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Stability and Bifurcation Analysis of Confection Model of Malaria and Zika Virus Diseases.

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Abstract

Malaria and zika virus disease are amongst the major causes of health burdens globally and efforts are still being made to control their spread. Studies have shown that both diseases can co-circulate in an environment where Anopheles and Aedes mosquitoes coexist. This portrays the possibility of coinfection of both diseases as studies have also proved. In this work, bifurcation analysis was carried out on a coinfection model of malaria and zika virus disease. The model incorporated vaccination against malaria, treatment of infectious humans and use of SIT to control the population of the vectors. The various equilibrium states obtainable in the system were shown and analyzed The existence of an endemic equilibrium is shown and conditions were obtained for the occurrence of backward bifurcation or not. The endemic equilibrium was shown to be globally asymptotically stable when it exists. Plots were also used to demonstrate the dynamics of the system. This study highlights the importance of taking into consideration, the occurrence of coinfection of diseases so that proper diagnosis should be carried out before treatment. It also shows the role that vaccination, treatment and use of sterile insect technique play in controlling the spread of malaria, zika virus disease and their coinfection. The study concludes that malaria, zika virus and their coinfection will be effectively controlled if the intervention measures focuses on both the human and mosquito populations simultaneously.

Keywords: Malaria; zika virus; co-infection; endemic equilibrium; bifurcation.
2020 Mathematics Subject Classification: 93A30, 34B60, 34D20, 34D23.

1 Introduction

Malaria is one of the diseases targeted by the United Nations' Sustainable Development Goals (SDGs) that should be fully combated by 2030 (United Nations, 2023). It is caused by the *Plasmodium parasite* and transmitted to humans through the bites of infectious female Anopheles mosquitoes (Onah et al., 2019; Nwankwo and Okounghae, 2019). Malaria has remained highly endemic in Asian and sub-Saharan African countries and still poses a global threat. One of the reasons for its endemicity in recent times is the increasing nature of drug resistance by the causative parasite thus highlighting the need for more preventive than controlling measures (WHO, 2022). According to WHO (2023), the mosquitoes have mutated to resist the effect of insecticides and thus remains ever-present in their host environment. It is estimated that there are about 247 million cases globally while the estimated number of deaths due to malaria was 619,000 (WHO, 2022). Tropical regions in Africa accounted for 92% cases and 93% deaths respectively out of which Nigeria had the highest with 25% and Uganda lowest with 4%. Symptoms of malaria include infant mortality, morbidity, headache, fever, shaking chills, bloody stools, jaundice, severe anaemia, profuse sweating, nausea, muscle pain, diarrhea, vomiting, abdominal pain, fatigue, convulsions, coma, etc (WHO, 2023).
Zika virus disease (ZIKV) on the hand is a flavivirus disease transmitted through the bites of infectious female Aedes mosquitoes (Atokolo and Mbah, 2020). It can also be transmitted through sex, blood transfusion or by infectious women to their newborns during pregnancy. It was reported in 2015 that over 69 countries had (ZIKV) infection through mosquito bites while human-to-human transmission cases occurred in 13 countries, 29 countries had congenital transmission cases and 20 countries had Guillain-Barre syndrome (GBs) cases (WHO, 2016). The symptoms of ZIKA include headache, maculopapular rash, fatigue, mild fever, muscle and joint pain, retroorbital pain, oadema, vomiting, conjunctivitis, lymphadenopathy malaise, arthralgia, sore throat and uveitis (CDC, 2022; Eguda et al., 2019).
Malaria and zika virus disease are amongst the diseases that can coinfect humans. Others include; COVID-19 and pneumonia, Hookworm and malaria, Chikungunya and Dengue, Dengue and HIV, Hepatitis C and HIV, Hepatitis C and D, COVID-19 and flu, Malaria and Zika virus, Ebola and malaria, Dengue and Zika virus, etc (WHO, 2016; McArdle et al., 2018). Studies have shown that in any environment where both malaria and ZIKV disease coexist, their coinfection is possible. Amaoh-Mensah et al. (2018) studied a coinfection model of malaria and zika virus disease where they showed that both diseases can be controlled by improving their rate of recovery. Otu et al. (2020) conducted a study on the prevalence of both diseases in hundred (100) patients with fever in nine (9) secondary healthcare facilities in south-east Nigeria. They tested blood samples of the patients and found out that 55% of the patients had malaria, 20% had zika infection while about 15% had the coinfection showing the high probability of the existence of the coinfection of both diseases. The authors in (Mac et al., 2023) conducted a sero-epidemiological and clinical studies to help understand the hidden endemicity and disease burden of zika virus, malaria and other arbovirus in humans. Their study showed the possibility of zika virus, malaria and other flavivirus co-circulating in Nigeria. Baba et al. (2023) carried out a cryptic study on Zika virus

infections arising from Malaria suspected cases. They tested 496 patients suspected to be infected with Malaria from choice health centers in Bauchi, Borno and Adamawa states. They discovered that 86% of Zika virus patients were found to be co-infected with other arbovirus diseases. Patients co-infected with Chikungunya (39.3%), dengue fever (60.7%), Yellow fever (7.1%) and West Nile viruses (23.2%). The authors in Duru et al. (2024) worked on a coinfection model that incorporates vaccination, treatment and using sterile insect technology to control the vectors. In their work, they assumed that some humans accepts vaccination against malaria while some refuses and simulated the scenario to show the dangers of not being vaccinated as the proportion of humans who accepts vaccination is varied. They also considered cases where infectious humans with malaria, zika virus disease and their coinfection are treated. It also looked at the effects of refusing treatment by infectious humans with malaria and coinfectious humans with both diseases on health burdens. Their work showed that treatment reduces the spread of the diseases in both human and mosquito populations. The work also considered the effect of using sterile insect technique (SIT) to control the vectors. Sterile insect technique is a proceedure that involves releasing certain number of sterile male mosquitoes into a target population so that when the sterile males mate with the females in the target population, they lay eggs that do not hatch. Duru et al. (2024) simulated the effect of varying the number of SIT mosquitoes interacting with the females in the wild with time and showed how successfully SIT can be employed to control the population of mosquitoes and thus the spread of malaria and zika virus disease. In this study, we will present the existence of endemic equilibrium, bifurcation analysis and more simulations of the system shown by Duru et al. (2024) to gain more insight into the dynamics of the coinfection.

2 Materials and Methods

The mathematical model for the coinfection by Duru et al. (2024) has twenty-two (22) compartments made up of the human and mosquito populations. The human population is divided into sixteen (16) compartments; Susceptible humans S_h, Vaccinated humans for malaria S_{hv}, Unvaccinated humans for malaria S_{hu}, Exposed humans to malaria E_{hm}, Exposed humans to zika E_{hz}, coinfected humans with both diseases E_{mz}, Infectious humans with malaria I_{hm}, symptomatic infectious humans with zika I_{hzS}, asymptomatic infectious humans with zika I_{hzA}, coinfectious humans with both diseases I_{mz}, Infectious humans undergoing treatment for malaria I_{hmT}, Infectious humans undergoing treatment for zika I_{hzT}, coinfectious humans undergoing treatment for both diseases I_{mzT}, Infectious humans not undergoing treatment for malaria I_{hmU}, coinfectious humans not undergoing treatment for both disease I_{mzU} and Recovered humans R_h. The mosquito population is subdivided into six (6) compartments; Susceptible Anopheles mosquitoes S_{mv}, Exposed Anopheles mosquitoes E_{mv}, Infectious Anopheles Mosquitoes I_{mv}, Susceptible Aedes mosquitoes S_{zv}, Exposed Aedes mosquitoes E_{zv} and Infectious Aedes mosquitoes I_{zv}. The details of the transmission dynamics and theoretical background of the model has been fully discussed in their work. The coinfection

model of Duru et al. (2024) is given by

$$
\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h + \theta R_h - (\rho_1 + \rho_2 + \tau_1)S_h \\
\frac{dS_{hu}}{dt} &= \rho_1 S_h - (\alpha_1\beta_1 I_{mv} + \alpha_2\eta_1 I_{zv} + \tau_1)S_{hu} \\
\frac{dS_{hv}}{dt} &= \rho_2 S_h - (\alpha_1\beta_2 I_{mv}\varphi + \alpha_2\eta_1 I_{zv} + \tau_1)S_{hv} \\
\frac{dE_{hm}}{dt} &= \alpha_1\beta_1 I_{mv} S_{hu} + \alpha_1\beta_2 I_{mv}\varphi S_{hv} + \phi_1 I_{hmU} + \phi_2 I_{mzU} - \alpha_2\eta_1 I_{zv} E_{hm} - (\delta_1 + \tau_1)E_{hm} \\
\frac{dE_{hz}}{dt} &= \alpha_2\eta_1 I_{zv}(S_{hu} + S_{hv}) - \alpha_1\beta_1 I_{mv} E_{hz} - ((\chi_1 + \chi_2)\delta_2 + \tau_1)E_{hz} \\
\frac{dE_{hmz}}{dt} &= \alpha_1\beta_1 I_{mv} E_{hz} + \alpha_2\eta_1 I_{zv} E_{hm} - (\delta_3 + \tau_1)E_{mz} \\
\frac{dI_{hm}}{dt} &= \delta_1 E_{hm} - \alpha_2\eta_1 I_{zv} I_{hm} - (\tau_1 + \tau_2 + \varepsilon_1 + \varepsilon_2)I_{hm} \\
\frac{dI_{hmT}}{dt} &= \varepsilon_1 I_{hm} - (\gamma_1 + \tau_1 + \tau_2)I_{hmT} \\
\frac{dI_{hmU}}{dt} &= \varepsilon_2 I_{hm} - (\phi_1 + \tau_1 + \tau_2)I_{hmU} \\
\frac{dI_{hzS}}{dt} &= \delta_2\chi_1 E_{hz} - \alpha_1\beta_1 I_{mv} I_{hzS} - (\tau_1 + \tau_3 + \psi + \omega_1)I_{hzS} \\
\frac{dI_{hzA}}{dt} &= \delta_2\chi_2 E_{hz} - \alpha_1\beta_1 I_{mv} I_{hzA} - (\tau_1 + \tau_3 + \omega_3)I_{hzA} \\
\frac{dI_{hzT}}{dt} &= \psi I_{hzS} - (\tau_1 + \tau_3 + \omega_2)I_{hzT} \qquad (1) \\
\frac{dI_{hmz}}{dt} &= \alpha_1\beta_1 I_{mv}(I_{hzS} + I_{hzA}) + \alpha_2\eta_1 I_{zv} I_{hm} + \delta_3 E_{mz} - (\tau_1 + \tau_4 + \sigma_1 + \sigma_2)I_{hmz} \\
\frac{dI_{hmzT}}{dt} &= \sigma_1 I_{mz} - (\tau_1 + \tau_4 + \gamma_2)I_{hmzT} \\
\frac{dI_{hmzU}}{dt} &= \sigma_2 I_{mz} - (\tau_1 + \tau_4 + \phi_2)I_{hmzU} \\
\frac{dR_h}{dt} &= \gamma_1 I_{hmT} + \gamma_2 I_{mzT} + \omega_1 I_{hzS} + \omega_2 I_{hzT} + \omega_3 I_{hzA} - (\tau_1 + \theta)R_h \\
\frac{dS_{mv}}{dt} &= \Lambda_{mv} - \alpha_1(\beta_3 I_{hm} + \beta_4 I_{hmT} + \beta_5 I_{hmU} + \beta_6 I_{hmz} + \beta_7 I_{hmzT} + \beta_8 I_{hmzU})S_{mv} - (\kappa_1 M_{SIT} + \mu_m)S_{mv} \\
\frac{dE_{mv}}{dt} &= \alpha_1(\beta_3 I_{hm} + \beta_4 I_{hmT} + \beta_5 I_{hmU} + \beta_6 I_{hmz} + \beta_7 I_{hmzT} + \beta_8 I_{hmzU})S_{mv} - (\nu_1 + \mu_m)E_{mv} \\
\frac{dI_{mv}}{dt} &= \nu_1 E_{mv} - \mu_m I_{mv} \\
\frac{dS_{zv}}{dt} &= \Lambda_{zv} - \alpha_2(\eta_2 I_{hzS} + \eta_3 I_{hzA} + \eta_4 I_{hzT} + \eta_5 I_{hmz} + \eta_6 I_{hmzT} + \eta_7 I_{hmzU})S_{zv} - (\kappa_2 Z_{SIT} + \mu_z)S_{zv} \\
\frac{dE_{zv}}{dt} &= \alpha_2(\eta_2 I_{hzS} + \eta_3 I_{hzA} + \eta_4 I_{hzT} + \eta_5 I_{hmz} + \eta_6 I_{hmzT} + \eta_7 I_{hmzU})S_{zv} - (\nu_2 + \mu_z)E_{zv} \\
\frac{dI_{zv}}{dt} &= \nu_2 E_{zv} - \mu_z I_{zv}
\end{aligned}
$$

