l_1l_3\mu_H} + \frac{l_6\sigma_2w_2+(\psi_3w_7+\alpha_2w_3+\alpha_3w_5)l_2}{l_2l_6},$$

$$\hat{X}_9 = \frac{\sigma_3w_4}{l_4} + \frac{(1-y_1)\beta_{MCD}(\phi_2w_3+\theta_2w_5)}{\beta_{MC}l_6}.$$

Hence, backward bifurcation occurs if and only if $a > 0$.

5. Analysis of the full Zika-Dengue-Chikungunya co-infection model

Having studied all the sub-models, our next step is to investigate the whole model (2.1) for its qualitative features. This analysis is carried out in this part.

5.1. Local stability of disease free equilibrium.

Following the analysis of Zika-Dengue and Chikungunya full model (2.1), we consider the Zika-Dengue-Chikungunya full model (2.1). Its disease free equilibrium point is given by:

$$\zeta_{CD} = \left({}^{\Lambda_H}/_{\mu_H}, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, {}^{\Lambda_M}/_{\mu_M} 0, , 0, 0, 0, 0\right).$$

It is more straightforward to establish, as mentioned in Sections 3 and 4, that the corresponding reproduction number for the Zika-Dengue-Chikungunya full model (2.1) is given by:

$$R_{ZDC} = max\left(R_{0Z}, R_{0D}, R_{0C}\right). \tag{5.1}$$

Thus, the following results are established based on Theorem 2 from [46].

Theorem 5.1. *The disease free equilibrium of the Zika-Dengue-Chikungunya full model (2.1) given by (5.1), is locally asymptotically stable if $R_{ZDC} < 1$ and unstable if$R_{ZDC} > 1$.*

Since Zika, Dengue and Chikungunya only model undergoes backward bifurcation, it follows that the Zika-Dengue-Chikungunya full model (2.1) equally undergoes backward bifurcation at $R_{ZDC} = 1$. Theorem 11. Zika-Dengue-Chikungunya model (2.1) undergoes backward bifurcation at $R_{ZDC} = 1$ as in section 3 and 4 above for sub model analysis as well as co-infections.

6. Sensitivity analysis and data fitting

We undertake sensitivity analysis to find the parameter(s) that influence the spread and control of infection in a given population. The sensitivity index of the reproduction number for Zika, Dengue, and Chikungunya viruses with respect to any parameter (say i) is given by

$$\chi_i^{R_0} = \frac{\partial R_0}{\partial i} \times \frac{i}{R_0}.$$

Thus the sensitivity index of the reproduction number of Zika (R_{0Z}) Dengue (R_{0D}) and Chikungunya (R_{0C}) with respect to the parameters i is given by:

$\chi_i^{R_{0Z}} = \frac{\partial R_{0Z}}{\partial i} \times \frac{i}{R_{0Z}}$, $\chi_i^{R_{0D}} = \frac{\partial R_{0D}}{\partial i} \times \frac{i}{R_{0D}}$ and$\chi_i^{R_{0C}} = \frac{\partial R_{0C}}{\partial i} \times \frac{i}{R_{0C}}$.

Considering Zika-only reproduction number as given below:

$$\chi_{\sigma_1}^{R_{0Z}} = \frac{\mu_H\left(m\beta_{MZ}\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}+\Lambda_H\beta_Z\mu_H\mu_M^2+\Lambda_H\beta_Z\mu_M^2\sigma_{MZ}\right)}{(\sigma_1+\mu_H)^2(\alpha_1+\delta_Z+\mu_H)(\sigma_{MZ}+\mu_H)\Lambda_H\mu_M^2}$$

$$\times\frac{(\sigma_1+\mu_H)(\alpha_1+\delta_Z+\mu_H)(\sigma_{MZ}+\mu_H)\Lambda_H\mu_M^2}{\beta_Z(\sigma_{MZ}+\mu_H)\Lambda_H\mu_M^2+m\beta_{MZ}\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}},$$

$$\chi_{\sigma_1}^{R_{0Z}} = \frac{\mu_h}{\sigma_1+\mu_h} = +0.2539,\ \chi_{\delta_Z}^{R_{0Z}} = -\frac{\delta_Z}{\alpha_1+\delta_Z+\mu_H} = -0.0159,$$

$$\chi_{\alpha_1}^{R_{0Z}} = -\frac{\alpha_1}{\alpha_1+\delta_Z+\mu_H} = -0.9712,$$

$$\chi_m^{R_{0Z}} = \frac{2m^2\beta_{MZ}\beta_{HZ}\Lambda_M\sigma_{MZ}\mu_H}{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2+m^2\beta_{MZ}\beta_{HZ}\Lambda_M\sigma_{MZ}\mu_H} = 1.9981,$$

$$\chi_{\Lambda_H}^{R_{0Z}} = -\frac{m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}}{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2+m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}} = -0.9991,$$

$$\chi_{\Lambda_M}^{R_{0Z}} = \frac{m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}}{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2+m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}} = +0.9991,$$

$$\chi_{\sigma_{MZ}}^{R_{0Z}} = \frac{m^2\beta_{MZ}\beta_{HZ}\Lambda_M\mu_H\mu_M\sigma_{MZ}}{(\sigma_{MZ}+\mu_M)(m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}+\Lambda_H\beta_Z\mu_M{}^3+\Lambda_H\beta_Z\mu_M{}^2\sigma_{MZ})} = +0.2806,$$

$$\chi_{\mu_H}^{R_{0Z}} = \frac{\sigma_1+\mu_H\left((\sigma_{MZ}+\mu_M)\Lambda_H\mu_M^2\sigma_1(1+\sigma_1\beta_Z)+m\beta_{MZ}\Lambda_M\sigma_{MZ}\beta_{HZ}\sigma_1\mu_H\right)}{\Lambda_H\beta_Z\mu_H^2\sigma_1(\sigma_{MZ}+\mu_M)+m\beta_{MZ}\Lambda_M\sigma_1\sigma_{MZ}\beta_{HZ}\mu_H} = +0.7321,$$

$$Z_{\beta_{MZ}}^{R_0^Z} = \frac{m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}}{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2+m^2\Lambda_M\sigma_{MZ}\mu_H\beta_{HZ}\beta_{MZ}} = +0.9991,$$

$$Z_{\beta_Z}^{R_0^Z} = \frac{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2}{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2+m^2\beta_{MZ}\beta_{HZ}\Lambda_M\sigma_{MZ}\mu_H} = +0.0009,$$

$$Z_{\beta_Z}^{R_0^Z} = \frac{m^2\beta_{MZ}\beta_{HZ}\Lambda_M\sigma_{MZ}\mu_H}{\beta_Z\Lambda_H(\sigma_{MZ}+\mu_M)\mu_M{}^2+m^2\beta_{MZ}\beta_{HZ}\Lambda_M\sigma_{MZ}\mu_H} = +0.9991.$$

