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Climate change potential impacts on mosquito-borne diseases: a mathematical modelling analysis

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Abstract. Climate change and global warming have caused catastrophic effects that are already being felt in Bangladesh. The rise in temperature associated with global warming, as well as the broader impacts of climate change, are damaging the planet. These effects are spatial and temporal and have led to unexpected outcomes, such as the coexistence of humans and mosquitoes in regions where it was previously unimaginable. Despite being the smallest animals on earth, mosquitoes are also the deadliest, killing thousands of humans each year. The Culex mosquito, a common type of mosquito in Bangladesh, is easily accessible and poses a significant threat to human health. The transmission of viruses to humans is a significant concern. This article introduces and discusses the LMSEI-SEIR mathematical model, which can help in understanding this process. The disease-free equilibrium point and its stability are presented, and the reproduction number is calculated. To further investigate the implications of this model, a numerical analysis is conducted using MATLAB. The resulting figures can be used to inform future measures aimed at protecting against human fatalities.

Keywords. Mosquitoes, human, disease free, reproduction number, stability

1 Introduction

Culex mosquitoes typically have a medium size and are brown in color, with some white markings visible on the abdomen. There are several different types of Culex mosquitoes, including Culex pipiens, Culex quinquefasciatus, Culex tritaeniorhynchus, and Culex tarsalis. Culex mosquitoes are commonly referred to as house mosquitoes and are known for spreading viruses such as West Nile virus, filariasis, and Japanese encephalitis. These diseases can affect humans, birds, and other animals. Culex mosquitoes have the ability to transmit viruses to birds, horses, and humans, making them a significant concern. These mosquitoes typically bite at night and rest during the day and can be found both indoors and outdoors. They tend to breed in areas such as containers, floodwater, fresh and polluted water, swamps, and tree holes. Interestingly, Culex mosquitoes tend to stay relatively close to their larval habitats and are capable of flying a distance of approximately 1.5 miles

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A mosquito has four stages of life. That is true for all existing mosquitos. The eggs are in the initial state, turns into larvae, and move to the second stage of their life. The adult is the final stage, known as the deadliest stage of life because it causes the most damage to human beings in such a stage. Before the final stage, larvae turn into pupa, widely known as the third stage of life. The duration of the entire life cycle varies, typically ranging from one week to one month. However, environmental factors such as temperature, rainfall, and humidity can influence this timeframe, sometimes causing the cycle to take less than two weeks or up to a year. The first three stages require water for completion, while adult mosquitoes fly away in search of a blood meal before beginning the cycle anew.

Adult Culex mosquitoes typically have a lifespan of one to two months, but in some cases, they can live for up to six months or longer by hibernating during the winter period. Interestingly, male mosquitoes tend to have a shorter lifespan than females. The development of these mosquitoes' life cycle is heavily influenced by temperature, with the optimal range falling between approximately 2^oC and 32^oC. Ciota et al. [1] conducted research on the development of Culex mosquitoes and found that the optimal temperature for their development is 16^oC. Mosquito development can still occur at temperatures below 24^oC, but as temperatures rise above this threshold, the mortality rate of the mosquitoes increases.

Chitnis et al. [2] introduced a human: SEIR and mosquitoes: SEI model for malaria and examined disease-free equilibrium points while calculating the reproductive number, R_0. They studied the various behaviors of R_0. Ducrot et al. [3] expanded upon the work of [2] by considering a non-immune host: SEIS, a semi-immune host: SEIRS, and a mosquito: SEI model. They derived an explicit formula for the reproductive number, R_0. Buonomo and Vargas-De-Leon [4] provided a condensed version of the studies conducted by [2, 3]. They introduced human: SI and mosquitoes: SI models for malaria, omitting the exposed class of both humans and mosquitoes. They also calculated the basic reproductive number and demonstrated that if $R_0 > 1$, the disease will spread and persist within its host population, while $R_0 < 1$ would result in the disease dying out. They further discussed local and global stability.

Later on, Li [5] examined a discrete-time model for malaria, which consisted of human: SEIR and mosquito: SEI components. The author analyzed the disease-free equilibrium point and derived an explicit expression for the reproductive number, R_0. Li and Jin [6] proposed a continuous-time model for humans: SIR and mosquitoes: SI, which applies to various diseases such as dengue, malaria, and WNV. The model incorporates the logistic growth of the mosquito population and examines the stability of the disease-free equilibrium when $R_0 < 1$. Additionally, the study investigates different types of bifurcations resulting from parameter changes. Ngonghala et al. [7] introduced an SI-SI model for malaria disease, which is an autonomous model. They computed the reproduction number, analyzed the stability of equilibria, and discussed various bifurcations and chaotic dynamics in the model.

Traore et al. [8] examined the effects of seasonal patterns on the transmission of malaria, both theoretically and through numerical simulations. They introduced a mathematical model that incorporated the dynamics of both humans (SEIR model) and mosquitoes (EgLSEI model). The results of their investigation indicated that decreasing the number of breeding sites could be an effective measure in reducing the spread of malaria. However, it is important to note that this research did not account for the influence of seasonal variations on the life cycle of mosquitoes. Bakary et al. [9] put forward an intricate mathematical model that divides the human population into two distinct groups: non-immune individuals and semi-immune individuals.

To represent the non-immune group, they utilized the SEI model, while the semi-immune group was represented by the SEIR model. Additionally, they incorporated a separate group to account for mosquitoes, employing the LSEI model. Their primary emphasis revolved around disease-free equilibrium and associated analytical methods. They discovered that the threshold parameter κ plays a crucial role in regulating disease transmission. Ibrahim et al. [10] examined the influence of knowledge and understanding of malaria and its significance in managing the disease. To explore the dynamics of malaria transmission, the researchers proposed a mathematical model that took into account both the human population and the mosquito population [11]. Specifically, they utilized the SEI_1I_2R model for humans, where I_1 represented the class of infected individuals who were unaware of their infection, and I_2 represented the class of infected individuals who were aware of their condition. Additionally, they employed the SEI model for mosquitoes. They found that awareness plays a crucial role in controlling malaria in regions with a high risk of infection.

In a later study, Al Basir and Abraha [12] introduced a mathematical model aimed at effectively managing and reducing the transmission of malaria. To achieve this, they employed simple yet effective modeling techniques, specifically targeting the interactions between humans and mosquitoes. By utilizing the well-established SIS (Susceptible-Infectious-Susceptible) model for humans and the SI (Susceptible-Infectious) model for mosquitoes, they were able to gain insights into the dynamics of malaria transmission. They identified social media as a highly effective tool for raising awareness about malaria transmission. They emphasized that utilizing social media platforms could result in widespread awareness at a relatively low cost.