where $S_h(0) = S_h^0, S_{hu}(0) = S_{hu}^0, S_{hv}(0) = S_{hv}^0, E_{hm}(0) = E_{hm}^0, E_{hz}(0) = E_{hz}^0, E_{hmz}(0) = E_{hmz}^0, I_{hm}(0) = I_{hm}^0, I_{hmz}(0) = I_{hmz}^0, I_{hmT}(0) = I_{hmT}^0, I_{hmU}(0) = I_{hmU}^0, I_{hzS}(0) = I_{hzS}^0, I_{hzA}(0) = I_{hzA}^0, I_{hzT}(0) =$

$I^0_{hzT}, I_{hmzT}(0) = I^0_{hmzT}, I_{hmzU}(0) = I^0_{hmzU}, R_h(0) = R^0_h, S_{mv}(0) = S^0_{mv}, E_{mv}(0) = E^0_{mv}, I_{mv}(0) = I^0_{mv}, S_{zv}(0) = S^0_{zv}, E_{zv}(0) = E^0_{zv}$ and $I_{zv}(0) = I^0_{zv}$ are the initial conditions of the system.

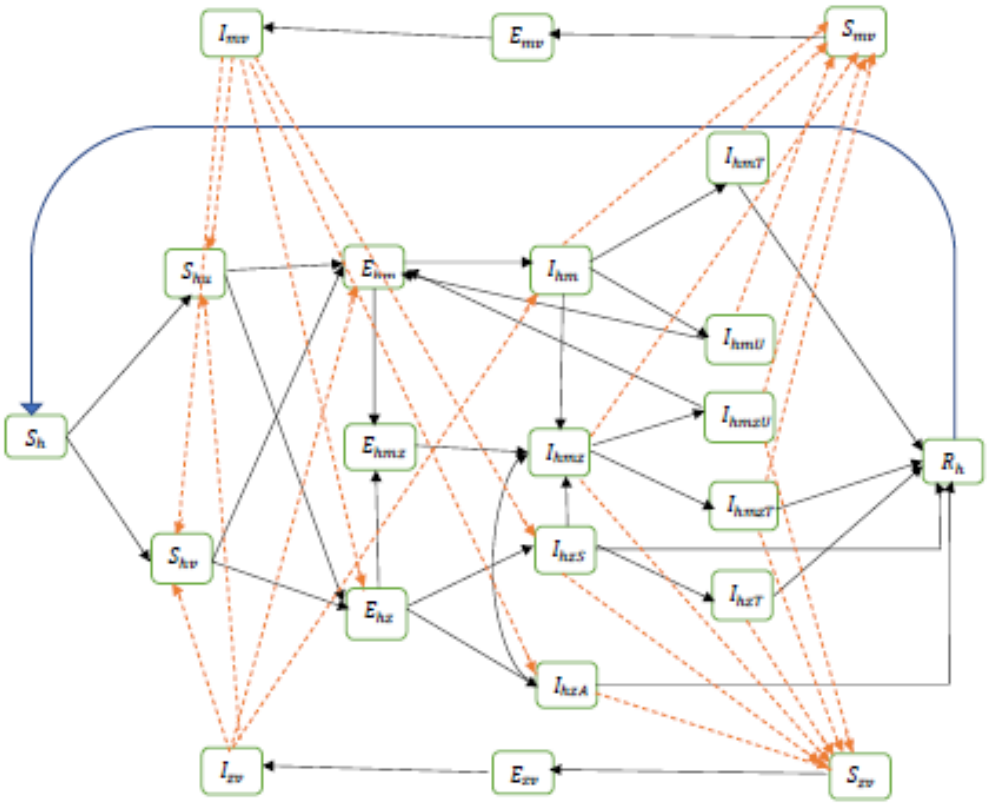


Figure 1: The flow diagram for the coinfection of malaria and zika virus disease.

2.1 Positivity of solutions and Invariant Region

Theorem 1. *Let the initial data set for the model be* $(S^0_h, S^0_{hu}, S^0_{hv}, E^0_{hm}, E^0_{hz}, E^0_{hmz}, I^0_{hm}, I^0_{hmz}, I^0_{hmT}, I^0_{hmU}, I^0_{hzS}, I^0_{hzA}, I^0_{hzT}, I^0_{hmzT}, I^0_{hmzU}, R^0_h, S^0_{mv}, E^0_{mv}, I^0_{mv}, S^0_{zv}, E^0_{zv})$ *which are all nonnegative at* $t = 0$. *Then, the solution set* $(S_h(t), S_{hu}(t), S_{hv}(t), E_{hm}(t), E_{hz}(t), E_{hmz}(t), I_{hm}(t), I_{hmz}(t), I_{hmT}(t), I_{hmU}(t), I_{hzS}(t), I_{hzA}(t), I_{hzT}(t), I_{hmzT}(t), I_{hmzU}(t), R_h(t), S_{mv}(t), E_{mv}(t), I_{mv}(t), S_{zv}(t), E_{zv}(t), I_{zv}(t))$ *of the model with the given initial data will remain positive for all time* $t > 0$.

Theorem 2. *The region,* $\Omega = \Omega_h \times \Omega_m \times \Omega_z$ *is positively invariant and is an attractor of all possible solutions to the system where* $\Omega_h = \{(S_h, S_{hu}, S_{hv}, E_{hm}, E_{hz}, E_{hmz}, I_{hm}, I_{hmz}, I_{hmT}, I_{hmU}, I_{hzS}, I_{hzA}, I_{hzT}, I_{hmzT}, I_{hmzU}, R_h) \in \mathcal{R}^{16}_+ : N_h \leq \frac{\Lambda_h}{\mu_h}\}, \Omega_m = \left\{(S_{mv}, E_{mv}, I_{mv}) \in \mathcal{R}^3_+ : N_{mv} \leq \frac{\Lambda_{mv}}{\mu_m}\right\}$ *and* $\Omega_z = \left\{(S_{zv}, E_{zv}, I_{zv}) \in \mathcal{R}^3_+ : N_{zv} \leq \frac{\Lambda_{zv}}{\mu_z}\right\}$.

Proof. The proofs of Theorem 2.1 and 2.2 have been succintly detailed in Duru et al. (2024) showing that the model is well-posed epidemioogically and hence can be analyzed. □

Table 1: Description of Variables and Parameters

Variables	**Description**
S_h	Susceptible human population
S_{hu}	Unvaccinated humans for Malaria
S_{hv}	Vaccinated humans for Malaria
E_{hm}	Exposed humans to Malaria only
E_{hz}	Exposed humans to Zika virus only
E_{hmz}	Exposed humans to Malaria and Zika
I_{hm}	Infectious humans with Malaria only
I_{hmT}	Infectious humans with Malaria only undergoing treatment
I_{hmU}	Infectious humans with Malaria not undergoing treatment
I_{hzS}	Symptomatic infectious humans with Zika
I_{hzA}	Asymptomatic infectious humans with Zika
I_{hzT}	Infectious humans with Zika only undergoing treatment
I_{hmz}	Co-infectious humans with Malaria and Zika
I_{hmzT}	Co-infectious humans with both Malaria and Zika undergoing treatment
I_{hmzU}	Co-infectious humans with both Malaria and Zika not undergoing treatment
R_h	Recovered humans from both diseases
S_{mv}	Susceptible Anopheles mosquito population
E_{mv}	Exposed Anopheles mosquito population
I_{mv}	Infectious Anopheles mosquito population
S_{zv}	Susceptible Aedes mosquito population
E_{zv}	Exposed Aedes mosquito population
I_{zv}	Infectious Aedes mosquito population
Parameters	**Description**
Λ_h	Level of recruitment of humans into susceptible population
Λ_{mv}	Level of recruitment of Anopheles mosquitoes
Λ_{zv}	Level of recruitment of Aedes mosquitoes
φ	Rate at which vaccinated humans loses immunity
θ	Rate of loss of immunity to Malaria from recovered class
ρ_1	Proportion of the susceptible humans that rejects vaccination
ρ_2	Proportion of the susceptible humans that accepts vaccination
τ_1	Natural death rate of humans
τ_2	Rate of death due to Malaria
τ_3	Rate of death due to Zika disease
τ_4	Rate of death due to co-infection
α_1	Contact rate of Anopheles mosquitoes with humans
α_2	Contact rate of Aedes mosquitoes with humans
β_1	Probability of transmission of malaria from infectious mosquitoes to unvaccinated humans
β_2	Probability of transmission of malaria from infectious mosquitoes to vaccinated humans
β_3	Probability of transmission of malaria from infectious humans to mosquitoes
β_4	Probability of transmission of malaria from humans undergoing treatment to mosquitoes
β_5	Probability of transmission of malaria from humans not undergoing treatment to mosquitoes

