Vol. 3, No. 1, pp. 85-108, (June 2025)
DOI: 10.21608/astb.2025.344137.1014
ASWAN SCIENCE AND TECHNOLOGY BULLETIN (ASTB)
Online ISSN: 3009-7916, Print ISSN: 1110-0184
Journal homepage: https://astb.journals.ekb.eg/ E-mail: essamshaalan@sci.aswu.edu.eg
Original Article

Buruli Ulcer Mathematical Modeling

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Received: 13/12/2024 Revised: 31/01/2025 Accepted: 24/02/2025

Abstract:

Buruli ulcer is classified as a neglected tropical disease that has emerged in various regions, including developed nations such as Australia. This condition primarily manifests as a skin disorder affecting the arms and legs. It has been detected in several mammalian species, notably in possums which in turn transmit the disease to humans. To effectively reduce the incidence and prevent the transmission of this disease to less developed countries, comprehensive eradication and control initiatives are essential before it escalates into an epidemic. This study introduces a SIR-type epidemic model specifically for humans. A detailed analysis of the model's properties has been conducted, leading to the establishment of its stability results. The stability at fixed points has been assessed, demonstrating that the model exhibits local asymptotic stability. The conditions for stability in the disease-free scenario are confirmed for $R_0 < 1$, while the endemic situation is analyzed for $R_0 > 1$.

Keywords: Buruli ulcer, Mathematical Modeling, Stability analysis, Reproduction number, Equilibria Points.

1. Introduction

An infection with Mycobacterium Ulcerans (MU) is thought to be the most common disease in human society that causes both disability and deformity. The MU is one of several that have been found to have the potential to be hazardous to both humans and animals (Bonyah et al. 2016). The pathogenic bacterium that causes Buruli Ulcers frequently causes large ulcers to form on the arms or legs, causing extensive destruction of soft tissue and skin. MU are the cause of this terrible illness. In many nations, ulcers are quickly becoming a crippling condition. It is named for the Buruli region of Uganda, which is close to the Nile River and where the first significant number of cases were documented in 1961 (Nyabadza and Bonyah 2015).

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The possibility of MU infection in wildlife has been the subject of numerous studies. In Australia, ringed-tailed opossums and an alpaca naturally infected koalas. The clinically identified lesions were identical to those found in humans. According to (Hayman and Hibble 2001), a clinically detected lesion in an adult ringed tail opossum (*Pseudocheirus Peregrinus*) in east Cows in January 1998 was consistent with an infection caused by MU. Nevertheless, no additional research regarding the PCR or culture of this infected animal has been presented for diagnosis. In their study of brushtail possum MU inoculation, the authors in (Bolliger et al. 1950) discovered that an uninoculated opossum in a different cage in the same room had contracted the infection. According to some recent findings, aquatic insects may be involved in the spread of infections among anemia populations and humans. For more information, see (Marsollier al. 2002). Koalas and possums, which are classified as small mammals, consume MU by transferring it through the environment through aerosols (Hayman and Hibble 2001). Individual possums may contract the disease from infected insect vectors or mosquitoes that feed on mammals and spread the infection. A vector may become infected if it attacks small infected mammals. MU is eventually released into the environment by infected mammals, who also increase infection. This cycle of disease transmission between vectors and mammals is underway, and vice versa (Khan et al. 2021). Additionally, it's necessary to Keep in mind that antibiotics can be used to treat Buruli ulcer. Daily administration of a combination of streptomycin and rifampin has the capacity to eradicate MU bacilli and encourage healing without recurrence for eight weeks (Nyabadza and Bonyah 2015).

A mathematical model is an abstract representation of a phenomenon created using equations that produce perspectives of the general behavior of an epidemic event. It also serves as a means of examining the impact of determinate factors on the spread of disease. It provides a primitive general behavior of an epidemic as addressed by epidemic curves, enabling predictions regarding the duration of an epidemic, its magnitude in the population, and the assessment of factors that affect the dynamics of transmission and, in turn, the number of cases. pointing out that the models can be improved mathematically to make them more similar to actual data (Van et al. 2017) and (Huppert 2013). Mathematical modeling is a highly flexible tool in infectious disease epidemiology that enables the identification of epidemic patterns, extrapolations of epidemic behaviors, and the dynamic effects of interventions like treatment needed, vaccination, quarantine, social distance, and hygiene measures. It is also inexpensive and allows for the simulation of experiments that are unethical in human subjects as well as experiments that have low economic viability in animal models (Opatowski L et al. 2011).

Ronald Ross, William Hamer, and others created the susceptible-infected-removed (SIR) model in the early 20th century. It is made up of three coupled non-linear ordinary differential equations without an explicit formula solution. On the other hand, we can learn a lot about the solutions using basic calculus tools. Along the way, we demonstrate how this straightforward model aids in providing a theoretical framework for public health interventions and how the discovery of several public health guiding principles requires the use of a model similar to this one. A number of strong assumptions are made in the derivation of the SIR disease transmission model. By easing some of the presumptions, the authors of hundreds of papers (and some books) expand this fundamental model in numerous ways.

In this paper, we employ mathematical modeling, especially SIR, to comprehend the behavior and spread of Buruli Ulcer in order to find solutions and raise awareness of the disease. The infection can then be avoided. Public health Organizations may find our hypothesis useful in containing the infection and fight the disease. In section 2 we offer a thorough mathematical modeling formulation for the specified issue. In section 3 we will take sub-model and deal with it by giving a brief analysis of the equilibrium points of the model, its stability locally also estimating its reproductive number. In section 4 we analyze the full model by studying its equilibrium points at free disease and in case of endemic also we find the reproductive number and study the local stability of the full model. Section 5 shows the numerical simulation of our model and we summarize our present work in Section 6. As far as the authors are aware, no research has been mathematically planned to comprehend Buruli Ulcer's human mathematical modeling and investigate its dynamics.

