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Mathematical Modeling and Analysis of Transmission Dynamics and Control of Hookworms in Obi Local Government Area of Nasarawa State, Nigeria

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Hookworms' infection is common among children living in rural areas in developing countries especially in Sub-Saharan Africa with serious public health significance. This study presents a mathematical modeling and analysis of transmission dynamics and control of hookworms in Obi

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Local Government Area of Nasarawa State, Nigeria. A mathematical model for the transmission of hookworms was developed in an effort to stop the disease. The presence of endemic and disease-free equilibrium points, as well as their stabilities, were the main focus of the model analysis. A mathematical model based on the Susceptible-Exposed-Infected-Treated-Public Health Education-Filariform Larvae (SEITPF) compartments for hookworm revealed that the unique endemic equilibrium point is locally asymptotically stable, provided R_0 >1. Furthermore, the sensitivity analysis of R_0 revealed that the parameters with positive index increases the burden of the diseases while those with negative index decreases the burden of the diseases in the study area. Therefore, the study determined the best way of curbing the spread of hookworm infection and other NTDs in the study area through combined application of treatment, public health education and personal hygiene.

Keywords: Hookworm; mathematical modeling; transmission dynamics; Control.

1. INTRODUCTION

"Hookworm is the most common cause of maternal and childhood illnesses in developing tropical and subtropical countries" [1]. "It is a soil-transmitted helminth infection caused primarily by the nematode parasites called *Ancylostoma duodenale* and *Necator americanus*. The latter is the predominant etiologic agent for hookworm infection [2]. "Hookworm is one of the neglected tropical diseases listed by WHO" [3]. "Neglected tropical diseases resulted in 46-57 million disability-adjusted life years lost and they account the top 4th leading cause of communicable diseases" [4]. "3000–6500 persons lose their lives to hookworm every year. Hookworm compromises an individual's immune system and raises the possibility of contracting diseases like HIV/AIDS, convulsions, portal hypertension, and diarrhea" [5]. "In sub-Saharan Africa, hookworm infection is the most common cause of anemia. *A. duodenale* consumes approximately 150 mL of blood daily, whereas *N. americanus* only consumes 30 mL. Hookworm can have a long-lasting effect on children's cognitive development and performance; it can reduce academic achievement in schools by 20%" (Eniola et al., 2019). "In sub-Saharan Africa, more than 200 million people have been infected with hook worm and 90 million of them were children. In Ethiopia, more than 11 million peoples were infected with hookworm, the third highest burden in sub-Saharan Africa" [6]. "Hookworm infection is endemic and highly prevalent among Nigerians living between latitudes 350 N and 300 S where the disposal of faeces is inadequate or where the environmental conditions such as humidity and temperature favour the development of the infective worm larvae" [7].

Hookworm transmission occurs when third-stage infective filariform larvae come into contact with skin. Hookworm larvae have the ability to actively penetrate the cutaneous tissues, most often those of the hands, feet, arms and legs due to exposure and usually through hair follicles or abraded skfin [8,9]. Following skin penetration, the larvae enter subcutaneous venules and lymphatics to gain access to the host's afferent circulation. Ultimately, they enter the pulmonary capillaries where they penetrate into the alveolar spaces, ascend the brachial tree to the trachea, traverse the epiglottis into the pharynx and are swallowed into the gastrointestinal tract. Larvae undergo two molts in the lumen of the intestine before developing into egg-laying adults approximately five to nine weeks after skin penetration [10-13].

"One of the main risk factors for hookworm infection is living in or travelling to areas with poor sanitation and hygiene" [14] These worms are transmitted through contact with contaminated soil or faeces, and people living in areas without access to clean water or proper sanitation are at a higher risk of infection. Research conducted by Eniola et al., (2019) "among school children in Lafia, Nasarawa State revealed that factors such as the absence of regular wearing of shoes and the absence of proper latrine utilization were significantly associated with hookworm infection. Another risk factor is poverty, as people living in poverty are more likely to live in areas with poor sanitation and may also have limited access to healthcare". Findings from a study by Muslim et al. [15] indicated that "low socioeconomic status was highly associated with Soil-Transmitted Helminth infections". Another study by Misikir et al. [16] also indicated that "poverty was associated with hookworm infection". "Other potential risk factors include walking barefoot, working in jobs that involve contact with soil, and having a weakened immune system" [17,18-20].

Over the years, mathematical models have aided public health officials and policy makers in making decisions about important intervention initiatives. They can also be used as guiding tools for studying the transmission and control of diseases. It has been thought to play a very useful function in the study and comprehension of the dynamics of transmission as well as the efficacy of the various control techniques of numerous infectious diseases. The World Health Organization lists hookworm as one of the deadliest neglected tropical diseases [21,22]. The disease is still widespread in many tropical and subtropical countries, especially in the impoverished African nations, despite multiple intervention efforts to stop its spread [23]. Numerous illnesses' regulation and dissemination have been modeled using mathematical techniques [23]. Therefore, the creation of a mathematical model that will aid in the explanation of the spread and management of hookworm is necessary [24].

2. MATERIALS AND METHODS

2.1 Model Formulation

A deterministic model that describes the transmission dynamics of the Neglected Tropical Diseases (Hookworm) was proposed. The work of Ebrima et al., [23] was extended. In their work, the human sub population was divided into four compartments i.e susceptible humans (S_h), exposed humans (S_h), infected humans (I_h) and treatment humans (T_h). We incorporated the public health Education human on drug treatment which is the compartment (P_h) and also the compartments for the Filariform larvae (F_L) based on the transmission of the diseases was added.