β_6	Probability of transmission of malaria from co-infectious humans to mosquitoes
β_7	Probability of transmission of malaria from co-infectious humans undergoing treatment to mosquitoes
β_8	Probability of transmission of malaria from co-infectious humans not undergoing treatment to mosquitoes
η_1	Probability of transmission of zika virus from infectious mosquitoes to humans
η_2	Probability of transmission of zika virus from symptomatic humans to mosquitoes
η_3	Probability of transmission of zika virus from asymptomatic humans to mosquitoes
η_4	Probability of transmission of zika virus from humans undergoing treatment to mosquitoes
η_5	Probability of transmission of zika virus from co-infectious humans to mosquitoes
η_6	Probability of transmission of zika virus from co-infectious humans undergoing treatment to mosquitoes
η_7	Probability of transmission of zika virus from co-infectious humans not undergoing treatment to mosquitoes
δ_1	Rate at which exposed humans with Malaria parasite become infectious with Malaria
δ_2	Rate at which exposed humans with Zika virus become infectious with Zika disease
δ_3	Rate at which co-infected humans become infectious with both diseases
ε_1	Rate at which infectious humans with Malaria accepts to be treated
ε_2	Rate at which infectious humans with Malaria refuse to be treated
σ_1	Rate at which co-infectious humans accept to be treated
σ_2	Rate at which co-infectious humans refuse to be treated
χ_1	Proportion of infectious humans with Zika that are symptomatic
χ_2	Proportion of infectious humans with Zika that are asymptomatic
ϕ_1	Proportion of infectious humans with Malaria not undergoing treatment that loses their infectiousness
ϕ_2	Proportion of co-infectious humans not undergoing treatment that loses their Malaria infectiousness
γ_1	Rate of recovery of infectious humans with Malaria undergoing treatment
γ_2	Rate of recovery of co-infectious humans with Malaria and Zika virus disease undergoing treatment
ω_1	Rate of recovery of symptomatic infectious humans with Zika virus not undergoing treatment
ω_2	Rate of recovery of infectious humans with Zika virus undergoing treatment
ω_3	Rate of natural recovery of asymptomatic humans with Zika virus
ψ	Rate at which symptomatic infectious humans with Zika accepts to be treated
κ_1	Rate of reduction of Anopheles mosquitoes
κ_2	Rate of reduction of Aedes mosquitoes
μ_m	Natural death rate of Anopheles mosquitoes
μ_z	Natural death rate of Aedes mosquitoes
ν_1	Rate of development of Infectiousness of Malaria parasite in Anopheles mosquitoes
ν_2	Rate of development of Infectiousness of Zika virus in Aedes mosquitoes
M_{SIT}	Population of Sterile males to control Anopheles population
Z_{SIT}	Population of Sterile males to control Aedes population

2.2 The disease reproduction number

The disease-free equilibrium (DFE) point of the model is the steady state solution of (1) where there is no malaria infection, zika virus infection nor coinfection in the human and mosquito populations. It is denoted by E^0 and given as

$$E^0 = \left(\frac{\Lambda_h}{\rho_1+\rho_2+\tau_1}, \frac{\rho_1\Lambda_h}{\tau_1(\rho_1+\rho_2+\tau_1)}, \frac{\rho_2\Lambda_h}{\tau_1(\rho_1+\rho_2+\tau_1)}, 0,0,0,0,0,0,0,0,0,0,0,0,0,0, \frac{\Lambda_{mv}}{\mu_m}, 0, 0, \frac{\Lambda_{zv}}{\mu_z}, 0, 0 \right),$$

The control reproduction number is defined as the average number of new cases of an infection caused by one typical infectious malaria, zika virus or coinfectious human or mosquito in a population consisting of susceptibles only (Ajao et al., 2023; Musa et al., 2023; Omede et al., 2023). The control reproduction number which corresponds to the dominant eigenvalue of FV^{-1} denoted in Duru et al. (2024) by R_{mz} is given by

$$R_{mz} = max(R_m, R_z). \tag{2}$$

where

$$R_m = \left(\frac{\nu_1\delta_1 A_1(A_2B_4B_3 + A_3\varepsilon_1B_4 + A_4\varepsilon_2B_3)}{\mu_m B_3B_5(B_1B_2B_4 - \varepsilon_2\delta_1\phi_1)} \right)\frac{1}{2}$$

and

$$R_z = \left(\frac{C_1\nu_2\delta_2(C_2\chi_1D_3D_4 + C_3\chi_2D_2D_4 + C_4\chi_1\psi D_3)}{\mu_z D_1D_2D_3D_4D_5} \right)\frac{1}{2},$$

$A_1 = \frac{\alpha_1\Lambda_h(\beta_1\rho_1+\beta_2\varphi\rho_2)}{\tau_1(\rho_1+\rho_2+\tau_1)}$, $A_2 = \frac{\alpha_1\beta_3\Lambda_{mv}}{\mu_m}, A_3 = \frac{\alpha_1\beta_4\Lambda_{mv}}{\mu_m}$, $A_4 = \frac{\alpha_1\beta_5\Lambda_{mv}}{\mu_m}, A_5 = \frac{\alpha_1\beta_6\Lambda_{mv}}{\mu_m}$,
$A_6 = \frac{\alpha_1\beta_7\Lambda_{mv}}{\mu_m}, A_7 = \frac{\alpha_1\beta_8\Lambda_{mv}}{\mu_m}, B_1 = \delta_1+\tau_1, B_2 = \tau_1+\tau_2+\varepsilon_1+\varepsilon_2, B_3 = \gamma_1+\tau_1+\tau_2, B_4 = \phi_1+\tau_1+\tau_2$,
$B_5 = \nu_1+\mu, B_6 = \delta_3+\tau_1, B_7 = \tau_1+\tau_4+\sigma_1+\sigma_2, B_8 = \tau_1+\tau_4+\omega_2, B_9 = \tau_1+\tau_4+\phi_2, C_1 = \frac{\alpha_2\eta_1\Lambda_h}{\tau_1}$,
$C_2 = \frac{\alpha_2\eta_2\Lambda_{zv}}{\mu_z}, C_3 = \frac{\alpha_2\eta_3\Lambda_{zv}}{\mu_z}, C_4 = \frac{\alpha_2\eta_4\Lambda_{zv}}{\mu_z}, C_5 = \frac{\alpha_2\eta_5\Lambda_{zv}}{\mu_z}, C_6 = \frac{\alpha_2\eta_6\Lambda_{zv}}{\mu_z}, C_7 = \frac{\alpha_2\eta_7\Lambda_{zv}}{\mu_z}$,
$D_1 = (\chi_1+\chi_2)\delta_2+\tau_1, D_2 = \tau_1+\tau_3+\psi+\omega_1, D_3 = \tau_1+\tau_3+\omega_3, D_4 = \tau_1+\tau_3+\omega_2, D_5 = \nu_2+\mu.$

The control reproduction number was obtained using the Next-generation matrix approach. R_m is the average number of humans and Anopheles mosquitoes that can be infected by one infectious humans or mosquito with malaria in a population of susceptible humans or mosquitoes. Similarly, R_z is the average number of humans and Aedes mosquitoes that can be infected by one infectious humans or mosquito with zika virus in a population of susceptible humans or mosquitoes.

3 Stability Analysis of the disease-free equilibrium

3.1 Local stability of the disease-free equilibrium

Theorem 3. *The DFE is locally asymptotically stable if $R_{mz} < 1$ and unstable if otherwise.*

Proof. See (Duru et al., 2024). □

3.2 Global stability of the disease-free equilibrium

Theorem 4. *Consider the system of differential equations*

$$\frac{dX}{dt} = F_1(X, 0). \tag{3}$$

$$\frac{dY}{dt} = F_2(X, Y), F_2(X, 0) = 0. \tag{4}$$

where (3) is the system of differential equations, satisfied by non-disease classes such that $X = (S_h, S_{hu}, S_{hv},$
$R_h, S_{mv}, S_{zv})$ *and (4) is the system of differential equations satisfied by the disease classes so that* $Y = (E_{hm}, E_{hz}, E_{hmz}, I_{hm}, I_{hmT}, I_{hmU}, I_{hzS}, I_{hzA}, I_{hzT}, I_{hmz}, I_{hmzT}, I_{hmzU}, E_{mv}, I_{mv}, E_{zv}, I_{zv})$. *The CFE,* E^0 *is GAS if (3) is GAS, and if in (4),* $BX_2 - F_2(X, Y) \geq 0$, *where* B *is the Jacobian matrix of* $F_2(X, Y)$, *evaluated at* E^0.

Theorem 4 was adapted from Castillo-Chavez and Song (2004).

Proof. See See (Duru et al., 2024). □

3.3 Coinfection endemic equilibrium point of the system

Coinfection Endemic equilibrium points (CEEP) are steady-state solutions in the population where malaria and zika virus disease persist, that is, where all state variables are positive. The endemic equilibrium points denoted in this work by E^* is gotten by changing all state variables to have the index '*', set each equation in the model to zero and find an expression for the state variables (Lutera et al., 2018; Mahato and Mishra, 201).

Theorem 5. *The positive endemic equilibrium exists and is unique if and only if* $R_{mz} > 1$.

Proof. To show the existence of the co-infection endemic equilibrium, the approach by (Massawe et al., 2015; Mpande et al., 2015) is adopted. Summing all the equations of the model at the endemic equilibrium gives

$$\begin{aligned}
&\Lambda_h - \tau_1(S_h^* + S_{hu}^* + S_{hv}^* + E_{hm}^* + E_{hz}^* + E_{hmz}^* + I_{hm}^* + I_{hm}^* + I_{hmT}^* + I_{hmU}^* + I_{hzS}^* + I_{hzA}^* \\
&\quad + I_{hzT}^* + I_{hmz}^* + I_{hmzT}^* + I_{hmzU}^* + R_h^*) - \tau_2(I_{hm}^* + I_{hmT}^* + I_{hmU}^*) - \tau_3(I_{hzS}^* + I_{hzA}^* + I_{hzT}^*) \\
&\quad - \tau_4(I_{hmz}^* + I_{hmzT}^* + I_{hmzU}^*) + \Lambda_{mv} - \mu_m(S_{mv}^* + E_{mv}^* + I_{mv}^*) - \kappa_1 M_{SIT} S_{mv}^* + \Lambda_{zv} \\
&\quad - \mu_z(S_{zv}^* + E_{zv}^* + I_{zv}^*) - \kappa_2 Z_{SIT} S_{zv}^* = 0
\end{aligned}$$

Simplifying further, we have

$$\begin{aligned}
&\Lambda_h - \tau_1 N_h^* - \tau_2(I_{hm}^* + I_{hmT}^* + I_{hmU}^*) - \tau_3(I_{hzS}^* + I_{hzA}^* + I_{hzT}^*) - \tau_4(I_{hmz}^* + I_{hmzT}^* + I_{hmzU}^*) \\
&+ \Lambda_{mv} - \mu_m N_{mv}^* - \kappa_1 M_{SIT} S_{mv}^* + \Lambda_{zv} - \mu_z N_{zv}^* - \kappa_2 Z_{SIT} S_{zv}^* = 0
\end{aligned} \tag{5}$$

The result (5) can be rearranged to obtain

$$\Lambda_h + \Lambda_{mv} + \Lambda_{zv} = \tau_1 N_h^* + \tau_2(I_{hm}^* + I_{hmT}^* + I_{hmU}^*) + \tau_3(I_{hzS}^* + I_{hzA}^* + I_{hzT}^*)$$
$$+ \tau_4(I_{hmz}^* + I_{hmzT}^* + I_{hmzU}^*) + \mu_m N_{mv}^* + \kappa_1 M_{SIT} S_{mv}^* + \mu_z N_{zv}^* + \kappa_2 Z_{SIT} S_{zv}^*$$