2. Mathematical Model Formulation

Here, we give a brief explanation of the model formulation by denoting the human population as N_h(t) and further dividing it into three compartments: S_h(t) represents the healthy or susceptible individuals who may be at risk of contracting an infection, $I_h(t)$ represents those who are infectious with MU, and $R_h(t)$ represents those who recover after becoming infected.

$$N_h(t) = S_h(t) + I_h(t) + R_h(t) .$$

Let N_p(t) be the possum population, Since S_p(t) is the healthy or the susceptible possums which are possibly to attract the infections , and I_p(t) is infectious with MU, which is determined by

$$N_p(t) = S_p(t) + I_p(t).$$

Let $N_v(t)$ be the vector (mosquitoes) population at time t which splits into two compartments: $S_v(t)$ represents the susceptible or healthy vector, and $I_v(t)$ is the infected vector

$$N_v(t) = S_v(t) + I_v(t) .$$

The density of the MU in the environment is shown by E.

The transformation diagram is given as following figure (1).

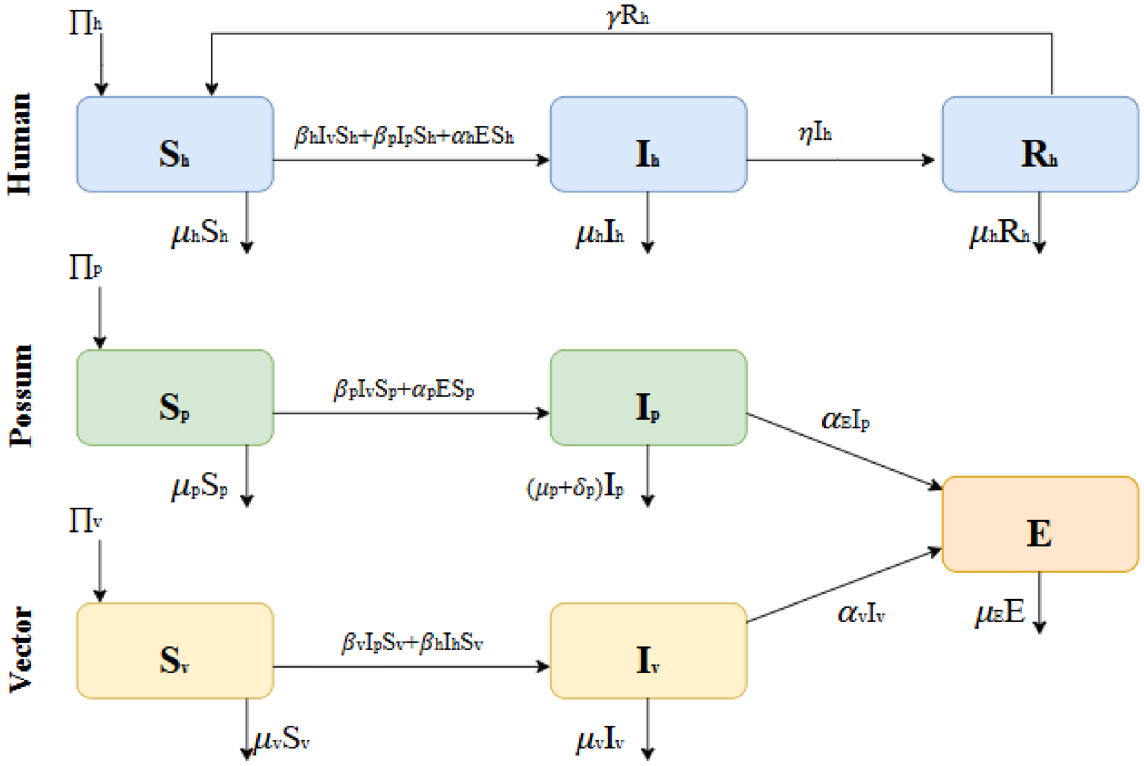

Figure 1. Transmission diagram

As we show in the figure (1), β_h is the transmission probability of contact through the infected possum and is given by the route $\beta_h I_v S_h$. The item α_h defines to be the probability of human getting infection due to the environment and is given by the route $\alpha_h E S_h$.

Including possum-related items, The infection spreads to the infected class of possums through the contact rate indicated by $\beta_p I_p S_h$. Additionally, The item α_p, which is determined by the route $\alpha_p E S_p$, is defined as the transmission probability of contact through MU from the environment. Moreover, δ_p is the number of individuals who die from possum-infected diseases.

Concerning vector (mosquito) object β_v is defines to be The contact rate between suseptable vectors and environment then the transmission route given by $\beta_v I_p S_v$.

Environment item are α_E which is The rate of shedding of infected individual in environment and $\mu_E$is the decay of environmental MU , all news born are supposed to be susceptible.

In the following table we define parameters we used in our model and its values which will be used lately in numerical results.