Similarly, we obtain the sensitivity indices of the basic reproduction number of Dengue as:

$$\chi_{\sigma_1}^{R_{0D}} = +0.0689,\ \chi_{\alpha_1}^{R_{0D}} = -0.3192,$$

$$\chi_{\sigma_{MD}}^{R_{0D}} = 0.0063,\ \chi_m^{R_{0D}} = +1,\ \chi_{\delta_D}^{R_{0D}} = -0.0957,\ \chi_{\beta_D}^{R_{0D}} = +0.5,$$

$$\chi_{\beta_{MD}}^{R_{0D}} = +0.5,\ \chi_{\Lambda_M}^{R_{0D}} = 0.5,$$

$$\chi_{\Lambda_H}^{R_{0D}} = -0.5,\ \chi_{\mu_M}^{R_{0D}} = -1$$

and $\chi_{\mu_H}^{R_{0D}} = 0.3396$.

Finally, we perform sensitivity analysis for Chikungunya virus in the same manner as we did for Zika and Dengue fever. The sensitivity indices for Chikungunya virus are as follows:

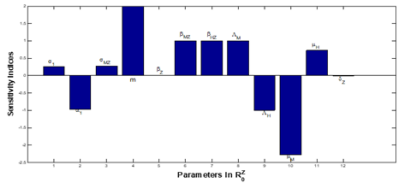


Figure 6. Sensitivity index of the basic reproduction number for Zika virus

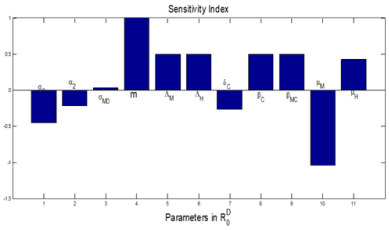


Figure 7. Sensitivity index of the basic reproduction number for Dengue fever

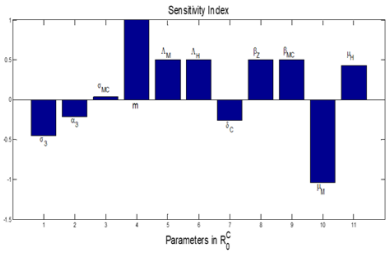


Figure 8. Sensitivity index of the basic reproduction number for Chikungunya

$$\chi_{\sigma_1}^{R_{0D}} = +0.4500,$$

$$\chi_{\alpha_3}^{RC} = -0.2139, \chi_{\sigma_{MC}}^{R_{0C}} = 0.03677,$$

$$\chi_{m}^{R_{0C}} = +1, \chi_{\delta_C}^{R_{0C}} = -0.2621,$$

$$\chi_{\beta_C}^{R_{0C}} = +0.5, \chi_{\beta_{MC}}^{R_{0C}} = +0.5,$$

$$\chi_{\Lambda_M}^{R_{0C}} = 0.5, \chi_{\Lambda_H}^{RC} = -0.5, \chi_{\mu_M}^{R_{0C}} = -1.03676,$$

$$\chi_{\mu_H}^{R_{0C}} = 0.4259.$$

6.1. Interpretation of sensitivity indices

Figures (6), (7), and (8) depict the sensitivity indices for the parameters of the models proposed and analyzed in this work. These indices quantify the extent to which each parameter contributes to the disease's spread. In the bar charts, parameters with positive values exert a greater impact on the spread of the disease, whereas those with negative values have a lesser impact. This implies that increasing the values of parameters with positive indices will lead to an increase in the number of infection cases, while decreasing the values of parameters with negative indices will result in a decrease in the number of cases. Based on the study's findings, for the Zika virus, the top-ranked parameters that should be targeted for controlling the spread of the disease are the death rate due to Zika virus (δ_Z), the recovery rate of infectious humans with Zika virus (α_1), and the recruitment rate of humans (Λ_H).

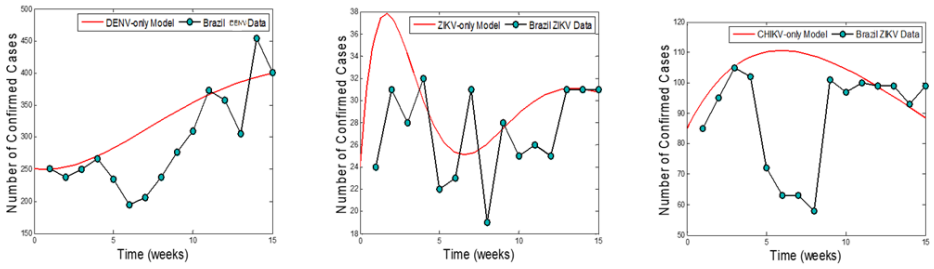
Similarly, for dengue fever, the key parameters for controlling the spread are the death rate due to dengue fever disease (δ_D), the recovery rate of infectious humans with dengue fever α_2, the natural death rate of mosquitoes (μ_M), and the recruitment rate for humans (Λ_H). Conversely, in the case of Chikungunya virus, the primary parameters to focus on for controlling the disease's spread are the death rate due to Chikungunya virus δ_C, the recovery rate of infectious humans with Chikungunya virus (α_3), the mortality rate for mosquitoes (μ_M), and the recruitment rate for humans (Λ_H). Taking proactive measures to ensure that the sensitivity indices for these key parameters consistently remain negative will significantly contribute to the effective control of disease transmission.

6.2. Data fitting for Zika, Dengue and Chikungunya virus

This section describes how the data for the study was carried out for some of the important parameters in the models. The data fitting is performed on the Zika, Dengue, and Chikungunya viral models using the fmincon method, which is a component of the optimization toolbox of MATLAB program. Weekly epidemiological data was gathered from Espirito Santo State, Brazil, where the three (3) vector-borne illnesses co-circulated [38]. The number of confirmed cases of Zika, Dengue, and Chikungunya is provided in Table 4 below.

Table 4. Real life data as obtained for the three diseases

Week	Period	Zika	Dengue	Chikungunya
1	03/01/2021–09/01/2021	24	251	85
2	10/01/2021–16/01/2021	31	238	95
3	17/01/2021–23/01/2021	28	250	105
4	24/01/2021–30/01/2021	32	267	102
5	31/01/2021–06/02/2021	22	235	72
6	07/02/2021–13/02/2021	23	195	63
7	14/02/2021–20/02/2021	31	206	63
8	21/02/2021–27/02/2021	19	238	58
9	28/02/2021–06/03/2021	28	277	101
10	07/03/2021–13/03/2021	25	310	97
11	14/03/2021–20/03/2021	26	373	100
12	21/03/2021–27/03/2021	25	358	99
13	28/03/2021–03/04/2021	31	306	99
14	04/04/2021–10/04/2021	31	454	93
15	11/04/2021–17/04/2021	31	401	99



(a) Dengue fever data fitting **(b)** Zika Virus data fitting **(c)** Chikungunya data fitting

Figure 9. Numbers of cases of Dengue, Zika and Chikungunya per epidemiological week in Espírito Santo State in Brazil from 3rd January, 2021 to 17th April, 2021 as extracted from [43].