Since $\Lambda_h + \Lambda_{mv} + \Lambda_{zv} > 0,\ \tau_1 > 0,\ \tau_2 > 0,\ \tau_3 > 0,\ \tau_4 > 0,\ \mu_m > 0,\ \mu_z > 0,\ \kappa_1 > 0,$ and $\kappa_2 > 0$ then, $\tau_1 N_h^* > 0,\quad \mu_m N_{mv}^* > 0\ ,\ \tau_2(I_{hm}^* + I_{hmT}^* + I_{hmU}^*) > 0,\quad \tau_3(I_{hzS}^* + I_{hzA}^* + I_{hzT}^*) > 0,$ $\tau_4(I_{hmz}^* + I_{hmzT}^* + I_{hmzU}^*) > 0$, and $\mu_z N_{zv}^* > 0$.
This implies that at least one malaria infectious state, one zika infectious state and one coinfectious state exist. Since the existence of I_{hmU}^* and I_{hmT}^* are dependent on I_{hm}^*, then it guarantees that if $\tau_2(I_{hm}^* + I_{hmT}^* + I_{hmU}^*) > 0$ then, $I_{hm}^* > 0$. Similarly, the same results holds for I_{hzS}^*, I_{hzA}^* and I_{hmz}^*. Thus, at the co-infection endemic equilibrium, $I_{hm}^* > 0, I_{hzS}^* > 0, I_{hzA}^* > 0, I_{hmz}^* > 0$. □

3.4 Bifurcation analysis

In this subsection, we conducted bifurcation analysis to check if the co-infection endemic equilibrium is locally asymptotically stable or not and obtain some conditions for the existence of forward or backward bifurcation in the system. The method of Castillo-Chavez and Song (2004) based on the Center Manifold Theorem is employed.

Theorem 6. *Given a system of ordinary differential equation with a bifurcation parameter ψ;*

$$x^{'}(t) = f(x, \psi), \quad f : \mathbb{R}^n \times \mathbb{R},\ f \in C^2(\mathbb{R}^n \times \mathbb{R}). \tag{6}$$

Let $J = \frac{\partial f_k(0,0)}{dx_j}$ be the Jacobian matrix of $f(x, \psi)$ evaluated at $(0, 0)$, where $x = 0$ is the equilibrium point of the system. Assuming the following hold;

1. *zero is a simple eigenvalue of the Jacobian matrix, and all other eigenvalues of J have negative real part.*
2. *J has a nonnegative right eigenvector w and a left eigenvector v corresponding to the zero eigenvalue.*

Let $f_k(x, \psi)$ denote the kth component of $f(x, \psi)$ and

$$q = \sum_{k,i,j}^{n} v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j}, \quad r = \sum_{k,i}^{n} v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_i \partial \psi}$$

then

1. *If $q > 0,\ r > 0$, then when $\psi < 0$ with $|\psi| \ll 1,\ x = 0$ is locally asymptotically stable and $\exists$ a positive unstable equilibrium; and when $0 < |\psi| \ll 1,\ x = 0$ is unstable, and $\exists$ a negative and locally asymptotically stable equilibrium.*

2. *If* $q < 0,\ r < 0$, *then when* $\psi < 0$ *with* $|\psi| \ll 1,\ x = 0$ *is unstable; and when* $0 < |\psi| \ll 1,\ x = 0$ *is locally asymptotically stable and* $\exists$ *a positive unstable equilibrium.*

3. *If* $q > 0,\ r < 0$, *when* $\psi < 0$ *with* $|\psi| \ll 1,\ x = 0$ *is unstable and* $\exists$ *a locally asymptotically stable negative equilibrium; and when* $0 < |\psi| \ll 1,\ x = 0$ *is stable and a positive unstable equilibrium appears.*

4. *If* $q < 0$ *and* $r > 0$, *when* ψ *changes from negative to positive,* $x = 0$ *changes from stable to unstable. correspondingly, a negative unstable equilibrium becomes positive and locally asymptotically stable.*

Particularly, if $q < 0$ and $r > 0$, then a forward bifurcation occurs at $\psi = 0$ and if $q > 0,\ r > 0$, a backward bifurcation occurs at $\psi = 0$.

Proof. To perform the bifurcation analysis on the co-infection model, we will have two case scenario since the co-infection reproduction number, $R_{mz} = \max(R_m, R_z)$. Hence, we need to consider a situation where R_m is the maximum and thus the co-infection reproduction number and when R_z is the co-infection reproduction number.

Case 1: Let R_m be the coinfection reproduction number and let our state variables be represented thus; $S_h = x_1, S_{hu} = x_2, S_{hv} = x_3, E_{hm} = x_4, E_{hz} = x_5, E_{hmz} = x_6, I_{hm} = x_7, I_{hmT} = x_8, I_{hmU} = x_9, I_{hzS} = x_{10}, I_{hzA} = x_{11}, I_{hzT} = x_{12}, I_{hmz} = x_{13}, I_{hmzT} = x_{14}, I_{hmzU} = x_{15}, R_h = x_{16}, S_{mv} = x_{17}, E_{mv} = x_{18}, I_{mv} = x_{19}, S_{zv} = x_{20}, E_{zv} = x_{21}, I_{zv} = x_{22}, M_{SIT} = x_{23}$ and $Z_{SIT} = x_{24}$.
If we choose β_3 as the bifurcation parameter, then $R_m = 1$ implies that

$$\beta_3 = \beta_3^* = \frac{\mu_m^2 B_3 B_5 (B_1 B_2 B_4 - \epsilon_2 \phi_1 \delta_1) - A_1 \nu_1 \delta_1 (A_3 \epsilon_1 B_4 + A_4 \epsilon_2 B_3) \mu_m}{\alpha_1 \Lambda_{mv} A_1 \nu_1 \delta_1 B_3 B_4},$$

Let $J(E^0, \beta_3^*)$ be the Jacobian matrix of $f(x, \beta_3^*)$ at the coinfection-free equilibrium E^0 where β_3 is now replaced with β_3^* which is the bifurcation parameter. The matrix $J(E^0, \beta_3^*)$ possesses one zero eigenvalue, while the remaining eigenvalues have negative real part. Therefore, $J(E^0, \beta_3^*)$ is non-hyperbolic, and we can apply the center manifold theorem to analyze the dynamics of the model around the bifurcation parameter value β_3^*. The right and left eigenvectors corresponding to the zero eigenvalues satisfying the systems is given by $J(E^0, \beta_3^*)\bar{w} = 0$ and $\bar{v} J(E^0, \beta_3^*) = 0$, respectively.
Case 2: Let R_z be the coinfection reproduction number and let our state variables be represented as in case 1. If we choose η_2 as the bifurcation parameter, then $R_z = 1$ implies that

$$\eta_= \eta_2^* = \frac{\mu_z^2 D_1 D_2 D_3 D_4 D_5 - C_1 \nu_2 \delta_2 (C_3 \chi_2 D_2 D_4 + C_4 \chi_1 \psi D_3) \mu_z}{\alpha_2 \Lambda_{zv} C_1 \nu_2 \delta_2 \chi_1 D_3 D_4},$$

Let $J(E^0, \eta_2^*)$ be the Jacobian matrix of $f(x, \eta_2^*)$ at the coinfection-free equilibrium E_1^0 where η_2 is now replaced with η_2^* which is the bifurcation parameter. The matrix $J(E^0, \eta_2^*)$ possesses one zero eigenvalue, while the remaining eigenvalues have negative real part. Therefore, $J(E^0, \eta_2^*)$ is non-hyperbolic, and we can apply the center manifold theorem to analyze the dynamics of the model around the bifurcation parameter value η_2^*.

The right and left eigenvectors corresponding to the zero eigenvalues satisfying the systems $J(E^0, \eta_2^*)\bar{w} = 0$ and $\bar{v}J(E^0, \eta_2^*) = 0$, respectively is the same as used in case one.
The Jacobian matrix $J(E^0, \eta_2^*)$ and $J(E^0)$ are the same, only that in C_2, η_2 is replaced with η_2^*.
For case one, using the Jacobian matrix, $J(E^0, \beta_3^*)$ and the vector $\bar{w} = (w_1, w_2, w_3, w_4,$
$w_5, w_6, w_7, w_8, w_9, w_{10}, w_{11},$
$w_{12}, w_{13}, w_{14}, w_{15}, w_{16}, w_{17}, w_{18}, w_{19}, w_{20}.w_{21}$ and $w_{22})$, then $J(E^0, \beta_3^*)\bar{w}$ will give

$$J(E^0, \beta_3^*)\bar{w} = \begin{pmatrix} -A_8w_1 + \theta w_{16} \\ \rho_1 w_1 - \tau_1 w_2 - A_9 w_{19} - A_{10} w_{22} \\ \rho_2 w_1 - \tau_1 w_3 - C_8 w_{19} - C_9 w_{22} \\ -B_1 w_4 + \phi_1 w_9 + \phi_2 w_{15} + A_1 w_{19} \\ -D_1 w_5 + C_1 w_{22} \\ -B_6 w_6 \\ \delta_1 w_4 - B_2 w_7 \\ \epsilon_1 w_7 - B_3 w_8 \\ \epsilon_2 w_7 - B_4 w_9 \\ D_6 w_5 - D_2 w_{10} \\ D_7 w_5 - D_3 w_{11} \\ \psi w_{10} - D_4 w_{12} \\ \delta_3 w_6 - B_7 w_{13} \\ \sigma_1 w_{13} - B_8 w_{14} \\ \sigma_2 w_{13} - B_9 w_{15} \\ \gamma_1 w_8 + \omega_1 w_{10} + \omega_2 w_{11} + \omega_3 w_{12} + \gamma_2 w_{14} - D_8 w_{16} \\ -A_2^* w_7 - A_3 w_8 - A_4 w_9 - A_5 w_{13} - A_6 w_{14} - A_7 w_{15} - \mu_m w_{17} \\ A_2^* w_7 + A_3 w_8 + A_4 w_9 + A_5 w_{13} + A_6 w_{14} + A_7 w_{15} - B_5 w_{18} \\ \nu_1 w_{18} - \mu_m w_{19} \\ -C_2 w_{10} - C_3 w_{11} - C_4 w_{12} - C_5 w_{13} - C_6 w_{14} - C_7 w_{15} - \mu_z w_{20} \\ C_2 w_{10} + C_3 w_{11} + C_4 w_{12} + C_5 w_{13} + C_6 w_{14} + C_7 w_{15} - D_5 w_{21} \\ \nu_2 w_{21} - \mu_z w_{22} \end{pmatrix} = 0.$$