Ndamuzi and Gahungu [13] examined how malaria transmission operates in Burundi, an East African nation. They utilized two models, namely the SLIR model for humans and the SI model for mosquitoes, to investigate this phenomenon. The study highlighted that a notable reduction in the transmission of malaria can be achieved by decreasing the frequency of mosquito bites, thereby leading to a significant decline in the mosquito population. Wyse et al. [14] examined the effects of genetically modified mosquitoes on the prevention of malaria. They analyzed various factors including human and mosquito populations using SEIS and SEI models, as well as heterozygous and homozygous transgenic mosquitoes using SEI models for each group. The researchers discovered that the introduction of transgenic mosquitoes is significant in reducing disease transmission. However, they also identified climate change as a potential limitation to their effectiveness.

Mosquito-borne diseases pose significant threats to public health, particularly in tropical and subtropical regions. Mathematical models play a crucial role in understanding the dynamics of these diseases and informing effective control strategies. One such model, the LMSEI-SEIR model, integrates the life stages of mosquitoes and humans to capture the complex interactions and transmission dynamics. The existing research on the LMSEI-SEIR model, highlighting its applications, extensions, and key findings is not enough to deal with the situations in the region where summer is the most frequent part for such insects. As far as the author is aware, there has been limited research done on the impact of intraspecific competition among aquatic mosquitoes and the presence of adult male mosquitoes in disease transmission models.

Therefore, the objective of this paper is to fill this research gap by proposing an LMSEI-SEIR mathematical model that takes into account these factors in the context of Bangladesh.

The primary aim of the model is to investigate the disease-free equilibrium point and its stability, as well as to calculate the reproduction number. The model will be developed by considering the interactions among different mosquito life stages, including eggs, larvae, pupae, and adults, and the impact of environmental factors such as temperature and humidity. The presence of adult male mosquitoes will also be taken into account, as they have a different life span than adult female mosquitoes and can play a role in disease transmission.

2 Framework of the Mathematical Model

The mosquito life cycle consists of four stages that can be subdivided into two parts: the aquatic phase, which includes the egg, larva, and pupa, and the adult phase. In this study, we utilized a logistic growth model to describe the population dynamics of aquatic mosquitoes, as suggested by Noden et al. [15] due to the realistic intraspecific competition rate. Additionally, we considered the adult mosquito stage in our model. This study assumes a constant population of both mosquitoes and humans. The human population is divided into four categories: susceptible, exposed, infected, and recovered. Meanwhile, the mosquito population is divided into five categories: aquatic, male adult, female susceptible, exposed, and infected. Let us consider the following state variables: with the parameters:

Symbol	**Description**
L_m	The population of aquatic mosquitoes
M_m	The population of male adult mosquitoes
S_m	The population of susceptible female adult mosquitoes
E_m	The population of exposed female adult mosquitoes
I_m	The population of infected female adult mosquitoes
S_h	The population of susceptible human
E_h	The population of exposed human
I_h	The population of infected human
R_h	The population of recovered human

Table 1: Description of Population Symbols

The LMSEI-SEIR model has been extensively applied to various mosquito-borne diseases, such as dengue, Zika, and Chikungunya. Researchers have utilized the model to analyze disease transmission dynamics, evaluate control strategies, and predict the impact of interventions. These applications have provided valuable insights into the key factors influencing disease spread, such as mosquito biting rates, transmission rates, and population sizes. Hence, the dynamics of the LMSEI-SEIR model can be mathematically modeled using the following system of differential equations:

Symbol	Description
r_m	The per-capita birth rate of mosquitoes
r_h	The per-capita birth rate of human
δ	The per-capita maturation rate of mosquitoes
d_l	The per-capita death rate of aquatic mosquitoes
$\bar{k}$	The intraspecific competition rate of aquatic mosquitoes
p	Total percentage population of male adult mosquitoes
b_m	The per-capita biting rate of mosquitoes
β_m	Transmission rate from an infected human to mosquitoes
β_h	Transmission rate from infected mosquitoes to human
k_1	Per-capita transition rate from exposure to infected mosquitoes
k_2	Per-capita transition rate from exposure to infected human
d_m	The per-capita death rate of adult mosquitoes
d_h	The per-capita death rate of human
ϵ	Per-capita transition rate from recovered to susceptible human
μ	The per-capita mortality rate due to the mosquito-borne disease
γ	Per-capita recovery rate due to the mosquito-borne disease
N_m	Total population of mosquitoes
N_h	Total population of human

Table 2: Description of Parameters

$$\begin{cases} \frac{dL_m}{dt} &= r_m N_m - \delta L_m - d_l L_m - \bar{k} L_m^2, \\ \frac{dM_m}{dt} &= p\delta L_m - d_m M_m, \\ \frac{dS_m}{dt} &= (1-p)\delta L_m - \frac{b_m \beta_m}{N_h} S_m I_h - d_m S_m, \\ \frac{dE_m}{dt} &= \frac{b_m \beta_m}{N_h} S_m I_h - k_1 E_m - d_m E_m, \\ \frac{dI_m}{dt} &= k_1 E_m - d_m I_m \\ \frac{dS_h}{dt} &= r_h N_h - \frac{b_m \beta_h}{N_m} S_h I_m - d_h S_h + \epsilon R, \\ \frac{dE_h}{dt} &= \frac{b_m \beta_h}{N_m} S_h I_m - d_h E_h - k_2 E_h, \\ \frac{dI_h}{dt} &= k_2 E_h - d_h I_h - \mu I_h - \gamma I_h, \\ \frac{dR_h}{dt} &= \gamma I_h - d_h R_h - \epsilon R_h, \end{cases} \tag{2.1}$$

where all the parameters are positive numbers with the initial values belonging to the set

$$R_+^9 = \left\{ (L_m, M_m, S_m, E_m, I_m, S_h, E_h, I_h, R_h) \in \mathbb{R}^9 \right\},$$

where

$$\left\{ L_m \geq 0, M_m \geq 0, S_m \geq 0, E_m \geq 0, I_m \geq 0, S_h \geq 0, E_h \geq 0, I_h \geq 0, R_h \geq 0 \right\}.$$

As the interaction functions on the right-hand side of the system (2.1) are continuous and possess continuous partial derivatives, it can be noted that a unique and existing solution of the system (2.1) is guaranteed.