7. Numerical simulations and discussion

It becomes imperative to conduct the numerical simulations of the co-infection model towards validation of results obtained from qualitative analysis of the model.

The initial conditions of the state variables used for the numerical simulations is given as follows:

$S_H(0)$=208463140,$E_Z(0)$=500,$I_Z(0)$=24,$E_D(0)$=1000,$I_D(0)$=251,

$E_C(0)$=700,$I_C(0)$=85,$E_{ZD}(0)$=450,$E_{ZC}(0)$=300,$E_{DC}(0)$=370,$E_{ZDC}(0)$=150,

I_{ZD}=15,I_{ZC}=10,

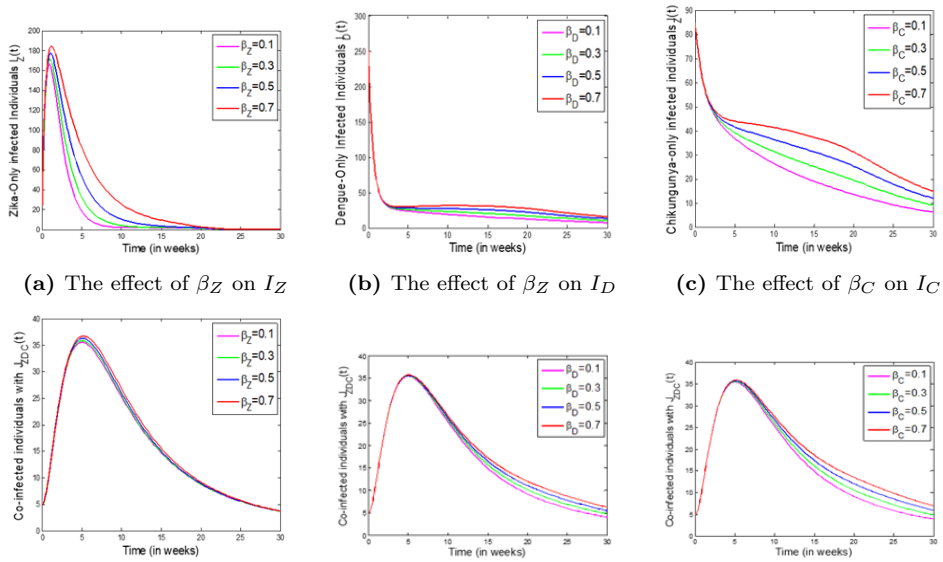
I_{DC}=25,$\Im_{ZDC}(0)$=5,R(0)=0,$S_M(0)$=5000,$E_{MZ}(0)$=150,

$E_{MD}(0)$=300,$E_{MC}(0)$=180,$I_{MZ}(0)$=4$I_{MD}(0)$=21and $I_{MD}(0)$=21.

These are the initial conditions we used in the simulation of the model towards validating some of the theoretical results obtained in this work, would be systematically discussed.

β_D	R_{OD}
0.1	0.4303
0.3	0.7453
0.5	0.9622
0.7	1.1285

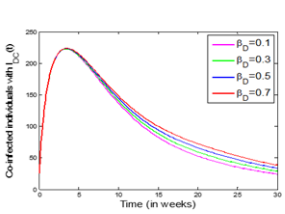
Table 5. β_D and R_{OD}



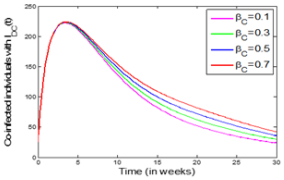
(a) The effect of β_Z on I_Z **(b)** The effect of β_Z on I_D **(c)** The effect of β_C on I_C

(d) The effect of β_Z on $J_{ZDC}(t)$ **(e)** The effect of β_D on $J_{ZDC}(t)$ **(f)** The effect of β_C on $J_{ZDC}(t)$

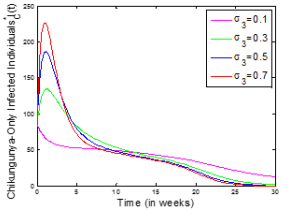
Figure 10. Simulations of the model (2.1) showing plots of (10a) Zika-only infected individuals (I_Z), (10b) Dengue-only infected individuals (I_D), (10c) Chikungunya-only infected individuals (I_C) and (10d), (10e), and (10f) infected individuals with the three diseases ($\Im_{ZDC}$), using initial conditions stated earlier. Parameters values used for the plots are found in Table 12 (in appendices); parameter values were varied for β_Z, β_D and β_C at different intervals with the corresponding values of their reproduction numbers as shown in Tables (5, 6 and 7), so that $R_{0Z} = 0.0061$, $R_{0D} = 0.3611$, $R_{0C} = 0.0907$ and $R_{ZDC} = 0.3611$.



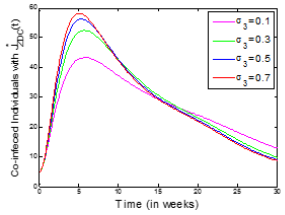
(a) The effects of β_Z on $I_{ZC}(t)$



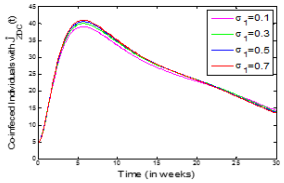
(b) The effects of β_D on β_Z



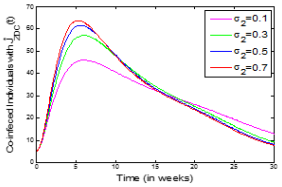
(c) The effects of β_D on $I_{DC}(t)$



(d) The effects of β_C on $I_{DC}(t)$



(e) The effects of σ_1 on I_Z^* for $R_{ZDC} > 1$



(f) The effects of σ_2 on I_D^* for $R_{ZDC} > 1$

Figure 11. The simulations of model (2.1) showing the plots (11a) and (11b) for co-infected individuals with Zika and Chikungunya (I_{ZC}), varying the transmission rate from infected humans with Zika to susceptible humans (β_Z) and infected mosquitoes with Dengue fever to susceptible humans, with the values of their reproduction numbers summarized in Tables (9, 10 and 11) respectively for the values of $R_{ZC} < 1$, using various initial conditions. The values of parameters used are as shown in Table 5 (in appendices), where ($R_{0Z} = 0.0061$, $R_{0C} = 0.0907$ and $R_{ZC} = 0.0907$). Similarly, plots (11c) and (11d) depict co-infected humans with Dengue fever and Chikungunya Virus, varying the transmission rate from infected mosquitoes with Dengue fever to susceptible humans and from infected mosquitoes with Chikungunya to susceptible humans for the value of $R_{ZC} < 1$; the parameter values used are in Table (5) above, where ($R_{0D} = 0.1155$, $R_{0C} = 0.0907$ and $R_{DC} = 0.1155$). Plots (11e) and (11f) display co-infected humans with Zika Virus and Dengue fever, varying the transmission rate from infected mosquitoes with Zika Virus to susceptible humans and from infected mosquitoes with Dengue fever to susceptible humans for the value of $R_{ZD} < 1$, where ($R_{0Z} = 0.0061$, $R_{0D} = 0.1155$ and $R_{DC} = 0.1155$); the parameter values used are in Table 12.

