

## NUMERICAL ANALYSIS OF THE EFFECTS OF MOSQUITO BITING RATE ON THE TRANSMISSION DYNAMICS OF MALARIA

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### Abstract

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*We conduct a simulation experiment on a mathematical model of malaria to access the impact of mosquito biting rate on malaria transmission. The analysis is based on reported malaria data from Baptist Medical Center, Saki, Oyo State from 2007 -2017. Simulation was run for 7 years while maple 18 was used for computations. The numerical results are displayed in tables and graphs. The obtained results showed that as mosquito biting rate increases, there is a decrease in the number of susceptible human population while the number of infected human increases. These results suggest that control strategies should focus more on reducing mosquito biting rate if we are to control malaria infection in the population.*

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**Keywords:** Simulation, Malaria, Equilibrium point, Disease free, Transmission.

### Introduction

Among the vector – borne diseases, malaria is the most prevalent and life – threatening disease and is caused by female anopheles mosquito bite. The mode of spread can be from human to human through blood transfusions, vertically from mother to child [1]. The World Health Organization (WHO) estimates that approximately 50% of the world is at risk of malaria [2].

The disease also causes serious adverse effects in pregnant women such as miscarriage, low birth weight and anemia [3]. Symptoms of malaria include fever, shivers, chills, headache, vomiting, diarrhea and loss of appetite [4].

The dynamics of malaria have been studied by various researchers. [5] developed a SEIR malaria model. They established a stable threshold below diseases – free equilibrium. The numerical results of the computer simulation performed on equations (1) – (4) are presented in the tables 4- 8. These results are plotted for  $S_h$ ,  $I_h$ ,  $S_m$  and  $I_m$  against time ( $t$ ). The graphs are displayed in figures 1 – 5.

### Model Formulation

The model of [6] is given by the following set of First order differential equations:

$$\frac{dS_h}{dt} = \Lambda_h - \beta_1 I_m S_h - \mu_h S_h \quad (1)$$

$$\frac{dI_h}{dt} = \beta_1 I_m S_h - (\delta_h + \mu_h) I_h \quad (2)$$

$$\frac{dS_m}{dt} = \Lambda_m - \beta_2 I_h S_m - \mu_m S_m \quad (3)$$

$$\frac{dI_m}{dt} = \beta_2 I_h S_m - (\delta_m + \mu_m) I_m \quad (4)$$

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The description of the variables and model parameters are given in table 1.

**Table 1: Variable and Model Parameters.**

$S_h$	Number susceptible humans at time t
$S_m$	Number of susceptible mosquitoes at time t
$I_h$	Number of infectious human at time t
$I_m$	Number of infectious mosquitoes at time t
$\Lambda_h$	Recruitment rate of susceptible human
$\Lambda_m$	Recruitment rate of susceptible mosquito
$\beta_1$	Transmission rate of malaria in susceptible human
$\beta_2$	Transmission rate of parasite in susceptible mosquito
$\mu_h$	Natural death rate of human
$\mu_m$	Natural death rate of mosquito
$\delta_h$	Disease-induced death rate human
$\delta_m$	Disease-induced death rate of mosquito

**Numerical Simulation**

The malaria model is fitted to malaria data collected from Baptist Medical Center, Saki, Oyo State using WHO infection rate formula [7]. Following the approach in [8], we perform numerical simulations on the data below.

**Table 2: number of malaria infections in Saki between 2007 – 2017**

Year	Number of infected persons (per 100 populations)
2007	61
2008	59
2009	55
2010	53
2011	52
2012	50
2013	71
2014	76
2015	81
2016	83
2017	88

Source: Baptist Medical Center, Saki, Oyo State.

Following WHO indicator whole country infection rate (biting rate) as given in [7]

$$\text{Infection rate (biting rate)} = \frac{\text{Number of infected cases}}{\text{Total Population}} \quad (5)$$

**Table 3: infection rate of malaria in Saki ( $\beta_1$ )**

Year	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
Infected rate ( $\beta_1$ )	0.61	0.59	0.55	0.53	0.52	0.50	0.71	0.76	0.81	0.83	0.88

**Discussion of Results**

The numerical results in the tables indicate that there is malaria infection. From table 2 to 6, it could be observe that the number of infected human population ( $I_h$ ) also increases with time. This increase in the number of  $I_h$  confirms malaria infection in the population. In addition, the reduction in the number of susceptible individuals as noted from the tables further suggests establishment of infection. The increase in the infection from the tables is consistent with the increase in mosquito biting rate ( $\beta_1$ ), showing the effect of this parameter on malaria transmission in the population. The plots of  $S_h, I_h, S_m, I_m$  against time further confirmed infection. As the value of  $\beta_1$  increased it is seen from the figures that there is a decrease in the population of susceptible humans while there is increase in the number of infected mosquitoes.