3 Basic Reproduction Number

The subsequent section presents a discussion and analysis of all feasible equilibrium points, their stability, and the basic reproduction number. The existence and uniqueness of the solution of Eq. (2.1) can be ensured since all interaction functions provided on the right-hand side of the system are continuous and possess continuous partial derivatives. Model (2.1) has a disease-free equilibrium point, which is referred to as

$$E_0 = (L_m^*, M_m^*, S_m^*, 0, 0, S_h^*, 0, 0, 0),$$

where L_m^*, M_m^*, and S_m^* are the equilibrium values of L_m, M_m, and S_m, respectively, and S_h^* is the equilibrium value of S_h.

$$M_m^* = \frac{p\delta L_m^*}{d_m}, \quad S_m^* = \frac{(1-p)\delta L_m^*}{d_m}, \quad S_h^* = \frac{r_h N_h}{d_h}.$$

$$L_m^* = \frac{-(\delta + d_l) + \sqrt{(\delta + d_l)^2 + 4r_m N_m \bar{k}}}{2\bar{k}}.$$

Now, to compute the basic reproduction number of the Eq. (2.1) using the next-generation matrix technique [16], [17], the non-negative matrix F of the infection terms (E_m, I_m, E_h, I_h) and the non-singular matrix V of transition terms are computed by

$$F = \begin{pmatrix} 0 & 0 & 0 & \frac{b_m \beta_m}{N_h} S_m \\ 0 & 0 & 0 & 0 \\ 0 & \frac{b_h \beta_h}{N_m} S_h & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} d_m + k_1 & 0 & 0 & 0 \\ -k_1 & d_m & 0 & 0 \\ 0 & 0 & d_h + k_2 & 0 \\ 0 & 0 & -k_2 & \gamma + \mu + d_h \end{pmatrix}.$$

Therefore, it is obtained that

$$V^{-1} = \begin{pmatrix} \frac{1}{(d_m + k_1)} & 0 & 0 & 0 \\ \frac{k_1}{d_m(d_m + k_1)} & \frac{1}{d_m} & 0 & 0 \\ 0 & 0 & \frac{1}{(d_h + k_2)} & 0 \\ 0 & 0 & \frac{k_2}{(\gamma + \mu + d_h)(d_h + k_2)} & \frac{1}{\gamma + \mu + d_h} \end{pmatrix}.$$

Then the basic reproduction number R_0 is defined as the spectral radius of the basic reproduction matrix FV^{-1} at the E_0 is

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{(1-p)\delta b_m k_2 \beta_m L_m^*}{(\gamma + \mu + d_h) d_m (d_h + k_2) N_h} & \frac{(1-p)\delta b_m \beta_m L_m^*}{(\gamma + \mu + d_h) d_m N_h} \\ 0 & 0 & 0 & 0 \\ \frac{b_m k_1 N_h r_h \beta_h}{d_h d_m (d_m + k_1) N_m} & \frac{b_m N_h r_h \beta_h}{d_h d_m N_m} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

Hence, the reproduction number is computed as

$$R_0 = \left(\frac{(1-p)\delta b_m^2 k_1 k_2 r_h \beta_h \beta_m L_m^*}{d_h d_m^2 (\gamma + \mu + d_h)(d_m + k_1)(d_h + k_2) N_m} \right)^{1/2}. \tag{3.1}$$

Endemic equilibrium point E_1:

$$E_1 = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9),$$

where $x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8$, and x_9 are the positive solutions of the system:

$$\begin{cases} r_m N_m - \delta L_m - d_l L_m - \bar{k} L_m^2 = 0, \\ p\delta L_m - d_m M_m = 0, \\ (1-p)\delta L_m - \frac{b_m \beta_m}{N_h} S_m I_h - d_m S_m = 0, \\ \frac{b_m \beta_m}{N_h} S_m I_h - k_1 E_m - d_m E_m = 0, \\ k_1 E_m - d_m I_m = 0, \\ r_h N_h - \frac{b_m \beta_h}{N_m} S_h I_m - d_h S_h + \epsilon R_h = 0, \\ \frac{b_m \beta_h}{N_m} S_h I_m - d_h E_h - k_2 E_h = 0, \\ k_2 E_h - d_h I_h - \mu I_h - \gamma I_h = 0, \\ \gamma I_h - d_h R_h - \epsilon R_h = 0. \end{cases} \tag{3.2}$$

Now, the local stability results of the disease-free equilibrium point can be summarized in the following theorem:

Theorem 3.1: The disease-free equilibrium point of the system (2.1) is locally asymptotically stable provided that $R_0 < 1$, and unstable for $R_0 > 1$.

Proof: Direct computation of the Jacobian matrix of the system (2.1) at E_0 is given by

$$J(E_0) = \begin{bmatrix} -\delta - d_l - 2\bar{k}L_m^* & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ p\delta & -d_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \delta - p\delta & 0 & -d_m & 0 & 0 & 0 & 0 & -\frac{(1-p)\delta b_m \beta_m L_m^*}{d_m N_h} & 0 \\ 0 & 0 & 0 & -d_m - k_1 & 0 & 0 & 0 & \frac{(1-p)\delta b_m \beta_m L_m^*}{d_m N_h} & 0 \\ 0 & 0 & 0 & k_1 & -d_m & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\frac{b_m N_h r_h \beta_h}{d_h N_m} & -d_h & 0 & \epsilon \\ 0 & 0 & 0 & 0 & 0 & \frac{b_m N_h r_h \beta_h}{d_h N_m} & 0 & -d_h - k_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & k_2 & -\gamma - \mu - d_h & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma & -\epsilon - d_h \end{bmatrix}.$$

Then the characteristic polynomial equation of $J(E_0)$ can be written as

$$(-\epsilon-\lambda-d_h)(\lambda+d_h)(-\lambda-d_m)(\lambda+d_m)(-\delta-\lambda-d_l-2\bar{k}L_m^*)\left(\lambda^4 + A_1\lambda^3 + A_2\lambda^2 + A_3\lambda + A_4\right) = 0, \tag{3.3}$$

where

$$A_1 = (\gamma + \mu + 2d_h + 2d_m + k_1 + k_2),$$

$$A_2 = (\gamma + \mu + d_h)(d_h + k_2) + (\gamma + \mu + 2d_h)(2d_m + k_1) + d_m^2 + d_m k_1 + (2d_m + k_1)k_2,$$

$A_3 = 2d_h d_m (\gamma + \mu + d_h)(d_h + k_2) + k_1 (\gamma + \mu + d_h)(d_h + k_2)(d_h + k_2) + (\gamma + \mu + 2d_h)$
$(d_h + k_2)(d_m^2 + d_m k_1) + (d_m^2 + d_m k_1)k_2),$
$A_4 = (\gamma + \mu + d_h)(d_m^2 + d_m k_1)(d_h + k_2) - \frac{((1-p)\delta b_m^2 k_1 k_2 N_h r_h L_m^* \beta_h \beta_m)}{d_h d_m N_h N_m}$
$= (\gamma + \mu + d_h)(d_m^2 + d_m k_1)(d_h + k_2)\left[1 - R_0^2\right].$

From the characteristic polynomial equation (3.3), it is obtained that

$$\lambda_1 = -\delta - d_l - 2\bar{k}L_m^*, \quad \lambda_2 = \lambda_3 = -d_m, \quad \lambda_6 = -d_h, \quad \text{and} \quad \lambda_9 = -\epsilon - d_h,$$

are negative eigenvalues. However, from the other factor of Eq.(3.3) it is observed that A_1, A_2, and A_3 are positive, while A_4 is positive provided that condition $R_0 < 1$ is satisfied. Moreover, direct computation shows that $R_0 < 1$ guarantees that the two expressions $A_1A_2 - A_3$

and $(A_1A_2 - A_3)A_3 - A_1^2A_4$ are positive. Hence, according to the Routh–Hurwitz criterion, the fourth-order polynomial equation in Eq.(3.3) has four roots (eigenvalues) with negative real parts. Thus, E_0 is a locally asymptotically stable point.