β_C	R_{OC}
0.1	0.5120
0.3	0.8194
0.5	1.0400
0.7	1.2070

Table 6. β_C and R_{OC}

β_C	R_{OC}
0.1	0.1282
0.3	0.2221
0.5	0.2867
0.7	0.3392

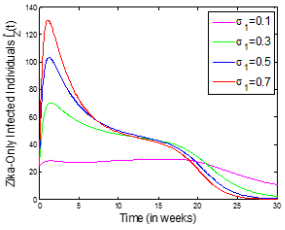
Table 7. β_C and R_{OC}

β_Z	R_{OZ}
0.1	0.0000
0.3	0.0000
0.5	0.0000
0.7	0.0000

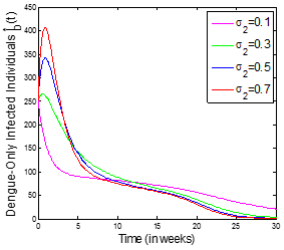
Table 8. β_Z and R_{OZ}

β_D	R_{0D}
0.1	1.1835
0.3	1.2139
0.5	1.2230
0.7	1.2230

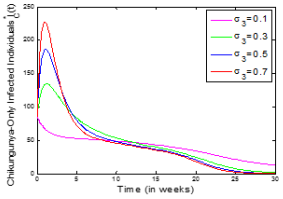
Table 9. Parameters for β_D and R_{0D}



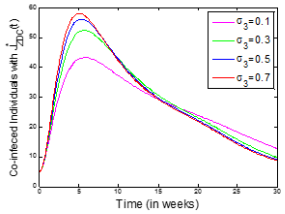
(a) The effects of σ_1 on I_Z^* for $R_{0Z} > 1$



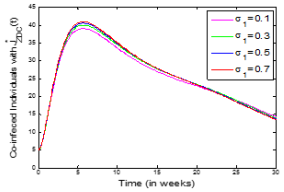
(b) The effect of σ_2 on I_D^* for $R_{0D} > 1$



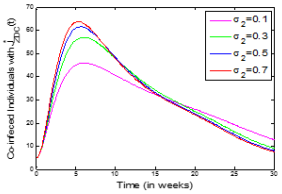
(c) The effect of σ_3 on I_C^* for $R_{0C} > 1$



(d) The effect of σ_3 on I_C^* for $R_{ZDC} > 1$



(e) The effect of σ_1 on I_Z^* for $R_{ZDC} > 1$



(f) The effect of σ_2 on I_D^* for $R_{ZDC} > 1$

Figure 12. The simulations of model (2.1) showing plots (12a) Zika-only infected individuals (I_Z^*), (12b) Dengue-only infected individuals (I_D^*), (12c) Chikungunya-only infected individuals (I_C^*) and (12d, 12e, and 12f) infected individuals with the three diseases ($\Im_{ZDC}^*$), using various initial conditions. Parameters and values used for the above plots are found in Tables 5, 6, and 7, with (12a) having ($\sigma_1 = 0.99$, $\beta_Z = 0.99$, $\beta_{MZ} = 0.93$, $\beta_{HZ} = 0.95$, $\alpha_1 = 0.99$ and $\delta_Z = 0.098$), (12b) ($\beta_D = 0.72$), (12c) ($\sigma_3 = 0.050$, $\beta_C = 0.90$, $\beta_{MC} = 0.99$ and $\alpha_3 = 0.09$), which applies to the co-infections by varying σ_1, σ_2 and σ_3 with their corresponding reproduction numbers tabulated in Tables (9), (10) and (11).

β_Z	R_{0Z}
0.1	1.0047
0.3	1.0569
0.5	1.0680
0.7	1.0728

Table 10. Parameters for β_Z and R_{0Z}

β_C	R_{0C}
0.1	1.7731
0.3	1.8186
0.5	1.8281
0.7	1.8323

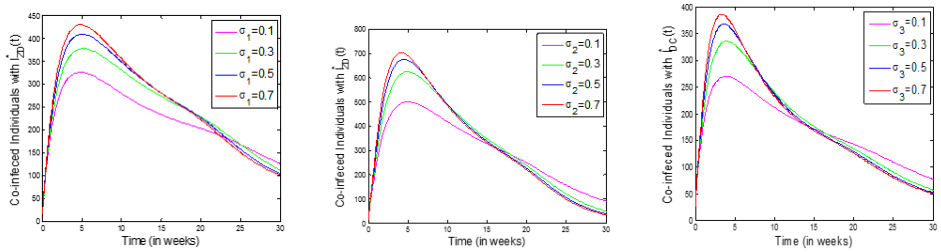
Table 11. Parameters for β_C and R_{0C}

7.1. Discussion and findings

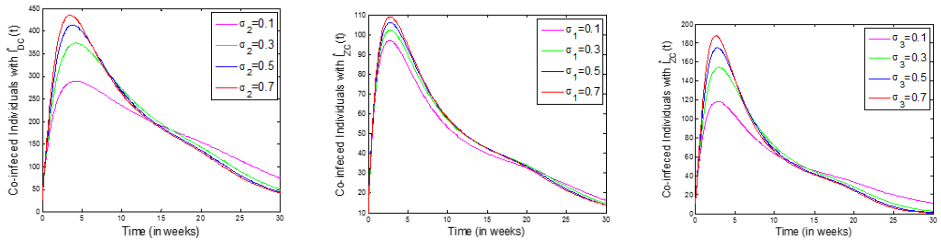
In an attempt to validate some of the analytical results obtained in these work, rigorous simulations of the model (2.1) were carried out, by using the sets of parameter values in Tables (5, 6, 7) in appendices. In Figure (10f), we explore the transmission dynamics of individuals infected with only Zika, Dengue fever and Chikungunya virus and individuals co-infected with the three diseases. Using various initial conditions and the parameter values in Table (4), we simulate the model by varying the transmission rates of each of the three diseases with respect to their associated changes in reproduction numbers as tabulated in Tables (5, 6 and 7) (so that $R_{0Z} = 0.0061$, $R_{0D} = 0.3611$, $R_{0C} = 0.0907$ and $R_{ZDC} = 0.3611$), which shows convergence to disease-free equilibrium. Similarly, Figure 13 depicts the effects of varying the transmission rates on the co-infected individuals with Zika-Dengue, Zika-Chikungunya and Dengue-Chikungunya virus with their corresponding reproduction numbers as tabulated in Tables (5, 6 and 7) and the parameter values used are as tabulated in Table (13), so that $R_{0Z} = 0.0061$, $R_{0D} = 0.3611$ and $R_{ZD} = 0.3611$; $R_{0Z} = 0.0061$, $R_{0C} = 0.0907$ and $R_{ZC} = 0.0907$; $R_{0D} = 0.3611$, $R_{0C} = 0.0907$ and $R_{DC} = 0.3611$.