Basic Model Assumptions:

1. All recruitment is carried out in the susceptible class.
2. It is assumed that hookworm transmission occurs when third stage infective filariform larvae come into contact with the skin.
3. Children are more prone and pregnant and lactating women also have an increased risk of anemia from hookworm infections.
4. Contact with the Filariform Larvae is the only means through which susceptible humans becomes exposed to the disease.
5. Treated human can become susceptible again on contact with Filariform Larvae.

2.2 A Compartmental Chart for the Mathematical Model of Hookworm

All recruitment is carried out in the S_h (susceptible compartment) which later moved to the E_h (exposed compartment) which the human population is been exposed with the disease. The infectious class compartment (I_h) is where the human population come in contact with the Filariform Larvae (F_L). The Filariform Larvae is the only means through which susceptible humans becomes exposed to the disease. Infectious humans are treated which is the class T_h (Treatment compartment) through Public Health Education compartment (P_h).

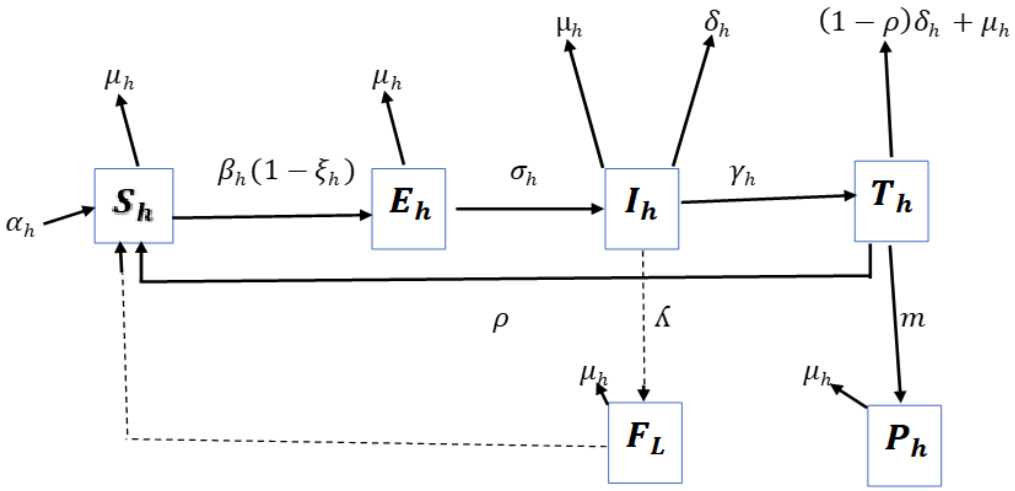


Chart 1. A Compartmental Chart for the Mathematical Model of Hookworm

Table 1. Variable Description

Variable	Description
S_h	Susceptible Human
E_h	Exposed Human
I_h	Infected Human
T_h	Treated Human
P_h	Public Health Education Human
F_L	Filariform Larvae

Table 2. Parameter description

Parameter	Description	Value	References
α_h	Recruitment rate of human	400	Estimate
μ_h	Natural death rate of human	0.00004379	Chiyak *et al.* 2009
β_h	Rate of transmission of humans from susceptible to exposed	0.09753	Kalinda *et al.* 2019
ξ_h	Preventive factor due to WASH	0.1	Ebrima *et al.* 2021
σ_h	Rate of transmission of human from exposure to infectious	0.0236	Ebrima *et al.* 2021
Λ	Rate at which human contact the Filariform Larvae	62	Estimate
ρ	Treatment efficacy	0.8	Ebrima *et al.* 2021
μ_F	Natural death rate of Filariform Larvae	0.2	Assumed
m	Transmission rate of humans from treatment to public health education	0.16	Assumed
γ_h	Transmission rate of humans from infection to treatment	0.3	Woolhouse 1991
δ_h	Death rate of human due to infection	0.002	Assumed

2.3 Model Equation

The model is represented by the following system of ODEs:

$$\frac{dS_h}{dt} = \alpha_h + \rho T_h - (1-\xi_h)\beta_h S_h - \mu_h S_h$$

$$\frac{dE_h}{dt} = (1-\xi_h)\beta_h S_h - \sigma_h E_h - \mu_h E_h$$

$$\frac{dI_h}{dt} = \sigma_h E_h - \gamma_h T_h - \delta_h I_h - \mu_h I_h$$

$$\frac{dT_h}{dt} = \gamma_h T_h - \rho I_h - (1-\rho)\delta_h T_h - \mu_h I_h - mT_h$$

$$\frac{dP_h}{dt} = mT_h - \mu_h P_h$$

$$\frac{dF_L}{dt} = \Lambda I_h - \mu_F F_L$$

With initial conditions $S_h(0) = 40, E_h(0) = 30, I_h(0) = 15, T_h(0) = 10, P_h(0) = 8$ and $F_L(0) = 5$

2.4 Data Analysis

The basic reproduction number R_0 was determined using the next generation matrix and the numerical analysis of the model was conducted using MATLAB.

3. RESULTS

3.1 Mathematical Analysis of the Model

$$\left.\begin{aligned}
\frac{dS_h}{dt} &= \propto_h + eT_h - (1-\xi_h)\beta_h F_L S_h - \mu_h \\
\frac{dB_h}{dt} &= (1-\xi_h)\beta_h F_L S_h - \sigma_h E_h - \mu_h E_h \\
\frac{dI_h}{dt} &= \sigma_h E_h - \gamma_h T_h - \delta_h I_h - \mu_h I_h \\
\frac{dT_n}{dt} &= \gamma_h T_h - (1-\rho)\delta_h T_h - \mu_h I_h - mI_h \\
\frac{dP_h}{dt} &= mT_h - \mu_h P_h \\
\frac{dF_L}{dt} &= \Lambda I_h - \mu_F F_L
\end{aligned}\right\} \quad (1)$$