On the other hand, when $R_0 > 1$ then $A_4 < 0$. Hence, according to Descartes's rules of signs, the fourth-order polynomial equation in Eq.(3.3) has at least one positive root. Thus, E_0 is an unstable point.

Theorem 3.2: The endemic equilibrium point of the system (2.1) is locally asymptotically stable provided that the following conditions are met:

$$\begin{cases} d_m + \frac{b_m x_8 \beta_m}{N_h} > \frac{b_m x_3 \beta_m}{N_h}, \\ d_m + k_1 > \left(\frac{b_m x_8 \beta_m}{N_h} + \frac{b_m x_3 \beta_m}{N_h} \right), \\ d_m > k_1 \\ d_h + \frac{b_m x_5 \beta_h}{N_m} > \left(\frac{b_m x_6 \beta_h}{N_m} + \epsilon \right), \\ d_h + k_2 > \left(\frac{b_m x_6 \beta_h}{N_m} + \frac{b_m x_5 \beta_h}{N_m} \right), \\ \gamma + \mu + d_h > k_2, \\ \epsilon + d_h > \gamma. \end{cases} \tag{3.4}$$

Proof. Direct computation of the Jacobian matrix of the system (2.1) at E_1 is given by

$$J(E_1) = \begin{bmatrix} -\delta - d_l - 2\bar{k}x_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ p\delta & -d_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \delta - p\delta & 0 & -d_m - \frac{b_m x_8 \beta_m}{N_h} & 0 & 0 & 0 & -\frac{b_m x_3 \beta_m}{N_h} & 0 & \\ 0 & 0 & \frac{b_m x_8 \beta_m}{N_h} & -d_m - k_1 & 0 & 0 & 0 & \frac{b_m x_3 \beta_m}{N_h} & 0 \\ 0 & 0 & 0 & k_1 & -d_m & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\frac{b_m x_6 \beta_h}{N_m} & -d_h - \frac{b_m x_5 \beta_h}{N_m} & 0 & 0 & \epsilon \\ 0 & 0 & 0 & 0 & \frac{b_m x_6 \beta_h}{N_m} & \frac{b_m x_5 \beta_h}{N_m} & -d_h - k_2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & k_2 & -\gamma - \mu - d_h & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma & -\epsilon - d_h \end{bmatrix}.$$

It is well known that the point E_1 is locally asymptotically stable if and only if all the eigenvalues of $J(E_1)$ lie entirely in the left half of the complex plane. Now, from Gershgorin's theorem (Allen, [18]), since the entries of $J(E_1)$ are real, if the diagonal elements of $J(E_1)$ satisfy $|a_{ii}| > r_i$, where $r_i = \sum_{j=1, j\neq i}^{n} |a_{ij}|$ with n being the size of the matrix, for $i = 1, 2, \ldots, n$, then the eigenvalues of $J(E_1)$ are negative or have negative real parts. Consequently, straightforward computation shows that the given conditions guarantee that Gershgorin's theorem condition is satisfied, and hence all the eigenvalues fall in the disks that lie in the left half of the complex plane. Thus the proof is done.

Studies utilizing the LMSEI-SEIR model have contributed significantly to our understanding of mosquito-borne diseases. Key findings include the identification of critical thresholds for disease persistence, the influence of mosquito control measures on disease prevalence, and the impact of human and mosquito demographic factors on disease dynamics [19]. These detections have substantial essences for conceiving effective prevention and control strategies, such as vector control interventions and vaccination campaigns.

4 Analysis of Endemic Equilibrium Points

Let us set the following equations to zero:

$$\frac{dL_m}{dt} = 0, \quad \frac{dM_m}{dt} = 0, \quad \frac{dS_m}{dt} = 0, \quad \frac{dE_m}{dt} = 0, \quad \frac{dI_m}{dt} = 0,$$

$$\frac{dS_h}{dt} = 0, \quad \frac{dE_h}{dt} = 0, \quad \frac{dI_h}{dt} = 0, \quad \frac{dR_h}{dt} = 0.$$

It gives that

$$\begin{cases} r_m N_m - \delta L_m - d_l L_m - \bar{k} L_m^2 = 0, \\ p\delta L_m - d_m M_m = 0 \\ (1-p)\delta L_m - \frac{b_m \beta_m}{N_h} S_m I_h - d_m S_m = 0, \\ \frac{b_m \beta_m}{N_h} S_m I_h - k_1 E_m - d_m E_m = 0, \\ k_1 E_m - d_m I_m = 0 \\ r_h N_h - \frac{b_m \beta_h}{N_m} S_h I_m - d_h S_h + \epsilon R_h = 0, \\ \frac{b_m \beta_h}{N_m} S_h I_m - d_h E_h - k_2 E_h = 0, \\ k_2 E_h - d_h I_h - \mu I_h - \gamma I_h = 0, \\ \gamma I_h - d_h R_h - \epsilon R_h = 0. \end{cases} \tag{4.1}$$

Let us assume that

$$a_1 = r_m N_m, \quad a_2 = \delta + d_l, \quad a_3 = \bar{k}, \quad a_4 = p\delta, \quad a_5 = d_m, \quad a_6 = (1-p)\delta,$$

$$a_7 = \frac{b_m \beta_m}{N_h}, \quad a_8 = k_1 + d_m, \quad a_9 = k_1, \quad a_{10} = \frac{b_m \beta_h}{N_h}, \quad a_{11} = d_h, \quad a_{12} = \epsilon,$$

$$a_{13} = r_h N_h, \quad a_{14} = d_h + k_2, \quad a_{15} = k_2, \quad a_{16} = d_h + \mu + \gamma,$$

$$a_{17} = \gamma, \quad a_{18} = d_h + \epsilon.$$

It gives us a simplified non-linear form of equations:

$$a_1 - a_2 L_m - a_3 L_m^2 = 0,$$

$$a_4 L_m - a_5 M_m = 0,$$

$$a_6 L_m - a_7 S_m I_h - a_5 S_m = 0,$$

$$a_7 S_m I_h - a_8 E_m = 0,$$

$$a_9 E_m - a_5 I_m = 0,$$

$$-a_{10} S_h I_m - a_{11} S_h + a_{12} R_h + a_{13} = 0,$$

$$a_{10} S_h I_m - a_{14} E_h = 0,$$

$$a_{15} E_h - a_{16} I_h = 0,$$

$$a_{17} I_h - a_{18} R_h = 0.$$

Solving this system of nonlinear equations for $(L_m, M_m, S_m, E_m, I_m, S_h, E_h, I_h, R_h)$, we get $E_1 = (x_1,\ x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$, where