From Figures (10) and (11a, 11b, 11c, 11d, 11e, 11f), it is obvious that an increase in the contact rates of co-infected individuals with any of the three diseases leads to convergence towards disease-free equilibrium. This could be related to natural death or the recovery rate resulting from people having antibodies that defend against re-infection or co-infection. These antibodies may also boost viral transmission through a method known as antibody-dependent enhancement, particularly when the reproduction number threshold reaches unity.

On the contrary, Figures (12a, 12b, 12c, 12d, 12e, 12f) and (13a, 13b, 13c, 13d, 13e, 13f) illustrate the effects of varying the progression rates of exposed individuals to Zika-only infected individuals, Dengue-only infected individuals, Chikungunya-only infected individuals, and co-infections such as Zika-Dengue, Zika-Chikungunya,

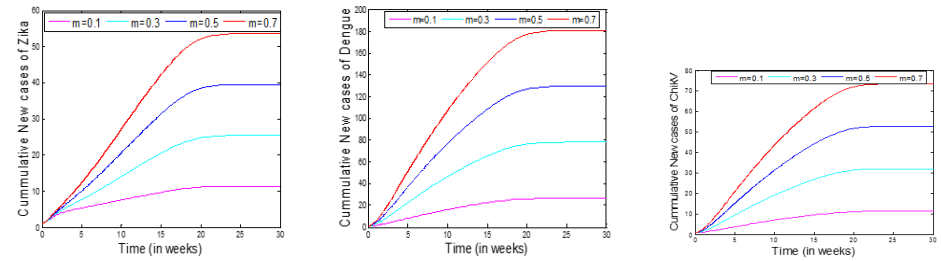


(a) The effect of σ_1 on $I_{ZD}(t)$ for $R_{ZD} > 1$ **(b)** The effect of σ_2 on $I_{ZD}(t)$ for $R_{ZD} > 1$ **(c)** The effect of σ_3 on $I_{DC}(t)$ for $R_{DC} > 1$



(d) The effect of σ_2 on $I_{DC}(t)$ for $R_{DC} > 1$ **(e)** The effects of σ_1 on $I_{ZC}(t)$ for $R_{ZC} > 1$ **(f)** The effects of σ_3 on $I_{ZC}(t)$ for $R_{ZC} > 1$

Figure 13. Simulations of the model (2.1) showing plots of (13a) Zika and Dengue fever co-infected individuals while varying σ_1, (13b) Zika and Dengue fever co-infected individuals while varying σ_2, (13c) Dengue fever and Chikungunya co-infected individuals while varying σ_3, (13d) Dengue fever and Chikungunya co-infected individuals while varying σ_2, (13e) Zika and Chikungunya co-infected individuals while varying σ_1, and (13f) Zika and Chikungunya co-infected individuals while varying σ_3.

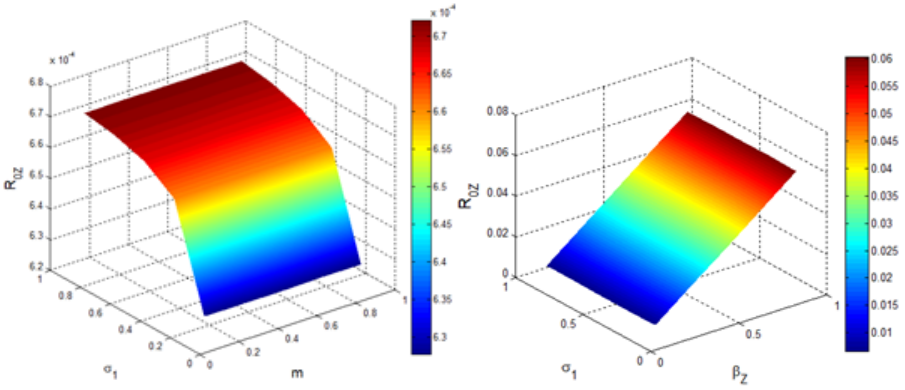


(a) The effects of m on cumulative number of new cases of Zika virus disease **(b)** The effects of m on cumulative number of new cases of Dengue fever disease **(c)** The effects of m on cumulative number of new cases of Chikungunya virus disease

Figure 14. The effects of biting rates (m) on the cumulative new cases of Zika, Dengue and ChikV.

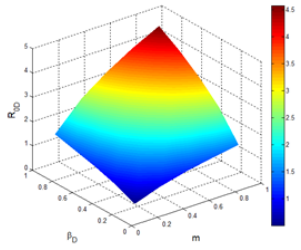
Dengue-Chikungunya, and Zika-Dengue-Chikungunya. The related values of the reproduction numbers are presented in Tables 9, 10, and 11, respectively. Numerous beginning circumstances were considered, and the parameter values utilized are given in Table 12, with $\sigma_1 = 0.99$, $\beta_Z = 0.99$, $\beta_{MZ} = 0.93$, $\beta_{HZ} = 0.95$, $\alpha_1 = 0.99$ and $\delta_Z = 0.098$: $\beta_D = 0.72$; $\sigma_3 = 0.050$, $\beta_C = 0.90$, $\beta_{MC} = 0.99$ and $\alpha_3 = 0.09$, (so that $R_0^Z = 1.0764$,$R_{0D} = 1.1420$, $R_{0D} = 1.7109$ and $R^*_{ZDC} = 1.7109$; $R_{0Z} = 1.0764$, $R_{0D} = 1.1420$ and $R_{ZD} = 1.1420$; $R_{0Z} = 1.0764$, $R_{0C} = 1.7109$ and $R_{ZC} = 1.7109$; $R_{0D} = 1.1420$, $R_{OC} = 0.0907$ and $R_{DC} = 1.7109$) which shows convergence to endemic equilibrium. Gumel et. al [56] ascertained that if two or more of the reproduction numbers are greater than unity, there is always co-existence of the two diseases no matter which of the reproduction numbers is greater. Figures (14a, 14b, 14c) illustrate the simulations portraying the impact of the mosquito biting rate m on the cumulative new cases of Zika-only infected individuals, Dengue-only infected individuals, and individuals infected with Chikungunya. The Figure suggest that an increase in the mosquito biting rate m directly and concurrently increases the new cases of Zika virus, Dengue fever, and Chikungunya virus co-dynamics. This phenomenon may be attributed to susceptible individuals not adopting accurate and effective preventive measures and controls, such as the application of insecticides and noncompliance with the use of mosquito-treated nets, among other factors.

