MATHEMATICAL MODELLING OF THE CAUSES, DYNAMIC TRANSMISSION AND CONTROL OF MALARIA DISEASE.

AKPUSUGH, Verse Ephraim

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Supervised By:

Prof. M. D. Shehu

OVERVIEW

- Introduction
- Problem
- Aims and Objectives
- Literature Review
- Methodology
- Results
- Conclusion
- Recommendation
- Thank You

INTRODUCTION

Malaria, a parasitic disease caused by plasmodium parasites, affects humans and monkey species. Despite being treatable and preventive, it results in 881,000 fatalities annually, with sub-Saharan Africa accounting for 85% of all deaths. The disease is caused by Plasmodium falciparum, while milder forms are caused by Plasmodium vivax, Plasmodium ovale, and Plasmodium malariae. Africa shares 80% of cases and 90% of deaths(Alhaji, 2023).

STATEMENT OF RESEARCH PROBLEM

Malaria has long been seen as a worldwide problem, and numerous experts, including epidemiologists, dedicate their time to understanding the disease’s dynamics and preventing its spread. Mathematicians use mathematical models to understand malaria dynamics, interactions, and eradicate the disease. These models optimize control interventions, resource allocation, and design targeted interventions for high-risk areas.

AIMS AND OBJECTIVES

AIMS

The aim of this study is to develop a mathematical model for malaria disease and derive the compartmental equations from the model and use it in establishing the relationship between the compartments and furthermore suggest the strategies to curb the disease.

AIMS AND OBJECTIVES

OBJECTIVES

Objective 1

The goal is to create a malaria disease model that clearly outlines its flowchart and transmission dynamics, and to derive human and vector compartmental equations from this model.

Objective 2

The study aims to determine reproduction number, disease-free and endemic equilibrium, and suggest solutions to balance disease transmission dynamics or eradicate the disease.

LITERATURE REVIEW

1. Plasmodium falciparum, the deadliest malaria parasite, dominates Africa, while Plasmodium vivax is the dominant parasite in non-Sub-Saharan African countries (Rezapour, 2023).

2. Ronald Ross' SIS-model, awarded a noble prize, revolutionized mathematical modelling of malaria, assuming distinct human compartments within the total population at any given time (Gwarinda, 2021).

3. Mosquito resistance is increasing, prompting the development of new insecticides and advanced malaria vector control tools, some nearing widespread implementation (Kokwaro, 2021).

METHODOLOGY

SEIR MODEL

The SEIR model is a mathematical tool used in epidemiology to mimic the transmission of infections illnesses. It is an extension of the basic SIR model that includes an exposed (E) compartment. The model separates a population into four compartments which are susceptible (S), Exposed (E), Infectious (I), and Recovered (R). The model uses differential equations to describe movement of individuals between compartments. Numerical analysis is employed to simulate the stability of this model

METHODOLOGY

Table 3.1: State variables, parameters and descriptions of malaria model.

Parameter	Parameter Description
μ_h	Natural mortality rate of humans
μ_v	Natural mortality rate of mosquitoes
β_h	Transmission rate from infectious mosquitoes to susceptible humans
β_v	Transmission rate from infectious humans to susceptible mosquitoes
σ_h	Rate at which exposed humans become infectious
σ_v	Rate at which exposed mosquitoes become infectious
γ_h	Recovery rate of infectious humans
N_h	Total human population