**Table 4: Numerical Values of  $S_h(t); S_m(t); I_h(t)$  and  $I_m(t)$  for DFE When  $\beta_1 = 0:61$ .**

t	$S_h(t)$	$S_m(t)$	$I_h(t)$	$I_m(t)$
0	100	60	25	30
1	0.00340298	14.72398624	121.68018891	144.42958143
2	0.04629671	7.3243030515	118.37828925	105.43965532
3	0.00799453	3.60604179	115.17184530	60.51474791
4	0.01508133	1.71844000	112.05644370	31.50683110
5	0.03012958	0.69664247	109.02515288	15.11229484
6	0.06757598	-0.00039543	106.06108063	5.72944348
7	0.25574778	-1.02139411	103.03443351	-1.51024207

**Table 5: Numerical Values of  $S_h(t)$ ;  $S_m(t)$ ;  $I_h(t)$  and  $I_m(t)$  for DFE When  $\beta_1 = 0:53$**

t	$S_h(t)$	$S_m(t)$	$I_h(t)$	$I_m(t)$
0	100	60	25	30
1	0.00465523	12.42483654	121.69158825	126.41310718
2	0.00639710	6.14497803	118.38882814	91.32320252
3	0.01107952	3.00014838	115.18074914	52.12643705
4	0.02098662	1.38107580	112.06225809	26.86952273
5	0.04272261	0.45702304	109.02410518	12.42136410
6	0.10475890	-0.29669530	106.03552973	3.67851091
7	0.69308098	-2.28161801	102.6198411	-5.17143797

**Table 6: Numerical Values of  $S_h(t)$ ;  $S_m(t)$ ;  $I_h(t)$  and  $I_m(t)$  for DFE When  $\beta_1 = 0:76$**

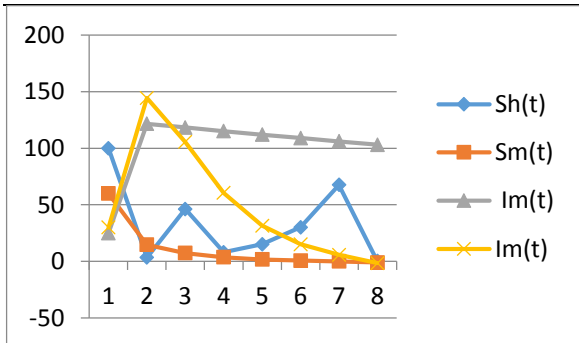
t	$S_h(t)$	$S_m(t)$	$I_h(t)$	$I_m(t)$
0	100	60	25	30
1	0.00234308	17.45619887	121.66596914	168.41381456
2	0.00316684	8.66689261	118.36550931	124.01685651
3	0.00546058	4.28943617	115.16051941	71.48528051
4	0.01028418	2.08760265	112.04772098	37.50220484
5	0.02032970	0.93728187	109.02169540	18.47405274
6	0.04319800	0.24525610	106.072286019	8.03701250
7	0.12156078	-0.43142306	103.15471018	1.38488099

**Table 7: Numerical Values of  $S_h(t)$ ;  $S_m(t)$ ;  $I_h(t)$  and  $I_m(t)$  for DFE When  $\beta_1 = 0:83$**

t	$S_h(t)$	$S_m(t)$	$I_h(t)$	$I_m(t)$
0	100	60	25	30
1	0.00204368	13.38439274	121.66178722	176.81257294
2	0.00275818	9.13080281	118.36095318	130.46894337
3	0.00475484	4.52445808	115.15639641	75.28027621
4	0.00895370	2.21259226	112.04434614	39.56254795
5	0.017661712	1.01510347	109.01975941	19.60750355
6	0.03707295	0.31687158	106.07386260	8.77113448
7	0.09785889	-0.29900380	103.17376129	2.15598414

**Table 8: Numerical Values of  $S_h(t)$ ;  $S_m(t)$ ;  $I_h(t)$  and  $I_m(t)$  for DFE When  $\beta_1 = 0:88$**

t	$S_h(t)$	$S_m(t)$	$I_h(t)$	$I_m(t)$
0	100	60	25	30
1	0.00187217	18.96056949	121.69877969	182.05114497
2	0.00252480	9.41862856	118.33580976	134.48011182
3	0.00435220	4.67004238	115.15379537	77.63602742
4	0.00819527	2.28961009	112.04217863	40.83860296
5	0.01614849	1.06230803	109.01841171	20.30499540
6	0.03367898	0.35879492	106.07443499	9.21421841
7	0.08597391	-0.22732865	103.18278301	2.59660474