Figures (15a, 15b, 16a, 16b, 17a, 17b) above shows the surface plots of Zika virus, Dengue Fever and Chikungunya virus. These demonstrate the transmission dynamics by identifying those key parameters that enhance the widespread and the prevalence of the diseases and vice versa.

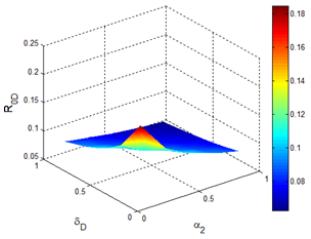


(a) Surface plot of R_{0Z} against σ_1 and β_D **(b)** Surface plot of R_{0Z} against σ_1 and β_Z

Figure 15. Surface plots of reproduction numbers against key parameters of the model

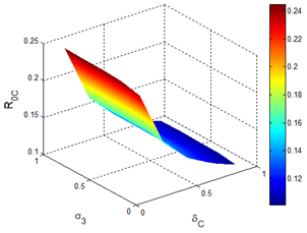


(a) Surface plot of R_{0D} against m and β_D

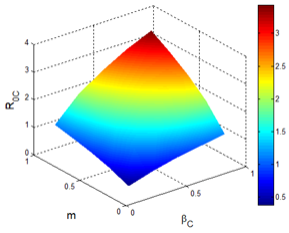


(b) Surface plot of R_{0D} against δ_D and α_2

Figure 16. Surface plots of reproduction numbers against key parameters of the model



(a) Surface plot of R_{0C} against δ_C and σ_3



(b) Surface plot of R_{0C} against m and β_C

Figure 17. Surface plots of reproduction numbers against key parameters of the model

8. Conclusion and recommendations

8.1. Conclusions

We have constructed and examined a mathematical model that determines the transmission dynamics of the co-infection combining Zika, Dengue fever, and Chikungunya virus. Our analysis involved examining the quality of the three different sub-models: one focusing entirely on the Zika virus, another specifically on Dengue fever, and the third exclusively on the Chikungunya virus. Our analysis has the following outcomes:

1. The fundamental reproduction number of Zika, Dengue, and Chikungunya infections was discovered to fall below one, which demonstrates the spatially asymptotic stability of their disease-free equilibrium points.
2. The entire co-infection model demonstrates local asymptotic stability at the disease-free equilibrium point when its basic reproduction number is below one.
3. The separate sub-models for Zika, Dengue fever, and Chikungunya, as well as the combinations of Zika and Dengue fever, Zika and Chikungunya, and Dengue and Chikungunya co-infection, all exhibit backward bifurcation at the disease-free equilibrium point.
4. We did numerical simulations of the model, wherein we systematically adjusted numerous parameters, including transmission rates for each of the diseases and progression rates from exposed individuals with Zika-only, Dengue-

only, and Chikungunya-only to their corresponding infected compartments. The goal was to comprehend the transmission dynamics of each of the three diseases and their co-infections. The research indicated that a heightened rate of interaction between susceptible and diseased people contributes to the enhanced transmission of all three diseases. Similarly, a large progression of exposed individuals to the infected class results in an escalation of individuals infected with one or more of the diseases.

5. Finally, it was noted that an increased biting rate among the vectors (mosquitoes) also adds to the heightened spread of the diseases and leads to an increase in the cumulative number of new infection cases for all three diseases.

8.2. Recommendations

Based on our findings, we make the following recommendations:

- An awareness campaign should be created so as to educate people on the actions that accelerate the transmission and multiplication of Zika, Dengue, and Chikungunya viruses.
- Construction of sufficient number of healthcare and treatment facilities to provide for people infected with Zika, Dengue, and Chikungunya viruses should be embarked upon. It is advised that governments in third-world countries undertake the distribution of mosquito nets to every household in the community. This initiative aims to safeguard vulnerable individuals from mosquito bites, thereby reducing the likelihood of contracting any or all three diseases. Consequently, healthcare policymakers are urged to take proactive measures to ensure that individuals in society protect themselves from mosquito bites, the sole mode of transmission for all three diseases. By doing this, it is predicted that the co-circulation of all three diseases can be effectively halted.

Conclusively, in this work, a comprehensive dynamical analysis of the transmission patterns involving Zika virus, Dengue fever, and Chikungunya viruses has been conducted. Nevertheless, there are multiple avenues for expanding this research work. These include the following:

- Integrating preventive measures such as the use of mosquito nets and launching public awareness campaigns on activities that contribute to mosquito breeding should be included in our disease control strategy. This approach aims to decrease the occurrence of Zika, Dengue fever, and Chikungunya infections, as well as their simultaneous presence in a population.
- Utilizing age-structure models to explore the transmission patterns of co-infections involving Zika, Dengue fever and Chikungunya virus.
- Incorporation of optimal control strategies into the Zika, Dengue, and Chikungunya co-infection model so as to reduce the disease burden in a population.
- Reformulating and analyzing the co-infection of Zika, Dengue, and Chikungunya disease model using fractional order model approach.

As mathematical models act as symbolic representations of real-life biological systems, they inherently possess the risk of losing critical information, potentially resulting in less precise predictions of model outcomes. Consequently, it becomes

crucial to undertake further research based on more reliable data, with the aim of refining our comprehension of the co-infection dynamics involving Zika virus, Dengue fever, and Chikungunya virus.

Conflict of interest

The authors declare that they have no known conflict of interest.

Availability of data

All the data used in this paper can be found in different literatures cited.