Let $k_1 = 1 - \xi_h$

$k_2 = 1 - \rho$

So that

$$\left.\begin{aligned}
\frac{dS_h}{dt} &= \propto_h + \rho T_h - k_1\beta_h F_L S_h - \mu_h S_h \\
\frac{dR_h}{dt} &= k_1\beta_h F_L S_h - \sigma_h E_h - \mu_h E_h \\
\frac{dI_h}{dt} &= \sigma_h E_h - \gamma_h T_h - \delta_h I_h - \mu_h I_h \\
\frac{dT_h}{dt} &= \gamma_h T_h - k_2\delta_h T_h - \mu_h I_h - mT_h \\
\frac{dP_h}{dt} &= mT_h - \mu_h P_h \\
\frac{dF_L}{dt} &= \Lambda I_h - \mu_F F_L
\end{aligned}\right\} \quad (2)$$

3.2 Steady States of Equilibrium

The system (2) has two equilibrium points namely, disease free equilibrium point (DFE) and endemic equilibrium point (EE).

1. The Disease-Free Equilibrium Point is defined by

$$\mathrm{E}_0 = (S_h^*, E_h^*, I_h^*, T_h^*, P_h^*, F_L^*)$$

At the disease- free equilibrium, there are no infection or recovering and thus Filariform Laevae is produced. Accordingly, at this point, I_h^* in the system (2) must be zero hence, the point is obtained as:

$$\mathrm{E}_0 = \left(\frac{\propto_h}{\mu_h}, 0, 0, 0, 0, 0\right)$$

Where $I_h^* = 0$

2. Endemic equilibrium Point (EE). At the endemic equilibrium point, all disease states in equation (2) are considered positive and consequently R_h^* must be greater than zero for all states to be positive, i.e $R_0 > 1$. We define by

$$\mathrm{E}_1 = (S_h^{**}, R_h^{**}, I_h^{**}, T_h^{**}, P_h^{**}, F_L^{**})$$

We set the LHS of equation (2) to be zero and solving we obtain

$$S_h^{**} = \frac{\propto_h + eT_h^{**}}{k_1\beta_h F_L^{**} + \mu_h} \tag{3}$$

$$E_h^{**} = \frac{k_1\beta_h F_L^{**} S_h^{**}}{\sigma_n + \mu_h} \tag{4}$$

$$I_h^{**} = \frac{\sigma_h E_h^{**} - \gamma_h T_h^{**}}{\sigma_n + \mu_h} \tag{5}$$

$$T_h^{**} = \frac{\mu_h I_h^{**} - \gamma_h T_h^{**}}{\gamma_n - m - k_2\delta_h} \tag{6}$$

$$P_h^{**} = \frac{mT_h^{**}}{\mu_h} \tag{7}$$

$$F_L^{**} = \frac{\varsigma T_h^{**}}{\mu_h} \tag{8}$$

3.3 Stability Analysis and Basic Reproduction Number (R_0)

The basic reproduction number is defined as the average number of secondary infections caused by the emergence of an infectious individual with a completely susceptible population (Van den Driessche *et al.* 2008). The method of Next Generation Matrix (Ebrima *et al*, 2021) was used.

The model equation (1) is rewritten starting with the new diseases in the system of equation

$$\left.\begin{aligned} \frac{dB_h}{dt} &= (1-\xi_h)\beta_h F_L S_h - \sigma_h E_h - \mu_h E_h \\ \frac{dI_h}{dt} &= \sigma_h E_h - \gamma_h T_h - \delta_h I_h - \mu_h I_h \\ \frac{dF_L}{dt} &= \Lambda I_h - \mu_F F_L \end{aligned}\right\} \tag{9}$$

From (9) f and v are deduced, where f refers to the new infections while v indicates other interactions in the infected compartment. This yield

$$f = \begin{pmatrix} k_1\beta_h F_L S_h \\ 0 \\ 0 \end{pmatrix} \text{ and } v = \begin{pmatrix} \sigma_h E_h + \mu_h E_h \\ \gamma_h T_h + \delta_h I_h + \mu_h I_h - \sigma_h E_h \\ \mu_F F_L - \Lambda I_h \end{pmatrix}$$

Now differentiate f and v partially to yield F and V respectively that is

$$F = \begin{pmatrix} \frac{\partial f_1}{\partial B_h} & \frac{\partial f_1}{\partial I_h} & \frac{\partial f_1}{\partial F_L} \\ \frac{\partial f_2}{\partial B_h} & \frac{\partial f_2}{\partial I_h} & \frac{\partial f_2}{\partial F_L} \\ \frac{\partial f_3}{\partial B_h} & \frac{\partial f_2}{\partial I_h} & \frac{\partial f_3}{\partial F_L} \end{pmatrix} \quad \text{and} \quad V = \begin{pmatrix} \frac{\partial v_1}{\partial E_h} & \frac{\partial v_1}{\partial I_h} & \frac{\partial v_1}{\partial F_L} \\ \frac{\partial v_2}{\partial E_h} & \frac{\partial v_2}{\partial I_h} & \frac{\partial v_2}{\partial F_L} \\ \frac{\partial v_3}{\partial E_h} & \frac{\partial v_2}{\partial I_h} & \frac{\partial v_3}{\partial F_L} \end{pmatrix}$$

$$F = \begin{pmatrix} 0 & 0 & k_1\beta_h S_h \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \sigma_h+\mu_h & 0 & 0 \\ -\sigma_h & \delta_h+\mu_h & 0 \\ 0 & -\Lambda & \mu_F \end{pmatrix} = \begin{pmatrix} k_3 & 0 & 0 \\ -\sigma_h & k_4 & 0 \\ 0 & -\Lambda & \mu_F \end{pmatrix}$$

