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Mathematical Modeling of the Coinfection Dynamics of Malaria-Toxoplasmosis in the Tropics

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Summary

Coinfection by *Plasmodium* species and *Toxoplasma gondii* in humans is widespread, with its endemic impact mostly felt in the tropics. A mathematical model is formulated as a first-order nonlinear system of ordinary differential equations to describe the coinfection dynamics of malaria-toxoplasmosis in the mainly human and feline susceptible host population in tropical regions. Comprehensive mathematical techniques are applied to show that the model system is bounded, positive and realistic in an epidemiological sense. Also, the basic reproduction number (R_{omt}) of the coinfection model is obtained. It is shown that if $R_{omt} < 1$, the model system at its malaria-toxoplasmosis absent equilibrium is both locally and globally asymptotically stable. The impact of toxoplasmosis and its treatment on malaria, and vice versa, is studied and analyzed. Sensitivity analysis was performed to investigate the impact of the model system parameters on the reproduction number of the transmission of malaria-toxoplasmosis coinfection. Simulations and graphical illustrations were made to validate the results obtained from the theoretical model.

Key words: malaria-toxoplasmosis, reproduction number, local stability, global stability, sensitivity analysis

1. Introduction

Malaria-toxoplasmosis coinfection occurs as a result of the simultaneous infection of a single individual by different causative agents with multiple pathogens, which possess different strains of the disease. Malaria is a deadly infectious disease that poses a threat globally and is highly endemic in sub-Saharan Africa and Asia. According to the World Health Organization (WHO) fact sheet from 2017 and the latest world report in November 2018 (WHO, 2018), it was estimated that $435,000$ individuals died of malaria,

and that the tropical regions of Africa accounted for 92 and 93 percent of malaria cases and deaths respectively. Among the African countries, Nigeria had the highest share of cases with 25 percent, while Uganda had the lowest with 4 percent. Malaria is transmitted through the blood bite of an infected female *Anopheles* mosquito, where *Plasmodium* parasites released by infected mosquitos are deposited in the human body. Out of the five parasites that cause malaria, *P.falciparum* and *P.vivax* are the most dangerous. Clinical symptoms associated with malaria include fever, headache, severe anaemia, infant mortality, morbidity, etc. Malaria can be treated and controlled with Artemisinin Combination Therapy (ACT) drugs, the use of insecticide-treated nets, prophylaxis and other means.

In turn, toxoplasmosis is an apicomplexian parasitic disease caused by *Toxoplasma gondii* (Montoya and Liesenfeld, 2004). It affects more than one-third of the world's population, the tropics being one of the major endemic regions. The primary reservoir of toxoplasmosis is cats (*Felis catus*) (Felicia et al., 2004), although other animals such as dogs, sheep, etc. are capable of carrying the disease. Toxoplasmosis is contracted through the oral ingestion of oocysts in vegetables, food, water and undercooked meat. Infection also occurs through contact with cats and cat faeces (Frenkel et al., 1989). Symptoms of toxoplasmosis infection include ocular problems, fetal death, fatigue, still birth, etc. (Ambrose-Thomas and Petersen, 2013; Avelino et al., 2014). Toxoplasmosis can be treated and prevention can be achieved through proper hygienic procedure.

Coinfections of malaria-toxoplasmosis have been epidemiologically proven and detected in the tropics (Nyamongo et al., 2015; Simon et al., 2007). Mathematical models have been formulated by many researchers, and the earliest malaria model was formulated by Ross (1911). Recent publications by Traore and Sangare (2018), Berretta and Capasso (1986), Beretta et al. (2018) and Gimba and Bala (2017) have proved valuable in this study. Also, mathematical models have been developed and analyzed to describe toxoplasmosis in humans and the zoonotic host. Gonzalez-Parra et al. (2009, 2010) studied the model of toxoplasmosis disease transmission in human and cat host populations. Sullivan (2012) also worked on within-host toxoplasmosis invasion dynamics, while Kelting (2015) investigated the stability and the dynamics of transfer between cats and the environment. In addition, several authors have formulated mathematical models describing the dynamics of coinfectious diseases. The works of Okosun and Makinde (2014), Bakare and Nwozo (2017), Mensah et al. (2018), Hanif (2018), Gumel et al.

(2009), Mutua and Vaidya (2015), and Fatmawati and Tasman (2016) on coinfection dynamics have proved very effective in mathematical model formulation and in the analysis performed in this study. Furthermore, the basic reproduction number is an important epidemic threshold used in determining the average number of secondary infections when an infected individual is introduced into an entirely susceptible host population (Anderson and May, 1999; Diekmann et al., 2010; Hethcote, 1994; Van den Driessche and Watmough, 2002). Established theorems and mathematical techniques from Cull (1986), Esteva-Peralta and Velasco-Hernandez (2002) and Shahu et al. (2013) have been useful in analyzing the stabilities of the model system in this work.

Having reviewed all of the aforementioned articles, it is the author's belief that this article presents a new model formulated to describe the transmission dynamics of malaria-toxoplasmosis coinfection in the susceptible human and feline population in the tropics. In this work, the co-endemic deterministic model is qualitatively and quantitatively analyzed. In Section 2, the coinfection model is formulated and analyzed to show that the coinfection model is positive, bounded and realistic in an epidemiological sense. Also, the equilibrium solutions with malaria-toxoplasmosis absent and present were obtained. In Section 3, the reproduction number R_{omt} is obtained, and the impact of toxoplasmosis on malaria, and vice versa, is investigated. Section 4 deals with the local and global stability analysis of the model at the equilibrium solutions with malaria-toxoplasmosis absent and present. Section 5 describes the performance of sensitivity analysis to identify the parameters that have the greatest or the least influence on the reproduction number R_{omt}. Section 6 contains numerical simulations, graphical illustrations and conclusions.

2. Model Formulation

The model considered in this section consists of sub-populations subdividing the total population N_h into susceptible individuals S_h; individuals infected with malaria only I_m; individuals infected with toxoplasmosis only I_t; individuals infected with malaria-toxoplasmosis only C_{mt}; and individuals who have recovered from malaria and toxoplasmosis – R_m and R_t respectively. There is an assumption in this model that the coinfected individuals recover either from malaria or toxoplasmosis, but not both simultaneously, such that $N_h = S_h + I_m + I_t + C_{mt} + R_m + R_t$. Also, the total *Anopheles* mosquito

population N_v is subdivided into susceptible and infected mosquitos, S_v and I_v, such that $N_v = S_v + I_v$. The total cat population N_c is subdivided into susceptible and infected cats, S_c and I_c, such that $N_c = S_c + I_c$. The concentration of oocysts in the environment population is denoted by J_e.