From the result of the product $J(E^0, \beta_3^*)\bar{w}$, we will take $w_5 = w_7 = 1 > 0$ so that the other terms can be easily obtained in terms of w_5 as follows;

$$w_6 = w_{13} = w_{14} = w_{15} = 0$$

$$w_1 = \frac{\theta[D_2D_3D_4\gamma_1\epsilon_1 w_7 + B_3D_3\omega_1D_4D_6w_5 + B_3D_2D_4\omega_2D_7w_5 + B_3D_3\omega_3\psi D_6w_5]}{A_8B_2D_2D_3D_4D_8},$$

$$w_2 = \frac{\rho_1\theta[D_2D_3D_4\gamma_1\epsilon_1 w_7 + B_3D_3\omega_1D_4D_6w_5 + B_3D_2D_4\omega_2D_7w_5 + B_3D_3\omega_3\psi D_6w_5]}{\tau_1 A_8B_2D_2D_3D_4D_8} - \frac{A_9\nu_1[A_2B_3B_4 + A_3\epsilon_1B_4 + A_4\epsilon_2B_3]w_7}{\tau_1\mu_mB_3B_4B_5} - \frac{A_{10}D_1w_5}{\tau_1C_1}$$

$$w_3 = \frac{\rho_2\theta[D_2D_3D_4\gamma_1\epsilon_1 w_7 + B_3D_3\omega_1D_4D_6w_5 + B_3D_2D_4\omega_2D_7w_5 + B_3D_3\omega_3\psi D_6w_5]}{\tau_1 A_8B_2D_2D_3D_4D_8} - \frac{C_8\nu_1[A_2B_3B_4 + A_3\epsilon_1B_4 + A_4\epsilon_2B_3]w_7}{\tau_1\mu_mB_3B_4B_5} - \frac{C_9D_1w_5}{\tau_1C_1}$$

$$w_4 = \frac{B_2 w_7}{\delta_1}, \quad w_8 = \frac{\epsilon_1 w_7}{B_3}, \quad w_9 = \frac{\epsilon_2 w_7}{B_4}, \quad w_{10} = \frac{D_6 w_5}{D_2}, \quad w_{11} = \frac{D_7 w_5}{D_3}, \quad w_{12} = \frac{\psi D_6 w_5}{D_2 D_4}$$

$$w_{16} = \frac{D_2 D_3 D_4 \gamma_1 \epsilon_1 w_7 + B_3 D_3 \omega_1 D_4 D_6 w_5 + B_3 D_2 D_4 \omega_2 D_7 w_5 + B_3 D_3 \omega_3 \psi D_6 w_5}{B_2 D_2 D_3 D_4 D_8},$$

$$w_{17} = \frac{-[A_2 B_3 B_4 + A_3 \epsilon_1 B_4 + A_4 \epsilon_2 B_3] w_7}{\mu_m B_3 B_4}, \; w_{18} = \frac{[A_2 B_3 B_4 + A_3 \epsilon_1 B_4 + A_4 \epsilon_2 B_3] w_7}{B_3 B_4 B_5},$$

$$w_{19} = \frac{\nu_1 [A_2 B_3 B_4 + A_3 \epsilon_1 B_4 + A_4 \epsilon_2 B_3] w_7}{\mu_m B_3 B_4 B_5}, w_{20} = \frac{-[C_2 D_3 D_4 D_6 + C_3 D_2 D_4 D_7 + C_4 \psi D_3 D_6] w_5}{\mu_z D_2 D_3 D_4},$$

$$w_{21} = \frac{\mu_z D_1 w_5}{C_1 \nu_2}, \quad w_{22} = \frac{D_1 w_5}{C_1}.$$

Likewise, the left eigenvectors corresponding to $\bar{v} J(E^0, \beta_3^*)$ now becomes;

$$\bar{v} J(E^0, \beta_3^*) = \begin{pmatrix} -v_1 A_8 + v_2 \rho_1 + v_3 \rho_2 \\ -v_2 \tau_1 \\ -v_3 \tau_1 \\ -v_4 B_1 + v_7 \delta_1 \\ -v_5 D_5 + v_{10} D_6 + v_{11} D_7 \\ -v_6 B_6 + v_{13} \delta_3 \\ -v_7 B_2 + v_8 \epsilon_1 + v_9 \epsilon_2 - v_{17} A_2^* + v_{18} A_2^* \\ -v_8 B_3 + v_{16} \gamma_1 - v_{17} A_3 + v_{18} A_3 \\ v_4 \phi_1 - v_9 B_4 - v_{17} A_4 + v_{18} A_4 \\ -v_{10} D_2 + v_{12} \psi + v_{16} \omega_1 - v_{20} C_2 + v_{21} C_2 \\ -v_{11} D_3 + v_{16} \omega_3 - v_{20} C_3 + v_{21} C_3 \\ -v_{12} D_4 + v_{16} \omega_2 - v_{20} C_4 + v_{21} C_4 \\ -v_{13} B_7 + v_{14} \sigma_1 + v_{15} \sigma_2 - v_{17} A_5 + v_{18} A_5 - v_{20} C_5 + v_{21} C_5 \\ -v_{14} B_8 + v_{16} \gamma_2 - v_{17} A_6 + v_{18} A_6 - v_{20} C_6 + v_{21} C_6 \\ -v_{15} B_9 - v_{17} A_7 + v_{18} A_7 - v_{20} C_7 + v_{21} C_7 \\ v_1 \theta - v_{16} B_8 \\ -v_{17} \mu_m \\ -v_{18} B_5 + v_{19} \nu_1 \\ -v_2 a_2 - v_3 a_3 + v_4 A_1 - v_{19} \mu_m \\ -v_{20} \mu_z \\ -v_{21} D_5 + v_{22} \nu_2 \\ -v_2 c_1 - v_3 c_2 + v_5 C_1 - v_{22} \mu_z \end{pmatrix} = 0.$$

Taking $v_4 = v_5 > 0$, we will have the following $v_1 = v_2 = v_3 = v_{16} = v_{17} = v_{20} = 0$,

$$v_6 = \frac{A_1 B_9 D_5 \nu_1 \mu_z v_4 \delta_3 [A_6 \sigma_1 + A_7 \sigma_2] + [A_1 A_5 D_5 \nu_1 \mu_z v_4 + C_1 C_5 B_5 \nu_2 \mu_m v_5] B_8 B_9 \delta_3}{\mu_m \mu_z B_5 B_6 B_7 B_8 B_9 D_5},$$

$$v_7 = \frac{v_4 B_1}{\delta_1}, \; v_8 = \frac{v_4 A_1 A_3 \nu_1}{\mu_m \gamma_1 B_5}, v_9 = \frac{(A_1 A_4 \nu_1 + \mu_m B_5 \phi_1) v_4}{\mu_m B_4 B_5}, \; v_{10} = \frac{\nu_2 C_1 (C_4 \psi + C_2 D_4) v_5}{\mu_z D_2 D_4 D_5},$$

$$v_{11} = \frac{v_5 C_1 C_3 \nu_2}{\mu_z D_3 D_5}, \; v_{12} = \frac{v_5 C_1 C_4 \nu_2}{\mu_z D_4 D_5},$$

$$v_{13} = \frac{A_1 B_9 D_5 \nu_1 \mu_z v_4 [A_6 \sigma_1 + A_7 \sigma_2] + [A_1 A_5 D_5 \nu_1 \mu_z v_4 + C_1 C_5 B_5 \nu_2 \mu_m v_5] B_8 B_9}{\mu_m \mu_z B_5 B_7 B_8 B_9 D_5},$$

$$v_{14} = \frac{v_4 A_1 A_6 \nu_1}{\mu_m B_5 B_8} + \frac{v_5 C_1 C_6 \nu_2}{\mu_z D_5 B_8}, \; v_{15} = \frac{v_4 A_1 A_7 \nu_1}{\mu_m B_5 B_9} + \frac{v_5 C_1 C_7 \nu_2}{\mu_z D_5 B_9}, \; v_{18} = \frac{v_4 A_1 \nu_1}{\mu_m B_5},$$

$$v_{19} = \frac{v_4 A_1}{\mu_m}, \quad v_{21} = \frac{v_5 C_1 \nu_2}{\mu_z D_5}, \quad v_{22} = \frac{v_5 C_1}{\mu_z}.$$

Also, let

$$f(X(t)) = \begin{bmatrix} f_1 \\ f_2 \\ f_3 \\ f_4 \\ f_5 \\ f_6 \\ f_7 \\ f_8 \\ f_9 \\ f_{10} \\ f_{11} \\ f_{12} \\ f_{13} \\ f_{14} \\ f_{15} \\ f_{16} \\ f_{17} \\ f_{18} \\ f_{19} \\ f_{20} \\ f_{21} \\ f_{22} \end{bmatrix} = \begin{bmatrix} \Lambda_h + \theta x_8 - (\rho_1 + \rho_2 + \tau_1)x_1 \\ \rho_1 x_1 - (\alpha_1\beta_1 x_{19} + \alpha_2\eta_1 x_{22} + \tau_1)x_2 \\ \rho_2 x_1 - (\alpha_1\beta_2 x_{19}\Phi + \alpha_2\eta_1 x_{22} + \tau_1)x_3 \\ \alpha_1\beta_1 x_{19}x_2 + \alpha_1\beta_2 x_{19}\Phi x_3 + \phi_1 x_9 + \phi_2 x_{15} - \alpha_2\eta_1 x_{22}x_4 - (\delta_1 + \tau_1)x_4 \\ \alpha_2\eta_1 x_{22}(x_2 + x_3) - \alpha_1\beta_1 x_{19}x_5 - ((\chi_1 + \chi_2)\delta_2 + \tau_1)x_5 \\ \alpha_1\beta_1 x_{19}x_5 + \alpha_2\eta_1 x_{22}x_4 - (\delta_3 + \tau_1)x_6 \\ \delta_1 x_4 - \alpha_2\eta_1 x_{22}x_7 - (\tau_1 + \tau_2 + \epsilon_1 + \epsilon_2)x_7 \\ \epsilon_1 x_7 - (\gamma_1 + \tau_1 + \tau_2)x_8 \\ \epsilon_2 x_7 - (\phi_1 + \tau_1 + \tau_2)x_9 \\ \delta_2\chi_1 x_5 - \alpha_1\beta_1 x_{19}x_{10} - (\tau_1 + \tau_3 + \psi + \omega_1)x_{10} \\ \delta_2\chi_2 x_5 - \alpha_1\beta_1 x_{19}x_{11} - (\tau_1 + \tau_3 + \omega_3)x_{11} \\ \psi x_{10} - (\tau_1 + \tau_3 + \omega_2)x_{12} \\ \alpha_1\beta_1 x_{19}(x_{10} + x_{11}) + \alpha_2\eta_1 x_{22}x_7 + \delta_3 x_6 - (\tau_1 + \tau_4 + \sigma_1 + \sigma_2)x_{13} \\ \sigma_1 x_{13} - (\tau_1 + \tau_4 + \gamma_2)x_{14} \\ \sigma_2 x_{13} - (\tau_1 + \tau_4 + \phi_2)x_{15} \\ \gamma_1 x_8 + \gamma_2 x_{14} + \omega_1 x_{10} + \omega_2 x_{12} + \omega_3 x_{11} - (\tau_1 + \theta)x_{16} \\ \Lambda_{mv} - \alpha_1(\beta_3 x_7 + \beta_4 x_8 + \beta_5 x_9 + \beta_6 x_{13} + \beta_7 x_{14} + \beta_8 x_{15})x_{17} - (\kappa_1 x_{23} + \mu_m)x_{17} \\ \alpha_1(\beta_3 x_7 + \beta_4 x_8 + \beta_5 x_9 + \beta_6 x_{13} + \beta_7 x_{14} + \beta_8 x_{15})x_{17} - (\nu_1 + \mu_m)x_{18} \\ \nu_1 x_{18} - \mu_m x_{19} \\ \Lambda_{zv} - \alpha_2(\eta_2 x_{10} + \eta_3 x_{11} + \eta_4 x_{12} + \eta_5 x_{13} + \eta_6 x_{14} + \eta_7 x_{15})x_{20} - (\kappa_2 x_{24} + \mu_z)x_{20} \\ \alpha_2(\eta_2 x_{10} + \eta_3 x_{11} + \eta_4 x_{12} + \eta_5 x_{13} + \eta_6 x_{14} + \eta_7 x_{15})x_{20} - (\nu_2 + \mu_z)x_{21} \\ \nu_2 x_{21} - \mu_z x_{22} \end{bmatrix}.$$