METHODOLOGY

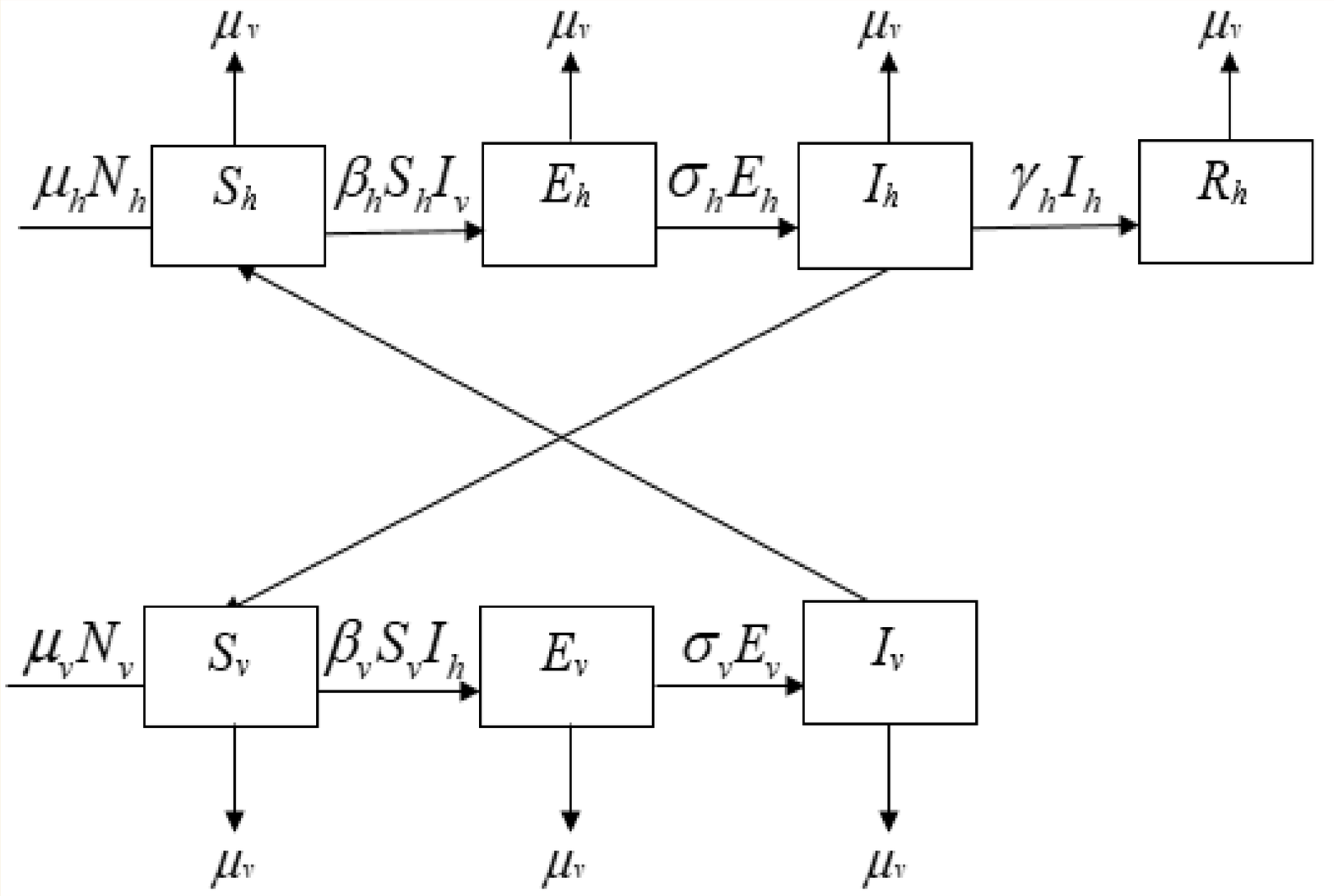

Figure 3.1: The compartmental model for malaria transmission.

METHODOLOGY

This SEIR model consists of four (4) compartments and seven (7) differential equations as shown below;

Human compartmental differential equations

$$\frac{dS_h}{dt} = \mu_h N_h - \beta_h S_h I_v - \mu_h S_h$$

$$\frac{dI_h}{dt} = \sigma_h E_h - (\gamma_h + \mu_h) I_h$$

$$\frac{dI_h}{dt} = \sigma_h E_h - (\gamma_h + \mu_h) I_h$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h$$

Vector compartmental differential equations

$$\frac{dS_v}{dt} = \mu_v N_v - \beta_v S_v I_h - \mu_v S_v$$

$$\frac{dE_v}{dt} = \beta_v S_v I_h - (\sigma_v + \mu_v) E_v$$

$$\frac{dI_v}{dt} = \sigma_v E_v - \mu_v I_v$$

METHODOLOGY

Determination of the Basic Reproduction number

There are two (2) major ways for determining the basic reproduction number, which are;