The sub-population of individuals susceptible to malaria-toxoplasmosis infection is recruited into the host population at a constant per capita rate M_h, while the quantities ϵR_t and αR_m increase the sub-population, where ϵ and α denote the rate at which individuals who have recovered from malaria and toxoplasmosis lose their immunities to toxoplasmosis and malaria infections by becoming susceptible. The susceptible sub-population is further decreased by the forces of infection (effective infectious contact rate) denoted by the quantity $(\beta_0 + \beta_*)S_h$. Hence the rate of change of the sub-population of susceptible individuals is given by

$$\frac{dS_h}{dt} = M_h - \beta_0 S_h - \beta_* S_h - \mu_1 S_h + \epsilon R_t + \alpha R_m. \tag{1}$$

The sub-population of individuals infected with malaria only is increased by the forces of infection (effective infectious contact rate) denoted by the quantity $\beta_0 S_h$ and decreased by $\beta_* I_m$. The sub-population of individuals infected with malaria only is reduced by the quantity $(\psi + \mu_1 + \phi)I_m$, where ψ denotes the recovery rate of individuals infected with malaria, while ϕ and μ_1 respectively denote the mortality induced by malaria infection and natural mortality. Thus, the rate of change of the sub-population of individuals infected with malaria only is given by

$$\frac{dI_m}{dt} = \beta_0 S_h - \beta_* I_m - (\psi + \mu_1 + \phi)I_m. \tag{2}$$

Also, the sub-population of individuals infected with toxoplasmosis only is increased by the quantity $\beta_* S_h$ and decreased by the quantity $\beta_0 C_{mt}$, where β_* and β_0 are forces of infection (effective infectious contact rate). It is further reduced by the quantity $(\omega + \mu_1 + \eta)I_t$, where ω is the recovery rate of individuals infected with toxoplasmosis, while μ_1 and η denote the natural mortality and mortality induced by toxoplasmosis. Hence, the rate of change of the sub-population of individuals infected with toxoplasmosis only is given by

$$\frac{dI_t}{dt} = \beta_* S_h - \beta_0 C_{mt} - (\omega + \mu_1 + \eta)I_t \tag{3}$$

The sub-population of individuals coinfected with malaria-toxoplasmosis is increased by the quantities $\beta_0 C_{mt}$ and $\beta_* I_m$ and reduced by the quantity

$(\delta+\mu_1+\eta+\phi)C_{mt}$, where δ is the recovery rate of individuals from malaria-toxoplasmosis coinfection. Hence, the rate of change of the sub-population of individuals infected with malaria-toxoplasmosis is given by

$$\frac{dC_{mt}}{dt} = \beta_0 C_{mt} + \beta_* I_m - (\delta + \mu_1 + \eta + \phi)C_{mt}. \tag{4}$$

The sub-population of individuals who have recovered from malaria is generated by progression from the malaria-infected to the recovered sub-population at the rate ψ, and reduced by α, which is the rate at which immunity to malaria infection is lost, thereby causing malaria-infected individuals to become susceptible after recovery, while the natural death rate is denoted μ_1. The sub-population is further increased by the quantity $f\delta C_{mt}$, where $f\delta$ denotes the rate at which coinfected individuals recover from malaria only. Hence, the rate of change of the sub-population of individuals who have recovered from malaria is given by

$$\frac{dR_m}{dt} = \psi I_m - (\alpha + \mu_1)R_m + f\delta C_{mt}. \tag{5}$$

The sub-population of individuals who have recovered from toxoplasmosis is increased by the quantity ωI_t, which represents progression from the sub-population of individuals infected with toxoplasmosis to the sub-population of individuals who have recovered from toxoplasmosis, at the rate ω. This group is decreased by the quantity $(\epsilon + \mu_1)R_t$, where ϵ denotes the loss of immunity to toxoplasmosis after recovery as individuals become susceptible again, and μ_1 denotes the natural mortality rate. This sub-population is further increased by the quantity $(1 - f)\delta C_{mt}$, which represents the fraction of individuals coinfected with malaria-toxoplasmosis who have recovered from toxoplasmosis only. Hence, the rate of change of the sub-population of individuals who have recovered from toxoplasmosis is given by

$$\frac{dR_t}{dt} = \omega I_t - (\epsilon + \mu_1)R_t + (1 - f)\delta C_{mt} \tag{6}$$

The susceptible sub-population of *Anopheles* mosquitos is increased by the recruitment rate of mosquitos denoted by M_v and decreased by the quantity $(\beta_k + \mu_v)S_v$, where β_k denotes the effective infectious contact rate and μ_v denotes the natural mortality rate of mosquitos. Hence, the rate of change of the sub-population of susceptible mosquitos is given by

$$\frac{dS_v}{dt} = M_v - \beta_k S_v - \mu_v S_v. \tag{7}$$

The sub-population of infected *Anopheles* mosquitos is increased by the quantity $\beta_k S_v$, where β_k is the effective infectious contact rate, and is decreased by the natural death of infected mosquitos at the rate μ_v. Hence, the rate of change of the sub-population of infected mosquitos is given by

$$\frac{dI_v}{dt} = \beta_k S_v - \mu_v I_a. \tag{8}$$

The sub-population of susceptible cats is increased by the recruitment rate M_c and decreased by the quantity $(\beta_g + \mu_c)I_c$, where β_g is the force of infection (effective contact rate) and μ_c denotes the natural death rate of susceptible cats. Hence, the rate of change of the sub-population of susceptible cats is given by

$$\frac{dS_c}{dt} = M_c - \beta_g S_c - \mu_c S_c. \tag{9}$$

The sub-population of infected cats is increased by the quantity $\beta_g S_c$, where β_g is the effective infectious contact rate, and decreased by the natural death of infected cats at the rate μ_c. Hence, the rate of change of the sub-population of infected cats is given by

$$\frac{dI_c}{dt} = \beta_g S_c - \mu_c I_c. \tag{10}$$

The sub-population of oocyst infestation in the environment is increased by the quantity $\pi(I_t + \theta_f C_{mt})$, where π is the rate of contribution of toxoplasmosis-infected individuals to the environment through unhygienic practices and θ_f is the modification parameter that takes into account the relative infectiousness of individuals who are asymptomatically coinfected with malaria-toxoplasmosis when exposed to toxoplasmosis. The subpopulation is further decreased by the quantity $\mu_c J_c$, where μ_c is the rate of natural degradation of infested oocysts present in the environment. Hence, the rate of change of this sub-population is given by

$$\frac{dJ_e}{dt} = \pi(I_t + \theta_f C_{mt}) - \mu_e J_e. \tag{11}$$

Equation (1) takes account of effective infectious contact between a susceptible individual (S_h) and an infected mosquito (I_v), which yields

$$\beta_0 = \frac{\beta_h a I_v}{N_h}. \tag{12}$$

Here, the mosquito biting rate is denoted β_h, and a is the probability of transmission of malaria in a susceptible individual per bite.

