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Approximate solution for a malaria model using the homotopy analysis method

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SUMMARY

Malaria as an infectious disease is caused by the Plasmodium parasite, and transmitted amongst humans through the bites of the female Anopheles mosquito. In this work, we used a system of nonlinear ordinary differential equations to present a new model for the disease. The model incorporated vaccination, treatment and vector control using sterile-insect technology. Sensitivity analysis was performed to identify the parameters which affect the endemicity of the disease. The approximate solutions of the system were obtained using the homotopy analysis method. The results obtained showed the region of convergence for the solutions. Plots were used to show this convergence region, highlighting the advantage of HAM over many other approximation methods. MATLAB and Maple were used in the simulation and mathematical analysis.

Key words: malaria, vaccination, sterile-insect technology, homotopy analysis method.

1. Introduction

Malaria is an infectious disease caused by the Plasmodium parasite and transmitted between humans through the bite of the female Anopheles mosquito (Chitnis et al, 2006; Onah et al., 2019). It is a deadly disease and highly endemic in sub-Saharan African and Asian countries, posing a threat globally. In 2020, it was reported that there are approximately 241 million malaria cases worldwide, while the number of deaths due to malaria was estimated as 627,000 (WHO, 2021). Africa had 95% of cases and 96% of deaths, and 80% of the total deaths were of children below 5 years (WHO, 2021). In 2021, almost half of the world's population was at risk of malaria, with an estimated 244 million cases globally

while the estimated number of deaths due to malaria was 619,000 (WHO, 2022). Tropical regions in Africa accounted for 92% of cases and 93% of deaths, of which Nigeria had the highest number (25%) and Uganda the lowest (4%). In 2022, the number of malaria cases stood at 249 million worldwide, with the number of deaths at 608,000 (WHO, 2023). Children under the age of 5 accounted for 76% of total deaths in 2022 (WHO, 2023). Associated symptoms of malaria include fever, which can be high or moderate, shaking chills, which can be severe or moderate, infant mortality, morbidity, headache, bloody stools, severe anaemia, profuse sweating, nausea, vomiting, abdominal pain, muscle pain, diarrhea, convulsions, coma, etc. (Amoah-Mensah et al., 2018). There are about five parasites that cause malaria, but the most dangerous are *Plasmodium falciparum* and *Plasmodium vivax* (Ogunmiloro, 2019). According to Ngwa and Shu (2000), the incubation period in humans is about twelve (12) days, while that for mosquitoes is about ten (10) days. The prevalence of malaria has been observed to be increasing due to increase in drug-resistance of the parasite and mosquito insecticide-resistance. Hence, there is a need to understand the various parameters involved in the transmission of the disease and set up effective control and preventive mechanisms. This underlines the need for vaccine control measures against malaria, as investigated in this work. By 2021, the only vaccine approved by the WHO was RTS,S, commercially known as Mosquirix (EMA, 2022). Large scale use of Mosquirix was recommended for the first time by the WHO in October 2021 for children living in areas with moderate-to-high malaria transmission, and it was stated that four injections are needed for full protection (EMA, 2022). Mosquirix is produced using genes from the outer protein of the *Plasmodium falciparum* Malaria parasite and a portion of a hepatitis B virus in addition to a chemical adjuvant to boost the immune response (ISE, 2022). Recently, it was reported that a new vaccine, R21/Matrix-M, developed by the University of Oxford and manufactured by the Serum Institute of India, has been approved by the WHO and found to give over 77% protection (Oxford, 2023). The vaccine has received regulatory clearance for use in Ghana and Nigeria (Oxford, 2023; Premium Times, 2023).

Sterile insect technology (SIT) is one of the methods of biologically controlling insects and pests (Vreysen et al., 2007; Atokolo and Mbah, 2020). It involves releasing an overwhelming number of sterile insects, preferably males, into the target population to mate with females (Dyck et al., 2021). In this method, females are not the preferred choice because they can start laying eggs and thus increasing the population, which is intended to be reduced further. When a female mosquito mates with a sterile male, it produces no offspring, as the resulting eggs do not hatch, thereby reducing the population of the next generation (Anguelov et al., 2012; Atokolo and Mbah, 2020). Sterile insects cannot replicate by themselves, hence cannot become established in the environment. When sterile insects are repeatedly introduced into an environment, the target population is either reduced or eliminated with time. At present, SIT is targeted at eradicating the Anopheles mosquito that causes malaria (Klassen, 2009), and the *Aedes aegypti* and *Aedes albopictus* mosquitoes causing dengue, yellow fever, filariasis, chikungunya and zika virus diseases (Chen and Hamer, 2016).

Mathematical modelling of infectious diseases has helped to study the mechanisms through which diseases spread, to make predictions on the future course of an outbreak and to evaluate methods of controlling them (Omale et al., 2020; Fatmawati, 2021; Collins and Duffy, 2022). It can project how infectious diseases progress, showing the likely outcome and helping to inform public health interventions (Omale et al., 2020; Mohammed, 2023). Aldila (2022) considered a malaria model that incorporated a preventive treatment against relapse as well as saturated fumigation. Specifically, their work suggested using tafenoquine treatment: when this is increased, the basic reproduction number decreases and vice versa. Their work further showed that it is possible to obtain two stable endemic equilibria when the basic reproduction number is greater than one. Collins and Duffy (2022) developed a mathematical model for the control of the spread of malaria incorporating treatment, drug resistance and the use of mosquito nets as preventive strategies. The model was fitted with data from the incidence of malaria in Nigeria. Their results showed that malaria will likely remain endemic in Nigeria unless there is widespread use of mosquito nets,

treatment of infectious humans is improved and the dominant resistant strain receives better control attention. Kamgang et al. (2022) incorporated the use of pyrethroid-treated bed-nets (PTNs) in developing a malaria model. Their work investigated cases of biting preferences of mosquitoes as well as repellent effects in the system. The work showed that an increase in the rate of mosquito choice of host or reduction in the rate of the repellent effect helps to remove the occurrence of backward bifurcation, leading to control of the disease. Keno et al. (2022) formulated a transmission model for malaria which included the role of climate variability and optimal control. Their optimal control showed that the use of treated bed nets, treatment of infected humans and application of insecticides will reduce the rate of infection. Kocabiyik (2022) developed a new mathematical model in terms of the Ross equation with distributed order incorporating a density function to study malaria. The model was numerically analyzed using a nonstandard finite difference scheme and compared with other numerical methods. Stability analyses of the various equilibrium points were also performed. Zhao et al. (2022) formulated and analyzed a delay transmission model for malaria that incorporates a control tool, ivermectin and seasonality. Their work showed that the dynamics of the model is determined totally by the basic reproduction number. They evaluated the effect of ivermectin using data from Kenya, and found that simulation of the effect of ivermectin confirms the existing clinical trial findings that it will take a minimum of 25 years to eradicate malaria from Kenya with malaria control measures intact. Al Basir and Abraha (2023) introduced the use of an awareness campaign against malaria, use of insecticides and treatment as intervention measures to control the spread of the disease. Optimal control analysis using the Pontryagin maximum principle was also carried out. Cost-effectiveness analysis revealed that using social media to organize an awareness campaign performed better than other control measures considered in their work. Mohammed (2023) formulated a deterministic mathematical model to simulate the transmission of malaria between human and mosquito populations. Through stability analysis, he showed that the model disease-free equilibrium point is both locally and globally asymptotically stable

when the reproduction number is less than one and unstable otherwise. Witbooi et al. (2023) worked on the stability and optimal control of malaria using a stochastic model. Their work proved the stability of the disease-free equilibrium in a stochastic sense and showed that the stability of that equilibrium in the stochastic model holds more generally than in a deterministic model. Unlike in the works reviewed here, our model incorporated SIT as a control measure for mosquitoes as well as vaccination and treatment as control measures in the human population. The remainder of this work is arranged thus: in section 2, the model is introduced and validated to be epidemiologically well-posed. The malaria-free equilibrium, malaria control number and sensitivity analysis are also obtained in this section. In section 3 the approximate solution is obtained, and conclusions appear in section 4.