Parameter	**Definition**	**Value**	**Refs**
$\prod_h$	The birth rate of humans	100	(Jin-Qiang et al.2021)

$\prod_p$	The birth rate of Possums	2	(Khan et al. 2021)
$\prod_v$	The birth rate of vectors	5	(Khan et al. 2021)
β_h	The contact rate between S_h and I_p	0.025	(Khan et al. 2021)
β_p	The contact rate between S_p and I_v	0.2	(Khan et al. 2021)
β_v	The contact rate between S_v and E	0.09	(Khan et al. 2021)
γ	Immunity warning recovery rate of infected humans	0.065	(Jin-Qiang et al.2021)
μ_h	Natural death (Mortality) rate in humans	0.00004	(Jin-Qiang et al.2021)
μ_p	Natural death(Mortality) rate in Possums	0.0000457	(Khan et al. 2021)
μ_v	Natural death (Mortality) rate in vectors	0.0714	(Khan et al. 2021)
μ_E	Natural death (Mortality) rate of MU in E	0.0714	(Khan et al. 2021)
η	The recovery rate of infected humans	0.05	(Khan et al. 2021)
α_h	Probability of human getting infection due to E	0.02	assumed
α_p	Probability of possum getting infection due to E	0.01	assumed
α_v	Probability of vector getting infection due to E	0.01	assumed
α_E	The rate of shedding of infected individual in E	0.0714	(Khan et al. 2021)
δ_p	The death rate due to infection in possum	0.0714	(Khan et al. 2021)

Table 1. The definition and values for variables and parameters of the model.

The system of differential equations that describe the mathematical model can be considered as the following:

$$\left\{\begin{aligned}
\frac{dS_h}{dt} &= \prod_h + \gamma R_h - \beta_h I_v S_h - \beta_p I_p S_h - \alpha_h E S_h - \mu_h S_h,\\
\frac{dI_h}{dt} &= \beta_h I_v S_h + \beta_p I_p S_h + \alpha_h E S_h - (\eta + \mu_h) I_h,\\
\frac{dR_h}{dt} &= \eta I_h - (\gamma + \mu_h) R_h,\\
\frac{dS_p}{dt} &= \prod_p - \beta_p I_v S_p - \alpha_p E S_p - \mu_p S_p,\\
\frac{dI_p}{dt} &= \beta_p I_v S_p + \alpha_p E S_p - (\mu_p + \delta_p) I_p,\\
\frac{dS_v}{dt} &= \prod_v - \beta_v I_p S_v - \beta_h I_h S_v - \mu_v S_v,\\
\frac{dI_v}{dt} &= \beta_v I_p S_v + \beta_h I_h S_v - \mu_v I_v,\\
\frac{dE}{dt} &= \alpha_E I_p + \alpha_v I_v - \mu_E E,
\end{aligned}\right\} \qquad (1)$$

refer to initial conditions that are not negative:

$$S_h(0) = S_{h_0} \geq 0, I_h(0) = I_{h0} \geq 0, R_h(0) = R_{h0}$$
$$S_p(0) = S_{p0} \geq 0, I_p(0) = I_{p0} \geq 0,$$
$$S_v(0) = S_{v0} \geq 0, I_v(0) = I_{v0} \geq 0 \text{ and } \mathrm{E}(0) = E_0 \geq 0$$

Mathematical analysis of the model

In this section, we will split the full model into two models to make our work little difficult first one is possum vector environment model and the other is the full model by adding human system to previous system.

3. Mathematical Analysis of only Possum, Vector and Environment (PVE) Model

The following system equations show the model of PVE

$$\left\{\begin{aligned} \frac{dS_p}{dt} &= \prod\nolimits_p - \beta_p I_v S_p - \alpha_p E S_p - \mu_p S_p, \\ \frac{dI_p}{dt} &= \beta_p I_v S_p + \alpha_p E S_p - (\mu_p + \delta_p) I_p, \\ \frac{dS_v}{dt} &= \prod\nolimits_v - \beta_v I_p S_v - \beta_h I_h S_v - \mu_v S_v, \\ \frac{dI_v}{dt} &= \beta_v I_p S_v + \beta_h I_h S_v - \mu_v I_v, \\ \frac{dE}{dt} &= \alpha_E I_p + \alpha_v I_v - \mu_E E, \end{aligned}\right\} (2)$$

3.1 Equilibria Points at Free Disease for only PVE Model

The only PVE model's infection free equilibrium, denoted by ε_{0PVE} for system (2), must be established before we can establish results for the basic reproduction number computations. The following method can be used to accomplish this:

$$\varepsilon_{0PVE} = (S_p^0, I_p^0, S_v^0, I_v^0, E^0)$$

free disease means there is no disease Then there is no infected items;

$$I_p = 0\ ,\ I_v = 0\ ,\ E = 0$$

Then the system will be

$$\frac{dS_p}{dt} = \prod\nolimits_p - \mu_p S_p^0 = 0 \quad \text{then } S_p^0 = \frac{\Pi_p}{\mu_p}$$

$$\frac{dS_v}{dt} = \prod\nolimits_v - \mu_v S_v^0 = 0 \quad \text{then } S_v^0 = \frac{\Pi_v}{\mu_v}$$

Then

$$\varepsilon_{0PVE} = \left(\frac{\Pi_p}{\mu_p}, 0, \frac{\Pi_v}{\mu_v}, 0, 0\right) \qquad \#$$

3.2 Basic Reproduction Number for only PVE Model

To obtain the expressions for R_{0PVE} , we employ the procedure and notation discussed in (Aatif Ali et al. 2022) as follows:

$$F = \begin{bmatrix} 0 & \beta_p S_p^0 & \alpha_p S_p^0 \\ \beta_v S_v^0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \qquad V = \begin{bmatrix} \mu_p + \delta_p & 0 & 0 \\ 0 & \mu_v & 0 \\ \alpha_E & \alpha_v & \mu_E \end{bmatrix},$$

Then

$$FV^{-1} = \begin{bmatrix} \frac{-\alpha_E \alpha_p S_p^0}{(\mu_p+\delta_p)\mu_E} & \frac{-\beta_p S_p^0}{\mu_v} + \frac{\alpha_p \alpha_v S_p^0}{\mu_E \mu_v} & \frac{\alpha_p S_p^0}{\mu_E} \\ \frac{\beta_v S_v^0}{(\mu_p+\delta_p)} & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

For our suggested model (2), the spectral radius of the above should be the required basic reproduction number following some calculations provided by:

$$R_{0PVE} = \sqrt{}\left(\frac{\Pi_p(\beta_v \Pi_v \alpha_v \alpha_p - \mu_v^2 \alpha_E \alpha_p - \mu_E \beta_v \beta_p \Pi_v)}{\mu_v^2 \mu_E \mu_p (\mu_p + \delta_p)}\right) \quad \#$$

3.3 Local Stability for only PVE Model at Free Disease

The following theorem establishes the local stability for the specified system (2).