Also, there is the effective infectious contact rate between a susceptible individual (S_h), oocyst-infested environment (J_e) and infected cat (I_c) with the quantity ($\beta_* S_h$). Susceptible individuals come into infectious contact with the oocyst-infested environment by ingesting oocysts in vegetables, foods, water sources, etc. Also, susceptible individuals come into infectious contact with infected cats reared and present in the host environment, generated by the quantity

$$\beta_* = \Big(\frac{v_o J_e}{K_m + J_e} + I_c\Big). \tag{13}$$

Here, v_o is the ingestion rate of oocysts shed by cats present in vegetables, foods and undercooked meat by susceptible individuals, and K_m denotes the concentration of infected oocysts in the environment.

Also, there is effective infectious contact between an individual infected with malaria (I_m) and β_*, which generates the quantity $\beta_* I_m$.

In addition, there is effective infectious contact between individuals coinfected with malaria-toxoplasmosis (C_{mt}) and β_*, which generates the quantity $\beta_* C_{mt}$.

Furthermore, there is effective infectious contact between susceptible and infected mosquitos, which generates the quantity $\beta_k S_v$, where

$$\beta_k = \frac{\beta_h a(I_m + kC_{mt})}{N_h} \tag{14}$$

Here, k is the modification parameter that accounts for the probability of infection of a mosquito from an individual with a coinfection of malaria-toxoplasmosis relative to the probability of acquiring infection from an individual with malaria only.

Moreover, there is effective infectious contact between susceptible cats, infected cats and the oocyst-infested environment, which generates the quantity $\beta_g S_c$, where

$$\beta_g = \frac{\beta_*(I_m + \theta C_{mt})}{N_h} \tag{15}$$

Here, θ is a modification parameter that takes into account the relative infectiousness of an asymptomatically infected individual with toxoplasmosis exposed to malaria.

The underlying assumptions behind the construction of the model are as follows;

- There exist birth and mortality rates.
- Malaria- or toxoplasmosis-infected individuals recover after treatment.
- Mortality-related cases of toxoplasmosis are small in number compared with mortality-related cases of malaria, i.e., ($\eta << \phi$).
- There is a loss of immunity to the disease, thereby making treated individuals susceptible to the co-disease again.
- Mosquitos and cats do not recover from malaria and toxoplasmosis infections.

Having incorporated all of the state variables, parameters and the assumptions involved in the model formulation, the malaria-toxoplasmosis coinfection model is given by

$$\begin{aligned}
\frac{dS_h}{dt} &= M_h - \beta_0 S_h - \beta_* S_h - \mu_1 S_h + \epsilon R_t + \alpha R_m,\\
\frac{dI_m}{dt} &= \beta_0 S_h - \beta_* I_m - (\psi + \mu_1 + \phi) I_m,\\
\frac{dI_t}{dt} &= \beta_* S_h - \beta_0 C_{mt} - (\omega + \mu_1 + \eta) I_t,\\
\frac{dC_{mt}}{dt} &= \beta_0 C_{mt} + \beta_* I_m - (\delta + \mu_1 + \eta + \phi) C_{mt},\\
\frac{dR_m}{dt} &= \psi I_m - (\alpha + \mu_1) R_m + f\delta C_{mt},\\
\frac{dR_t}{dt} &= \omega I_t - (\epsilon + \mu_1) R_t + (1 - f)\delta C_{mt},\\
\frac{dS_v}{dt} &= M_v - \beta_k S_v - \mu_v S_v,\\
\frac{dI_v}{dt} &= \beta_k S_v - \mu_v I_v,\\
\frac{dS_c}{dt} &= M_c - \beta_g S_c - \mu_c S_c,\\
\frac{dI_c}{dt} &= \beta_g S_c - \mu_c I_c,\\
\frac{dJ_e}{dt} &= \pi(I_t + \theta_f C_{mt}) - \mu_e J_e.
\end{aligned} \tag{16}$$

subject to the initial conditions $S_h(0) = S_{ho}$, $I_m(0) = I_{mo}$, $I_t(0) = I_{to}$, $C_{mt}(0) = C_{mto}, R_m(0) = R_{mo}, R_t(0) = R_{to}, S_v(0) = S_{vo}, I_v(0) = I_{vo}, S_c(0) = S_{co}, I_c(0) = I_{co}, J_e(0) = J_{eo}$.

2.1. Analysis of the Model System

In this section, it is aimed to show that the model system (16) is positive, bounded, realistic and meaningful in an epidemiological and a mathematical sense.

2.1.1. Positivity of the Model System

To show that the model is positive, all solutions of (1) with nonnegative initial data remain nonnegative for all positive times, i.e., $t > 0$.

Theorem 1. Assume that all of the parameters involved in (16) are positive constants. The nonnegative solutions of state variables $(S_h(t), I_m(t), I_t(t), C_{mt}(t), R_m(t), R_t(t), S_v(t), I_v(t), S_c(t), I_c(t), J_e(t))$ exist for all state variables with nonnegative initial data, i.e., $S_h(0) = S_{ho} \geqslant 0$, $I_m(0) = I_{mo} \geqslant 0$, $I_t(0) = I_{to} \geqslant 0$, $C_{mt}(0) = C_{mto} \geqslant 0$, $R_m(0) = R_{mo} \geqslant 0, R_t(0) = R_{to} \geqslant 0, S_v(0) = S_{vo} \geqslant 0, I_v(0) = I_{vo} \geqslant 0, S_c(0) = S_{co} \geqslant 0, I_c(0) = I_{co} \geqslant 0, J_e(0) = J_{eo} \geqslant 0$ for all $t > 0$.

2.1.2. Boundedness and Invariant Region

Theorem 2. All solutions of $(S_h(t), I_m(t), I_t(t), C_{mt}(t), R_m(t), R_t(t), S_a(t), I_a(t), S_c(t), I_c(t), J_e(t))$ in the model system (16) are bounded.

2.1.3. Equilibrium Solutions

The equilibrium solutions of the model system (16) are investigated to analyze the model system's asymptotic behavior. The malaria-toxoplasmosis model system is made static, i.e., it obtains time-independent solutions. The model system (16) has two equilibrium solutions, namely, the malaria-toxoplasmosis absent equilibrium solution, given by

$$Q^0 = (S_h^0, I_m^0, I_t^0, C_{mt}^0, R_m^0, R_t^0, S_a^0, I_a^0, S_c^0, I_c^0, J_e^0) = \Big(\frac{M_h}{\mu_1}, 0, 0, 0, 0, 0, \frac{M_v}{\mu_v}, 0, \frac{M_c}{\mu_c}, 0, 0\Big). \tag{17}$$

and the malaria-toxoplasmosis present equilibrium solution, at $S_h^* = I_m^* = I_t^* = C_{mt}^* = S_a^* = I_a^* = S_c^* = I_c^* = J_e^* \neq 0$, given by