2. Mathematical model

The mathematical model for malaria presented here has eleven (11) compartments made up of human and mosquito populations. The human population is divided into eight (8) compartments: Susceptible humans S_h, Vaccinated humans S_{hv}, Unvaccinated humans S_{hu}, Exposed humans E_{hm}, Infectious humans I_{hm}, Infectious humans undergoing treatment I_{hmT}, Infectious humans not undergoing treatment I_{hmU}, and Recovered humans R_h. The mosquito population is subdivided into three (3) compartments: Susceptible mosquitoes S_{mv}, Exposed mosquitoes E_{mv}, and Infectious Mosquitoes I_{mv}.

The susceptible human population S_h is increased by the level of recruitment through births and migration denoted by Λ_h and the rate of recovery θ from the disease. The susceptible human population is partitioned into the vaccinated class, S_{hv} and unvaccinated class, S_{hu}. The unvaccinated human population S_{hu} is increased by the proportion of the susceptible human population that refused vaccination for malaria, ρ_1, and reduced by movement into the exposed classes

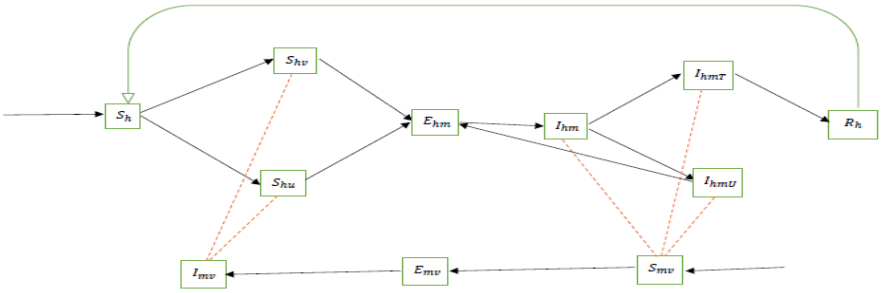

Figure 1. Flow diagram for the transmission of malaria

as well as the natural death rate, τ_1. The vaccinated human population S_{hv} is increased by the proportion of the susceptible human population that accepted vaccination ρ_2, and reduced by movement into the exposed class as well as the natural death rate, τ_1. The exposed human population E_{hm} is increased by the rate of movement from both the vaccinated and unvaccinated class as humans are bitten and infected by mosquitoes with malaria parasites. It is further increased by the proportion of untreated infectious humans that lose their infectiousness with time due to their immunity, ϕ_1, but have not recovered. It is reduced by the rate of movement, δ_1 into to the infectious class as well as natural death τ_1. The infectious human population, I_{hm} is increased by the rate of development of infectiousness from E_{hm} represented by δ_1 and reduced by the natural death rate τ_1, death due to the disease τ_2, the rate at which infectious persons accept treatment, ε_1 and the rate at which some infectious persons refuse to go for treatment. The human population undergoing treatment for malaria, I_{hmT} is increased by the proportion of those that accept treatment, ε_1 and reduced by the natural death rate, τ_1 as well as the rate of recovery from malaria γ_1 and the level of death due to the disease τ_2. The untreated human population, I_{hmU} is increased by the proportion of those that refuse to go for treatment, ε_2 and reduced by the natural death rate, τ_1 as well as movement into the exposed class, ϕ_1 and the level of death due to the disease τ_2. The recovered human population R_h is increased by the rate of recovery from those undergoing treatment, γ_1. It is reduced by the natural death rate, τ_1 and the rate at which recovered persons lose immunity

against the disease, ϕ and return to the susceptible class. The susceptible malaria vector population S_{mv} is increased by the level of recruitment denoted by Λ_{mv} and reduced by the natural death rate of mosquitoes μ, the rate of reduction κ_1 in the mosquito population due to SIT, as well as rate of exposure of susceptible mosquitoes to infectious humans with malaria parasites. The SIT technique reduces the mosquito population with time, since a sterile male introduced into the environment mating with Anopheles mosquitoes produces no offspring. The exposed malaria vector population E_{mv} is increased by the rate of exposure of Anopheles mosquitoes to infectious humans with malaria and reduced by natural death μ and the rate of infectiousness. The infectious malaria vector population I_{mv} is increased by the rate of development of infectiousness from E_{mv} and reduced by natural death μ. Thus, the model for the system becomes;

$$
\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h + \theta R_h - (\rho_1 + \rho_2 + \tau_1)S_h \\
\frac{dS_{hu}}{dt} &= \rho_1 S_h - (\alpha_1\beta_1 I_{mv} + \tau_1)S_{hu} \\
\frac{dS_{hv}}{dt} &= \rho_2 S_h - (\alpha_1\beta_2\Phi I_{mv} + \tau_1)S_{hv} \\
\frac{dE_{hm}}{dt} &= \alpha_1\beta_1 I_{mv}S_{hu} + \alpha_1\beta_2\Phi I_{mv}S_{hv} + \phi_1 I_{hmU} - (\delta_1 + \tau_1)E_{hm} \\
\frac{dI_{hm}}{dt} &= \delta_1 E_{hm} - (\tau_1 + \tau_2 + \varepsilon_1 + \varepsilon_2)I_{hm} \\
\frac{dI_{hmT}}{dt} &= \varepsilon_1 I_{hm} - (\gamma_1 + \tau_1 + \tau_2)I_{hmT} \\
\frac{dI_{hmU}}{dt} &= \varepsilon_2 I_{hm} - (\phi_1 + \tau_1 + \tau_2)I_{hmU} \\
\frac{dR_h}{dt} &= \gamma_1 I_{hmT} - (\tau_1 + \theta)R_h \\
\frac{dS_{mv}}{dt} &= \Lambda_{mv} - \alpha_1(\beta_3 I_{hm} + \beta_4 I_{hmT} + \beta_5 I_{hmU})S_{mv} - (\kappa_1 I_{SIT} + \mu)S_{mv} \\
\frac{dE_{mv}}{dt} &= \alpha_1(\beta_3 I_{hm} + \beta_4 I_{hmT} + \beta_5 I_{hmU})S_{mv} - (\nu_1 + \mu)E_{mv} \\
\frac{dI_{mv}}{dt} &= \nu_1 E_{mv} - \mu I_{mv}
\end{aligned}
\tag{1}
$$

where $S_h(0) = S_h^0,\ S_{hu}(0) = S_{hu}^0,\ S_{hv}(0) = S_{hv}^0,\ E_{hm}(0) = E_{hm}^0,\ I_{hm}(0) = I_{hm}^0, I_{hmT}(0) = I_{hmT}^0, I_{hmU}(0) = I_{hmU}^0, R_h(0) = R_h^0, S_{mv}(0) = S_{mv}^0, E_{mv}(0) =$

E_{mv}^0, $I_{mv}(0) = I_{mv}^0$ are the initial conditions for the system with the total human and mosquito populations given by;

$$N_h = S_h + S_{hu} + S_{hv} + E_{hm} + I_{hm} + I_{hmT} + I_{hmU} + R_h,$$

and

$$N_{mv} = S_{mv} + E_{mv} + I_{mv}.$$

We assume that the solution to the system exists in the region Ω described by $\Omega = \Omega_h \times \Omega_m$ where $\Omega_h = \left\{(S_h, S_{hu}, S_{hv}, E_{hm}, I_{hm}, I_{hmT}, I_{hmU}, R_h) \in \mathcal{R}_+^8 : S_h + S_{hu} + S_{hv} + E_{hm} + I_{hm} + I_{hmT} + I_{hmU} + R_h \leq \frac{\Lambda}{\tau_1}\right\}$ and $\Omega_m = \left\{(S_{mv}, E_{mv}, I_{mv}) \in \mathcal{R}_+^3 : S_{mv} + E_{mv} + I_{mv} \leq \frac{\Lambda}{\mu}\right\}$ respectively. The model uses the variables and parameters described in Tables 1 and 2, respectively.