**Figure 1: Graph of ( $S_h, I_h, S_m, I_m$ ) against time for disease-free equilibrium when  $\beta_1 = 0.61$   
Parameter values were chosen as follow:  $\beta_1 = 0.61, \Lambda_m = 0.03, \mu_m = 0.7, \mu_h = 0.01, \beta_2 = 0.1, \delta_m = 0.6, \delta_h = 0.02, \Lambda_h = 0.3$**

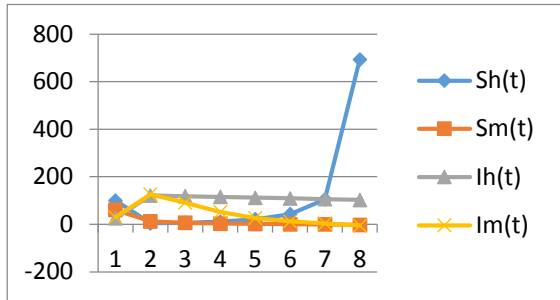


Figure 2: Graph of  $(S_h, I_h, S_m, I_m)$  against time for disease-free equilibrium when  $\beta_1 = 0.53$   
 Parameter values were chosen as follow:  $\beta_1 = 0.53, \Lambda_m = 0.03, \mu_m = 0.7, \mu_h = 0.01, \beta_2 = 0.1, \delta_m = 0.6, \delta_h = 0.02, \Lambda_h = 0.3$

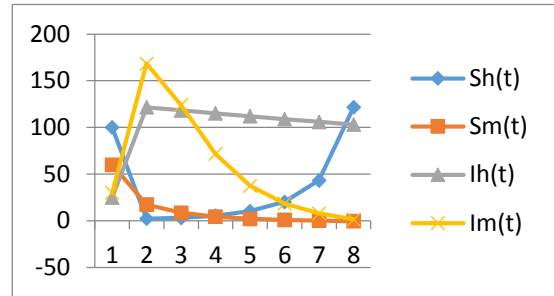


Figure 3: Graph of  $(S_h, I_h, S_m, I_m)$  against time for disease-free equilibrium when  $\beta_1 = 0.76$   
 Parameter values were chosen as follow:  $\beta_1 = 0.76, \Lambda_m = 0.03, \mu_m = 0.7, \mu_h = 0.01, \beta_2 = 0.1, \delta_m = 0.6, \delta_h = 0.02, \Lambda_h = 0.3$

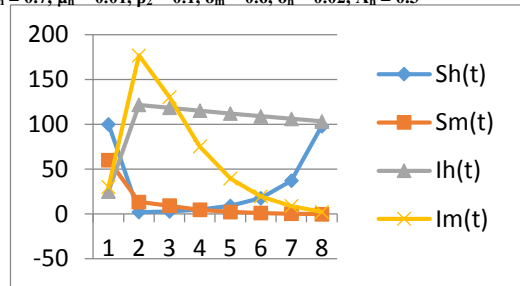


Figure 4: Graph of  $(S_h, I_h, S_m, I_m)$  against time for disease-free equilibrium when  $\beta_1 = 0.83$   
 Parameter values were chosen as follow:  $\beta_1 = 0.83, \Lambda_m = 0.03, \mu_m = 0.7, \mu_h = 0.01, \beta_2 = 0.1, \delta_m = 0.6, \delta_h = 0.02, \Lambda_h = 0.3$

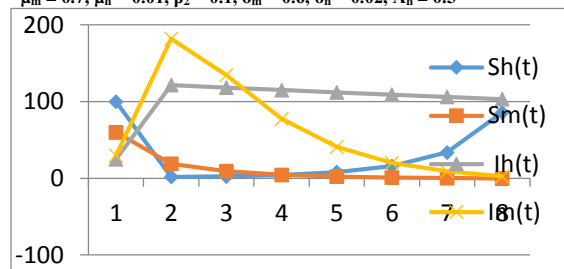


Figure 5: Graph of  $(S_h, I_h, S_m, I_m)$  against time for disease-free equilibrium when  $\beta_1 = 0.88$   
 Parameter values were chosen as follow:  $\beta_1 = 0.88, \Lambda_m = 0.03, \mu_m = 0.7, \mu_h = 0.01, \beta_2 = 0.1, \delta_m = 0.6, \delta_h = 0.02, \Lambda_h = 0.3$

**Conclusion**

The simulation experiment in this paper showed that mosquito biting rate plays a significant role in malaria transmission. Hence, public health practitioners and all malaria stakeholders should formulate policies and evolve strategies towards efficient treatment measures to reduce mosquito biting rate necessary for malaria eradication at the population level.

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