$$S_h^* = \frac{\alpha R_t^* + \epsilon R_m^* + M_h}{\beta_0 + \mu_1 + \beta_*}, \quad I_m^* = \frac{\beta_0 S_h^*}{\beta_* + \psi + \mu_1 + \phi}, \quad I_t^* = \frac{\beta_* S_h^* S_c^* - \beta_0 C_{mt}^*}{\omega + \mu_1 + \eta}$$

$$C_{mt}^* = \frac{\beta_* I_m^*}{\beta_0 + \delta + \mu_1 + \eta + \phi}, \quad R_m^* = \frac{\psi I_m^*}{-\delta f + \alpha + \mu - 1},$$

$$R_t^* = \frac{(\delta f - f) R_m^* + \omega I_t^*}{\epsilon + \mu_1}, \quad S_v^* = \frac{M_v}{\beta_k - \mu_v}, \quad I_v^* = \frac{\beta_k S_v^*}{\mu_v},$$

$$S_c^* = \frac{M_c}{\beta_g + \mu_c}, \quad I_c^* = \frac{\beta_g S_c^*}{\mu_c}, \quad J_e^* = \frac{\pi(I_t^* + \theta C_{mt}^*)}{\mu_e} \tag{18}$$

3. Basic Reproduction Number

The next generation matrix method (Diekmann et al., 2010) is employed to obtain R_{omt}. Say, $\dot{x} = f(x)$, where the components $f_i(x) = F_i(x) - V_i(x)$ for $i = 1, \cdots, n$. Then $F_i(x)$ is the rate of appearance of new infections in compartment i, while $V_i^-(x) - V_i^+(x)$, with $V_i^+(x)$ the rate of transfer of individuals into compartment i by any other means, and $V_i^-(x)$ is the rate of transfer out of compartment i, such that

$$F = \begin{pmatrix} 0 & 0 & 0 & \beta_0 S_h & 0 & 0 \\ 0 & 0 & 0 & 0 & \beta_* S_h & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \psi & 0 & 0 & 0 & 0 & 0 \\ 0 & \omega & 0 & 0 & 0 & 0 \\ 0 & \pi & \pi\theta & 0 & 0 & 0 \end{pmatrix}, \tag{19}$$

$$V = \begin{pmatrix} m_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & m_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & m_3 & 0 & 0 & 0 \\ 0 & 0 & f\delta & m_4 & 0 & 0 \\ 0 & 0 & (1-f)\delta & 0 & m_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & m_6 \end{pmatrix}, \tag{20}$$

and

$$V^{-1} = \begin{pmatrix} \frac{1}{m_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{m_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{m_3} & 0 & 0 & 0 \\ 0 & 0 & -\frac{f\delta}{m_3 m_4} & \frac{1}{m_4} & 0 & 0 \\ 0 & 0 & \frac{(1-f)\delta}{m_3 m_5} & 0 & \frac{1}{m_5} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{m_6} \end{pmatrix}. \tag{21}$$

Thus, the matrix product of F and V^{-1} is given by

$$FV^{-1} = \begin{pmatrix} 0 & 0 & -\frac{\beta_0 M_h f\delta}{\mu_1 m_3 m_4} & \frac{\beta_0 M_h}{\mu_1 m_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_* M_h}{\mu_1 m_5} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{\psi}{m_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\omega}{m_2} & 0 & 0 & 0 & 0 \\ 0 & \frac{\pi}{m_2} & \frac{\pi\theta}{m_3} & 0 & 0 & 0 \end{pmatrix}. \tag{22}$$

The values R_{om} for malaria and R_{ot} for toxoplasmosis are thus given by

$$R_{om}^2 = \frac{m_1 m_4 \psi \beta_0 M_h}{m_1 \mu_1 m_4} \tag{23}$$

and

$$R_{ot}^2 = \frac{m_2 m_6 \pi \omega \beta_* M_h}{m_2 m_6 \mu_1}. \tag{24}$$

Therefore, the reproduction number R_{omt} of the malaria-toxoplasmosis model (16) is given by

$$R_{omt} = \sqrt{\frac{m_1 m_4 \psi \beta_0 M_h^2 m_2 m_6 \pi \omega \beta_*}{m_1 m_2 m_4 m_6 \mu_1^2}}. \tag{25}$$

and

$$R_{omt}^2 = \frac{m_1 \mu_1 m_4 \psi \beta_0 M_h^2 m_2 m_6 \pi \omega \beta_*}{m_1 m_2 m_4 m_6 \mu_1^2}. \tag{26}$$

where $m_1 = (\psi + \mu_1 + \phi)$, $m_2 = (\omega + \mu_1 + \eta)$, $m_3 = (\delta + \mu_1 + \eta + \phi)$, $m_4 = \mu_v$, $m_5 = \mu_c$, $m_6 = \mu_e$.

3.1. Investigating the Impact of Toxoplasmosis on Malaria and Vice Versa

The impact of toxoplasmosis on malaria can be analyzed by expressing R_{om} in terms of R_{ot}. From (23), μ_1 is solved to obtain

$$\frac{R_{om}^2 m_1 m_4}{m_1 m_4 \psi \beta_0 M_h} = \mu_1. \tag{27}$$

If $m_1 m_4 = Q_1$ and $\psi \beta_0 M_h = Q_2$, substituting (27) into (24) yields

$$R_{ot} = \sqrt{\frac{m_2 m_6 \omega \pi \beta_* M_h}{m_2 m_6 Q_1 R_{om}^2} . \frac{1}{Q_1 Q_2}}. \tag{28}$$

Expressing (28) as a partial differential equation of R_{ot} with respect to R_{om} yields

$$\frac{\partial R_{ot}}{\partial R_{om}} = \frac{m_2 \omega \pi \beta_* M_h}{\sqrt{\frac{m_2 \omega \beta_0 M_h}{m_2 Q_1^2 R_{om}^2 Q_2}} m_2 Q_1^2 R_{om}^3 Q_2}. \tag{29}$$

If (29) is greater than 0, then an increment in cases of malaria results in an increase in cases of toxoplasmosis in the susceptible host population. If (29) equals zero, cases of malaria have no effect on the transmission of toxoplasmosis. If (29) is less than zero, an increment in malaria cases results in a decrease in toxoplasmosis cases in the susceptible host population.
Furthermore, the impact of malaria on toxoplasmosis can be analyzed by expressing R_{ot} in terms of R_{om}. From (24), μ_1 is solved to obtain

$$\mu_1 = \frac{m_2 m_5 \omega \pi \beta_* M_h}{R_{ot}^2 m_2 m_5}. \tag{30}$$

Let $Q_3 = m_2 m_5,\ Q_4 = \omega \pi \beta_* M_h$, so that

$$\mu_1 = \frac{Q_3 Q_4}{R_{ot}^2 Q_3}. \tag{31}$$

Substituting (31) into (23) yields

$$R_{om} = \sqrt{\frac{m_1 Q_3 m_4 \psi \beta_0 M_h}{m_1 R_{ot}^2 Q_3^2 Q_4 m_4} . \frac{1}{R_{ot}^2 Q_3}}. \tag{32}$$

Expressing (32) as a partial differential equation of R_{om} with respect to R_{ot} yields

$$\frac{\partial R_{om}}{\partial R_{ot}} = \frac{2m_1\psi\beta_0 M_h}{\sqrt{\frac{m_1\psi\beta_0 M_h}{m_2 R_{ot}^4 Q_4^2} m_2 R_{ot}^5 Q_4^2}}. \tag{33}$$

There is an increase in toxoplasmosis cases, which results in an increase in malaria cases in the susceptible host population whenever (33) is greater than zero. If (33) is equal to 0, toxoplasmosis has no effect on malaria dynamics. If (33) is less than zero, an increase in toxoplasmosis results in a decrease in malaria cases in the host population.