$$\begin{cases} x_8 = B_1 x_7, \\ x_9 = B_2 x_7, \\ x_6 = B_3 x_7 + B_4, \\ x_5 = \frac{x_7}{B_5 x_7 + B_6}, \\ x_4 = \frac{B_7 x_7}{B_5 x_7 + B_6}, \\ x_3 = \frac{B_8}{B_5 x_7 + B_6}, \\ x_1 = B_9 \left(\frac{B_{10} x_7 + a_5}{B_5 x_7 + B_6} \right), \\ x_2 = B_{11} \left(\frac{B_{10} x_7 + a_5}{B_5 x_7 + B_6} \right), \end{cases}$$

where

$$B_1 = \frac{a_{15}}{a_{16}},\ B_2 = \frac{a_{17} a_{15}}{a_{18} a_{16}}, B_3 = \frac{a_{12} B_2 - a_{14}}{a_{11}}, B_4 = \frac{a_{13}}{a_{11}},\ B_5 = \frac{a_{10} B_3}{a_{14}}, B_6 = \frac{a_{10} B_4}{a_{14}}$$

$$B_7 = \frac{a_5}{a_9},\ B_8 = \frac{a_8 B_7}{a_7 B_1},\ B_9 = \frac{B_8}{a_6},\ B_{10} = a_7 B_1,\ B_{11} = \frac{a_4 B_9}{a_5},$$

while x_7 is a positive root of the second-order equation:

$$a_1 (B_5 x_7 + B_6)^2 - a_2 B_9 \left(B_{10} x_7 + a_5\right) \left(B_5 x_7 + B_6\right) - a_3 {B_9}^2 (B_{10} x_7 + a_5)^2 = 0.$$

5 Construction of Lyapunov Function

In this section, a Lyapunov function has been constructed to establish the conditions of the global asymptotic stability of the endemic equilibrium point, as shown in the following theorem.

Theorem 5.1: The endemic equilibrium point is globally asymptotically stable under the following sufficient conditions

$$(p\delta)^2 < 2 d_m \left(\delta + d_l + \overline{k} x_1\right).$$

$$\left((1-p)\,\delta\right)^2 < \frac{4}{6} \left[\delta + d_l + \overline{k} x_1\right] \left(d_m + \frac{b_m \beta_m}{N_h}\right).$$

$$\left(\frac{b_m \beta_m}{N_h} N_m\right)^2 < \min \left\{ \frac{1}{3} \left(d_m + \frac{b_m \beta_m}{N_h}\right) \left(d_h + \mu + \gamma\right),\ \frac{1}{3} \left(k_1 + d_m\right) \left(d_h + \mu + \gamma\right) \right\}.$$

$$\left(\frac{b_m \beta_m}{N_h} x_8\right)^2 < \frac{4}{9} \left(d_m + \frac{b_m \beta_m}{N_h}\right) \left(k_1 + d_m\right).$$

$${k_1}^2 < \frac{4}{9} d_m \left(k_1 + d_m\right).$$

$$\left(\frac{b_m \beta_h}{N_m} x_6\right)^2 < \frac{4}{9} d_m d_h.$$

$$\epsilon^2 < \frac{4}{6} \left(d_h + \frac{b_m \beta_h}{N_m} I_m\right) \left(d_h + \epsilon\right).$$

$$\left(b_m \beta_h\right)^2 < \frac{4}{9} d_h \left(d_h + k_2\right).$$

$$k_2{}^2 < \frac{1}{3}\left(d_h + k_2\right)\left(d_h + \mu + \gamma\right).$$
$$\gamma^2 < \frac{1}{2}\left(d_h + \mu + \gamma\right)\left(d_h + \epsilon\right).$$

Proof. Consider the proposed Lyapunov function

$$V = \tfrac{(L_m - x_1)^2}{2} + \tfrac{(M_m - x_2)^2}{2} + \tfrac{(S_m - x_3)^2}{2} + \tfrac{(E_m - x_4)^2}{2} + \tfrac{(I_m - x_5)^2}{2} + \tfrac{(S_h - x_6)^2}{2} + \tfrac{(E_h - x_7)^2}{2} + \tfrac{(I_h - x_8)^2}{2} + \tfrac{(R_h - x_9)^2}{2}.$$

The function V is a positive definite function concerning the endemic equilibrium point. Moreover, computing the time derivative for V gives after simplification steps that:

$$\begin{aligned}
\tfrac{dV}{dt} = &-\left[\delta + d_l + \overline{k}\left(L_m + x_1\right)\right]\left(L_m - x_1\right)^2 + p\delta\left(L_m - x_1\right)\left(M_m - x_2\right) \\
&-d_m(M_m - x_2)^2 + (1-p)\,\delta\left(L_m - x_1\right)\left(S_m - x_3\right) - \tfrac{b_m\beta_m}{N_h} S_m\left(S_m - x_3\right)\left(I_h - x_8\right) \\
&-\left(d_m + \tfrac{b_m\beta_m}{N_h}\right)\left(S_m - x_3\right)^2 + \tfrac{b_m\beta_m}{N_h} S_m\left(E_m - x_4\right)\left(I_h - x_8\right) \\
&+\tfrac{b_m\beta_m}{N_h} x_8\left(S_m - x_3\right)\left(E_m - x_4\right) - \left(k_1 + d_m\right)\left(E_m - x_4\right)^2 \\
&+k_1\left(E_m - x_4\right)\left(I_m - x_5\right) - d_m(I_m - x_5)^2 - \tfrac{b_m\beta_h}{N_m} x_6\left(I_m - x_5\right)\left(S_h - x_6\right) \\
&-\left(d_h + \tfrac{b_m\beta_h}{N_m} I_m\right)\left(S_h - x_6\right)^2 + \epsilon\left(S_h - x_6\right)\left(R_h - x_9\right) + \tfrac{b_m\beta_h}{N_m} I_m\left(S_h - x_6\right)\left(E_h - x_7\right) \\
&+\tfrac{b_m\beta_h}{N_m} x_6\left(I_m - x_5\right)\left(E_h - x_7\right) - \left(d_h + k_2\right)\left(E_h - x_7\right)^2 \\
&+k_2\left(E_h - x_7\right)\left(I_h - x_8\right) - \left(d_h + \mu + \gamma\right)\left(I_h - x_8\right)^2 \\
&+\gamma\left(I_h - x_8\right)\left(R_h - x_9\right) - \left(d_h + \epsilon\right)\left(R_h - x_9\right)^2.
\end{aligned}$$