Appendix

The associated non-zero partial derivatives of the transformed model (4.4) is given by:

$$\begin{aligned}\frac{\partial^2 h_1}{\partial x_2 \partial x_{12}} =& \frac{\partial^2 h_1}{\partial x_{12} \partial x_2} = \frac{\partial^2 h_1}{\partial x_3 \partial x_{12}} = \frac{\partial^2 h_1}{\partial x_{12} \partial x_3} = \frac{\partial^2 h_1}{\partial x_4 \partial x_{12}} \\ =& \frac{\partial^2 h_1}{\partial x_{12} \partial x_4} = \frac{\partial^2 h_1}{\partial x_5 \partial x_{12}} \\ =& \frac{\partial^2 h_1}{\partial x_{12} \partial x_5} = \frac{\partial^2 h_1}{\partial x_6 \partial x_{12}} = \frac{\partial^2 h_1}{\partial x_{12} \partial x_6} \\ =& \frac{\partial^2 h_1}{\partial x_7 \partial x_{12}} = \frac{\partial^2 h_1}{\partial x_{12} \partial x_7} = \frac{\partial^2 h_1}{\partial x_8 \partial x_{12}} \\ =& \frac{\partial^2 h_1}{\partial x_{12} \partial x_8} = \frac{2m\beta_D \mu_H}{\Lambda_H},\end{aligned}$$

$$\begin{aligned}\frac{\partial^2 h_1}{\partial x_2 \partial x_{13}} =& \frac{\partial^2 h_1}{\partial x_{13} \partial x_2} = \frac{\partial^2 h_1}{\partial x_3 \partial x_{13}} = \frac{\partial^2 h_1}{\partial x_{13} \partial x_3} \\ =& \frac{\partial^2 h_1}{\partial x_4 \partial x_{13}} = \frac{\partial^2 h_1}{\partial x_{13} \partial x_4} = \frac{\partial^2 h_1}{\partial x_5 \partial x_{13}} \\ =& \frac{\partial^2 h_1}{\partial x_{13} \partial x_5} = \frac{\partial^2 h_1}{\partial x_6 \partial x_{13}} = \frac{\partial^2 h_1}{\partial x_{13} \partial x_6} \\ =& \frac{\partial^2 h_1}{\partial x_7 \partial x_{13}} = \frac{\partial^2 h_1}{\partial x_{13} \partial x_7} \\ =& \frac{\partial^2 h_1}{\partial x_8 \partial x_{13}} = \frac{\partial^2 h_1}{\partial x_{13} \partial x_8} = \frac{2m\beta_C \mu_H}{\Lambda_H},\end{aligned}$$

$$\begin{aligned}\frac{\partial^2 h_2}{\partial x_2 \partial x_{12}} =& \frac{\partial^2 h_2}{\partial x_{12} \partial x_2} = \frac{\partial^2 h_2}{\partial x_3 \partial x_{12}} = \frac{\partial^2 h_2}{\partial x_{12} \partial x_3} = \frac{\partial^2 h_2}{\partial x_4 \partial x_{12}} \\ =& \frac{\partial^2 h_2}{\partial x_{12} \partial x_4} = \frac{\partial^2 h_2}{\partial x_5 \partial x_{12}} \\ =& \frac{\partial^2 h_2}{\partial x_{12} \partial x_5} = \frac{\partial^2 h_2}{\partial x_6 \partial x_{12}} = \frac{\partial^2 h_2}{\partial x_{12} \partial x_6}\end{aligned}$$

$$
\begin{aligned}
&=\frac{\partial^2 h_2}{\partial x_7 \partial x_{12}} = \frac{\partial^2 h_2}{\partial x_{12} \partial x_7} = \frac{\partial^2 h_2}{\partial x_8 \partial x_{12}} = \frac{\partial^2 h_2}{\partial x_{12} \partial x_8} \\
&=\frac{\partial^2 h_4}{\partial x_4 \partial x_{12}} = \frac{\partial^2 h_4}{\partial x_{12} \partial x_4} = -\frac{m\beta_D \mu_H}{\Lambda_H},
\end{aligned}
$$

$$
\begin{aligned}
\frac{\partial^2 h_4}{\partial x_2 \partial x_{13}} &=\frac{\partial^2 h_4}{\partial x_{13} \partial x_2} = \frac{\partial^2 h_4}{\partial x_3 \partial x_{13}} = \frac{\partial^2 h_4}{\partial x_{13} \partial x_3} \\
&=\frac{\partial^2 h_4}{\partial x_4 \partial x_{13}} = \frac{\partial^2 h_4}{\partial x_{13} \partial x_4} = \frac{\partial^2 h_4}{\partial x_5 \partial x_{13}} \\
&=\frac{\partial^2 h_4}{\partial x_{13} \partial x_5} = \frac{\partial^2 h_4}{\partial x_6 \partial x_{13}} = \frac{\partial^2 h_4}{\partial x_{13} \partial x_6} \\
&=\frac{\partial^2 h_4}{\partial x_7 \partial x_{13}} = \frac{\partial^2 h_4}{\partial x_{13} \partial x_7} = \frac{\partial^2 h_4}{\partial x_8 \partial x_{13}} \\
&=\frac{\partial^2 h_4}{\partial x_{13} \partial x_8} = \frac{\partial^2 h_2}{\partial x_2 \partial x_{13}} = \frac{\partial^2 h_2}{\partial x_2 \partial x_{13}} = -\frac{m\beta_C \mu_H}{\Lambda_H},
\end{aligned}
$$

$$
\begin{aligned}
\frac{\partial^2 h_6}{\partial x_2 \partial x_{13}} &=\frac{\partial^2 h_6}{\partial x_{13} \partial x_2} \\
&=\frac{m\beta_{MC} \mu_H}{\Lambda_H}, \frac{\partial^2 h_6}{\partial x_4 \partial x_{12}} = \frac{\partial^2 h_6}{\partial x_{12} \partial x_4} = \frac{m\beta_D \mu_H}{\Lambda_H},
\end{aligned}
$$

$$
\begin{aligned}
\frac{\partial^2 h_{10}}{\partial x_1 \partial x_7} &=\frac{\partial^2 h_{10}}{\partial x_7 \partial x_1} = \frac{\partial^2 h_{10}}{\partial x_2 \partial x_7} = \frac{\partial^2 h_{10}}{\partial x_7 \partial x_2} \\
&=\frac{\partial^2 h_{10}}{\partial x_4 \partial x_7} = \frac{\partial^2 h_{10}}{\partial x_7 \partial x_4} = \frac{\partial^2 h_{10}}{\partial x_5 \partial x_7} = \frac{\partial^2 h_{10}}{\partial x_7 \partial x_5} \\
&=\frac{\partial^2 h_{10}}{\partial x_6 \partial x_7} = \frac{\partial^2 h_{10}}{\partial x_7 \partial x_6} = \frac{\partial^2 h_{10}}{\partial x_7 \partial x_8} \\
&=\frac{\partial^2 h_{10}}{\partial x_8 \partial x_7} = \frac{\partial^2 h_{10}}{\partial {x_7}^2} = -\frac{m y_1 \beta_{MCD} \Lambda_M \mu_H^2}{\Lambda_H^2 \mu_M},
\end{aligned}
$$