Where $k_3 = \sigma_h+\mu_h$ and $k_4 = \delta_h+\mu_h$

$$V^{-1} = \frac{1}{|V|}.AdjV$$

$$V^{-1} = \begin{pmatrix} \frac{1}{k_3} & 0 & 0 \\ \frac{\sigma_h}{k_3k_4} & \frac{1}{k_4} & 0 \\ \frac{\Lambda\sigma_h}{k_3k_4\mu_F} & \frac{\varsigma}{k_4\mu_F} & \frac{1}{\mu_F} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} 0 & 0 & k_1\beta_hS_h \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{k_3} & 0 & 0 \\ \frac{\sigma_h}{k_3k_4} & \frac{1}{k_4} & 0 \\ \frac{\Lambda\sigma_h}{k_3k_4} & \frac{\Lambda}{k_4\mu_F} & \frac{1}{\mu_F} \end{pmatrix}$$

$$\begin{pmatrix} \frac{k_1\beta_hS_h^*\Lambda T_h}{k_3k_4\mu_F} & \frac{k_1\beta_hS_h}{k_3\mu_F} & \frac{k_1\beta_hS_h}{\mu_F} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$$R_0 = e(FV^{-1}) = |FV^{-1} - \Lambda I| = 0$$

$$R_0 = \frac{k_1\beta_h\varsigma\sigma_hS_h^*}{k_3k_4\mu_F} > 1 \quad (10)$$

R_0 is positive, $R_0 > 1$ ⇒ Endemic Equilibrium

3.4 Sensitivity Analysis

In this section we determine the significant parameters that increase or decrease the burden of the disease. To do this, we will consider the parameters involved in R_0 and compute;

$$\psi_P R_0 = \frac{\partial R_0}{\partial P} \times \frac{P}{R_0}$$

Where P represents the parameters in R_0

Hence $\psi_{k_1}R_0 = 1$, $\psi_{\beta_h}R_0 = 1$, $\psi_{\varsigma}R_0 = 1$, $\psi_{\delta_h}R_0 = 1$, $\psi_{k_3}R_0 = -1$, $\psi_{k_4}R_0 = -1$, $\psi_{\mu_F}R_0 = -1$

Table 3. Sensitivity analysis

Parameter	Description	Value	Sensitivity Index
k_1	Preventive factor due to WASH (ξ_h)	0.9	+1
β_h	Rate of transmission of humans from susceptible to exposed	0.9153	+1
α_h	Recruitment rate of human	400	+1
δ_h	Death rate of human due to infection	0.002	+1
k_3	Rate of transmission of human from exposure to infectious (σ_h)	0.023644	−1
k_4	Natural death rate of human (μ_h)	0.002044	−1
μ_F	Natural death rate of Filariform Larvae	0.2	−1

Where k_1 = 1-ξ_h, k_3= σ_h + μ_h, k_4= δ_h + μ_h

In Table 3, the parameter with positive sensitivity index are those parameters that have great impact on the expansion or spread of the disease in the community because their values are increasing i.e the increase in the parameters will result in the increase in the burden of the disease. A reduction of these parameters will also reduce the spread of the diseases. On the other hand, the parameters with negative sensitivity index have capacity of minimizing or reducing the burden of the disease.

3.5 Numerical Simulation of the Mathematical Modelling

The numerical simulation results are shown in Figs. 1, 2, 3, 4 and 5 respectively.

Fig. 1 shows the behavior of all the populations of values shown on Table 2. A continuous increase in the filariform larvae and susceptible humans compartment was observed.

There was also a steady rise in the exposed human compartment and stability in other compartments. It can be observed in Fig. 2a that the susceptible humans have risen or increase within the first few days but gradually falls later as they continuously come in contact with the filariform larvae in the soil thereby leading to the greater rise of the filariform larvae compartment (Fig. 2b and Fig. 2c).

We also experienced a steady and then a quick rise in the exposed and infected human compartments. In Fig. 3a, it was observed that there was a great increase in the filariform larvae compartment and stability in all other compartments when 10 people are recruited to the population. In Fig. 3b, there was also an increase in the filariform larvae, susceptible humans and exposed compartments when 400 individuals are been recruited to the population but stability in all other compartments. Similarly, there was also continuous increase in the filariform larvae, susceptible humans and exposed compartments when 900 individuals are been recruited to the population but stability in all other compartments in Fig. 3c.

Also, in Figs. 4a and 4b, there was a steady increase in the susceptible humans and the filariform larvae compartments while in Fig. 4c the treatment human compartments show steady rise within the first few days and later gain stability.

It can be observed from Fig. 5a that there was a continuous increase in the susceptible humans and Filariform Larvae compartments but in Fig. 5b and 5c, the treatment humans compartment maintains a great stability.