Theorem 1. The model (2) is locally asymptotically stable, if $R_{0PVE} < 1$ at the disease free case ε_{0PVE}.

Proof. At ε_{0PVE} , we have the following Jacobian system:

$$J(\varepsilon_{0PVE}) = \begin{bmatrix} -\mu_p & 0 & 0 & -\beta_p \frac{\Pi_p}{\mu_p} & -\alpha_p \frac{\Pi_p}{\mu_p} \\ 0 & -(\mu_p + \delta_p) & 0 & \beta_p \frac{\Pi_p}{\mu_p} & \alpha_p \frac{\Pi_p}{\mu_p} \\ 0 & \frac{-\beta_v \Pi_v}{\mu_v} & -\mu_v & 0 & 0 \\ 0 & \frac{\beta_v \Pi_v}{\mu_v} & 0 & -\mu_v & 0 \\ 0 & \alpha_E & 0 & \alpha_v & -\mu_E \end{bmatrix}$$

The respective characteristics equation of $J(\varepsilon_{0PVE})$ is given by

$$\lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0 \qquad (3)$$

where

- $a_1 = \mu_E + \mu_v + \mu_p + \delta_p$,
- $a_2 = \mu_E \mu_v + (\mu_E + \mu_v)(\mu_p + \delta_p) - \frac{\Pi_p(\alpha_p \alpha_E \mu_v - \Pi_v \beta_p \beta_v)}{\mu_v \mu_p}$,
- $a_3 = (\mu_E + \mu_v)(\mu_p + \delta_p)\left(1 - \frac{\Pi_p(\beta_v \Pi_v \alpha_v \alpha_p - \mu_v^2 \alpha_E \alpha_p - \mu_v \beta_v \beta_p \Pi_v)}{\mu_E \mu_p \mu_v^2 (\mu_p + \delta_p)}\right)$.

while $\mu_E = \mu_v$ numerically, then

$$a_3 = (\mu_E + \mu_v)(\mu_p + \delta_p)\,(1 - R_{0pve}^2)$$

we obtain the roots for Eq. (3) as follows: $-\mu_p < 0, -\mu_v < 0$.

Using the Routh-Hurwitz criteria ($a_j > 0$ for j = 1,2,3 and further ($a_1 a_2 > a_3$). Therefore, the model (2) is locally asymptotically stable when $R_{0PVE} < 1$ at the infection free equilibrium. #

3.4 Endemic Equilibria for only PVE Model

In order to obtain the expressions for the endemic case of model (2), we indicate its endemic equilibrium by $\varepsilon_{1PVE} = (S_p^*, I_p^*, S_v^*, I_v^*, E^*)$ and is given by

- $S_p^* = \dfrac{(\mu_E+\mu_v)(\mu_p+\delta_p)\,(\beta_v I_p^*+\mu_v)}{\beta_v \prod_v \alpha_v \alpha_p + \mu_E \beta_p \beta_v \prod_v + \alpha_E \alpha_p \mu_v (\beta_v I_p^* + \mu_v)}$,
- $S_v^* = \dfrac{\prod v}{(\beta_v I_p^* + \mu_v)}$,
- $I_v^* = \dfrac{\prod_v \beta_v I_p^*}{\mu_v \beta_v I_p^* + \mu_v^2}$,
- $E^* = \dfrac{\alpha_E I_p^*}{\mu_E} + \dfrac{\alpha_v}{\mu_E}\left(\dfrac{\prod_v \beta_v I_p^*}{\mu_v \beta_v I_p^* + \mu_v^2}\right)$.

using above equations and substituting in first equation in model (2):

$$f(I_p) = a I_p^{*2} + b I_p^* + c = 0 \qquad (4)$$

where

- $a = \beta_v \alpha_E \alpha_p \mu_v (\mu_p + \delta_p)$,
- $b = \prod_p \beta_v \alpha_E \alpha_p \mu_v + \prod_v \mu_E \beta_p \beta_v (\mu_p + \delta_p) + \mu_v^2 \alpha_E \alpha_p (\mu_p + \delta_p) + \prod_v \beta_v \alpha_v \alpha_p (\mu_p + \delta_p) + \mu_E \mu_p \mu_v \beta_v (\mu_p + \delta_p)$,
- $c = \mu_E \mu_p \mu_v^2 (\mu_p + \delta_p)\left(1 - \left(\dfrac{\prod_p (\beta_v \prod_v \alpha_v \alpha_p - \mu_v^2 \alpha_E \alpha_p - \mu_E \beta_v \beta_p \prod_v)}{\mu_v^2 \mu_E \mu_p (\mu_p + \delta_p)}\right)\right) = \mu_E \mu_p \mu_v^2 (\mu_p + \delta_p)(1 - R_{0pve}^2)$

#

In (4), the coefficient a is positive, but the coefficient c 's positivity depends on whether R_{0pve}<1 or negative. Therefore, the positive solution of (4) can be determined by the sign of b and c. Two solutions, one positive and one negative, can be found for (4) in the case where R_{0pve}>1. There is a solution of the form $I_p^* = -b/a$ for the case where $c = 0$ if and only if $R_{0pve} = 1$, when $b < 0$. There is an interval for R_{0pve} with two equilibria, indicating that the equilibria depend on the changing value of R_{0pve},

$$I_{p1,2}^* = \frac{-b + \sqrt{(b^2 - 4ac)}}{2a}, \frac{-b - \sqrt{(b^2 - 4ac)}}{2a}$$

We have no solution for the Eq. (4) in such a case when c > 0 and either b ≥ 0 or $b^2 < 4ac$. #

3.5 Local Stability of the Endemic Equilibrium of only PVE Model:

Theorem 2. The possum model (2) at ε_{1PVE} is locally asymptotically stable if R_{0pve}>1.