1. The formula method

$$R_0 = \sqrt{\frac{\beta_h S_h \beta_v S_v}{(\sigma_h + \mu_h)(\gamma_h + \mu_h)(\sigma_v + \mu_v)\mu_v}}$$

2. The next-generation matrix approach

$$G = FV^{-1}$$

METHODOLOGY

Jacobian matrix for disease free equilibrium (DFE)

$$J_{DFE}=\begin{bmatrix} -\mu_h & 0 & 0 & 0 & 0 & 0 & -\beta_h N_h \\ 0 & -(\sigma_h+\mu_h) & 0 & 0 & 0 & 0 & \beta_h N_h \\ 0 & \sigma_h & -(\gamma_h+\mu_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_h & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & -\beta_v N_v & 0 & -\mu_v & 0 & 0 \\ 0 & 0 & \beta_v N_v & 0 & 0 & -(\sigma_v+\mu_v) & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_v & -\mu_v \end{bmatrix}$$

METHODOLOGY

Jacobian matrix for disease endemic equilibrium (EE)

$$J_{EE} = \begin{bmatrix} -(\beta_h I_v^* + \mu_h) & 0 & 0 & 0 & 0 & 0 & -\beta_h S_h^* \\ \beta_h I_v^* & -(\sigma_h + \mu_h) & 0 & 0 & 0 & 0 & \beta_h S_h^* \\ 0 & \sigma_h & -(\gamma_h + \mu_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_h & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & -\beta_v S_v^* & 0 & -(\beta_v I_h^* + \mu_v) & 0 & 0 \\ 0 & 0 & \beta_v S_v^* & 0 & \beta_v I_h^* & -(\sigma_v + \mu_v) & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_v & -\mu_v \end{bmatrix}$$

DISCUSSION OF RESULTS

Making use of numerical simulations to determine the basic reproduction number we have;

1. Formula method

$$R_0 = 20.8$$

2. Next-generation matrix approach

$$R_0 = 12.5$$

The formula method simplifies R_0, while the next-generation matrix approach offers a comprehensive analysis, ensuring the most accurate reproduction number calculation.

DISCUSSION OF RESULTS

Table 4.1: Iteration table for the endemic equilibrium values of the model compartments.

	$I_h^* = 1$	$I_h^* = 10$	$I_h^* = 50$	$I_h^* = 100$	$I_h^* = 500$
S_v^*	9091	5000	1667	910	196
S_v^*	303	1667	2778	3030	3267
I_v^*	606	3334	5556	6061	6532
S_h^*	32	6	4	3	0.3
E_h^*	179	181	181	181	18
I_h^*	298	302	302	302	151
R_h^*	1491	1510	1512	1512	757

DISCUSSION OF RESULTS

Making use of python software to further compute the eigenvalues of the endemic equilibrium and by satisfying the relation $(J - \lambda I) = 0$

We have,

$\lambda_1 = -0.02$

$\lambda_2 = -3.73030739$

$\lambda_3 = -13.08400012$

$\lambda_4 = -0.09921692$

$\lambda_5 = -0.1198067$

$\lambda_6 = -0.22006886$

$\lambda_7 = -0.2$

Since all eigenvalues have negative real parts, the EE is stable, implying that the disease will remain in the population without producing huge outbreaks.