3. Analysis of the model

3.1. Positivity and boundedness of solutions

Lemma 1: Let the initial data set for the model be $\left\{S_h^0 \geq 0, S_{hu}^0(0) \geq 0, S_{hv}^0(0) \geq 0, E_{hm}^0(0) \geq 0, I_{hm}^0 \geq 0, I_{hmT}^0 \geq 0, I_{hmU}^0 \geq 0, R_h^0 \geq 0, S_{mv}^0 \geq 0, E_{mv}^0 \geq 0, I_{mv}^0 \geq 0\right\}$, that is, at $t = 0$. Then, the solution set $\{S_h(t), S_{hu}(t), S_{hv}(t), E_{hm}(t), I_{hm}(t), I_{hmT}(t), I_{hmU}(t), R_h(t), S_{mv}(t), E_{mv}(t), I_{mv}(t)\}$ of the model with the given initial data will remain positive and bounded for all time $t > 0$.

Proof: It can be shown from eqn. (1) that

$$\frac{dS_h}{dt} \geq -(\rho_1 + \rho_2 + \tau_1)S_h,$$

$$\frac{dS_{hu}}{dt} \geq -(\alpha_1\beta_1 I_{mv} + \tau_1)S_{hu},$$

$$\vdots$$

$$\frac{dI_{mv}}{dt} \geq -\mu I_{mv}. \qquad (2)$$

Hence, solving the differential inequality (2) with given initial solutions gives

$$S_h \geq S_h^0 e^{-\int (\rho_1+\rho_2+\tau_1)dt} > 0\,,$$

Table 1. Description of state variables used in the model

Variables	Description
S_h	Susceptible human population
S_{hu}	Unvaccinated humans
S_{hv}	Vaccinated humans
E_{hm}	Exposed humans to malaria only
I_{hm}	Infectious humans with malaria only
I_{hmT}	Infectious humans with malaria only undergoing treatment
I_{hmU}	Infectious humans that refuse 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

Table 2. Description of parameters used in the model

Parameters	Description
Φ	Rate at which vaccinated humans lose immunity
Λ_h	Recruitment level of humans into susceptible population
Λ_{mv}	Recruitment level of Anopheles mosquitoes
θ	Rate of loss of immunity to malaria from recovered class
ρ_1	Rate at which susceptible humans refuse vaccination
ρ_2	Vaccinated proportion of the susceptible humans
τ_1	Natural death rate of humans
τ_2	Death rate due to malaria disease
μ	Natural death rate of mosquitoes
α_1	Contact rate of mosquitoes with humans
β_1	Effective rate of transmission of malaria parasite from infectious mosquitoes to unvaccinated humans
β_2	Effective rate of transmission of malaria parasite from infectious mosquitoes to vaccinated humans
β_3	Effective rate of transmission of malaria parasite from infectious humans to mosquitoes
β_4	Effective rate of transmission of malaria parasite from humans undergoing treatment to mosquitoes
β_5	Effective rate of transmission of malaria parasite from humans not undergoing treatment to mosquitoes
δ_1	Rate at which exposed humans with malaria parasite become infectious with malaria
v_1	Infectious rate of malaria parasite in mosquitoes
ε_1	Rate at which infectious humans accept treatment
ε_2	Rate at which infectious humans refuse to be treated
γ_1	Rate of recovery of infectious humans undergoing treatment
ϕ_1	Level of movement from Untreated humans to Exposed class
κ_1	Mating rate of SIT mosquitoes with Anopheles
I_{SIT}	Population of sterile males to control Anopheles population

$$S_{hu} \geq S_{hu}^{0} e^{-\int (\alpha_1 \beta_1 I_{hm}^{0} + \tau_1) dt},$$

$$\vdots$$

$$I_{mv} \geq I_{mv}^{0} e^{-\int \mu dt}.$$

Hence, given initial solutions that are individually positive, the solution to the model system remains positive $\forall\, t > 0$. Also, the region Ω is positively invariant and is an attractor of all positive solutions to the system.

The total human and mosquito populations satisfy the differential equations

$$\frac{dN_h}{dt} = \Lambda_h - \tau_1 N_h - \tau_2 (I_{hm} + I_{hmT} + I_{hmU})$$

$$\frac{dN_{mv}}{dt} = \Lambda_{mv} - \mu I_{mv}$$

respectively. Integrating both differential equations and solving as $t \to \infty$ gives $0 \leq N_{hm} \leq \frac{\Lambda_h}{\tau_1}$ and $0 \leq N_{mv} \leq \frac{\Lambda_{mv}}{\mu}$. This shows that all solutions of the system are positive and bounded, thus the model is epidemiologically well-posed and can be analyzed.

3.2. Malaria-control number

The malaria-free equilibrium (MFE) of the model is the steady state solution of (1) when there is no malaria infection in the human and mosquito populations. The MFE is denoted by E^0 and given by

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

The method for obtaining the malaria control number is defined in Van Den Driessche and Watmough (2002) as well as Diekmann et al. (2010). For our malaria model, the infectious class consists of the following compartments: $Y = (E_{hm}, I_{hm}, I_{hmT}, I_{hmU}, E_{mv}, I_{mv})$, with the corresponding differential equations;

$$\frac{dE_{hm}}{dt} = \alpha_1 I_{mv} (\beta_2 \Phi S_{hv} + \beta_1 S_{hu}) + \phi_1 I_{hmU} - (\delta_1 + \tau_1) E_{hm},$$

$$\frac{dI_{hm}}{dt} = \delta_1 E_{hm} - (\tau_1 + \tau_2 + \varepsilon_1 + \varepsilon_2) I_{hm},$$

$$\frac{dI_{hmT}}{dt} = \varepsilon_1 I_{hm} - (\tau_1 + \tau_2 + \gamma_1) I_{hmT},$$
$$\frac{dI_{hmU}}{dt} = \varepsilon_2 I_{hm} - (\phi_1 + \tau_1 + \tau_2) I_{hmU},$$
$$\frac{dE_{mv}}{dt} = \alpha_1(\beta_3 I_{hm} + \beta_4 I_{hmT} + \beta_5 I_{hmU}) S_{mv} - (\nu_1 + \mu) E_{mv},$$
$$\frac{dI_{mv}}{dt} = \nu_1 E_{mv} - \mu I_{mv}.$$

Let $\mathcal{F}$ denote the rate of appearance of new infection in the disease class and $\mathcal{V}$ denote the rate of inflow and outflow from the compartments through other means in the class; then

$$\mathcal{F} = \begin{bmatrix} \alpha_1 I_{mv}(\beta_2 \Phi S_{hv} + \beta_1 S_{hu}) \\ 0 \\ 0 \\ 0 \\ \alpha_1(\beta_3 I_{hm} + \beta_4 I_{hmT} + \beta_5 I_{hmU}) S_{mv} \\ 0 \end{bmatrix} \text{ and } \mathcal{V} = \begin{bmatrix} -\phi_1 I_{hmU} + (\delta_1 + \tau_1) E_{hm} \\ -\delta_1 E_{hm} + (\tau_1 + \tau_2 + \varepsilon_1 + \varepsilon_2) I_{hm} \\ -\varepsilon_1 I_{hm} + (\tau_1 + \tau_2 + \gamma_1) I_{hmT} \\ -\varepsilon_2 I_{hm} + (\tau_1 + \tau_2 + \phi_1) I_{hmU} \\ (\nu_1 + \mu) E_{mv} \\ -\nu_1 E_{mv} + \mu I_{mv} \end{bmatrix}.$$