1. Impact of the rate of behavior of all the populations

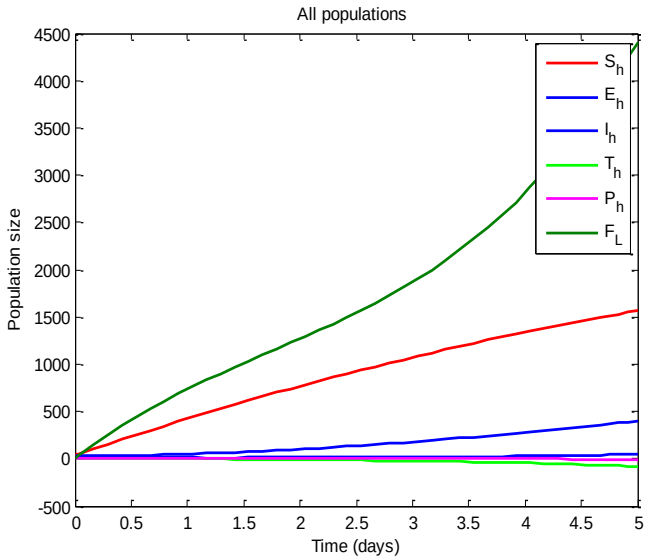
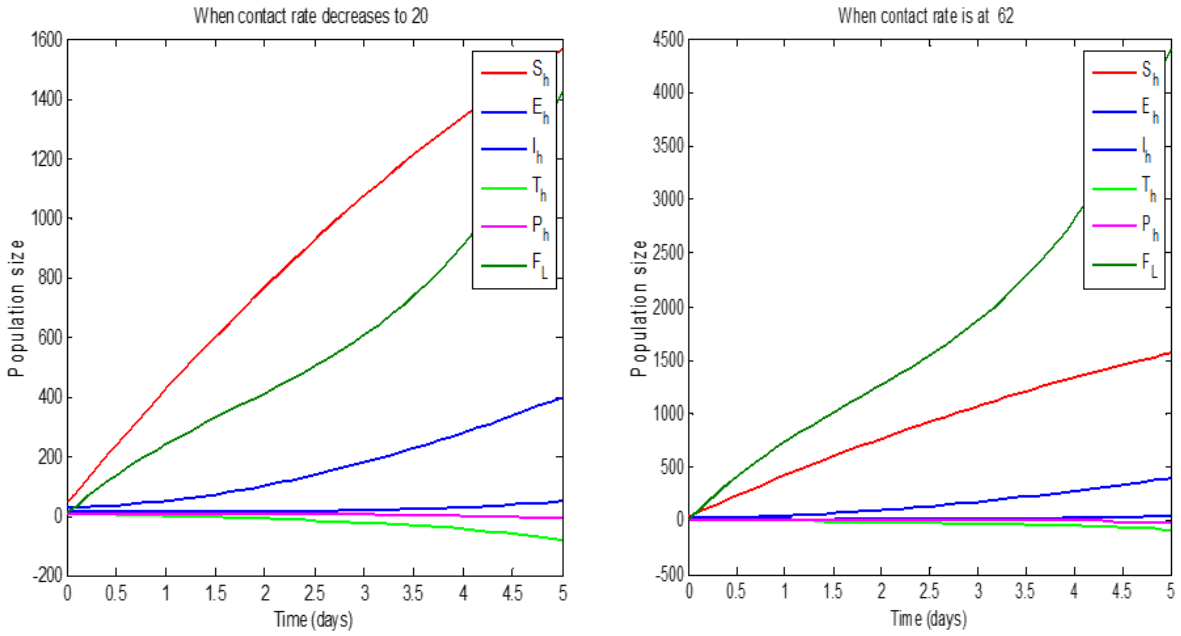
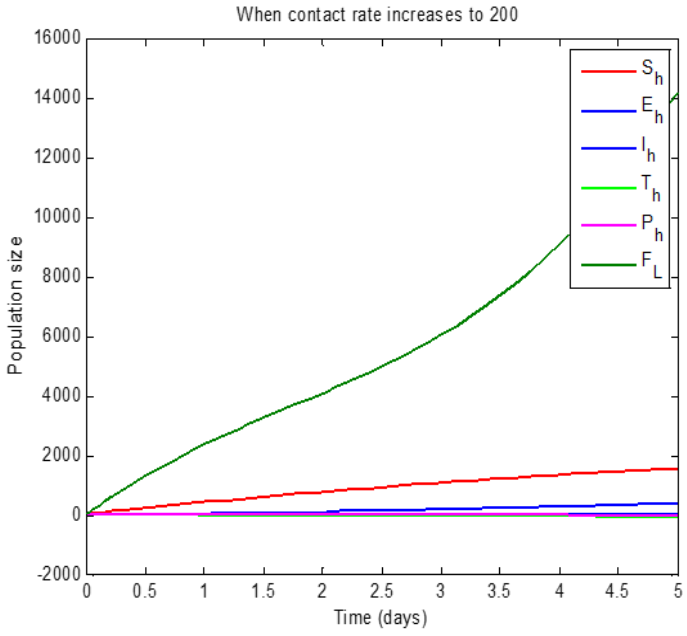


Fig. 1. Illustrate the behavior of all the populations of values shown on the Table 2

2. Impact of the Rate at Which Human Contact Filariform Larvae



(a) **(b)**



(c)

Fig. 2. The rate at which contact rate was varied from 20 to 200 with filariform larvae and all other parameter remains the same as given in Table 2