From Castillo-Chavez and Song [9] theorem on bifurcation analysis using the Center Manifold theorem, we require some second partial derivatives of the $f_i^{'}s$ with respect to the $x_i^{'}s$ for $i = 1, 2, 3, ..., 22$. From $f(X)$, we can only obtain second partial derivatives which are not zeroes from $f_2, f_3, f_4, f_5, f_6, f_7, f_{10}, f_{11}, f_{13}, f_{17}$,
f_{18}, f_{20} and f_{21}. Therefore, expanding q and r in terms of $\bar{v}$, the left-eigenvectors and $\bar{w}$, the right-eigenvectors with the associated derivatives of f, we will have

$$q = \sum_{k,i,j}^{n} v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j} = 2w_{19}\alpha_1\beta_1[v_4 w_2 + v_6 w_5 + v_{13}w_{10} + v_{13}w_{11} - v_5 w_5 - v_{10}w_{10} - v_{11}w_{11}]$$
$$+ 2v_4 w_3 w_{19}\alpha_1\beta_2\Phi + 2w_{22}\alpha_2\eta_1[v_5 w_2 + v_5 w_3 + v_6 w_4 + v_{13}w_7 - v_4 w_4 - v_7 w_7] + 2v_{18}w_7 w_{17}\alpha_1\beta_3$$
$$+ 2v_{18}w_8 w_{17}\alpha_1\beta_4 + 2v_{18}w_9 w_{17}\alpha_1\beta_5 + 2v_{21}w_{10}w_{20}\alpha_2\eta_2 + 2v_{21}w_{11}w_{20}\alpha_2\eta_3 + 2v_{21}w_{12}w_{20}\alpha_2\eta_4,$$

and

$$r = \sum_{k,i}^{n} v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_i \partial \psi} = v_{18}w_7\alpha_1 x_{17} + v_{18}w_{17}\alpha_1 x_7$$
$$= \frac{v_4 w_7 \alpha_1[B_4 A_1 \nu_1 \delta_1 x_{17} - B_5(B_1 B_2 B_4 - \epsilon_2\delta_1\phi_1)R_{0m}^2 x_7]}{\mu_m B_4 B_5 \delta_1}.$$

The endemic equilibrium of the coinfection model will be locally asymptotically stable if $q < 0$ and $r > 0$. In this case, a forward bifurcation occurs. But, if otherwise then backward bifurcation occurs

and the endemic equilibrium will not be locally asymptotically stable. In the analysis, we saw that the values of both the left and right-eigenvectors, $\bar{v}$ and $\bar{w}$ could not be determined except assuming that two left eigenvectors (v_4, v_5) or two right-eigenvectors, (w_5, w_7) are positive and then obtain others in terms of them. This is an indication also that the model may not have a unique endemic equilibrium.

For case 2, the product of the Jacobian matrix $J(E^0, \eta_2^*)$ with the right and left-eigenvectors will yield similar results as in case one since the only change required is to substitute η_2 with η_2^* in C_2 and obtain $r = \sum_{k,i}^{n} v_k w_i \dfrac{\partial^2 f_k(0,0)}{\partial x_i \partial \eta_2^*}$.

In this case, the equation for r becomes

$$r = v_{21}w_{10}\frac{\partial^2 f_{21}(0,0)}{\partial x_{10}\partial \eta_2^*} + v_{21}w_{20}\frac{\partial^2 f_{21}(0,0)}{\partial x_{20}\partial \eta_2^*} = \frac{\alpha_2 w_5 v_5[C_1 D_6 \nu_2 x_{20} - D_2 D_5 x_{10} R_{0z}^2]}{\mu_z D_2 D_5}.$$

The endemic equilibrium of the co-infection model in this case will be locally asymptotically stable if $q < 0$ and $r > 0$. The parameter $r > 0$ if $C_1 D_6 \nu_2 x_{20} > D_2 D_5 x_{10} R_{0z}^2$. Hence, the occurence of backward bifurcation or not depends on the signs of q and r as shown above. □

3.5 Global stability of the coinfection endemic equilibrium

The global stability of the coinfection endemic equilibrium is ascertained by means of Lyapunov function as demonstrated in the works of Mpande et al. (2015) and Ozioko et al. (2024).

Consider the Lyapunov function

$$\mathcal{V} = \frac{1}{2}\bar{X}^2, \tag{7}$$

where $\bar{X} = (S_h + S_{hu} + S_{hv} + E_{hm} + E_{hz} + E_{mz} + I_{hm} + I_{hmT} + I_{hmU} + I_{hzS} + I_{hzA} + I_{hzT} + I_{hmz} + I_{hmzT} + I_{hmzU} + R_h + S_{mv} + E_{mv} + I_{mv} + S_{zv} + E_{zv} + I_{zv})$.

Then,

$$\frac{d\mathcal{V}}{dt} = \bar{X}\dot{\bar{X}}, \tag{8}$$

where $\dot{\bar{X}} = (\dot{S}_h + \dot{S_{hu}} + \dot{S_{hv}} + \dot{E}_{hm} + \dot{E}_{hz} + \dot{E}_{hmz} + \dot{I}_{hm} + \dot{I}_{hmT} + \dot{I}_{hmU} + \dot{I}_{hzS} + \dot{I}_{hzA} + \dot{I}_{hzT} + \dot{I}_{hmz} + \dot{I}_{hmzT} + \dot{I}_{hmzU} + \dot{R}_h + \dot{S}_{mv} + \dot{E}_{mv} + \dot{I}_{mv} + \dot{S}_{zv} + \dot{E}_{zv} + \dot{I}_{zv})$.

Equation (8) becomes

$$\begin{aligned}
\frac{d\mathcal{V}}{dt} &= \bar{X}(\Lambda_h - \tau_1(S_h + S_{hu} + S_{hv} + E_{hm} + E_{hz} + E_{hmz} + I_{hm} + I_{hm} + I_{hmT} + I_{hmU} + I_{hzS} \\
&+ I_{hzA} + I_{hzT} + I_{hmz} + I_{hmzT} + I_{hmzU} + R_h) - \tau_2(I_{hm} + I_{hmT} + I_{hmU}) \\
&- \tau_3(I_{hzS} + I_{hzA} + I_{hzT}) - \tau_4(I_{hmz} + I_{hmzT} + I_{hmzU}) + \Lambda_{mv} - \mu_m(S_{mv} + E_{mv} + I_{mv}) \\
&- \kappa_1 M_{SIT} S_{mv} + \Lambda_{mv} - \mu_z(S_{zv} + E_{zv} + I_{zv}) - \kappa_2 Z_{SIT} S_{zv}) \\
&= \bar{X}(\Lambda_h - \tau_1 N_h - \tau_2(I_{hm} + I_{hmT} + I_{hmU}) - \tau_3(I_{hzS} + I_{hzA} + I_{hzT}) \\
&- \tau_4(I_{hmz} + I_{hmzT} + I_{hmzU}) + \Lambda_{mv} - \mu_m N_{mv} - \kappa_1 M_{SIT} S_{mv} + \Lambda_{mv} - \mu_z N_{zv} - \kappa_2 Z_{SIT} S_{zv})
\end{aligned}$$

Clearly, $0 \leq N_h \leq \frac{\Lambda_h}{\tau_1}$, $0 \leq N_{mv} \leq \frac{\Lambda_{mv}}{\mu_m}$ and $0 \leq N_{zv} \leq \frac{\Lambda_{zv}}{\mu_z}$ as shown in section 4.1.3, which means that $\tau_1 N_h \leq \Lambda_h$, $\mu_m N_{mv} \leq \Lambda_{mv}$ and $\mu_z N_{zv} \leq \Lambda_{zv}$. Using $\tau_1 N_h = \Lambda_h$, $\mu_m N_{mv} = \Lambda_{mv}$ and $\mu_z N_{zv} = \Lambda_{zv}$, then

$$\frac{d\mathcal{V}}{dt} = -(\tau_2(I_{hm} + I_{hmT} + I_{hmU}) + \tau_3(I_{hzS} + I_{hzA} + I_{hzT}) + \tau_4(I_{hmz} + I_{hmzT} + I_{hmzU}) + \kappa_1 M_{SIT} S_{mv} + \kappa_2 Z_{SIT} S_{zv})\bar{X} < 0$$

This shows that the co-infection endemic endemic equilibrium point is globally asymptotically stable since $\frac{d\mathcal{V}}{dt} < 0$. The global stability of the endemic equilibrium indicates that the co-infection will persist in the system at a stable level irrespective of the size of the initial infected populations. It also means that the number of infected humans with malaria and zika can never be zero. It also means that the system will converge to the co-infection endemic equilibrium point with time irrespective of the initial conditions.

4 Results and Discussion

In this section, we investigate the effects of the various controls employed in the system on the populations studied. The effects of the individual controls as well as when they are combined are analyzed. The simulation is shown in Figures 2–12.