Thus,

$$F = \frac{\partial \mathcal{F}}{\partial Y} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & A_1 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & A_2 & A_3 & A_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \text{ and } V = \frac{\partial \mathcal{V}}{\partial Y} = \begin{bmatrix} B_1 & 0 & 0 & -\phi_1 & 0 & 0 \\ -\delta_1 & B_2 & 0 & 0 & 0 & 0 \\ 0 & -\varepsilon_1 & B_3 & 0 & 0 & 0 \\ 0 & -\varepsilon_2 & 0 & B_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & B_5 & 0 \\ 0 & 0 & 0 & 0 & -\nu_1 & \mu \end{bmatrix}$$

where $A_1 = \frac{\alpha_1 \Lambda_h (\beta_2 \varphi \rho_2 + \beta_1 \rho_1)}{\tau_1(\tau_1 + \rho_1 + \rho_2)}$, $A_2 = \frac{\alpha_1 \beta_3 \Lambda_{mv}}{\mu}$, $A_3 = \frac{\alpha_1 \beta_4 \Lambda_{mv}}{\mu}$, $A_4 = \frac{\alpha_1 \beta_5 \Lambda_{mv}}{\mu}$, $B_1 = \delta_1 + \tau_1$, $B_2 = \tau_1 + \tau_2 + \varepsilon_1 + \varepsilon_2$, $B_3 = \tau_1 + \tau_2 + \gamma_1$, $B_4 = \tau_1 + \tau_2 + \phi_1$, $B_5 = \nu_1 + \mu$. Finding the inverse of the matrix V gives

$$V^{-1} = \begin{bmatrix} \frac{B_4 B_2}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & \frac{\phi_1 \varepsilon_2}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & 0 & \frac{\phi_1 B_2}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & 0 & 0 \\ \frac{\delta_1 B_4}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & \frac{B_4 B_1}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & 0 & \frac{\phi_1 \delta_1}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & 0 & 0 \\ \frac{\varepsilon_1 \delta_1 B_4}{(B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1) B_3} & \frac{\varepsilon_1 B_4 B_1}{(B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1) B_3} & \frac{1}{B_3} & \frac{\varepsilon_1 \delta_1 \phi_1}{(B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1) B_3} & 0 & 0 \\ \frac{\varepsilon_2 \delta_1}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & \frac{\varepsilon_2 B_1}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & 0 & \frac{B_1 B_2}{B_4 B_2 B_1 - \varepsilon_2 \delta_1 \phi_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{B_5} & 0 \\ 0 & 0 & 0 & 0 & \frac{\nu_1}{B_5 \mu} & \frac{1}{\mu} \end{bmatrix}$$

The malaria control number which corresponds to the dominant eigenvalue of the matrix, FV^{-1} is

$$R_{0m} = \left(\frac{\nu_1\delta_1 A_1(A_2B_4B_3+A_3\varepsilon_1B_4+A_4\varepsilon_2B_3)}{\mu B_3B_5(B_4B_2B_1-\varepsilon_2\delta_1\phi_1)}\right)^{\frac{1}{2}} \quad (3)$$

The first term in (3) is the total expected number of humans and mosquitoes that will be infected at the malaria-free equilibrium by a single newly infected human or mosquito whilst infectious but before deciding to accept or refuse treatment, the second term is the total expected number of humans or mosquitoes that will be infected at the malaria-free equilibrium by a single newly infected human whilst undergoing treatment for malaria, while the third term is the total expected number of humans that will be infected at the malaria-free equilibrium by a single newly infected human not undergoing treatment.

3.3. Sensitivity analysis

The sensitivity analysis of parameters in the malaria reproduction number is carried out here using the normalized forward sensitivity index of R_m that depends on the parameter p given by

$$S_p^{R_m} = \frac{\partial R_m}{\partial p} \times \frac{p}{R_m}$$

The sensitivity indices help to understand the parameters that affect R_m for more effective control of malaria. Malaria endemicity is increased by the parameters with positive sensitivity indices and decreased by the parameters with negative sensitivity indices. Hence, the parameters with positive values need to be reduced while those with negative values need to be increased in order to control malaria. The contact rate of humans with mosquitoes, denoted by α_1, is the parameter with the highest impact on the spread of the disease, with a sensitivity index of 1. This means that malaria will be successfully controlled by ensuring that humans have limited contact with mosquitoes. When the rate of contact between mosquitoes and humans is reduced, the probability of transmission of malaria within both populations will also be reduced. The recruitment rates for humans, Λ_h and Anopheles mosquitoes, Λ_{mv} respectively have sensitive indices of 0.5. This shows that controlling malaria will also require

humans to avoid areas where Anopheles mosquitoes are prevalent, hence efforts should be made to reduce the continuous recruitment of mosquitoes into the human environment.

Table 3. Sensitivity indices for $\boldsymbol{R_m}$

Parameter	Values	Sensitivity index	Parameter	Values	Sensitivity index
Λ_h	30	0.5	δ_1	0.0833	0.0004
Λ_{mv}	100	0.5	ρ_1	0.65	0.1495
α_1	0.5	1	ρ_2	0.28	-0.1495
β_1	0.321	0.4990	ν_1	0.1	0.1787
β_2	0.12	0.0010	Φ	0.0125	0.0010
β_3	0.24	0.0900	μ	0.0556	-1.1787
β_4	0.12	0.1960	ϵ_1	0.62	-0.3028
β_5	0.24	0.2140	ϵ_2	0.31	0.2131
τ_1	0.0000432	-0.5007	γ_1	0.142	0.1954
τ_2	0.0003454	-0.0020	ϕ_1	0.13	-0.2126

The rate at which humans refuse treatment for malaria, ϵ_2 and the vaccination rate ρ_1 also increase malaria endemicity. The parameters with negative values do not increase the persistence of malaria. The parameter with the least negative value is μ, which represents the natural death rate of mosquitoes. This means that to control the disease, efforts should also be focused on ensuring that mosquitoes die more often, as this will also reduce the contact rate of mosquitoes with humans.

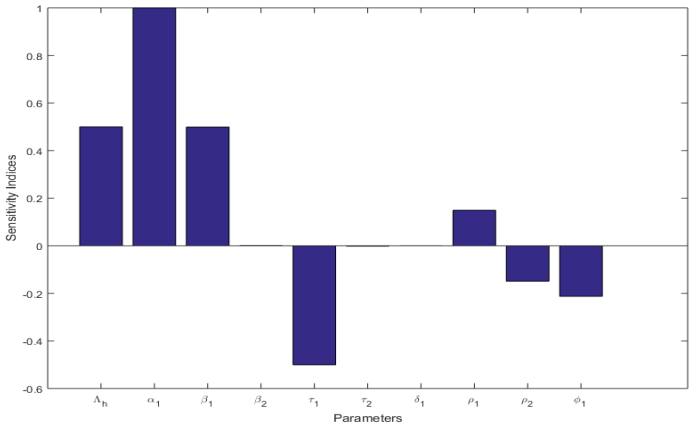

Figure 2. Sensitivity plots of parameters of $\boldsymbol{R_m}$

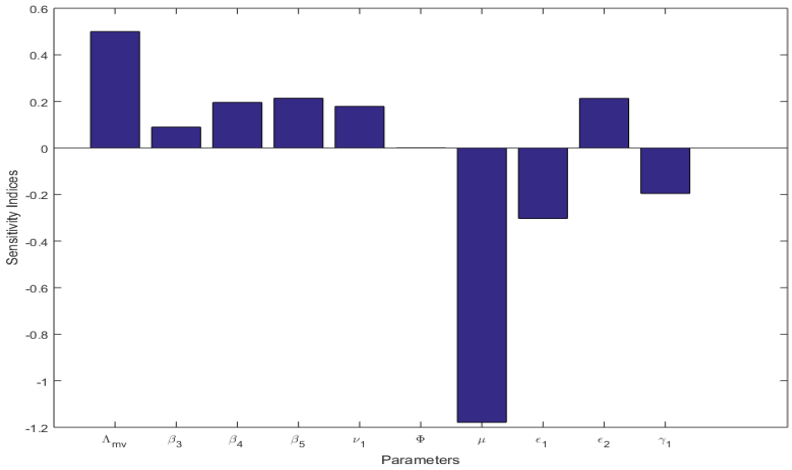

Figure 3. Sensitivity plots of parameters of $\boldsymbol{R_m}$

The sensitivity indices for the parameters representing the rate at which humans accept vaccination, ρ_2 and treatment, ϵ_1 are both negative, and also need to be increased. Conclusively, the sensitivity analysis suggests that every effort at controlling the spread of malaria should target reducing the contact rates of humans with mosquitoes. This could be successfully done by increasing the death rates of mosquitoes, increasing the rate of vaccination and treatment of infectious humans, and reducing the recruitment rate of mosquitoes into the human environment, which is the role of SIT as introduced in this work.