DISCUSSION OF RESULTS

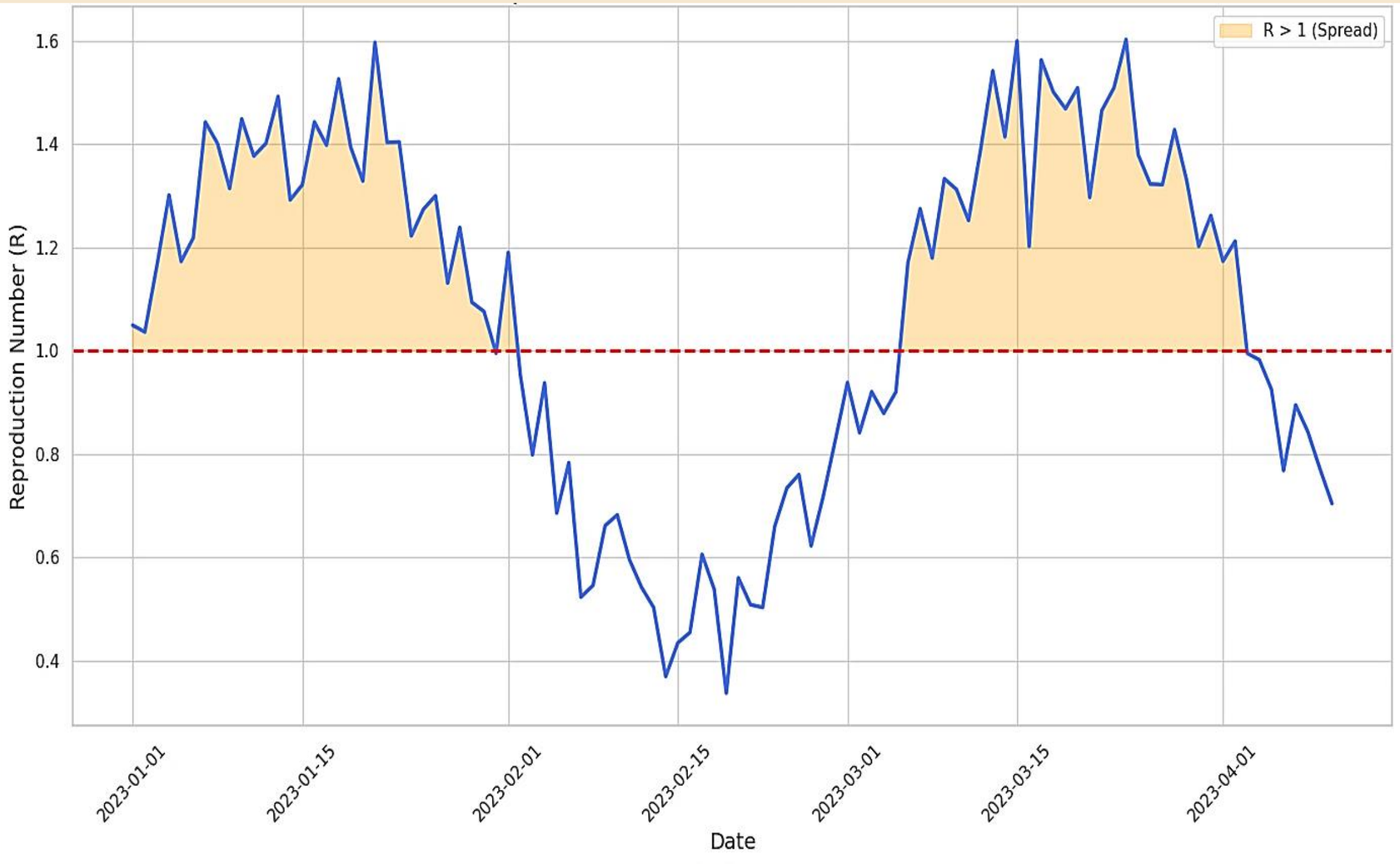

Figure 4.3: Visualization of the behavior of the reproduction number over time using the computed numerical values.