Moreover, the effect of the treatment of malaria on toxoplasmosis is investigated by partially differentiating (33) with respect to the recovery parameter ψ, to give

$$\frac{\partial R_{om}}{\partial \psi} = \frac{1}{2}\frac{m_1\beta_0 M_h}{\sqrt{\frac{m_1\psi\beta_0 M_h}{m_2 R_{ot}^4 Q_4^2}} m_2 R_{ot}^4 Q_4^2}. \tag{34}$$

From (34), R_{om} is a strictly decreasing function of ψ, which implies that the treatment of malaria will have a positive effect on the coinfection dynamics of malaria-toxoplasmosis in the susceptible host population.

4. Stability Analysis of the Model

In this section, the stability analysis of the malaria-toxoplasmosis absent equilibrium of the model is studied with theorems and proofs (see Appendix). The local stability of the malaria-toxoplasmosis absent equilibrium implies that if there is a small disturbance of the model system, that is, if a small number of malaria-toxoplasmosis coinfected individuals are introduced into the host population, then after some time, the model system will return to the malaria-toxoplasmosis equilibrium. If the stability of the model system is also global, no matter what the size of the change, malaria-toxoplasmosis infection will not persist in the host population.

4.1. Local Stability Analysis of Malaria-Toxoplasmosis Absent Equilibrium

Theorem 3. The malaria-toxoplasmosis absent equilibrium solution (17) of (16) is locally asymptotically stable if $R_{omt} < 1$.

4.2. Global Stability Analysis of the Malaria-Toxoplasmosis Absent Equilibrium

Theorem 4. The malaria-toxoplasmosis absent equilibrium is locally asymptotically stable if $R_{otm} < 1$.

5. Sensitivity Analysis

In this section, sensitivity analysis is carried out to show that each parameter in the model considered is sensitive to the prevalence of malaria-toxoplasmosis coinfection. The sensitivity index measures the relative change in a variable with respect to the relative change in the parameters involved. It will be of utmost importance to study the impact of the parameters on the basic reproduction number R_{omt}, determining which increase or decrease it the most, to enable implementation of the proper measures needed to control effectively the spread of malaria-toxoplasmosis.

Definition 1. *The normalized forward sensitivity index of a variable h with respect to parameter z_q is given by $\xi = \frac{\partial h}{\partial z_q} \times \frac{z_q}{h}$ (see Bakare and Nwozo, 2017).*

Definition 2. *The sensitivity and elasticity of the basic reproduction number R_{omt} with respect to β_o are given by $\xi_{\beta_o}^{R_{omt}} = \frac{\partial R_{omt}}{\partial \beta_o} \times \frac{\beta_o}{R_{omt}}$ (see Bakare and Nwozo, 2017)*

Table 1. Numerical values of sensitivity indices

Parameters	Parameter values	Sensitivity to R_{omt}
M_h	100	1.000
β_o	0.0034	0.5000
β_*	0.025	0.5000
η	0.134	0.16066375
ω	0.7	0.83928828
π	0.00598	0.50000
ψ	0.142	0.50000
μ_c	0.00004	1.0000
μ_e	0.002	1.0000
μ_v	0.0000569	1.0000

The positive signs of the sensitivity indices of the parameters of the basic reproduction number show that increases in the values of all of the

parameters lead to an increase in the reproduction number of the disease. The forces of infection parameters β_o, β_k positively increase the reproduction number. This calls for appropriate control strategies to be adopted by public health administrators, in order to control the spread of these two co-endemic diseases in the human and environmental host population.

6. Numerical Simulations

In this section, the parameters used were obtained from the baseline values used in the literature cited.

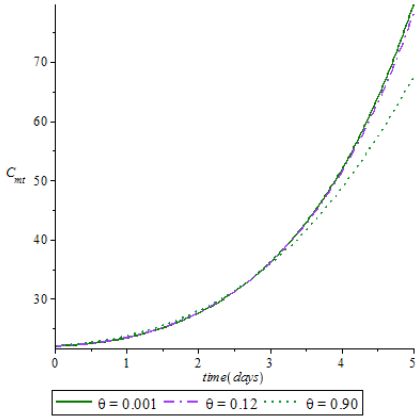

Figure 1. C_{mt} against Time (t) varying θ

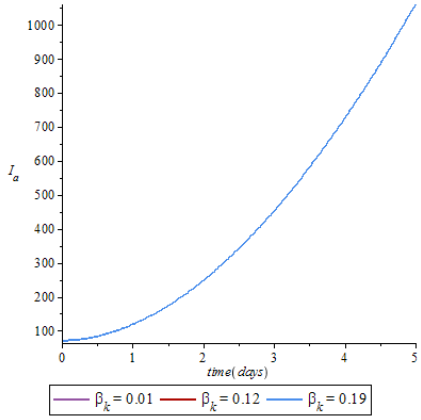

Figure 2. I_a against Time (t) varying β_k

Figure 1: Shows the variation of θ. The graphical behavior shows the increase of individuals infected with toxoplasmosis exposed to malaria. As time increases in the absence of control, more individuals acquire toxoplasmosis infection and exposure to malaria in the presence of mosquitos.

Figure 2: Depicts the graphical behavior of increased cases of infected mosquitos in the absence of control measures, with varying β_k. As time increases, infected mosquitos become predominant in the host population.

Figure 3: Shows the variation of ψ when there is recovery from malaria through treatment with Artemisinin Combination Therapy (ACT), Chloroquine and Artemether. As time increases and more individuals take the drugs, malaria infection becomes low in the host community.