4. Approximate analytical solutions by HAM

The homotopy analysis method (HAM) was proposed by S.J. Liao in his PhD thesis in 1992 and has been cited in many articles (e.g. Liao, 2004; Ghoreishi et al. 2011; Cherif and Djelioui, 2018; Massoun and Benzine, 2018; Al-Hayani and Fahad, 2019; Turq, 2020 and many others). HAM is an analytical method for computing the solutions of linear and nonlinear differential equations in terms of a convergent series (Sadaf and Akram, 2017). Before the advent of HAM, perturbation techniques were mostly in use, before some non-perturbation

methods such as the artificial small parameter method, δ-expansion method and ADM were introduced (Liao, 2004).

Consider the non-linear differential equation

$$\mathcal{N}[u(x)] = 0 \tag{4}$$

where $\mathcal{N}$ is a non-linear differential operator, x denotes the independent variable, and $u(x)$ is an unknown function. Then, the zeroth-order deformation equation of (4) can be constructed as

$$(1-p)\mathcal{L}[\phi(x;p) - u_0(x)] = hpH(x)\{N[\pi(x,p)]\},$$

where $\mathcal{L}$ is an auxillary linear operator with the property $\mathcal{L}[0] = 0$, N is the nonlinear operator related to (4), $p \in [0;1]$ is the homotopy parameter also known as the embedding parameter in topology, h is the convergence control parameter, u_0 is an initial guess, and $H(x)$ is an auxillary function.

When $p = 0, \pi(x;0) = u_0(x)$ and when $p = 1, \pi(x;1) = u(x)$. This means that, as p grows from 0 to 1, the solution $\pi(x;p)$ varies from the initial guesses $u_0(x)$ to the exact solution $u(x)$. $\pi(x;p)$ depends on the parameter p and so can be expanded by Maclaurin series about p as

$$\pi(x;p) = \pi(x;0) + \sum_{n=1}^{\infty} u\,(x)p^n, \tag{5}$$

or

$$\pi(x;p) = u_0 + \sum_{n=1}^{\infty} u\,(x)p^n, \tag{6}$$

where

$$u_n = \frac{1}{n!}\frac{\partial^n \pi(x;p)}{\partial p^n}, \qquad q = 0.$$

From (6), if we set $p = 1$, we will have

$$\pi(x;1) = u_0 + \sum_{n=1}^{\infty} u_n\,(x). \tag{7}$$

The unknown function, $u_n(x)$ can be determined using the zero-order deformation equation. By differentiating (7) n times with respect to p, setting $p = 0$ and dividing by $n!$, we obtain

$$\mathcal{L}[u_n(x) - \chi_n u_{n-1}(x)] = cD_{n-1}\big[\mathcal{N}\big(\pi(x;p)\big)\big],$$

called the n^{th} order deformation equation.

The term

$$D_{n-1}\big[\mathcal{N}\big(\pi(x;p)\big)\big] = \frac{1}{(n-1)!}\frac{\partial^{n-1}\mathcal{N}[\pi(x;p)]}{\partial p^{n-1}}$$

and

$$\chi_n = \begin{cases} 0, & if\ n \le 1 \\ 1, & if\ n > 1 \end{cases}.$$

4.1. Solution of the malaria model by HAM

Given the system (1) and equation (7), assuming that the auxiliary parameter h, the auxiliary function $H(t)$, the initial approximation and the auxiliary operator L are properly chosen, the series form of the solutions is given by;

$\pi_1(t;p) = S_h^0(t) + \sum_{i=1}^{\infty} S_h^i(t)p^i,$ $\pi_2(t;p) = S_{hu}^0(t) + \sum_{i=1}^{\infty} S_{hu}^i(t)p^i,$

$\pi_3(t;p) = S_{hv}^0(t) + \sum_{i=1}^{\infty} S_{hv}^i(t)p^i,$ $\pi_4(t;p) = E_{hm}^0(t) + \sum_{i=1}^{\infty} E_{hm}^i(t)p^i,$

$\pi_5(t;p) = I_{hm}^0(t) + \sum_{i=1}^{\infty} I_{hm}^i(t)p^i,$ $\pi_6(t;p) = I_{hmT}^0(t) + \sum_{i=1}^{\infty} I_{hmT}^i(t)p^i,$

$\pi_7(t;p) = I_{hmU}^0(t) + \sum_{i=1}^{\infty} I_{hmU}^i(t)p^i,$ $\pi_8(t;p) = R_h^0(t) + \sum_{i=1}^{\infty} R_h^i(t)p^i,$

$\pi_9(t;p) = S_{mv}^0(t) + \sum_{i=1}^{\infty} S_{mv}^i(t)p^i,$ $\pi_{10}(t;p) = E_{mv}^0(t) + \sum_{i=1}^{\infty} E_{mv}^i(t)p^i,$

$\pi_{11}(t;p) = I_{mv}^0(t) + \sum_{i=1}^{\infty} I_{mv}^i(t)p^i.$

We define the continuous mappings: $S_h \to \pi_1(t;p)$, $S_{hu} \to \pi_2(t;p)$, $S_{hv} \to \pi_3(t;p)$, $E_{hm} \to \pi_4(t;p)$, $I_{hm} \to \pi_5(t;p)$, $I_{hmT} \to \pi_6(t;p)$, $I_{hmU} \to \pi_7(t;p)$, $R_h \to \pi_8(t;p)$, $S_{mv} \to \pi_9(t;p)$, $E_{mv} \to \pi_{10}(t;p)$, $I_{mv} \to \pi_{11}(t;p)$ such that as p moves from $0\ to\ 1$, $\pi_i, i = 1,2,3,\ldots,11$ moves from the initial conditions, $S_h^0, S_{hu}^0, S_{hv}^0, \ldots, I_{mv}^0$ to the exact solution, $S_h(t), S_{hu}(t), S_{hv}(t), \ldots, I_{mv}(t)$. The auxilliary linear operator is chosen to be

$$\mathcal{L}_i[\,\pi_i(t;p)] = \frac{d\pi_i(t;p)}{dt},\ i = 1,2,3,\ldots,11 \qquad (8)$$

with the property that $L_i[f_i] = 0$ where f_i are integral constants. The nonlinear operator is defned as;

$$\mathcal{N}_1[\pi_i(t;p)] = \frac{\partial \pi_1(t;p)}{\partial t} - \Lambda_h - \theta\pi_8(t;p) + (\rho_1 + \rho_2 + \tau_1)\pi_1(t;p),$$

$$\mathcal{N}_2[\pi_i(t;p)] = \frac{\partial \pi_2(t;p)}{\partial t} - \rho_1\pi_1(t;p) + (\alpha_1\beta_1\pi_{11}(t;p) + \tau_1)\pi_2(t;p),$$

$$\mathcal{N}_3[\pi_i(t;p)] = \frac{\partial \pi_3(t;p)}{\partial t} - \rho_2\pi_1(t;p) + (\alpha_1\beta_2\Phi\pi_{11}(t;p) + \tau_1)\pi_3(t;p),$$