$$
\begin{aligned}
\frac{\partial^2 f_{10}}{\partial x_3 \partial x_9} &=\frac{\partial^2 f_{10}}{\partial x_9 \partial x_3} = \frac{m\beta_{MD} \mu_H}{\Lambda_H} = \frac{\partial^2 h_{10}}{\partial x_7 \partial x_9} \\
&=\frac{\partial^2 h_{10}}{\partial x_9 \partial x_7} = \frac{m y_1 \beta_{MCD} \Lambda_M \mu_H}{\Lambda_H},
\end{aligned}
$$

$$
\begin{aligned}
\frac{\partial^2 h_{11}}{\partial x_1 \partial x_7} &=\frac{\partial^2 h_{11}}{\partial x_7 \partial x_1} = \frac{\partial^2 h_{11}}{\partial x_2 \partial x_7} = \frac{\partial^2 h_{11}}{\partial x_7 \partial x_2} = \frac{\partial^2 h_{11}}{\partial x_3 \partial x_7} \\
&=\frac{\partial^2 h_{11}}{\partial x_7 \partial x_3} = \frac{\partial^2 h_{11}}{\partial x_4 \partial x_7} = \frac{\partial^2 h_{11}}{\partial x_7 \partial x_4} \\
&=\frac{\partial^2 h_{11}}{\partial x_6 \partial x_7} = \frac{\partial^2 h_{11}}{\partial x_7 \partial x_6} = \frac{\partial^2 h_{11}}{\partial x_8 \partial x_7}
\end{aligned}
$$

$$=\frac{\partial^2 h_{11}}{\partial x_7 \partial x_8} = \frac{\partial^2 h_{11}}{\partial {x_7}^2} = -\frac{m\left(1-y_1\right)\beta_{MCD}\Lambda_M \mu_H^2}{\Lambda_H^2 \mu_M},$$

$$\begin{aligned}\frac{\partial^2 h_{11}}{\partial x_1 \partial x_5} =& \frac{\partial^2 h_{11}}{\partial x_5 \partial x_1} = \frac{\partial^2 h_{11}}{\partial x_2 \partial x_5} = \frac{\partial^2 h_{11}}{\partial x_5 \partial x_2} = \frac{\partial^2 h_{11}}{\partial x_3 \partial x_5} \\ =& \frac{\partial^2 h_{11}}{\partial x_5 \partial x_3} = \frac{\partial^2 h_{11}}{\partial x_4 \partial x_5} = \frac{\partial^2 h_{11}}{\partial x_5 \partial x_4} \\ =& \frac{\partial^2 h_{11}}{\partial x_6 \partial x_5} = \frac{\partial^2 h_{11}}{\partial x_5 \partial x_6} = \frac{\partial^2 h_{11}}{\partial x_8 \partial x_5} \\ =& \frac{\partial^2 h_{11}}{\partial x_5 \partial x_8} = -\frac{m\beta_{MC}\Lambda_M \mu_H^2}{\Lambda_H^2 \mu_M}, \\ & \frac{\partial^2 h_{11}}{\partial {x_5}^2} \\ =& -\frac{2m\beta_{MC}\Lambda_M \mu_H^2}{\Lambda_H^2 \mu_M},\end{aligned}$$

$$\begin{aligned}\frac{\partial^2 h_{11}}{\partial x_5 \partial x_9} =& \frac{\partial^2 h_{11}}{\partial x_9 \partial x_5} = \frac{m\beta_{MC}\mu_H}{\Lambda_H} = \frac{\partial^2 h_{11}}{\partial x_5 \partial x_7} = \frac{\partial^2 h_{11}}{\partial x_7 \partial x_5} \\ =& -\left(\frac{m\Lambda_M \mu_H^2\left(\beta_{MC}+\left(1-y_1\right)\beta_{MCD}\right)}{\Lambda_H^2 \mu_M}\right) = \frac{\partial^2 h_{11}}{\partial x_7 \partial x_9} \\ =& \frac{\partial^2 h_{11}}{\partial x_9 \partial x_7} = \frac{m\left(1-y_1\right)\beta_{MCD}\mu_H}{\Lambda_H} = \frac{\partial^2 f_2}{\partial x_{12}\partial \beta_D} = m.\end{aligned}$$

Table 12. Tables of parameter values and Sensitivity Index

Parameters	Values	References	Sensitivity Index
Λ_H	100	[38]	$(-0.9991, -0.5, -0.5)$
Λ_M	100	[42]	$(0.9991, 0.5, 0.5)$
σ_1	0.0235	Fitted	$+0.2539$
σ_2	0.05	Fitted	$+0.0689$
σ_3	0.049	Fitted	$+0.4500$
σ_4	$1/4.5$	Assumed	–
σ_5	$1/4.5$	Assumed	–
σ_6	$1/4.5$	Assumed	–
α_1	$0.09 - 0.15$	[43]	-0.9712
α_2	$0.09 - 0.15$	[43]	-0.3192
α_3	$0.09 - 0.15$	[43]	-0.2139
$m(Z, D, C)$	0.45		$(+1.9981, +1, +1)$
$\delta_1, \delta_2, \delta_3$	$0.0098, 0.04, 0.089$	Assumed	–
β_Z	0.01	Fitted	$+0.0009$
β_{HZ}	0.065	Fitted	$+0.9991$
β_{MZ}	0.0441	Fitted	$+0.9991$
β_D	0.072	Fitted	$+0.5$
β_{MD}	0.140	[43]	$+0.5$
$(\delta_{ZD}, \delta_{ZC}, \delta_{DC})$	$(0.0098, 0.089, 0.0098)$	Assumed	–

Table 13. Tables of parameter values and Sensitivity Index

Parameters	Values	References	Sensitivity Index
$\mu_H(Z,D,C)$	$1/(365\times 67)$	[42]	$(0.7321, 0.3396, 0.4259)$
$\mu_M(Z,D,C)$	$1/14$	[42]	$(-2.2787, -1, -1.0369)$
σ_{MZ}	$1/8.2$	[51]	$+0.2806$
σ_{MD}	0.1	Assumed	$+0.0063$
σ_{MC}	0.3	Assumed	$+0.0368$
δ_Z	0.0098	Assumed	-0.0159
δ_D	0.04	[42]	-0.0957
δ_C	0.05	Assumed	-0.2621
η_1	0.5	Assumed	–
η_2	0.1	Assumed	–
ψ_1	0.2	Assumed	–
ψ_2	0.45	Assumed	–
θ_1	0.42	Assumed	–
θ_2	0.53	Assumed	–
ϕ_1	0.51	Assumed	–
ϕ_2	0.41	Assumed	–
β_C	0.0423	Fitted	0.5
β_{MC}	0.25	Fitted	0.5
δ_{ZCD}	0.0089	Assumed	–

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