Using the method of completing the square with the help of the given conditions, we obtain the following:

$$\begin{aligned}
\tfrac{dV}{dt} \le &-\left[\sqrt{\tfrac{\left[\delta + d_l + \overline{k}(L_m + x_1)\right]}{2}}\left(L_m - x_1\right) - \sqrt{d_m}\left(M_m - x_2\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\left[\delta + d_l + \overline{k}(L_m + x_1)\right]}{2}}\left(L_m - x_1\right) - \sqrt{\tfrac{\left(d_m + \frac{b_m\beta_m}{N_h}\right)}{3}}\left(S_m - x_3\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\left(d_m + \frac{b_m\beta_m}{N_h}\right)}{3}}\left(S_m - x_3\right) + \sqrt{\tfrac{\left(d_h + \mu + \gamma\right)}{4}}\left(I_h - x_8\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\frac{b_m\beta_m}{N_h} S_m}{3}}\left(E_m - x_4\right) - \sqrt{\tfrac{\left(d_h + \mu + \gamma\right)}{4}}\left(I_h - x_8\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\left(d_m + \frac{b_m\beta_m}{N_h}\right)}{3}}\left(S_m - x_3\right) - \sqrt{\tfrac{\left(k_1 + d_m\right)}{3}}\left(E_m - x_4\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\left(k_1 + d_m\right)}{3}}\left(E_m - x_4\right) - \sqrt{\tfrac{d_m}{3}}\left(I_m - x_5\right)\right]^2 \\
&-\left[\sqrt{\tfrac{d_m}{3}}\left(I_m - x_5\right) + \sqrt{\tfrac{\left(d_h + \frac{b_m\beta_h}{N_m} I_m\right)}{3}}\left(S_h - x_6\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\left(d_h + \frac{b_m\beta_h}{N_m} I_m\right)}{3}}\left(S_h - x_6\right) - \sqrt{\tfrac{\left(d_h + \epsilon\right)}{2}}\left(R_h - x_9\right)\right]^2 \\
&-\left[\sqrt{\tfrac{\left(d_h + \frac{b_m\beta_h}{N_m} I_m\right)}{3}}\left(S_h - x_6\right) - \sqrt{\tfrac{\left(d_h + k_2\right)}{3}}\left(E_h - x_7\right)\right]^2
\end{aligned}$$

$$-\left[\sqrt{\frac{d_m}{3}}\,(I_m - x_5) - \sqrt{\frac{(d_h+k_2)}{3}}\,(E_h - x_7)\right]^2$$
$$-\left[\sqrt{\frac{(d_h+k_2)}{3}}\,(E_h - x_7) - \sqrt{\frac{(d_h+\mu+\gamma)}{4}}\,(I_h - x_8)\right]^2$$
$$-\left[\sqrt{\frac{(d_h+\mu+\gamma)}{4}}\,(I_h - x_8) - \sqrt{\frac{(d_h+\epsilon)}{2}}\,(R_h - x_9)\right]^2.$$

It is clear that $\frac{dV}{dt}$ is negative definite and hence the endemic equilibrium point is globally asymptotically stable.

6 Sensitivity Analysis

The basic reproduction number is a crucial factor to examine when studying infectious disease models. Equation (3.1) was derived as the model's basic reproduction number, which is now being analyzed in a sensitivity analysis (3.1) [20]. This investigation helps us understand the impact of each variable on the spread of the disease [21]. Given the potential for errors in data collection and parameter assumptions, sensitivity analysis is a common tool to evaluate the model's robustness to changes in parameter values. This method is employed to pinpoint variables that require intervention efforts, as they strongly influence R_0. Sensitivity indices allow for an evaluation of the extent to which a variable changes when a parameter is modified. Specifically, the normalized forward sensitivity index for a variable concerning a particular parameter is utilized. This index is defined as the ratio of the variable's relative change to the relative change in the parameter. If the variable is differentiable concerning the parameter, the sensitivity index is expressed using partial derivatives as follows.

Given a parameter θ, the normalized forward sensitivity index of R_0 is differentiable and is defined by [22]

Accordingly, the normalized forward sensitivity index of R_0 with respect to system's parameters can be calculated as:

$$\mathrm{SS}_{\theta}^{R_0} = \frac{\theta}{R_0}\frac{\partial R_0}{\partial \theta},$$

$$\mathrm{SS}_{r_m}^{R_0} = -\frac{r_m \bar{k} N_m}{\sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}(\delta + d_l - \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m})},$$

$$\mathrm{SS}_{\delta}^{R_0} = \frac{-\delta + \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}}{2\sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}},$$

$$\mathrm{SS}_{d_l}^{R_0} = -\frac{d_l}{2\sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}},$$

$$\mathrm{SS}_{\bar{k}}^{R_0} = \frac{d_l^2 + 2\bar{k}N_m r_m + \delta(\delta - \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}) - d_l(-2\delta + \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m})}{2\sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}(\delta + d_l - \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m})},$$

$$\mathrm{SS}_{d_m}^{R_0} = -\frac{3d_m + 2k_1}{2(d_m + k_1)},$$

$$\mathrm{SS}_{b_m}^{R_0} = 1, \quad \mathrm{SS}_{\beta_m}^{R_0} = \frac{1}{2}, \quad \mathrm{SS}_{\beta_h}^{R_0} = \frac{1}{2}, \quad \mathrm{SS}_{r_h}^{R_0} = \frac{1}{2}, \quad \mathrm{SS}_{\epsilon}^{R_0} = 0, \quad \mathrm{SS}_{N_h}^{R_0} = 0,$$

$$\mathrm{SS}_{p}^{R_0} = -\frac{p}{2(1-p)}, \quad \mathrm{SS}_{k_1}^{R_0} = \frac{d_m}{2(d_m+k_1)}, \quad \mathrm{SS}_{k_2}^{R_0} = \frac{d_h}{2(d_h+k_2)},$$

$$\mathrm{SS}_{d_h}^{R_0} = -\frac{3d_h^2 + (\gamma+\mu)k_2 + 2d_h(\gamma+\mu+k_2)}{2(\gamma+\mu+d_h)(d_h+k_2)},$$

$$\mathrm{SS}_{\mu}^{R_0} = -\frac{\mu}{2(\gamma+\mu+d_h)}, \quad \mathrm{SS}_{\gamma}^{R_0} = -\frac{\gamma}{2(\gamma+\mu+d_h)},$$

$$\mathrm{SS}_{N_m}^{R_0} = \frac{d_l^2 + 2\bar{k}N_m r_m + \delta(\delta - \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}) - d_l(-2\delta + \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m})}{2\sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m}(\delta + d_l - \sqrt{(\delta+d_l)^2 + 4\bar{k}N_m r_m})}.$$

Accordingly, using data given in Table (1), it is obtained that

$$\mathrm{SS}_{r_m}^{R_0} = 0.31417, \ \mathrm{SS}_{r_h}^{R_0} = 0.5, \ \mathrm{SS}_{\delta}^{R_0} = 0.48326, \ \mathrm{SS}_{d_l}^{R_0} = -0.111601, \ \mathrm{SS}_{\bar{k}}^{R_0} = -0.185828,$$

$$\mathrm{SS}_{k_1}^{R_0} = 0.2222218, \ \mathrm{SS}_{k_2}^{R_0} = 0.0711834, \ \mathrm{SS}_{d_m}^{R_0} = -1.2222202, \ \mathrm{SS}_{d_h}^{R_0} = -0.7419400, \ \mathrm{SS}_{\epsilon}^{R_0} = 0,$$

$$\mathrm{SS}_{p}^{R_0} = -0.75, \ \mathrm{SS}_{b_m}^{R_0} = 1, \ \mathrm{SS}_{\beta_m}^{R_0} = 0.5, \ \mathrm{SS}_{\beta_h}^{R_0} = 0.5,$$

$$\mathrm{SS}_{\mu}^{R_0} = -0.0000699, \ \mathrm{SS}_{\gamma}^{R_0} = -0.324171908, \ \mathrm{SS}_{N_m}^{R_0} = -0.1858292, \ \mathrm{SS}_{N_h}^{R_0} = 0.$$

7 Computer Simulations

To analyze the behavior of the suggested model and identify the key parameters that impact the spread of the disease, a numerical simulation is conducted utilizing the dataset presented in Table 1.