Proof. at ε_{1PVE} , the following Jacobian matrix is presented,

$$J(\varepsilon_{1PVE}) = \begin{bmatrix} -Q_1 & 0 & 0 & -Q_5 & -Q_6 \\ Q_2 & -Q_3 & 0 & Q_5 & Q_6 \\ 0 & -Q_7 & -Q_4 & 0 & 0 \\ 0 & Q_7 & Q_8 & -\mu_v & 0 \\ 0 & \alpha_E & 0 & \alpha_v & -\mu_E \end{bmatrix}$$

where

$Q_1 = \beta_p I_v^* + \alpha_p E^* + \mu_p$, $Q_2 = \beta_p I_v^* + \alpha_p E^*$, $Q_3 = (\mu_p + \delta_p)$,

$Q_4 = \beta_v I_p^* - \mu_v$, $Q_5 = \beta_p S_p^*$, $Q_6 = \alpha_p S_p^*$,

$Q_7 = \beta_v S_v^*$ and $Q_8 = \beta_v I_p^*$.

The characteristics equation of J(ε_{1PVE}) is

$$\lambda^5 + k_1 \lambda^4 + k_2 \lambda^3 + k_3 \lambda^2 + k_4 \lambda + k_5 = 0$$, where

- $k_1 = \mu_E + \mu_v + Q_1 + Q_3 + Q_4$,
- $k_2 = (\mu_E + \mu_v)Q_4 + (Q_1 + Q_3)Q_4 + \mu_E\mu_v + (\mu_E + \mu_v) + (Q_1 + Q_3) + Q_1Q_3$,
- $k_3 = \mu_E\mu_v Q_4 + (\mu_E + \mu_v)(Q_1 + Q_3)Q_4 + Q_1Q_3Q_4 - (\mu_E + \mu_v)Q_1Q_3 - \alpha_E Q_6(Q_2 - Q_1)$,
- $k_4 = (\mu_E + \mu_v)Q_1Q_3Q_4 - \mu_E\mu_v Q_1Q_3 - \mu_E\mu_v(Q_1 + Q_3) + Q_5Q_7(Q_1 - Q_2)(Q_4 - Q_8) + \alpha_E Q_6(Q_2 - Q_1)(Q_4 - \mu_v)$,
- $k_5 = \mu_E\mu_v Q_1Q_3Q_4 + \mu_E\mu_v Q_4(Q_1 + Q_3) + Q_5Q_7\mu_E(Q_1 - Q_2)(Q_4 - Q_8) - \alpha_v Q_6Q_7(Q_2 - Q_1)(Q_4 - Q_8) + \alpha_E Q_6(Q_2 - Q_1)Q_4\mu_v$. #

$k_i > 0$ *for* $i = 1, 2, ...5$ where

$$H_1 = k_1 \ , \ H_2 = \begin{bmatrix} k_1 & 1 \\ k_3 & k_2 \end{bmatrix}, H_3 = \begin{bmatrix} k_1 & 1 & 0 \\ k_3 & k_2 & k_1 \\ k_5 & k_4 & k_3 \end{bmatrix}$$

$$,H_4 = \begin{bmatrix} k_1 & 1 & 0 & 0 \\ k_3 & k_2 & 1 & 0 \\ k_5 & k_4 & k_3 & k_2 \\ 0 & 0 & k_5 & k_4 \end{bmatrix}, H_5 = \begin{bmatrix} k_1 & 1 & 0 & 0 & 0 \\ k_3 & k_2 & k_1 & 1 & 0 \\ k_5 & k_4 & k_3 & k_2 & k_1 \\ 0 & 0 & k_5 & k_4 & k_3 \\ 0 & 0 & 0 & 0 & k_5 \end{bmatrix}$$

These requirements can be met by using algebraic computation software to ensure that $k_i > 0 \; for \; i = 1, 2, \ldots 5$. The system PVE (2) is proven to be locally asymptotically stable at the endemic state if each of these requirements is met. #

4. Mathematical Analysis of the Full Model

In the following section, we will deal with full model (1) at free disease and in case of disease.

4.1 Equilibria Points at Free Disease of the Full Model

The infection free equilibrium, represented by ε_0 for system (1), must be obtained before we can establish results for the basic reproduction number computations. This can be done in the following manner:

$$\varepsilon_0 = (S_h^0, I_h^0, R_h^0, S_p^0, I_p^0, S_v^0, I_v^0, E^0)$$

free disease means there is no disease Then there is no infected items;

$$I_h = 0 \; , I_p = 0 \; , I_v = 0 \; , E = 0$$

Then the system will be

$$\frac{dS_h}{dt} = \prod\nolimits_h - \mu_h S_h^0 = 0 \qquad \text{then } S_h^0 = \frac{\Pi_h}{\mu_h}$$

$$\frac{dR_h}{dt} = -(\gamma + \mu_h) R_h^0 = 0 \qquad \text{then } R_h^0 = 0$$

$$\frac{dS_p}{dt} = \prod\nolimits_p - \mu_p S_p^0 = 0 \qquad \text{then } S_p^0 = \frac{\Pi_p}{\mu_p}$$

$$\frac{dS_v}{dt} = \prod\nolimits_v - \mu_v S_v^0 = 0 \qquad \text{then } S_v^0 = \frac{\Pi_v}{\mu_v}$$

$$\text{then } \varepsilon_0 = \left(\frac{\Pi_h}{\mu_h}, 0, 0, \frac{\Pi_p}{\mu_p}, 0, \frac{\Pi_v}{\mu_v}, 0, 0\right)$$