Figure 4: Describes the variation of the force of infection parameter β_0. This leads to an increase in infected mosquitos in the human host environ-

Table 2. Parameter values of model

Parameter Descriptions	Symbols	Values	Source
Per capita human recruitment rate	M_h	100	Bakare and Nwozo (2017)
Contact rate between susceptible humans and mosquitos	β_0	0.034	Okosun and Makinde (2014)
Contact rate between humans, cats and oocyst-infested environment	β_*	0.025	Frenkel et al. (1989)
Natural mortality rate in human population	μ_1	0.00004	Okosun and Makinde (2014)
Immunity loss to malaria after recovery	ϵ	0.7902	Bakare and Nwozo (2017)
Immunity loss to toxoplasmosis after recovery	α	0.11	Avelino et al. (2014)
Rate of recovery from malaria	ψ	0.142	Okosun and Makinde (2014)
Mortality rate related to malaria	ϕ	0.05	Bakare and Nwozo (2017)
Rate of recovery from toxoplasmosis	ω	0.7	Ambrose-Thomas and Petersen (2013)
Mortality rate related to toxoplasmosis	η	0.134	Gonzalez-Parra et al. (2010)
Rate of recovery from malaria-toxoplasmosis coinfection	δ	0.245	Simon et al. (2007)
Rate of recovery from toxoplasmosis in coinfected individuals	$(1-f)$	0.014	Montoya and Liesenfeld (2004)
Rate of recovery from malaria in coinfected individuals	f	0.21	Bakare and Nwozo (2017)
Contact rate between susceptible mosquitos and infected mosquitos	β_k	0.09	Bakare and Nwozo (2017)
Natural mortality rate in mosquitos	μ_v	0.0000569	Bakare and Nwozo (2017)
Contact rate between susceptible and infected cats	β_g	0.015	Gonzalez-Parra et al. (2009)
Natural mortality rate of cats	μ_c	0.00004	Frenkel et al. (1989)
Recruitment rate of mosquitos	M_v	1000	Bakare and Nwozo (2017)
Recruitment rate of cats	M_c	0.576	Frenkel et al. (1989)
Rate of contribution of toxoplasmosis infected to environment	π	0.00598	Gonzalez-Parra et al. (2010)
Rate of natural degradation of oocyst	μ_e	0.002	Gonzalez-Parra et al. (2010)

ment as they come into contact with individuals infected with malaria as time increases.

Figure 5: Shows the variation of π. As time increases in the absence

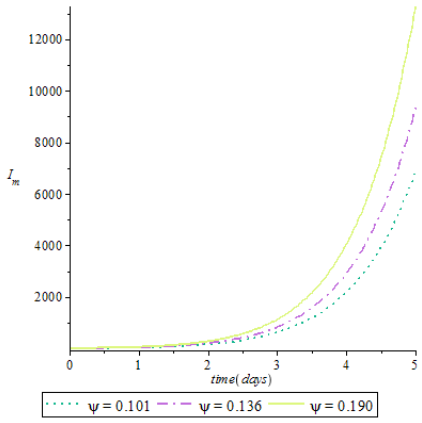

Figure 3. I_m against Time (t) varying ψ

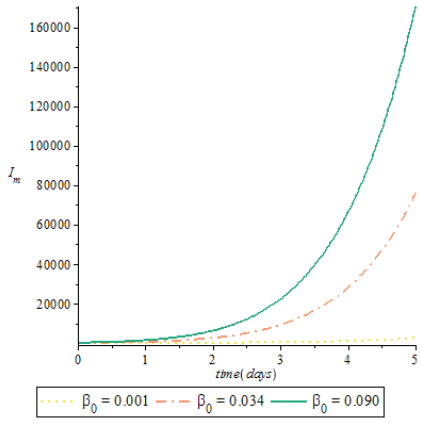

Figure 4. I_m against Time (t) varying β_0

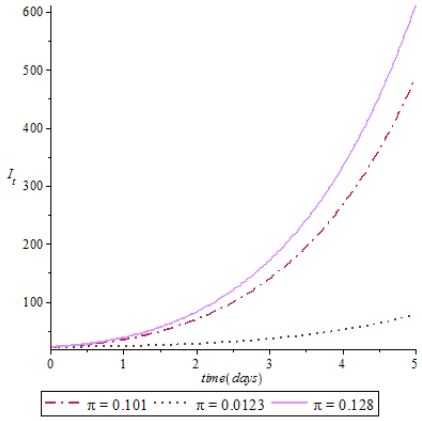

Figure 5. I_t against Time (t) varying π

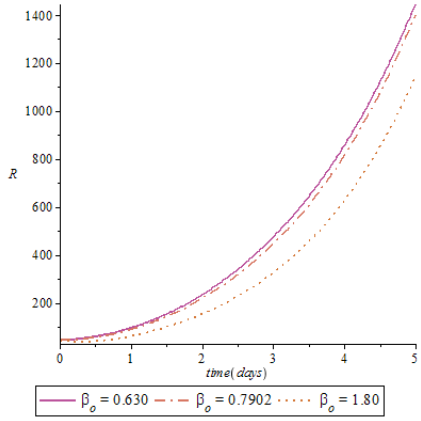

Figure 6. R against Time (t) varying β_0

of control interventions, toxoplasmosis infection increases due to human infectious contribution to the host environment.

Figure 6: Shows the variation of parameter β_o. As time increases, individuals who have undergone treatment recover from the codisease.

Figure 7: Shows the variation of parameter β_k. As time increases, the human environment is saturated with cat oocysts in the absence of control measures. If sanitation is applied, the environmental host is free of infected oocysts.

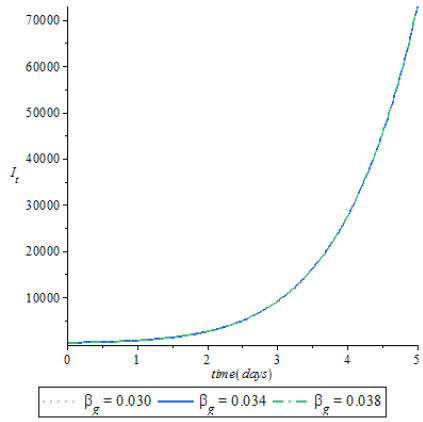

Figure 7. I_t against time(t) varying β_g

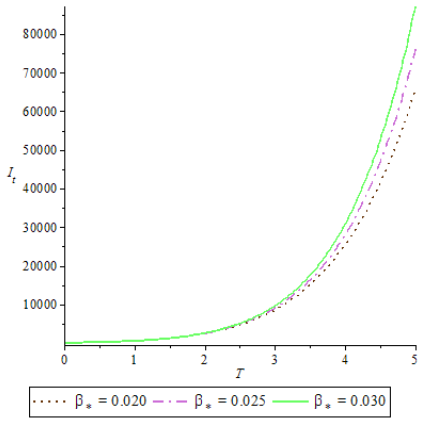

Figure 8. I_t against time(t) varying β_*

Figure 8: Depicts the variation of parameter β_k. As time increases, infection increases due to infectious contact between humans and infected cats.