We have used the values from different references and got the following results.

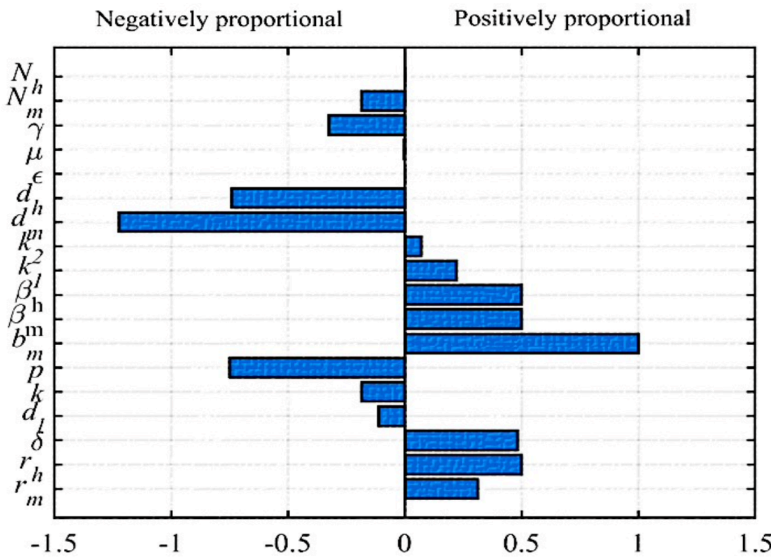

Figure 1: Sensitivity of basic reproduction number using data set given in Table 1

Parameter	Description	Value
r_m	Per-capita birth rate of mosquitoes	0.6
r_h	Per-capita birth rate of human	0.035
δ	Per-capita maturation rate of mosquitoes	0.06
d_l	Per-capita death rate of aquatic mosquitoes	0.4
$\bar{k}$	Intraspecific competition rate of aquatic mosquitoes	0.005
p	Total percentage population of male adult mosquitoes	0.6
b_m	Per-capita biting rate of mosquitoes	0.5
β_m	Transmission rate from infected human to mosquitoes	0.63
β_h	Transmission rate from infected mosquitoes to human	1.12
k_1	Per-capita transition rate from exposed to infected mosquitoes	0.125
k_2	Per-capita transition rate from exposed to infected human	0.5
d_m	Per-capita death rate of adult mosquitoes	0.1
d_h	Per-capita death rate of human	0.083
ϵ	Per-capita transition rate from recovered to susceptible human	0.1
μ	Per-capita mortality rate due to the mosquitoes born disease	0.000034
γ	Per-capita recovery rate due to the mosquitoes born disease	0.16
N_m	Total population of mosquitoes	250
N_h	Total population of human	10,000

According to Fig. 1, the set of parameters that are positively proportional to R_0 is given by $r_m, r_h, \delta, b_m, \beta_m, \beta_h, k_1, k_2$, while the set of parameters that are negatively proportional to R_0 includes $d_l, \bar{k}, p, d_m, d_h, \mu, \gamma, N_m$. However, the parameters ϵ and N_h do not affect R_0.

Fig. 2 illustrates the impact of the parameters β_h and β_m on infected humans and mosquitoes, respectively. The results indicate that an increase in the value of β_h from 0.75 to 1.5 leads to a rise in the number of infected humans from approximately 1700 to 2500 within the first 60 days. Subsequently, all profiles of infected humans exhibit a decreasing trend over time [23].

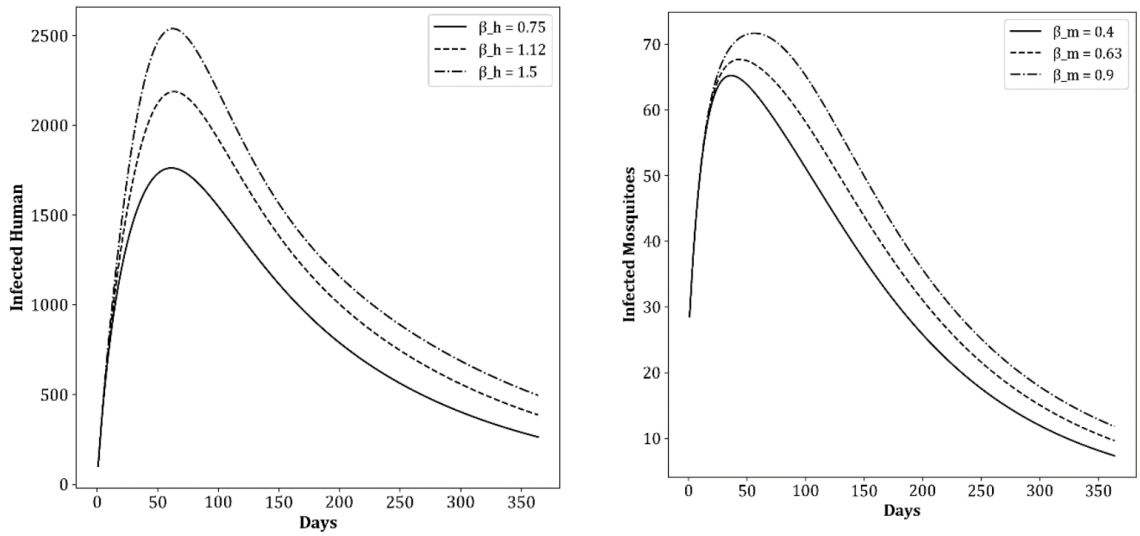

Figure 2: Effect of β_h and $\beta_m$on infected human and mosquitoes respectively.

Additionally, an increase in the value of β_m from 0.4 to 0.9 results in a rise in the number of infected mosquitoes from approximately 63 to 72 within the initial 60 days. This suggests that as the number of infected humans increases during the $[0, 60]$ day period, susceptible mosquitoes become infected, leading to a peak in the number of infected mosquitoes during this timeframe. These findings underscore the importance of controlling mosquito populations to mitigate transmission and manage the spread of malaria.