4.2 Basic Reproduction Number of the Full Model

To obtain the expressions for R_0, we employ the procedure and notation discussed in (Aatif Ali et al. 2022) as follows:

$$F = \begin{bmatrix} 0 & \beta_p S_h^0 & \beta_h S_h^0 & \alpha_h S_h^0 \\ 0 & 0 & \beta_p S_p^0 & \alpha_p S_p^0 \\ \beta_h S_v^0 & \beta_v S_v^0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} \eta + \mu_h & 0 & 0 & 0 \\ 0 & \mu_p + \delta_p & 0 & 0 \\ 0 & 0 & \mu_v & 0 \\ 0 & -\alpha_E & -\alpha_v & \mu_E \end{bmatrix}$$

Inverse of V:

$$V^{-1}=\begin{bmatrix} \frac{1}{\eta+\mu_h} & 0 & 0 & 0 \\ 0 & \frac{1}{\mu_p+\delta_p} & 0 & 0 \\ 0 & 0 & \frac{1}{\mu_v} & 0 \\ 0 & \frac{\alpha_E}{\mu_E(\mu_p+\delta_p)} & \frac{-\alpha_v}{\mu_E\mu_v} & \frac{1}{\mu_E} \end{bmatrix}$$

Then

$$FV^{-1}=\begin{bmatrix} 0 & \frac{\prod_h(\mu_E\beta_p+\alpha_E\alpha_h)}{\mu_h\mu_E(\mu_p+\delta_p)} & \frac{\prod_h(\mu_E\beta_h-\alpha_v\alpha_h)}{\mu_h\mu_E\mu_v} & \frac{\prod_h\alpha_h}{\mu_h\mu_E} \\ 0 & \frac{\prod_p\alpha_p\alpha_E}{\mu_p\mu_E(\mu_p+\delta_p)} & \frac{\prod_p(\mu_E\beta_p-\alpha_p\alpha_v)}{\mu_p\mu_E\mu_v} & \frac{\prod_p\alpha_p}{\mu_p\mu_E} \\ \frac{\prod_v\beta_p}{\mu_v(\eta+\mu_h)} & \frac{\prod_v\beta_v}{\mu_v(\mu_p+\delta_p)} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

This gives R_0 as the positive root of the cubic polynomial :

$$G(Z)=Z^3-a\,Z^2-bZ-c\ =0$$

then $G(1)=\ 1\ -\ (a+b+c)\ =0$

then $R_0\ =\ (R_{0a}+R_{0b}+R_{0c})$

where

- $R_{0a}=\frac{\prod_p\alpha_p\alpha_E}{\mu_p\mu_E(\mu_p+\delta_p)}$,
- $R_{0b}=\frac{\prod_v\prod_h\beta_p}{\mu_v\mu_h(\eta+\mu_h)}\ (\frac{\mu_E\beta_h-\alpha_v\alpha_h}{\mu_v\mu_E})$,
- R_{0c}=$\frac{\prod_p}{\mu_v^2\mu_E\mu_p\mu_h(\eta+\mu_h)(\mu_p+\delta_p)}[\mu_E\beta_v\beta_p\prod_v\mu_E\mu_v\mu_h\beta_v(\eta+\mu_h)-\prod_v\alpha_v\alpha_p\mu_E\mu_v\mu_h(\eta+\mu_h)$

$$-\mu_v^2\alpha_E\alpha_p(\mu_p\mu_v\mu_h\beta_p(\eta+\mu_h)(\mu_p+\delta_p)(\mu_E\beta_h-\alpha_v\alpha_h))-\mu_v\beta_p\prod_v\prod_h(\alpha_v\alpha_p-\mu_E\beta_p)(\mu_E\beta_p+\alpha_E\alpha_h)] \qquad \#$$

you can see R_{0PVE} inside c.

4.3 Local Stability of the Full Model

The local stability for the given system (1) has been established in the following theorem.

Theorem 3. The model (1) is locally asymptotically stable, if $R_0<1$ **at the disease free case** ε_0.

Proof. At ε_0 , we have the following Jacobian system:

$$J(\varepsilon_0)=\begin{bmatrix} -\mu_h & 0 & \gamma & 0 & -\beta_p\dfrac{\Pi_h}{\mu_h} & 0 & -\beta_h\dfrac{\Pi_h}{\mu_h} & -\alpha_h\dfrac{\Pi_h}{\mu_h} \\ 0 & -(\eta+\mu_h) & 0 & 0 & \beta_p\dfrac{\Pi_h}{\mu_h} & 0 & \beta_h\dfrac{\Pi_h}{\mu_h} & \alpha_h\dfrac{\Pi_h}{\mu_h} \\ 0 & \eta & -(\gamma+\mu_h) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\mu_p & 0 & 0 & -\beta_p\dfrac{\Pi_p}{\mu_p} & -\alpha_p\dfrac{\Pi_p}{\mu_p} \\ 0 & 0 & 0 & 0 & -(\mu_p+\delta_p) & 0 & \beta_p\dfrac{\Pi_p}{\mu_p} & \alpha_p\dfrac{\Pi_p}{\mu_p} \\ 0 & -\beta_h\dfrac{\Pi_v}{\mu_v} & 0 & 0 & -\beta_v\dfrac{\Pi_v}{\mu_v} & -\mu_v & 0 & 0 \\ 0 & \beta_h\dfrac{\Pi_v}{\mu_v} & 0 & 0 & \beta_v\dfrac{\Pi_v}{\mu_v} & 0 & -\mu_v & 0 \\ 0 & 0 & 0 & 0 & \alpha_E & 0 & \alpha_v & -\mu_E \end{bmatrix}$$