$$\mathcal{N}_4[\pi_i(t;p)] = \frac{\partial \pi_4(t;p)}{\partial t} - \alpha_1\beta_1\pi_{11}(t;p)\pi_2(t;p) + \alpha_1\beta_2\Phi\pi_{11}(t;p)\pi_3(t;p)$$

$$+\phi_1\pi_7(t;p) + (\delta_1 + \tau_1)\pi_4(t;p),$$

$$\mathcal{N}_5[\pi_i(t;p)] = \frac{\partial \pi_5(t;p)}{\partial t} - \delta_1\pi_4(t;p) + (\tau_1 + \tau_2 + \epsilon_1 + \epsilon_2)\pi_5(t;p),$$

$$\mathcal{N}_6[\pi_i(t;p)] = \frac{\partial \pi_6(t;p)}{\partial t} - \epsilon_1\pi_5(t;p) + (\gamma_1 + \tau_1 + \tau_2)\pi_6(t;p),$$

$$\mathcal{N}_7[\pi_i(t;p)] = \frac{\partial \pi_7(t;p)}{\partial t} - \epsilon_2\pi_5(t;p) + (\phi_1 + \tau_1 + \tau_2)\pi_7(t;p),$$

$$\mathcal{N}_8[\pi_i(t;p)] = \frac{\partial \pi_8(t;p)}{\partial t} - \gamma_1\pi_6(t;p) + (\tau_1 + \theta)\pi_8(t;p),$$

$$\mathcal{N}_9[\pi_i(t;p)] = \frac{\partial \pi_9(t;p)}{\partial t} - \Lambda_{mv} + \alpha_1\big(\beta_3\pi_5(t;p) + \beta_4\pi_6(t;p) +$$

$$+\beta_5\pi_7(t;p)\big)\pi_9(t;p) + (\kappa_1 q + \mu)\pi_9(t;p),$$

$$\mathcal{N}_{10}[\pi_i(t;p)] = \frac{\partial \pi_{10}(t;p)}{\partial t} - \alpha_1\big(\beta_3\pi_5(t;p) + \beta_4\pi_6(t;p) + \beta_5\pi_7(t;p)\big)\pi_9(t;p)$$

$$+(\nu_1 + \mu)\pi_{10}(t;p),$$

$$\mathcal{N}_{11}[\pi_i(t;p)] = \frac{\partial \pi_{11}(t;p)}{\partial t} - \nu_1\pi_{10}(t;p) + \mu\pi_{11}(t;p), \qquad i = 1,2,3,\ldots,11.$$

The eleven zero-order deformation equations can be constructed following (8) as

$$\begin{aligned}
&(1-p)\mathcal{L}[\pi_1(t;p) - S_h^0(t)] = phH(t)\mathcal{N}_1[\pi_i(t;p)],\\
&(1-p)\mathcal{L}[\pi_2(t;p) - S_{hu}^0(t)] = phH(t)\mathcal{N}_2[\pi_i(t;p)], \qquad (9)\\
&\quad\vdots\\
&(1-p)\mathcal{L}[\pi_{11}(t;p) - I_{mv}^0(t)] = phH(t)\mathcal{N}_{11}[\pi_i(t;p)], \quad i = 1,2,3,\ldots,11.
\end{aligned}$$

We can see that if $p = 0, then\ \pi_1(t;0) = S_h^0(t),\ \pi_2(t;0) = S_{hu}^0(t), \cdots \pi_{11}(t;0) = I_{mv}^0(t)$ and if $p = 1$, then $\pi_1(t;1) = S_h(t), \pi_2(t;1) = S_{hu}(t), \cdots \pi_{11}(t;1) = I_{mv}(t)$.

Thus, from these zero-order deformation equations, the 11 high-order deformation equations are as follows;

$$\mathcal{L}[S_h^n(t) - \chi_n S_h^{n-1}(t)] = hH(t)D_{n-1}[\mathcal{N}_1[\pi_i(x;q)],$$

$$\mathcal{L}[S_{hu}^n(t) - \chi_n S_{hu}^{n-1}(t)] = hH(t)D_{n-1}[\mathcal{N}_2[\pi_i(x;q)],$$

$$\mathcal{L}[S_{hv}^n(t) - \chi_n S_{hv}^{n-1}(t)] = hH(t)D_{n-1}[\mathcal{N}_3[\pi_i(x;q)], \tag{10}$$

$$\vdots$$

$$\mathcal{L}[I_{mv}^n(t) - \chi_n I_{mv}^{n-1}(t)] = hH(t)D_{n-1}[\mathcal{N}_{11}[\pi_i(x;q)], \quad i = 1,2,3,\ldots,11,$$

where $D_{n-1}\left[\mathcal{N}_i\left(\pi_i(x_i;p)\right)\right] = \frac{1}{(n-1)!}\frac{\partial^{n-1}\mathcal{N}_i[\pi_i(x_i;p)]}{\partial p^{n-1}},\ i = 1,2,3,\ldots,11.$

From (9)–(10), $D_{n-1}\left[\mathcal{N}_i\left(\pi_i(x_i;p)\right)\right]$ becomes

$$D_{n-1}[\mathcal{N}_1(\pi(x_i;p))] = \frac{dS_h^{n-1}}{dt} - \Lambda_h - \theta R_h^{n-1} + (\rho_1 + \rho_2 + \tau_1)S_h^{n-1},$$

$$D_{n-1}[\mathcal{N}_2(\pi(x_i;p))] = \frac{dS_{hu}^{n-1}}{dt} - \rho_1 S_h^{n-1} + \sum_{i=0}^{n-1}\alpha_1\beta_1 S_{hu}^i I_{mv}^{n-1-i} + \tau_1 S_{hu}^{n-1},$$

$$D_{n-1}[\mathcal{N}_3(\pi(x_i;p))] = \frac{dS_{hv}^{n-1}}{dt} - \rho_2 S_h^{n-1} + \sum_{i=0}^{n-1}\alpha_1\beta_2\Phi S_{hv}^i I_{mv}^{n-1-i} + \tau_1 S_{hv}^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_4\left(\pi(x_i;p)\right)\right] = \frac{dE_{hm}^{n-1}}{dt} - \sum_{i=0}^{n-1}\alpha_1\beta_1 S_{hu}^i I_{mv}^{n-1-i} - \sum_{i=0}^{n-1}\alpha_1\beta_1 S_{hu}^i I_{mv}^{n-1-i}$$
$$-\phi_1 I_{hmU}^{n-1} + (\delta_1 + \tau_1)E_{hm}^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_5\left(\pi(x_i;p)\right)\right] = \frac{dI_{hm}^{n-1}}{dt} - \delta_1 E_{hm}^{n-1} + (\tau_1 + \tau_2 + \varepsilon_1 + \varepsilon_2)I_{hm}^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_6\left(\pi(x_i;p)\right)\right] = \frac{dI_{hmU}^{n-1}}{dt} - \varepsilon_1 I_{hm}^{n-1} + (\gamma_1 + \tau_1 + \tau_2)I_{hmU}^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_7\left(\pi(x_i;p)\right)\right] = \frac{dI_{hmT}^{n-1}}{dt} - \varepsilon_2 I_{hm}^{n-1} + (\phi_1 + \tau_1 + \tau_2)I_{hmT}^{n-1},$$

$$D_{n-1}[\mathcal{N}_8(\pi(x_i;p))] = \frac{dR_h^{n-1}}{dt} - \gamma_1 I_{hmT}^{n-1} + (\tau_1 + \theta)R_h^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_9\left(\pi(x_i;p)\right)\right] = \frac{dS_{mv}^{n-1}}{dt} - \Lambda_{mv} + \sum_{1=0}^{n-1}\alpha_1\left(\beta_3 I_{hm}^i + \beta_4 I_{hmT}^i + \beta_5 I_{hmU}^i\right)S_{mv}^{n-1-i}$$
$$+(\kappa_1 I_{SIT} + \mu)S_{mv}^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_{10}\left(\pi(x_i;p)\right)\right] = \frac{dE_{mv}^{n-1}}{dt} - \sum_{1=0}^{n-1}\alpha_1\left(\beta_3 I_{hm}^{i} + \beta_4 I_{hmT}^{i} + \beta_5 I_{hmU}^{i}\right)S_{mv}^{n-1-i} + \\ +(\nu_1 + \mu)E_{mv}^{n-1},$$

$$D_{n-1}\left[\mathcal{N}_{11}\left(\pi(x_i;p)\right)\right] = \frac{dI_{mv}^{n-1}}{dt} - \nu_1 E_{hm}^{n-1} + \mu I_{mv}^{n-1}.$$