Fig. 3 demonstrates the impact of the parameters k_2 and k_1 on infected humans and mosquitoes, respectively. The results indicate that an increase in the value of k_2 from 0.1 to 1.0 leads to a rise in the number of infected humans from approximately 1000 to 2500 within the first 80 days. Following this, the profiles of infected humans consistently show a decline over time. Additionally, an increase in the value of k_1 from 0.1 to 1.0 results in a rise in the number of infected mosquitoes from approximately 35 to 78 within the initial 60 days. This implies that with an increase in the number of exposed susceptible humans, there is a higher likelihood of mosquito bites, resulting in a rise in the infected human population. Conversely, an increase in the number of mosquitoes poses a greater risk of infection for the human population during this period. These observations highlight the significance of implementing additional measures to control exposure to mosquito bites among humans, ultimately reducing the transmission of malaria.

Fig. 4 demonstrates the impact of the parameters β_h and k_2 on recovered humans. The results indicate that an increase in the value of β_h from 0.75 to 1.5 leads to a rise in the number of recovered humans from approximately 1100 to 1700 within the first 100 days. Following this, the profiles of recovered humans consistently show a decline over time. Additionally, an increase in the value of k_2 from 0.1 to 1.0 results in a rise in the number of recovered humans from approximately 700 to 1600 within the initial 130 days. These observations are linked to the results depicted in Fig. 2 and 3, indicating a higher number of infected humans in the early days. Subsequently,

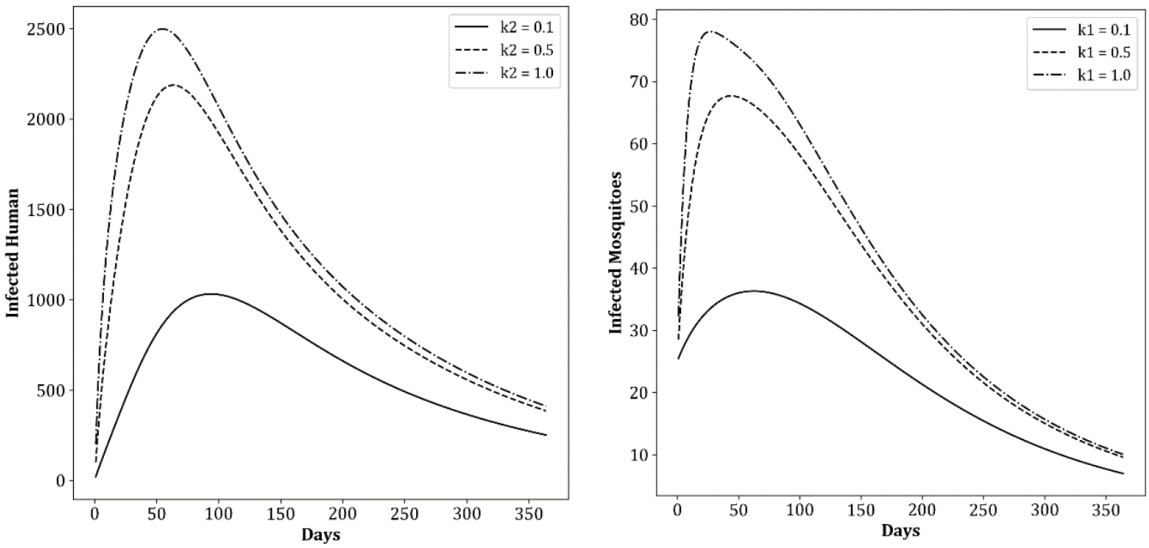

Figure 3: Effect of k_2 and k_1 on infected humans and mosquitoes respectively.

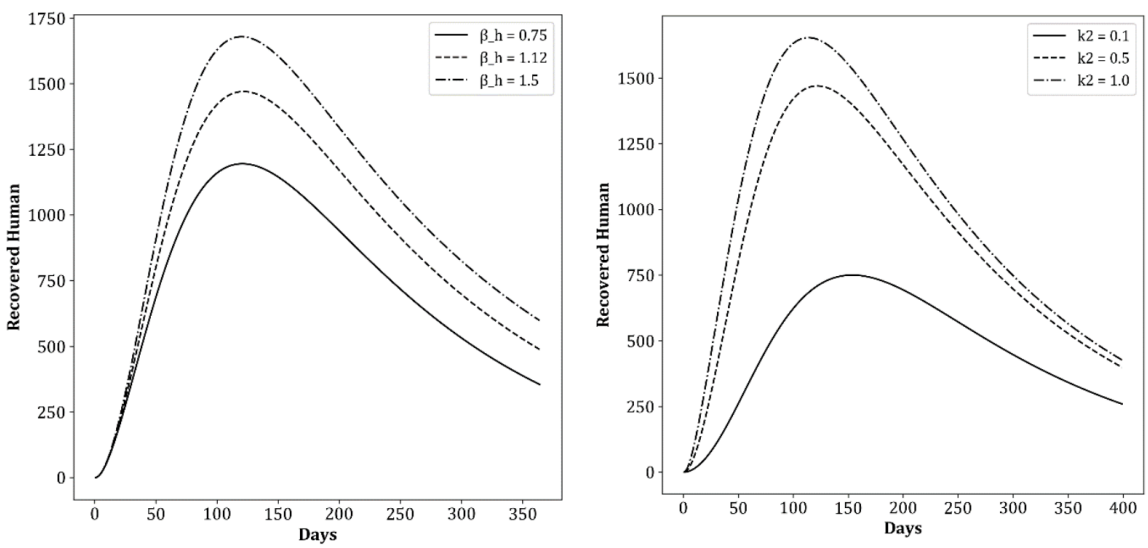

Figure 4: Effect of β_h and k_2 on recovered human.

these individuals recover, contributing to the peak observed in the recovered human class, as illustrated in Fig. 4 However, over time, the number of recovered humans decreases for both β_h and k_2, associated with the transition from the recovered human class to the susceptible human class. This transition is influenced by the fact that all recovered individuals have the potential to be infected by malaria again.

8 Discussion and Concluding Remarks

The LMSEI-SEIR model has emerged as a valuable tool for studying mosquito-borne disease dynamics. Its applications have provided insights into disease transmission, control strategies, and the impact of interventions. The model's extensions have improved its realism, enabling a better understanding of the complexities of disease dynamics. However, further research is needed to address the model's limitations and refine its applicability in real-world scenarios. While the LMSEI-SEIR model provides valuable insights, it also has certain limitations. These include assumptions regarding homogeneous mixing, constant parameter values, and lack of consideration for behavioural changes. Future research should focus on refining the model to incorporate these aspects and explore the impacts of interventions in real-world settings. Additionally, data-driven approaches for parameter estimation and model validation should be pursued to enhance the model's accuracy and applicability.

Declaration of competing interest The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability The data that has been used is confidential.

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