3. Impact of Recruitment

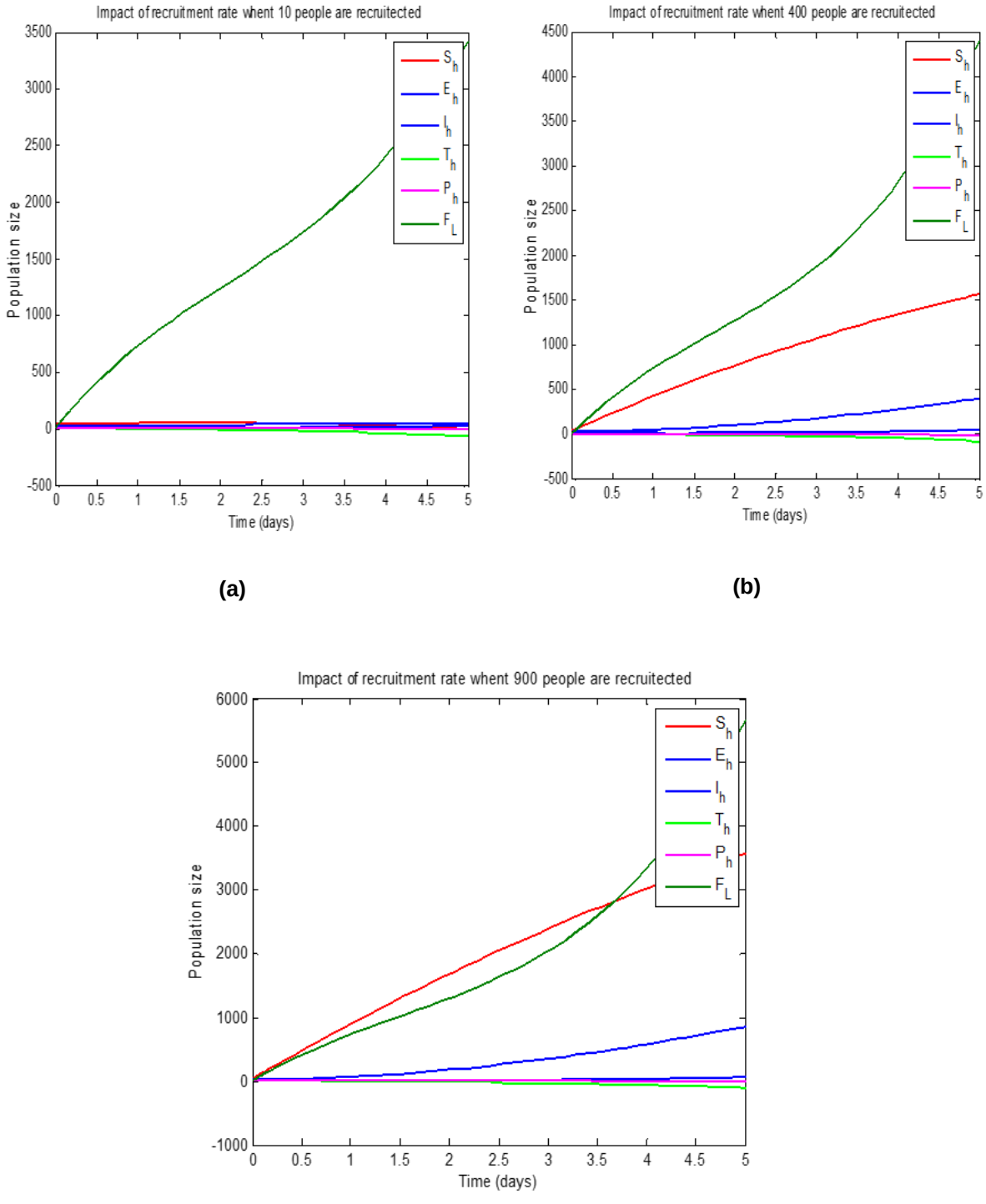
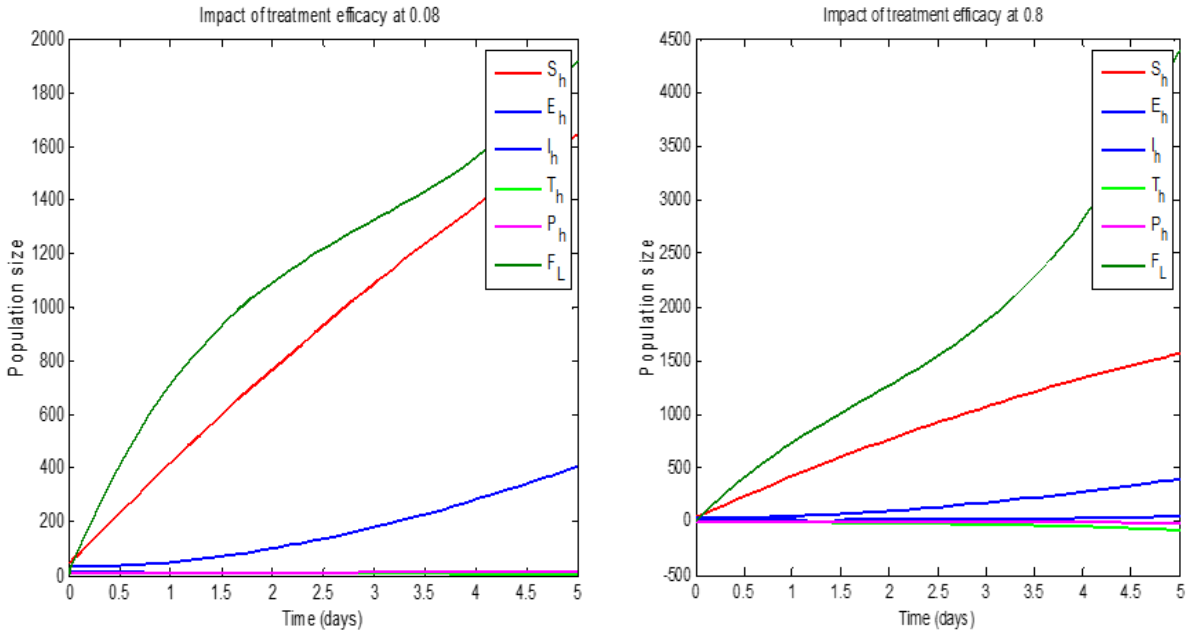
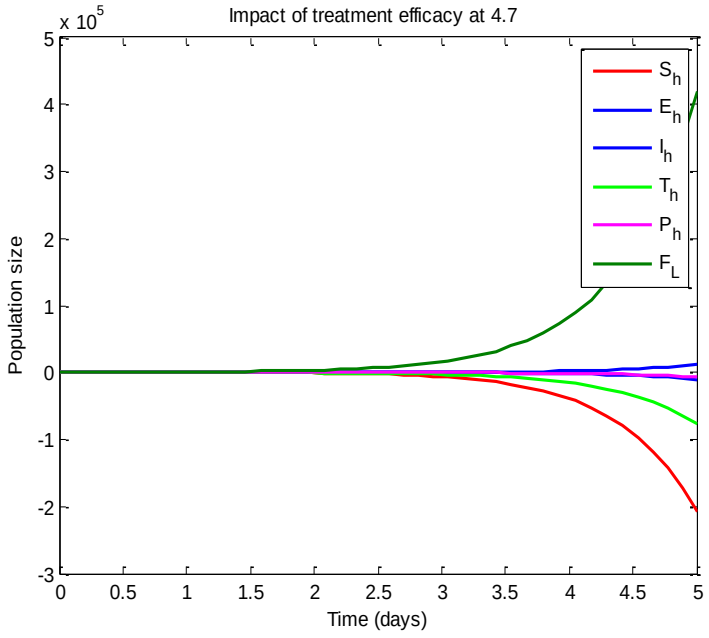