Table 2: Parameters, Values and Sources

Parameters	Values	Sources	Parameters	Values	Sources
Λ_h	100	Assumed	β_3	0.0044	Fatmawati et al. (2021)
Λ_{mv}	100	Assumed	β_4	0.0022	Assumed
Λ_{zv}	100	Assumed	β_5	0.0044	Collins and Duffy (2022)
Φ	0.0125	Duru et al. (2024)	β_6	0.0022	Assumed
θ	0.0146	Onah et al. (2019)	β_7	0.0044	Assumed
ρ_1	0.65	Duru et al. (2024)	β_8	0.0022	Assumed
ρ_2	0.28	Duru et al. (2024)	ω_1	0.1429	Andayani et al. (2019)
γ_1	0.25	Onah et al. (2019)	ω_2	0.1667	Lamwong and Pongsumpun (2018)
γ_2	0.111	Duru et al. (2024)	ω_3	0.118	Dantas et al. (2017)
τ_3	0.0003	Duru et al. (2024)	χ_1	0.31	Assumed
τ_4	0.0006454	Duru et al. (2024)	χ_2	0.62	Assumed
ϕ_1	0.13	Assumed	α_1	0.4	Onah et al. (2019)
α_2	0.1	Assumed	β_1	0.034	Amaoh-Mensah et al. (2018)
ϕ_2	0.1	Assumed	τ_1	0.00004	Bonyah and Okosun (2016)
β_2	0.013	Anyanwu et al. (2021)	τ_2	0.00032338	Nwankwo and Okuonghae (2019)
η_1	0.0009	Lamwong and Pongsumpun (2018)	η_2	0.07	Lamwong and Pongsumpun (2018)
η_3	0.07	Lamwong and Pongsumpun (2018)	η_4	0.05	Assumed
η_5	0.03	Assuned	η_6	0.02	Assumed
η_7	0.03	Assumed	ψ	0.85	Andayani et al. (2019)
ϵ_1	0.62	Duru et al. (2024)	ϵ_2	0.31	Assumed
σ_1	0.72	Duru et al. (2024)	σ_2	0.18	Duru et al. (2024)
κ_1	0.25	Duru et al. (2024)	κ_2	0.25	Duru et al. (2024)
ν_1	0.1	Onah et al. (2019)	δ_1	0.0833	Duru et al. (2024)
ν_2	0.1	Anyanwu et al. (2021)	δ_2	0.125	Andayani et al. (2019)
M_{SIT}	500	Assumed	δ_3	0.0833	Duru et al. (2024)
Z^*_{SIT}	500	Assumed	μ_m	0.0556	Lamwong and Pongsumpun (2018)
μ_z	0.0556	Lamwong and Pongsumpun (2018)			

4.1 Effects of treatment

The effect of employing treatment only is shown in Figure 2. Here, the populations of the coinfectious humans with both diseases reduced with treatment as compared to when there was no treatment. This shows that employing treatment of infectious persons is critical in the control of infectious

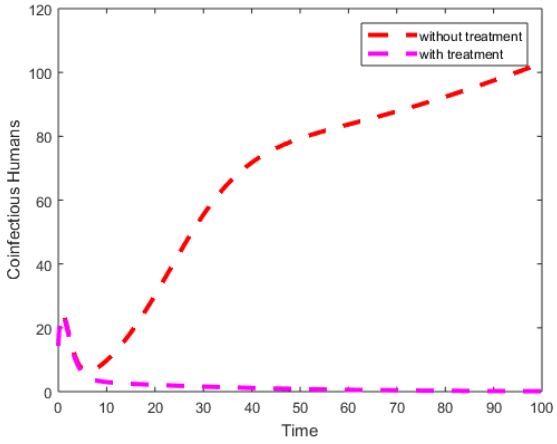
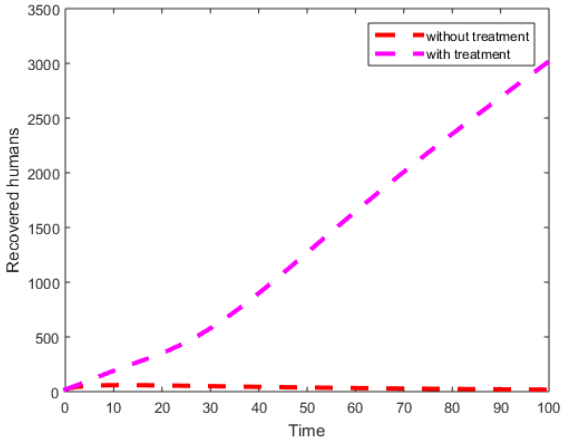


Figure 2: (i) Coinfectious humans



(ii) Recovered humans under treatment

diseases. As the infectious classes are treated, the population of recovered humans increases as shown in Figure 3(ii). The increase is because treatment increases the rate of recovery and reduces the time spent in the infectious class.

4.2 Effects of vaccination

The effect of vaccination is shown in Figures 3. In this Figure, vaccination was seen to reduce the population of susceptible humans as shown in Figure 3(i).

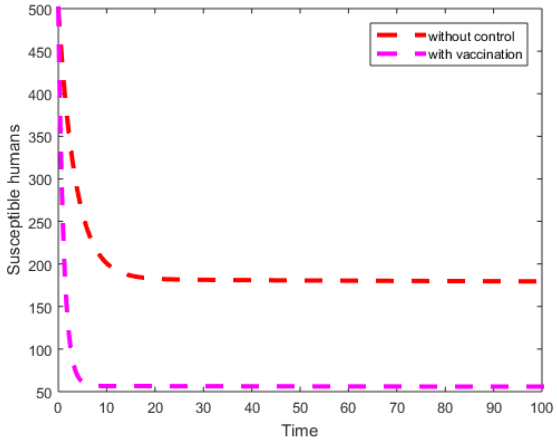
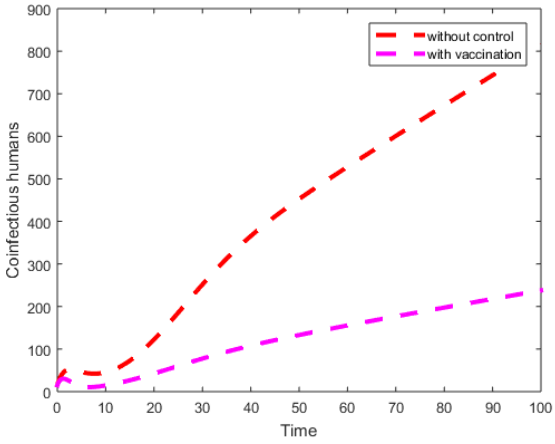


Figure 3: (i) Susceptible humans



(ii) Coinfectious humans

This is because vaccination protects more humans from malaria thus reducing the susceptible

population of humans. The population of coinfectious humans (Figure 3(ii)) also reduced as more people are protected from malaria by vaccination.

4.3 Effects of SIT

The effects of employing only sterile insect technique are shown in Figures 4. In this Figure, the infectious mosquito populations were reduced under the application of SIT. The reduction in the population of the mosquitoes reducing the number of possible contacts and infection with humans. This underlines how powerful sterile insect technology is in controlling the malaria and zika virus disease.

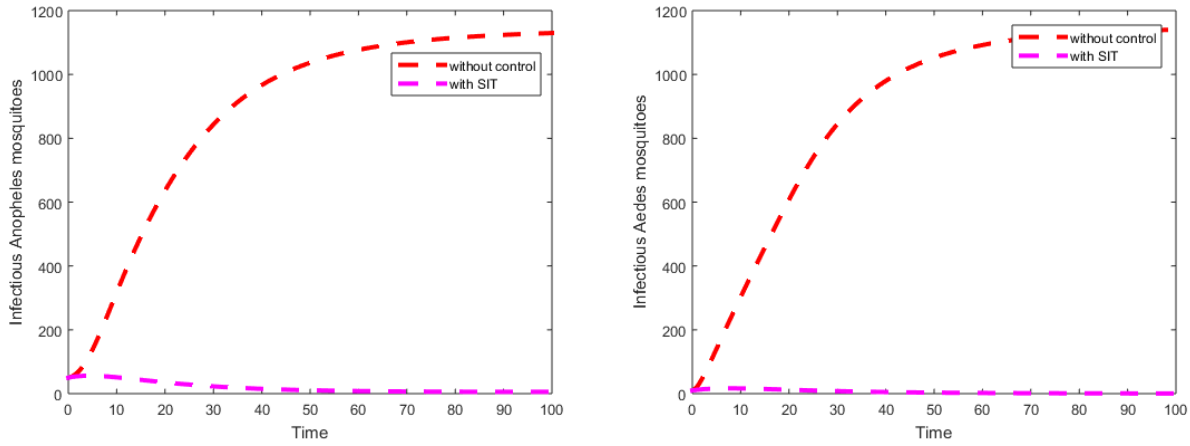


Figure 4: Infectious Anopheles and Infectious Aedes mosquitoes

4.4 Effects of treatment and vaccination only

The effects of treatment and vaccination in the system are shown in Figures 5 – 6. In these Figures, vaccination and treatment were seen to reduce the population coinfectious human significantly but the mosquito population reduced slightly. The slight reduction in the mosquito population was because the control measures employed here were not directly on the mosquito population hence does not affect the population of the susceptible mosquitoes.

4.5 Effects of treatment and SIT only

The effects of treatment and SIT are shown in Figures 7–8. Employing treatment and sterile insect technique as a control measure reduce coinfectious population significantly as well as the infectious mosquito populations.

The reduction of the infectious mosquitoes is due to the reduction in the susceptible mosquito population thus reducing the coinfectious human population as the number of mosquitoes that can infect humans are reduced.