The characteristics equation of $J(\varepsilon_0)$ is

$$\lambda^4+a_1\lambda^3+a_2\lambda^2+a_3\lambda+a_4=0$$

where

- $a_1 = \eta+\mu_h+\mu_E+\mu_v+\mu_p+\delta_p$,
- $a_2 = (\eta+\mu_h)(\mu_E+\mu_v+(\mu_p+\delta_p))-\alpha_E\alpha_p\frac{\Pi_p}{\mu_p}+\mu_E\mu_v+(\mu_E+\mu_v)(\mu_p+\delta_p)+\beta_v\beta_p\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v}-\beta_h^2\frac{\Pi_h}{\mu_h}\frac{\Pi_v}{\mu_v}$,
- $a_3 = (\eta+\mu_h)[(\mu_E\mu_v+\mu_E(\mu_p+\delta_p)+\mu_v(\mu_p+\delta_p)-\alpha_E\alpha_p\frac{\Pi_p}{\mu_p}+\beta_v\beta_p\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v})]-\alpha_v\alpha_p\beta_v\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v}-\alpha_E\alpha_p\mu_v\frac{\Pi_p}{\mu_p}+\mu_E\mu_v(\mu_p+\delta_p)-\beta_v\beta_p\mu_E\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v}-\alpha_v\alpha_h\beta_h\frac{\Pi_h}{\mu_h}\frac{\Pi_v}{\mu_v}-\beta_h^2\mu_E\frac{\Pi_h}{\mu_h}\frac{\Pi_v}{\mu_v}-\beta_p^2\beta_h\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v}\frac{\Pi_h}{\mu_h}-\beta_h^2\frac{\Pi_h}{\mu_h}\frac{\Pi_v}{\mu_v}(\mu_p+\delta_p)$,
- $a_4 = (\eta+\mu_h)\mu_E\mu_v(\mu_p+\delta_p)-(\eta+\mu_h)\alpha_v\alpha_p\beta_v\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v}-(\eta+\mu_h)\alpha_E\alpha_p\mu_v\frac{\Pi_p}{\mu_p}-(\eta+\mu_h)\beta_v\beta_p\mu_E\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v}-\frac{\Pi_h}{\mu_h}\frac{\Pi_v}{\mu_v}[\alpha_v\alpha_h\beta_h(\mu_p+\delta_p)+\alpha_E\alpha_h\beta_h\beta_p\frac{\Pi_p}{\mu_p}+\alpha_v\alpha_p\beta_p\beta_h-\alpha_E\alpha_p\beta_h^2\frac{\Pi_p}{\mu_p}+\mu_E\beta_h\beta_p^2\frac{\Pi_p}{\mu_p}+\beta_h^2\mu_E(\mu_p+\delta_p)]$

then $a_4 = (\eta+\mu_h)[\mu_v - \alpha_v\alpha_p\beta_v\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v} - \beta_v\beta_p\frac{\Pi_p}{\mu_p}\frac{\Pi_v}{\mu_v(\mu_p+\delta_p)} - R_{0a}] + \alpha_E\alpha_p\beta_h^2\frac{\Pi_p\Pi_h\Pi_v}{\mu_p\mu_E\mu_h\mu_v(\mu_p+\delta_p)} - \alpha_E\alpha_h\beta_h\beta_p\frac{\Pi_p\Pi_v\Pi_h}{\mu_p\mu_h\mu_v\mu_E(\mu_p+\delta_p)} - \alpha_v\alpha_p\beta_p\beta_h\frac{\Pi_v\Pi_h}{\mu_h\mu_v\mu_E(\mu_p+\delta_p)} - \frac{\Pi_v\Pi_h\beta_p}{\mu_h\mu_v^2\mu_E(\eta+\mu_h)}[\alpha_v\alpha_h(\frac{-\mu_v\beta_h(\eta+\mu_h)}{\beta_p} - \mu_E\beta_h\frac{\Pi_p\mu_v\beta_p(\eta+\mu_h)}{\mu_p(\mu_p+\delta_p)})]$

You can also see R_{0b} in the last term of a_4 .

Applying Routh-Hurwitz criteria($a_j > 0$ for j = 1, ..., 4 and further $a_1a_2a_3 > a_4$).

Thus, the model when $R_0 < 1$ at the infection free equilibrium is locally asymptotically stable.