Fig. 3. Graphs showing the effect of recruitment into the entire population

4. Impact of Treatment Efficacy



(a) **(b)**



(c)

Fig. 4. The plots of the treatment rate efficacy varied from 0.08 to 4.7

1. The Effect of Prevention Measure by Wash

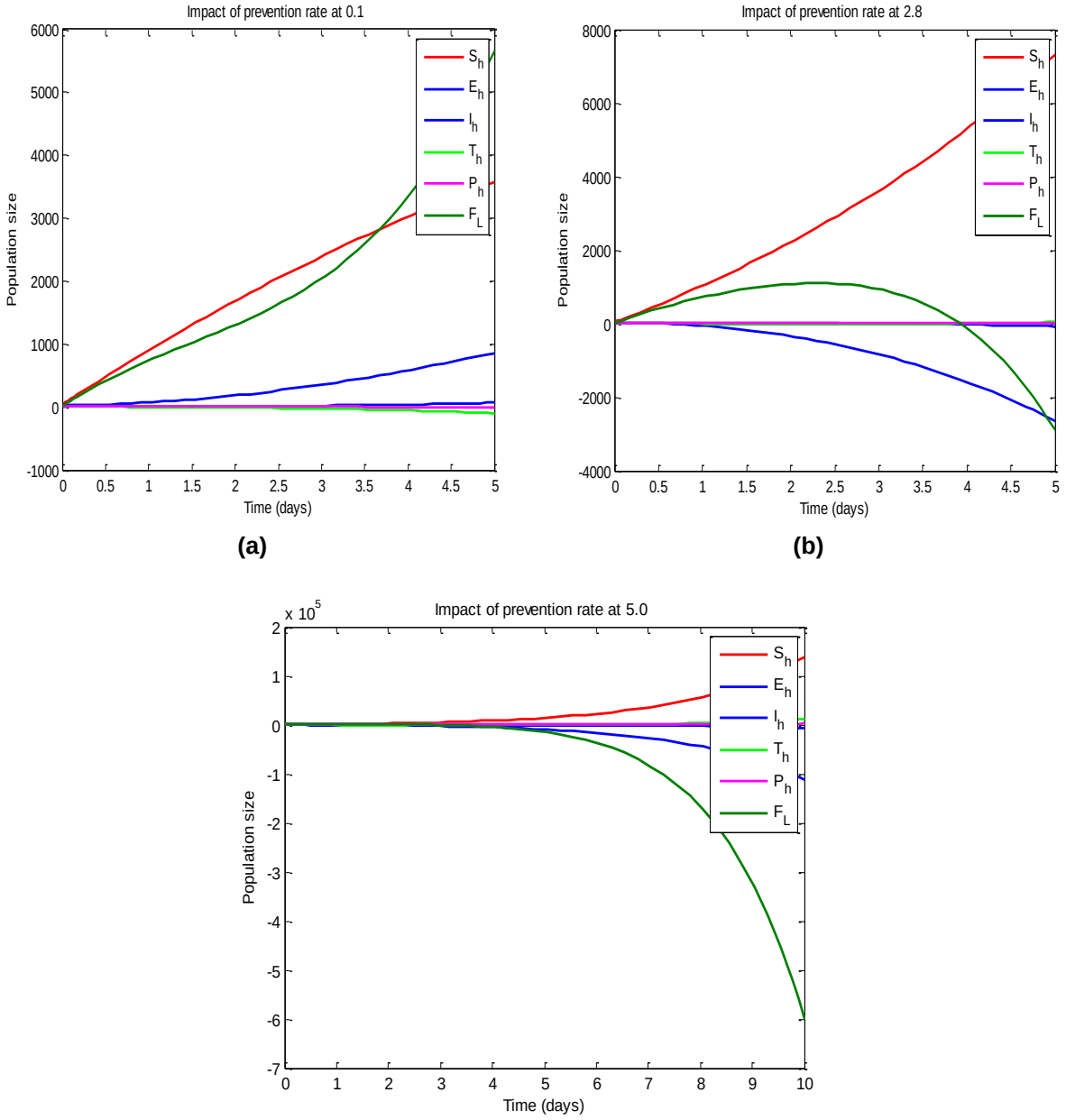


Fig. 5. Demonstrate the prevention measure on the entire population

4. DISCUSSION

In mathematical modelling of epidemiology, it is encouraging and sometimes, imperative to validate the analytical results obtained with numerical simulation. Also, wherever models is/are formulated in the mathematical sense, it is usually required to check the agreement between abstraction of the model and mathematical language formulation which is done using mathematical concepts band properties such as existence and uniqueness solution, equilibrium states etc. Depending on interest, further analysis such as threshold parameter for the spread of diseases, control criteria, the most sensitive conditions that could lead to an outbreak of diseases may be examined. In this study, a mathematical model was proposed to

reveal the dynamics of hookworm. Properties like existence and uniqueness of solution was investigated which shows that the models were well posed in the biological and mathematical senses. An establishment of a disease control parameter popularly referred to as reproduction number (R_0) which proved the chances for successful eradication of Hookworm outbreak.