6.1. Conclusion and Recommendations

The coinfection of malaria-toxoplasmosis is modeled based on a system of nonlinear ordinary differential equations. The model system is shown to be positive, bounded and mathematically well posed. Also, the reproduction number of the codisease is obtained, where the impact of toxoplasmosis on malaria and vice versa is analyzed. It was shown that if $R_{omt} < 1$, malaria-toxoplasmosis becomes absent in the system, and the model system becomes locally and globally asymptotically stable. Furthermore, if $R_{omt} > 1$, coinfection is present and becomes a full-blown epidemic in the absence of control. Sensitivity analysis was performed on the parameters of R_{omt} and gave all positive values, indicating the need for proper optimum medical strategies such as availability of drugs, treated bed nets, disinfectants, hygienic compliance, etc., to minimize and stop the spread of malaria-toxoplasmosis coinfections. This work is recommended to be continued by extending it into an optimal control problem, with age structure, seasonality and climatic factors, etc.

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Appendix

Appendix 1

Considering the first state equation in model system (16),

$$\dot{S}_h = M_h - \beta_0 S_h - \beta_* S_h - \mu_1 S_h + \epsilon R_t + \alpha R_m,$$

$$\dot{S}_h \geqslant M_h - (\beta_0 + \beta_* + \mu_1) S_h.$$

Integrating the equality above with the initial condition $S_h(0) = S_{ho} \geqslant 0$ yields

$$S_h(t) = exp\Big(- \int_0^t (\beta_0(s) + \beta_*(s) + \mu_1) ds \Big) \Big[S_h(0) +$$

$$\int_0^t (M_h + \epsilon R_t(s) + \alpha R_m(s)) * exp\Big(\int_0^s (\beta_0(s) + \beta_*(s) + \mu_1) dc \Big) ds \Big] \geqslant$$

$$\geqslant \Big(- \int_0^t (\beta_0(s) + \beta_*(s) + \mu_1) ds \Big) *$$

$$\int_0^t (M_h + \epsilon R_t(s) + \alpha R_m(s)) * exp\Big(\int_0^s (\beta_0(s) + \beta_*(s) + \mu_1) dc \Big) ds > 0,$$

for all $t > 0$. Following the same procedure for the remaining ten state equations in (16), the following are obtained such that

$$I_m(t) = e^{-(\beta_* - (\psi + \mu_1 + \phi))t} \Big(I_m(0) + \int_0^t \beta_0 S_h(s) e^{(\beta_* - (\psi + \mu_1 + \phi))s} ds \Big) \geqslant$$

$$\geqslant e^{-(\beta_* - (\psi + \mu_1 + \phi))t} \Big(\int_0^t \beta_0 S_h(s) e^{(\beta_* - (\psi + \mu_1 + \phi))s} ds \Big) > 0,$$

$$I_t(t) = e^{-(\omega + \mu_1 + \eta))t} \Big(I_t(0) + \int_0^t \beta_* S_h(s) - \beta_0 C_{mt}(s) e^{(\omega + \mu_1 + \eta)s} ds \Big) \geqslant$$

$$\geqslant e^{-(\omega + \mu_1 + \eta))t} \Big(\int_0^t \beta_* S_h(s) - \beta_0 C_{mt}(s) e^{(\omega + \mu_1 + \eta)s} ds \Big) > 0,$$

$$C_{mt}(t) = e^{-(\beta_0+(\delta+\mu_1+\eta+\phi))t}\Big(C_{mt}(0) + \int_0^t \beta_* I_m(s) e^{((\beta_0+(\delta+\mu_1+\eta+\phi))s} ds\Big)$$

$$\geqslant e^{-(\beta_0+(\delta+\mu_1+\eta+\phi))t}\Big(\int_0^t C_{mt}(s) e^{(\beta_0+(\delta+\mu_1+\eta+\phi))s} ds\Big) > 0,$$

$$R_m(t) = e^{-(\alpha+\mu_1)t}\Big(R_m(0) + \int_0^t e^{(\alpha+\mu_1)s} ds\Big) \geqslant e^{-(\alpha+\mu_1)t}\Big(\int_0^t e^{(\alpha+\mu_1)s} ds\Big) > 0,$$

$$R_t(t) = e^{-(\epsilon+\mu_1)t}\Big(R_t(0) + \int_0^t e^{(\epsilon+\mu_1)s} ds\Big) \geqslant e^{-(\epsilon+\mu_1)t}\Big(\int_0^t e^{(\epsilon+\mu_1)s} ds\Big) > 0,$$

$$S_v(t) = e^{-(\beta_k+\mu_v)t}\Big(S_v(0) + \int_0^t e^{(\beta_k+\mu_v)s} ds\Big) \geqslant e^{-(\beta_k+\mu_v)t}\Big(\int_0^t e^{(\beta_k+\mu_v)s} ds\Big) > 0,$$

$$I_v(t) = e^{-(\mu_v)t}\Big(I_v(0) + \int_0^t e^{(\mu_v)s} ds\Big) \geqslant e^{-(\mu_v)t}\Big(\int_0^t e^{(\mu_v)s} ds\Big) > 0,$$

$$S_c(t) = e^{-(\beta_g+\mu_v)t}\Big(S_c(0) + \int_0^t e^{(\beta_g+\mu_v)s} ds\Big) \geqslant e^{-(\beta_g+\mu_v)t}\Big(\int_0^t e^{(\beta_k+\mu_v)s} ds\Big) > 0,$$

$$I_c(t) = e^{-(\mu_c)t}\Big(I_c(0) + \int_0^t e^{-(\mu_c)s} ds\Big) \geqslant e^{-(\mu_c)t}\Big(\int_0^t e^{-(\mu_c)s} ds\Big) > 0,$$

$$J_e(t) = e^{-(\mu_e)t}\Big(J_e(0) + \int_0^t e^{-(\mu_e)s} ds\Big) \geqslant e^{-(\mu_e)t}\Big(\int_0^t e^{-(\mu_e)s} ds\Big) > 0.$$

Appendix 2

The Jacobian of model system (16) at malaria-toxoplasmosis equilibrium solution (17) is given by

$$J = \begin{bmatrix} -d_1 & 0 & 0 & 0 & \alpha & \epsilon & 0 & 0 & 0 & 0 & 0 \\ 0 & -d_2 & 0 & 0 & 0 & 0 & 0 & \beta_0\left(\frac{M_h}{\mu_1}\right) & 0 & 0 & 0 \\ 0 & 0 & -d_3 & -\beta_0 & 0 & 0 & 0 & 0 & 0 & \beta_*\left(\frac{M_h}{\mu_1}\right) & 0 \\ 0 & \beta_* & 0 & -d_4 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \psi & 0 & f\delta & -d_5 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \omega & (1-f)\delta & 0 & -d_6 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -d_7 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_k & -d_8 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -d_9 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \beta_g & -d_{10} & 0 \\ 0 & 0 & \pi & \pi\theta & 0 & 0 & 0 & 0 & 0 & 0 & -d_{11} \end{bmatrix}, \quad (35)$$