Using $H = 1$, the nth-order deformation equations (10) will have the following solutions for $n \geq 1$;

$$S_h^n(t) = \chi_n S_h^{n-1}(t) + h\int_0^t D_{n-1}\left[\mathcal{N}_1\left(\pi(x_i;p)\right)\right],$$

$$S_{hu}^n(t) = \chi_n S_{hu}^{n-1}(t) + h\int_0^t D_{n-1}\left[\mathcal{N}_2\left(\pi(x_i;p)\right)\right],$$

$$S_{hv}^n(t) = \chi_n S_{hv}^{n-1}(t) + h\int_0^t D_{n-1}\left[\mathcal{N}_3\left(\pi(x_i;p)\right)\right], \quad (11)$$

$$\vdots$$

$$I_{mv}^n(t) = \chi_n I_{mv}^{n-1}(t) + h\int_0^t D_{n-1}\left[\mathcal{N}_{11}\left(\pi(x_i;p)\right)\right].$$

Equation (11) gives us the iteration scheme to obtain the series solution of the system for any n terms.

Using three-term approximations, that is, $n = 1,2,3$, with the parameter values in Table 4 and the following assumed values for the state variables $S_h^0 = 500, S_{hu}^0 = 362, S_{hv}^0 = 9, E_{hm}^0 = 48, I_{hm}^0 = 35, I_{hmT}^0 = 21, I_{hmU}^0 = 8, R_h^0 = 10, S_{mv}^0 = 500, E_{mv}^0 = 320, I_{mv}^0 = 170$; the series solution by HAM is then given by

Table 4. Parameter values and sources

Parameter	Values	Sources	Parameter	Values	Sensitivity index
Λ_h	50	Assumed	δ_1	0.0833	[9]
Λ_{mv}	100	Assumed	ρ_1	0.65	[44]
α_1	0.4	[2]	ρ_2	0.28	[44]
β_1	0.034	[2,13]	ν_1	0.1	[9]
β_2	0.013	[13]	Φ	0.0125	[44]
β_3	0.0044	[2,13]	μ	0.0556	[24]
β_4	0.0022	[44]	ϵ_1	0.62	[44]
β_5	0.0044	[2.13]	ϵ_2	0.31	[44]
τ_1	0.0000391	[13,29]	γ_1	0.142	[32]
τ_2	0.0003454	[29]	ϕ_1	0.13	[44]
κ_1	0.25	[44]	θ	0.0146	[13]

$$S_h(t) = 500 + 1{,}119.622ht + 1{,}012.185h^2t + 470.7794h^2t^2 + \\ 192.9618h^3t^2 + 29.9052h^3t^3 + 207.437h^3t,$$

$$S_{hu}(t) = 362 + 1{,}535.8755ht + 1{,}279.8963h^2t + 1{,}011.8655h^2t^2 + \\ +468.9132h^3t^2 + 255.9793h^3t + 107.0171h^3t^3,$$

$$S_{hv}(t) = 9 - 419.7003ht - 349.7503h^2t - 143.6886h^2t^2 - 69.9501h^3t \\ -58.4754h^3t^2 - 9.0853h^3t^3,$$

$$E_{hm}(t) = 48 - 2{,}502.2496ht - 2{,}085.208h^2t - 1{,}287.3047h^2t^2 - \\ -417.0416h^3t - 535.5136h^3t^2 - 134.7344h^3t^3,$$

$$I_{hm}(t) = 35 + 75.1929ht + 62.6608h^2t + 112.8648h^2t^2 + 12.5322h^{3t} \\ +45.1461h^3t^2 + 13.2065h^3t^3,$$

$$I_{hmT}(t) = 21 - 49.3272ht - 41.106h^2t - 24.5709h^2t^2 - 8.2212h^3t \\ -9.8285h^3t^2 - 5.0753h^3t^3, \qquad (12)$$

$$I_{hmU}(t) = 8 - 18.9213ht - 15.7678h^2t - 7.6073h^2t^2 - 3.1536h^3t - \\ -3.043h^3t^2 - 1.6463h^3t^3,$$

$$R_h(t) = 10 - 15.3108ht - 12.759h^2t + 5.3075h^2t^2 - 2.5518h^3t + \\ +2.0837h^3t^2 + 0.4148h^3t^3,$$

$$S_{mv}(t) = 500 + 187{,}174.64ht + 156{,}137.2h^2t + 9{,}770{,}342.155h^2t^2 + \\ +31{,}187.44h^3t + 3{,}906{,}264.83h^3t^2 + 81{,}544{,}499.35h^3t^3,$$

$$E_{mv}(t) = 320 + 8.136ht + 6.78h^2t - 7{,}395.4132h^2t^2 + 1.356h^3t \\ -2{,}976.8086h^3t^2 - 63{,}024.9192h^3t^3,$$

$$I_{mv}(t) = 170 - 67.644ht - 56.37h^2t - 1.9063h^2t^2 - 11.274h^3t \\ -0.7625h^3t^2 + 49.0885h^3t^3.$$

Equation (12) is the sum of three terms of the series solution obtained using (11) taking $\chi_n = 0$ when $n = 1$ and $\chi_n = 1$ when $n > 1$. The HAM gives an analytical approximate solution in infinite power series form. Equation (12) provides the numerical values of the infinite power series. The consequent series truncation and practical procedure are conducted to accomplish this task. The series solution contains the auxiliary parameter h, which offers a simple way to adjust and control the convergence of the series solution. In fact, it is very

important to ensure that the series (12) are convergent. We then plot the approximate solutions of the various state variables with respect to values of h in the interval $-1.5 \leq h \leq 1$ to ascertain the region of admissibility where the solutions will converge. Figures 4–9 shows the range of admissible values of h where the state variables converge. According to Ghoreishi et al, (2011) and Huseen (2020), the valid region of values of h is where the line segment is almost parallel to the horizontal axis. These ranges of values are tabulated for easy understanding in Table 5 below.