Initial values for parameters of model were drawn from literature to ensure the reliability and competence of the simulation results with biological framework for the proposed models and where values were not available assume values were adopted. The assigned initial values are presented in Table 2. The equilibrium analysis established two equilibrium states for the model, disease free equilibrium and endemic equilibrium. For the human population. Interestingly, these results are in line with the fact of hookworms in line with Ebrima et al. [12]. The interpretation of the results are: in a state when the society or community will be free of the parasites and a state where there is a persistence of disease in the humans population which is as a results of exposure to filariform larvae.

The results of the threshold parameter for successful management of hookworm is obtained in equation 1 and 2. The implication is that the society will enjoy sound health provided equilibrium (ii) can be well managed (i.e ability to reduce infection and treated already infected individuals). Alternatively, restricting the movement of infected individuals (quarantine) while receiving treatment will go a long way to manage the spread of hookworms. In mathematical sense to force of infection must be less than the removal rate.

Using the ordinary differential equation (ODE) in MATLAB, some numerical simulations were performed using the values of the model parameters in Table 2. Many of the parameters are obtained from existing literature and are rightly cited while some are taken from real life data. Other parameters are estimated based on convenience using what is generally known about the dynamics of the studied population and the parasite. The numerical simulation results are shown in Figs. 1, 2, 3, 4 and 5 respectively.

Fig. 1 shows the behavior of all the populations of values shown on Table 2. A continuous increase in the filariform larvae and susceptible humans compartment was observed. There was a steady rise in the exposed human compartment and stability in other compartments. The study revealed the behaviors of each compartment of the model in the study population.

It can be observed in Fig. 2a that the susceptible humans have risen or increase within the first few days but gradually falls later as they continuously come in contact with the filariform larvae in the soil thereby leading to the greater rise of the filariform larvae compartment (Fig. 2b and Fig. 2c). We also experienced a steady and then a quick rise in the exposed and infected human compartments due to the introduction of the parasite both of which later had a slow rise as the disease spread. This finding revealed that increase contact or exposure of susceptible humans to the filariform larvae can result to the infection of the parasite.

In Fig. 3a, it was observed that there was a great increase in the filariform larvae compartment and stability in all other compartments when 10 people are recruited to the population. In Fig. 3b, there was also an increase in the filariform larvae, susceptible humans and exposed compartments when 400 individuals are been recruited to the population but stability in all other compartments. Similarly, there was also continuous increase in the filariform larvae, susceptible humans and exposed compartments when 900 individuals are been recruited to the population but stability in all other compartments in Fig. 3c. This shows that the greater the number of individuals in a given population, the greater increase and exposure of the susceptible humans to the filariform larvae.

Also, in Fig. 4a and 4b, there was a steady increase in the susceptible humans and the filariform larvae compartments when there was no or little public health awareness or education while in Fig. 4c the treatment human compartments show steady rise within the first few days and later gain stability. This shows that human population who obtained serious public health education maintain stability and reduce rate of contact with filariform larvae which is responsible for the infection of the parasite i.e increase in the public health education can lead to decrease in the contact of susceptible humans to the filariform larvae.

We also observed the effect of treatment in Fig. 5 as the treatment rate efficacy varied from 0.1 to 5.0. Here, we look into how increase in the number of treated infected humans can affect the

number of infected humans and also the production rates of the pathogens. It can be observed from Fig. 5a that there was a continuous increase in the susceptible humans and Filariform Larvae compartments simply because there was no or little preventive measures to reduce the rate of the contact with filariform larvae. But in Fig. 5b and 5c, the treatment humans compartment maintains a great stability simply because a greater prevention rate was introduced and that lead to the greater decreased of the Filariform Larvae compartment. This revealed that Individuals will continue to get infected or re-infected even when treatment is due without combining of with preventive strategies like WASH. WASH is a preventive mechanism in controlling the spread of hookworms. As a result, the susceptible and treated individuals should be educated on WASH procedures to effectively curtail the spread of the disease.

Results of the sensitivity analysis in Table 3 revealed that, the parameters k_1, β_h, α_h, and δ_h have positive indices and therefore, are each directly proportional to the value of R_0. Thus, increasing the value of any of these parameters will lead to the disease remaining endemic within the studied population and vice versa. However, the parameters k_3, k_4, and μ_F have each a negative sensitivity index, which means that each of them varies inversely as the value of R_0. Therefore, a continuous decrease in these parameters will lead to a continuous decrease in the burden of the disease and, hence, contribute to the elimination of the parasite and vice versa.

5. CONCLUSION

A mathematical model that explains the transmission dynamics of the disease (hookworm) involving humans and the dynamics of the free-living filariform larvae has been presented. The disease-free equilibrium and endemic equilibrium points were obtained and analyzed for local stabilities. The existence of a unique endemic equilibrium point when R_0 >1 was established and it is confirmed that the basic reproduction number (R_0) is positive, $R_0 > 1$ which revealed the endemicity of the parasite in the study area. To validate these analytic results, a numerical simulation was carried out. Hence, the mathematical model was able to provide a better control measure which is the Public Health Education for the control and possible eradication of the parasite and other NTDs.
However, Optimal control analysis and cost effectiveness are recommended for further study in order to help decision makers understand best strategies and cost implication to manage the spread of this parasite. Also, global stability analysis is suggested to ensure complete eradication of this parasite.

6. CONTRIBUTION TO KNOWLEDGE

1. The study incorporated the public health Education which is the compartment (P_h) and also the compartments for the Filariform larvae (F_L) based on the transmission of the diseases in the compartmental Chart for the Mathematical Modelling of Hookworm.
2. The use of Mathematical Model in the study has helped to identified public health Education as the most effective control measures against Hookworm and possibly other NTDs.
3. This research work also provided data base information about mathematical modeling and analysis of transmission dynamics and control of hookworms in Obi Local Government Area of Nasarawa State, which other researchers can use for further studies.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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