DISCUSSION OF RESULTS

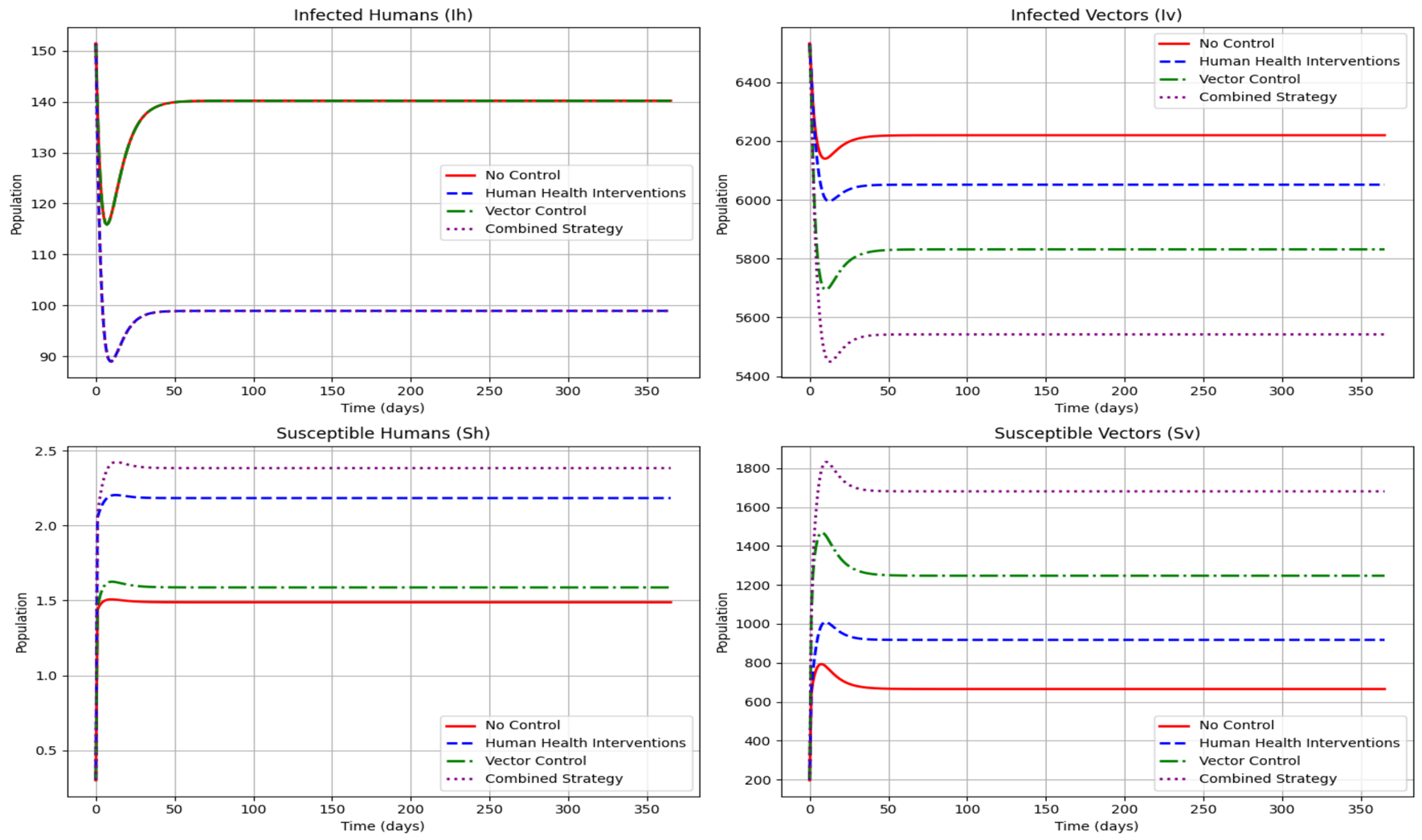

Figure 4.4: Visualization of the control of the I_h, I_v, S_h and S_v compartments using the computed numerical values.

CONCLUSION

The model demonstrates that the disease-free equilibrium point (DFE) is stable if (R_0<0) and the Jacobian matrix eigenvalues have negative real parts, so the disease dies out. If (R_0>0), the equilibrium becomes unstable, while the endemic state emerges. The study suggests that intervention strategies should focus on treatment and reducing contact between mosquito vectors and humans, using drugs, bed nets and insecticides.

RECOMMENDATIONS

- This SEIR model will aid researchers and public health officials in understanding infectious disease dynamics, guiding treatment decisions, and determining DFEs to reduce reproduction numbers and balance disease in the population.

- This study advocates for improved malaria management through training healthcare professionals, infrastructure improvements and adequate diagnostic equipment. It also recommends securing funds for control programs and using higher compartments in disease modeling.

THANK YOU