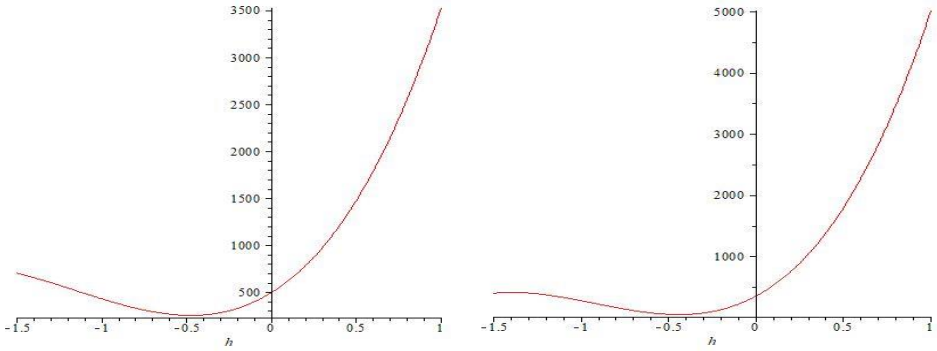

Figure 4. Susceptible and Unvaccinated humans against h

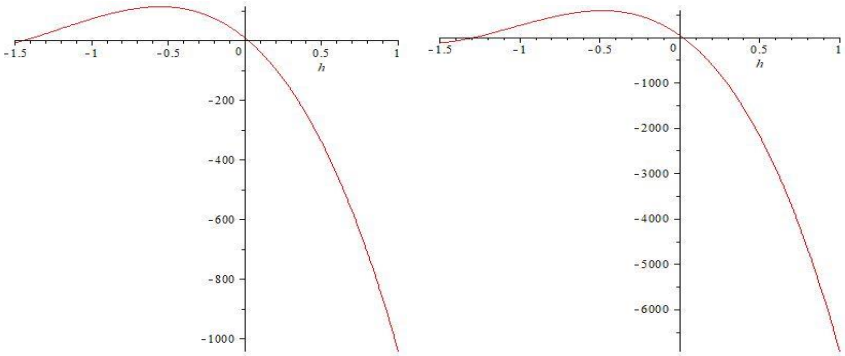

Figure 5. Vaccinated and Exposed humans against h

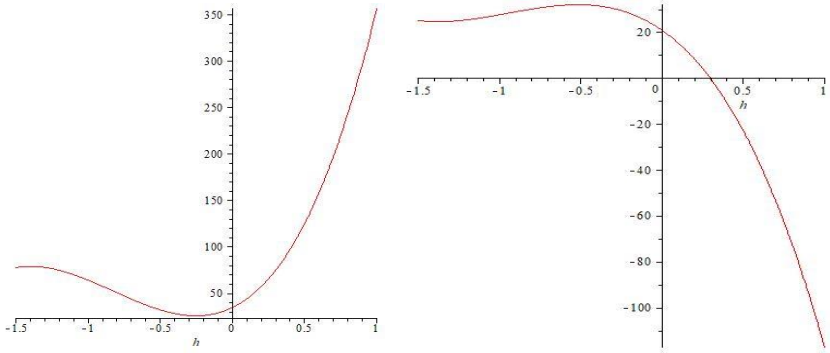

Figure 6. Infectious and Treated humans against h

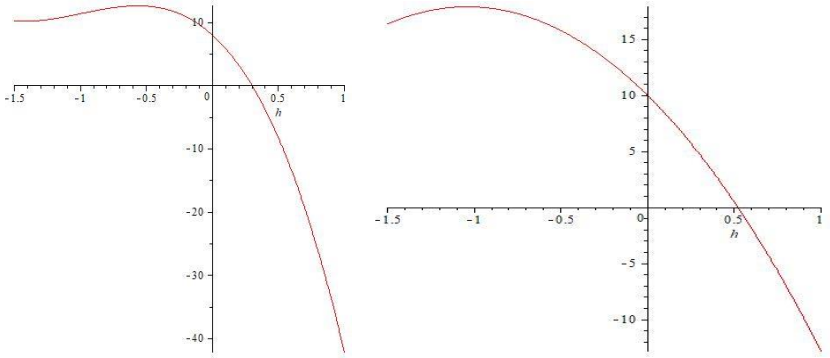

Figure 7. Untreated and Recovered humans against h

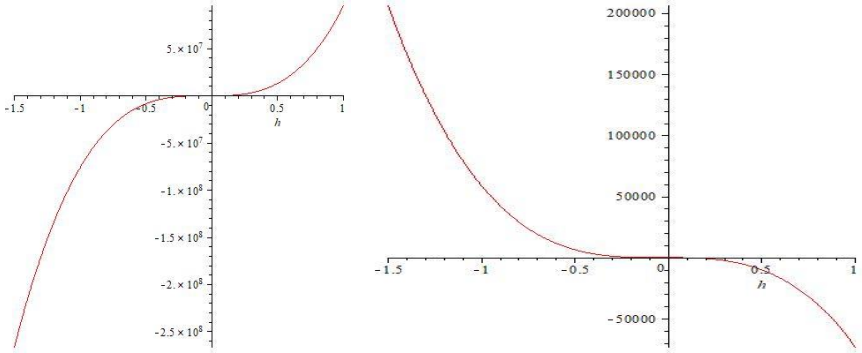

Figure 8. Susceptible and Exposed mosquitoes against h

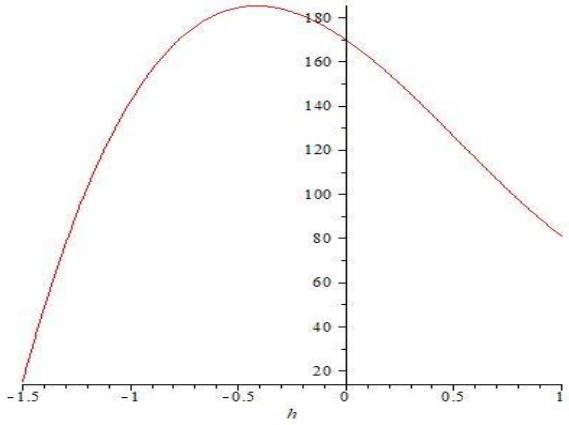

Figure 9. Infectious mosquitoes against h

Table 5. Admissible values of h for the solutions

S_h	$-0.7 < h < -0.3$	I_{hmU}	$-1.5 \leq h \leq -0.4$
S_{hu}	$-1.5 < h < -0.3$	R_h	Centered around -1
S_{hv}	$-0.7 \leq h \leq -0.4$	S_{mv}	$-0.3 \leq h \leq 0.2$
E_{hm}	$-1.5 \leq h \leq -0.4$	E_{mv}	$-0.3 \leq h \leq 0.2$
I_{hm}	$-1.5 \leq h \leq -0.3$	I_{mv}	Centered around -0.5
I_{hmT}	$-1.5 \leq h \leq -0.3$		

The plots show that the population of Anopheles decreases within the region of convergence, showing the effect of the controls employed. Practically, this shows that use of the sterile insect technique ensures that the population of susceptible, exposed and infectious mosquitoes continues to fall. This is because as more SIT mosquitoes mate with females in the wild, the females lay eggs without hatching, thereby reducing the future generation. The implication of this is that the spread of malaria will be reduced as there are fewer mosquitoes which can infect humans. In the human population, we see that the population of the infectious class reduces over time, which is attributed to the controls introduced in the human population to reduce the spread of the disease. Increasing the rate at which humans accept vaccination and treatment, as well as the probability of wild female mosquitoes mating with the SIT mosquitoes will certainly reduce the spread of malaria in the system.

5. Conclusion

In this work, we have proposed a new model for control of the spread of malaria in human and mosquito populations. The model incorporates vaccination, treatment, and the use of insect sterile technology to control the vectors. The model was shown to be epidemiologically well-posed. The malaria-free equilibrium and the malaria control number were obtained. Then, sensitivity analysis was performed using the normalized forward sensitivity index approach to determine the parameters which most affect the dynamics of the disease. The results showed that recruitment of humans and mosquitoes, the contact rate of humans and mosquitoes, probabilities of disease transmission, and the rates at which humans refuse vaccination and treatment increase the endemicity of malaria in the system, hence must be reduced to ensure that the disease is controlled. The homotopy analysis method (HAM) was used to obtain approximate analytical solutions to the system of equations in the model. The choice of HAM is made because the method can be used to approximate a nonlinear problem by selecting different sets of base functions effectively. It can also provide an easy way of adjusting and controlling the convergence region and approximation rate when necessary. HAM can be employed even when a nonlinear problem does not contain small/large parameters at all. Thereafter, we presented the h-values where the solutions will converge. The solutions showed that the h-values can be adjusted effectively to obtain the solutions to the system. All mathematical simulations were performed using Maple 14 and MATLAB 2015b. In future research, other methods of approximate analytical solution can be obtained and compared with the solutions obtained here, as well as with numerical solutions. Also, error analysis can be used to determine the degree of accuracy of HAM compared with other methods.

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