where $d_1 = \mu_1,\ d_2 = -(\psi + \mu_1 + \phi),\ d_3 = (\omega + \mu_1 + \eta),\ d_4 = -(\delta + \mu_1 + \eta + \phi),\ d_5 = (\alpha + \mu_1),\ d_6 = (\epsilon + \mu_1),\ d_7 = (\beta_k + \mu_v),\ d_8 = \mu_v,\ d_9 = (\beta_g + \mu_c),\ d_{10} = \mu_c,\ d_{11} = \mu_e$.
It is however observed that, in the trace determinant plane of (35),

$$T_r(J) = -(d_1 + d_2 + d_3 + d_4 + d_5 + d_6 + d_7 + d_8 + d_9 + d_{10} + d_{11}) < 0 \quad (36)$$

and

$$Det(J) = d_9 d_2 d_4 d_5 d_{10} d_{11} d_3 d_6 d_1 d_7 d_8 > 0, \quad (37)$$

where the characteristic polynomial of (35) is given by

$$\begin{aligned} &(\lambda + d_8)(\lambda + d_7)(\lambda + d_6)(\lambda + d_5)(\lambda + d_3)(\lambda + d_2)(\lambda + d_1)(\lambda + d_{10}) \\ &(\lambda + d_9)(\lambda + d_{11})(1 - R_{otm}). \end{aligned} \quad (38)$$

For (38) to be stable, $1 - R_{otm} > 0$. This implies that, $-R_{otm} > -1$ and $R_{otm} < 1$. Since all of the real part of (35) is negative, (36) and (37) hold. Hence, the malaria-toxoplasmosis absent equilibrium is locally asymptotically stable.

Appendix 3

From the theorem given that

$$\dot{W} = F(W, Y), \quad (39)$$

$$\dot{Y} = G(W, Y), \tag{40}$$

where $W = (S_h, R_m, R_t, S_v, S_c)$ represents the compartments without malaria and toxoplasmosis infections, such that $W \in \Re^{+5}$, and $Y = (I_m, I_t, C_{mt}, I_v, I_c, J_e)$ represents the compartments with malaria and toxoplasmosis infections, such that $Y \in \Re^{+5}$. The malaria-toxoplasmosis absent equilibrium solution is denoted by $E^0 = (W^*, Y^*) = (W^*, 0)$, where $W^* = (\frac{M_h}{\mu_1}, \frac{M_v}{\mu_v}, \frac{M_c}{\mu_c})$. The following conditions hold.

i $\dot{W} = F(W, 0)$, W^* is globally asymptotically stable.

ii $G(W, Y) = D_Y(W^*, 0)Y - \hat{G}(W, Y) \geqslant 0$ for all $(W, Y) \in \Delta$, where Δ is a region where the model system (1) makes epidemiological sense.

where $D_Y G(W^*, 0)$ denotes the Metzler matrix with nonnegative off-diagonal elements.
Therefore,

$$F(W,0) = \begin{pmatrix} M_h - \mu_1 S_h + \epsilon R_t + \alpha R_m \\ -(\alpha + \mu_1) R_m \\ -(\epsilon + \mu_1) R_t \\ M_v - \mu_v S_v \\ M_c - \mu_c S_c \end{pmatrix},$$

and

$$G(W,Y) = \begin{pmatrix} \beta_0 S_h - \beta_* I_m - (\psi + \mu_1 + \phi) I_m \\ \beta_* S_h - \beta C_{mt} - (\omega + \mu_1 + \eta) I_t \\ \beta_0 C_{mt} + \beta_* I_m - (\delta + \mu_1 + \eta + \phi) C_{mt} \\ \beta_k S_v - \mu_v I_v \\ \beta_g - \mu_c I_c \\ \pi(I_t + \theta C_{mt} - \mu_e J_e) \end{pmatrix}.$$

In the absence of malaria-toxoplasmosis disease, it is clear that $G(W, 0) = 0$. Also

$$D_Y G(W^*, 0) = \begin{pmatrix} -m_1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -m_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & m_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -m_4 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -m_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -m_6 \end{pmatrix},$$

where $m_1 = -(\psi + \mu_1 + \phi)$, $m_2 = -(\omega + \mu_1 + \eta)$, $m_3 = -(\delta + \mu_1 + \eta + \phi)$, $m_4 = \mu_v$, $m_5 = -\mu_c$, $m_6 = -\mu_e$, so that

$$\hat{G}(W,Y) =$$

$$\begin{pmatrix} \beta_*(S_h^o - S_h) - \beta_*(I_m^o - I_m) - (\psi + \mu_1 + \phi)(I_m^o - I_m) \\ \beta_*(S_h^o - S_h) - \beta_0(C_{mt}^o - C_{mt}) - (\omega + \mu_1 + \eta)(I_t^o - I_t) \\ \beta_*(C_{mt}^o - C_{mt}) - \beta_*(I_m^o - I_m) - (\delta + \mu_1 + \eta + \phi)(C_{mt}^o - C_{mt}) \\ \beta_k(S_a^o - S_v) - \mu_v(I_v^o - I_v) \\ \beta_g(S_c^o - S_c) - \mu_c(I_c^o - I_c) \\ \pi((I_t^o - I_t) + \theta(C_{mt}^o - C_{mt})) - \mu_c(I_e^o - J_e \end{pmatrix}.$$

From the first condition in the stated proof above, $S_h(t) = \frac{M_h}{\mu_1} + \Big(S_h(0) - \frac{M_h}{\mu_1}\Big)e^{-\mu_1 t} \to \frac{M_h}{\mu_1}$ as $t \to \infty$, $S_v(t) = \frac{M_v}{\mu_v} + \Big(S_v(0) - \frac{M_v}{\mu_v}\Big)e^{-\mu_v t} \to \frac{M_v}{\mu_v}$ as $t \to \infty$ and $S_c(t) = \frac{M_c}{\mu_c} + \Big(S_c(0) - \frac{M_c}{\mu_c}\Big)e^{-\mu_c t} \to \frac{M_c}{\mu_c}$ as $t \to \infty$. Since $W^* = \Big(\frac{M_h}{\mu_1}, \frac{M_v}{\mu_v}, \frac{M_c}{\mu_c}\Big)$, the convergence of the solutions of W^* is globally asymptotically stable.

Also, if $I_m^o = I_m, I_t^o = I_t, C_{C_{mt}}^o = C_{mt}, I_v^o = I_v, I_c^o = I_c, J_e^o = J_e$. The malaria-toxoplasmosis absent equilibrium solutions denoted as I_m^o, I_f^o, I_{mf}^o, E_v^o, I_v^o, are all zeros. Then, $\hat{G}(W,Y) \geqslant 0$. Therefore, from the second condition in the stated theorem, that $G(W,Y) = D_Y(W^*,0)Y - \hat{G}(W,Y) \geqslant 0$, the malaria-toxoplasmosis absent equilibrium $E^0 = (X^*,0)$ is globally asymptotically stable.