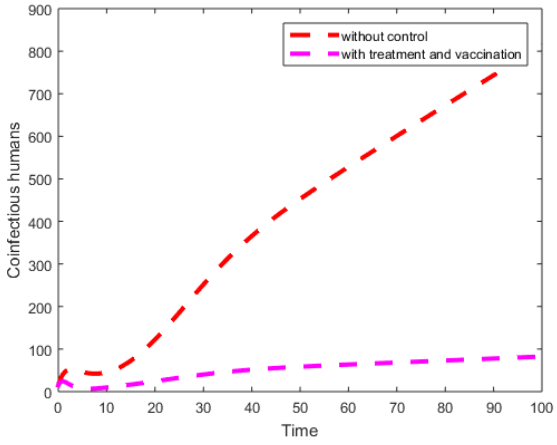


Figure 5: Coinfectious humans under treatment and vaccination only

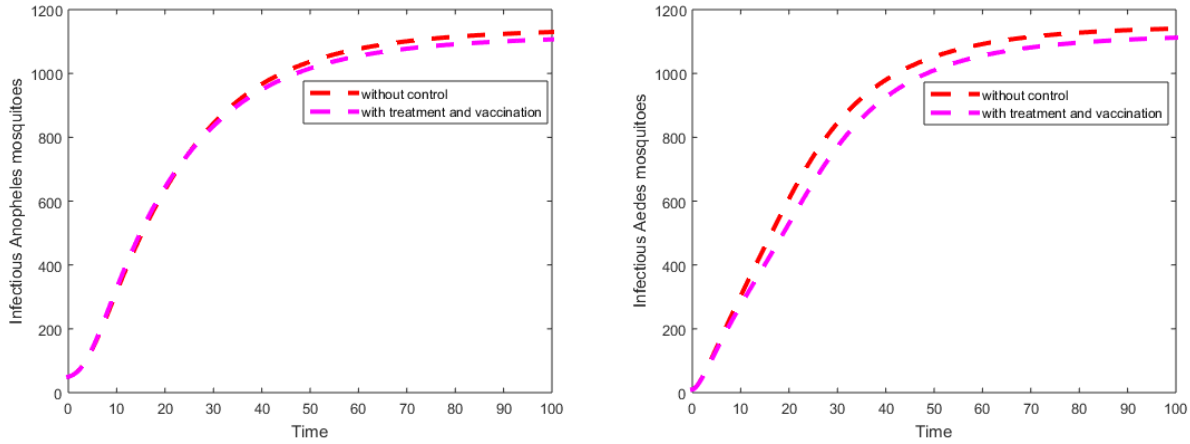


Figure 6: Infectious Anopheles and Infectious Aedes mosquitoes

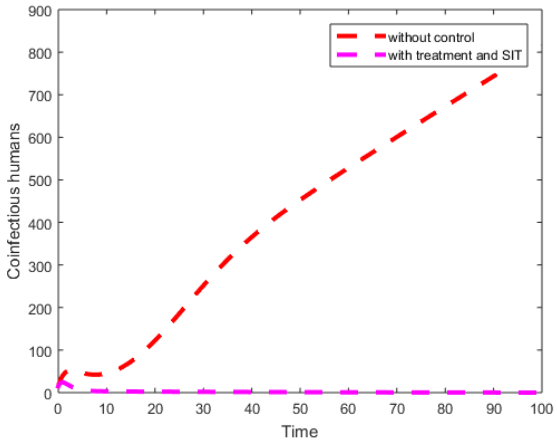


Figure 7: Coinfectious humans under treatment and SIT only

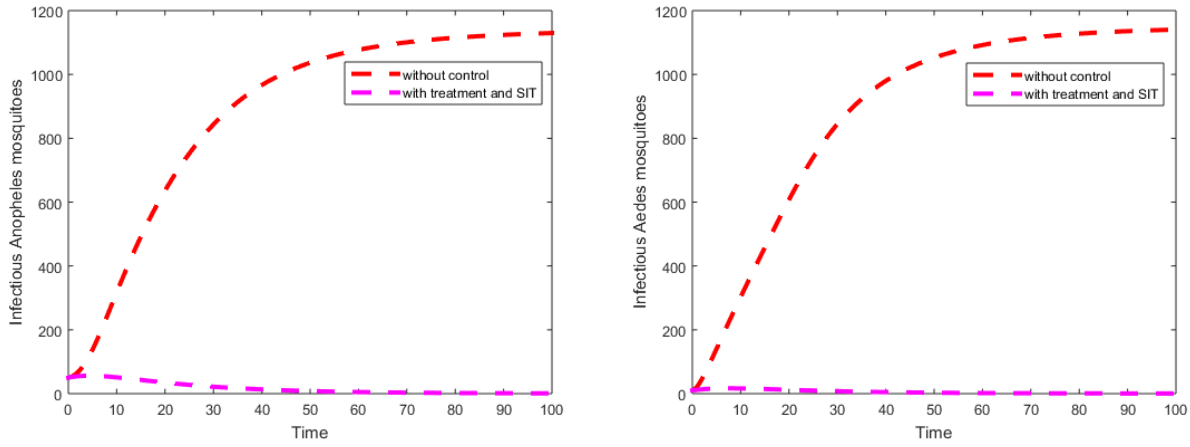


Figure 8: Infectious Anopheles and Infectious Aedes mosquitoes

4.6 Effects of vaccination and SIT only

The effects of vaccination and SIT are shown in Figures 9 – 10. In these Figures, vaccination and SIT were seen to reduce the population of coinfectious humans as shown in Figure 9. The population of the infectious mosquitoes were also reduced in this case showing that SIT and vaccination offers significant option in reducing the infectious human populations.

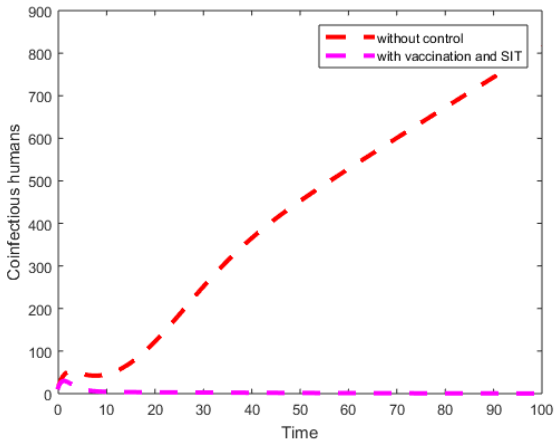


Figure 9: Coinfectious humans under vaccination and SIT only

4.7 Effects of treatment, SIT and vaccination

Figures 11 – 12 show the effect of employing the three controls which are treatment, vaccination and use of SIT to control the vectors. The simulation also showed that the combination of these three control measures performed relatively better when compared to using only one or two control measures. In this case, combining the three controls ensured that the three different populations had a measure employed to help control them. This will ensure rapid and efficient control of the

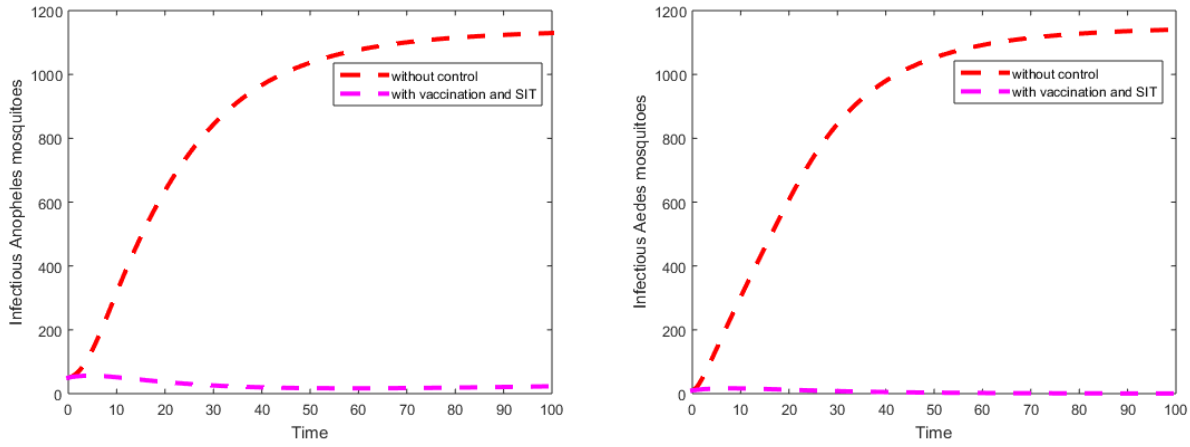


Figure 10: Infectious Anopheles and Infectious Aedes mosquitoes

diseases. Hence, we suggest that the three controls should be incorporated simultaneously in the fight against malaria and zika virus disease. The analyses performed in this work has shown the

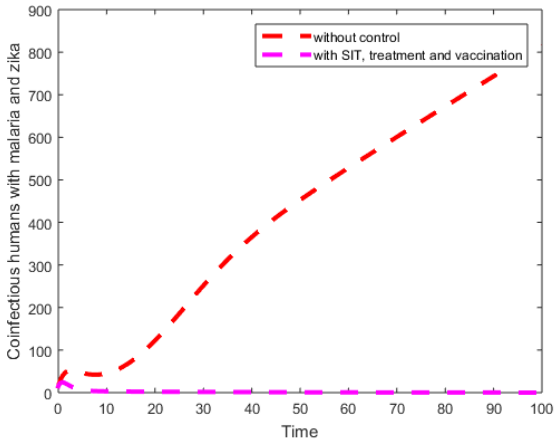


Figure 11: Coinfectious humans under treatment, SIT and vaccination

importance of vaccination against infectious diseases such as malaria. It was shown that in the presence of vaccination in all cases where it was employed in the simulation, the population of infectious and coinfectious humans reduced drastically. The reduction is because the number of humans susceptible to the disease was reduced significantly by vaccination. This underlines the importance of vaccination and the need for health practitioners to keep encouraging people to embrace vaccination. Efforts should be made to ensure that every barrier against vaccination such as religious and ethnic sentiments as well as some conspiracy theories are overcome. Also, people should be educated that refusing to be vaccinated does not only put them at risk but those around them thereby causing a global health burden. The importance of treatment was equally shown in this work. Treatment of infectious humans helped significantly to improve the rate of recovery and reduce the time infectious humans spent being sick. This ensures that there are few infectious

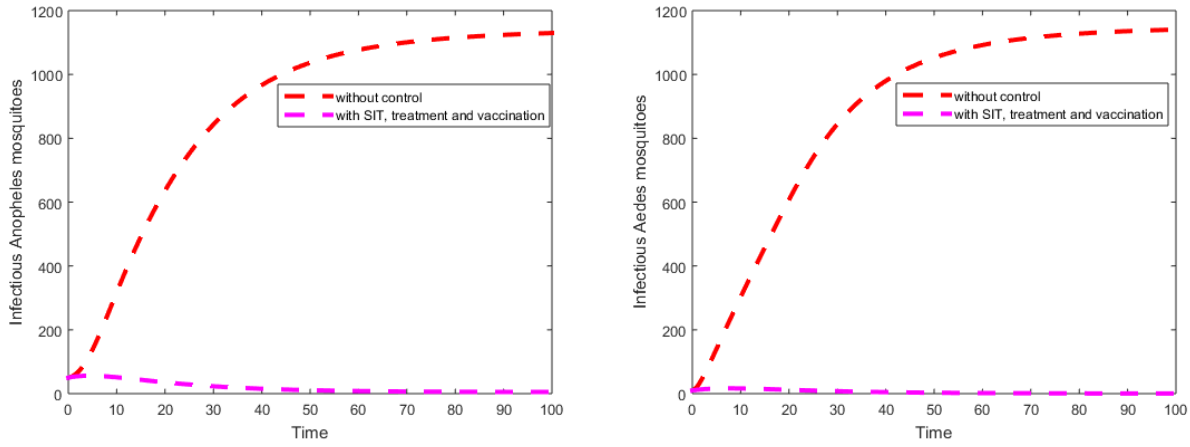


Figure 12: Infectious Anopheles and Infectious Aedes mosquitoes

humans who can infect the mosquitoes and renew the cycle of the spread of the diseases. Thus refusing to be treated when sick is not an option that should be entertained. Moreover, as proposed in Duru et al. (2024), using sterile insect technique as a control measure against the continuous growth of mosquitoes was shown to be highly successful.

5 Conclusion

In this work, the coinfection model proposed by Duru et al. (2024) was studied to provide more insight into the dynamics of the coinfection and its control. The model incorporated vaccination, treatment and sterile insect technique as control measures against the spread of malaria, zika virus disease and their coinfection. The model was shown to be well-posed epidemiologically by proving that the solutions to the system are always positive and bounded. Then, the existence of an endemic equilibrium was also shown and using bifurcation analysis, the conditions for having forward or backward bifurcation were obtained. Also, the global stability of the coinfection endemic equilibrium was shown by means of Lyapunov method. Furthermore, numerical simulations were performed to show the effects of the various controlled adopted in the work. The results showed that each of the three controls contributed to the reduction of the coinfectious population. This shows that malaria, zika virus disease and their coinfection will be effectively controlled by ensuring that intervention efforts should not only be focused on humans nor mosquitoes seperately but simultaneously on both humans and mosquito population. In future studies, the performance of different incidence functions can also be employed and compared to the results obtained here. Furthermore, different controls such as physical and chemical procedures can also be incorporated into the system to see if better results will be obtained.

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Conflict of Interest

The authors declare that they have no conflicts of interest.

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