4.4 Endemic Equilibria of the Full Model

To have the expressions for the model (1) at the endemic case, we denote its endemic equilibrium by

$$\varepsilon_1 = (S_h^*, I_h^*, R_h^*, S_p^*, I_p^*, S_v^*, I_v^*, E^*)$$

and is given by

- $S_h^* = \frac{1}{\mu_h}(\prod_h + [\frac{\gamma\eta}{\gamma+\mu_h} - (\eta+\mu_h)]I_h^*)$,
- $R_h^* = \frac{\eta}{\gamma+\mu_h}I_h^*$,
- $S_p^* = \frac{\Pi_p}{\mu_p} - \frac{(\mu_p+\delta_p)}{\mu_p}[\frac{I_h^*(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})+\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}}{\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}}]$,
- $I_p^* = \frac{I_h^*(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})+\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}}{\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}}$,
- $S_v^* = \frac{\Pi_v}{\mu_v} - [\frac{\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$
  $[\frac{I_h^*(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})+\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}}{(\mu_p+\delta_p)}] - \frac{\frac{\mu_p}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}]$,
- $I_v^* = \frac{\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$

$[\frac{I_h^*(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})+\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}}{(\mu_p+\delta_p)}] - \frac{\frac{\mu_p}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}$,

- $$E^*= \frac{1}{\mu_E}[\frac{\frac{\mu_p\alpha_v}{\Pi_p}-\frac{\alpha_E\alpha_p\alpha_v}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]} - \frac{\frac{\mu_p\alpha_v}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}$$
$$+\frac{\alpha_E}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}][\frac{I_h^*(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})+\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}}{(\mu_p+\delta_p)}],$$

substituting in I_h (second equation in model(1))

$$f(I_h) = aI_h^{*2} + bI_h^* + c = 0 \qquad \text{where,}$$

- $$a = \frac{(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}]\beta_h}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]\mu_h}[\frac{\gamma\eta}{(\gamma+\mu_h)}-(\eta+\mu_h)]$$
$$+\frac{(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})\beta_p}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]\mu_h}[\frac{\gamma\eta}{(\gamma+\mu_h)}-(\eta+\mu_h)]$$
$$+\frac{\alpha_h}{\mu_h\mu_E}(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})[\frac{\frac{\mu_p\alpha_v}{\Pi_p}-\frac{\alpha_E\alpha_p\alpha_v}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$$
$$-\frac{\frac{\mu_p\alpha_v}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}+\frac{\alpha_E}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}][\frac{\gamma\eta}{(\gamma+\mu_h)}-(\eta+\mu_h)],$$

- $$b = \frac{\prod_h\beta_h}{\mu_h}\frac{(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})(\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)})}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$$
$$+\frac{(\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)})(\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)})}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}[\frac{\gamma\beta_h\eta}{\mu_h(\gamma+\mu_h)}-\frac{\beta_h(\eta+\mu_h)}{\mu_h}]$$
$$-\frac{\frac{\mu_p}{(\mu_p+\delta_p)}\beta_h}{\mu_h[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p]}[\frac{\gamma\eta}{(\gamma+\mu_h)}-(\eta+\mu_h)]+\frac{(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})\prod_h\beta_p}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]\mu_h}$$
$$+\frac{(\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)})\beta_p}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]\mu_h}[\frac{\eta}{(\gamma+\mu_h)}-(\eta+\mu_h)]$$
$$+\frac{(\frac{\Pi_v\beta_p\beta_h}{\mu_v^2(\mu_p+\delta_p)}+\frac{\Pi_v\beta_h\alpha_v\alpha_p}{\mu_v^2})\alpha_h}{\mu_h\mu_E}[\frac{\frac{\mu_p\alpha_v}{\Pi_p}-\frac{\alpha_E\alpha_p\alpha_v}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$$

$$-\frac{\frac{\mu_p\alpha_v}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}+\frac{\alpha_E}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}][\prod_h+\frac{\gamma\eta}{(\gamma+\mu_h)}]\ -$$

$$\frac{(\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)})(\eta+\mu_h)\alpha_h}{\mu_h\mu_E}[\frac{\frac{\mu_p\alpha_v}{\Pi_p}-\frac{\alpha_E\alpha_p\alpha_v}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$$

$$-\frac{\frac{\mu_p\alpha_v}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}+\frac{\alpha_E}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}][\prod_h+\frac{\gamma\eta}{(\gamma+\mu_h)}]-(\eta+\mu_h),$$

- $$c=\frac{\prod_h\beta_h}{\mu_h}(\frac{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}][\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}]}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}-\frac{\frac{\mu_p}{(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p]})$$

$$+\frac{\prod_h[\frac{\Pi_v\beta_p}{\mu_v(\mu_p+\delta_p)}+\frac{\Pi_v\alpha_v\alpha_p}{\mu_v}+\frac{\mu_p}{(\mu_p+\delta_p)}]}{\mu_h}[\frac{\beta_P}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}$$

$$+\ \frac{\alpha_h}{\mu_E}\ [\frac{\frac{\mu_p\alpha_v}{\Pi_p}-\frac{\alpha_E\alpha_p\alpha_v}{\mu_E(\mu_p+\delta_p)}}{[\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p][\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}\quad-\frac{\frac{\mu_p\alpha_v}{(\mu_p+\delta_p)}}{\frac{\beta_p}{(\mu_p+\delta_p)}+\alpha_v\alpha_p}+$$

$$\frac{\alpha_E}{[\frac{\mu_p}{\Pi_p}-\frac{\alpha_E\alpha_p}{\mu_E(\mu_p+\delta_p)}-\frac{\Pi_v\beta_p\beta_v}{\mu_v^2(\mu_p+\delta_p)}-\frac{\Pi_v\beta_v\alpha_v\alpha_p}{\mu_v^2}]}]]$$

The coefficient a, b and c is positive. For the case when considering c = 0, then a solution of the form exists $I_h^*=-b/a$, when $b<0$.

$$I_{h1,2}^*=\frac{-b+\sqrt(b^2-4ac)}{2a},\frac{-b-\sqrt(b^2-4ac)}{2a}\qquad\#$$

4.5 Stability of the endemic equilibrium of the Full Model

At the endemic case ε_1, the following Jacobian matrix is presented,

$$J(\varepsilon_1)=\begin{bmatrix}-Q_1 & 0 & \gamma & 0 & -Q_6 & 0 & -Q_{10} & -Q_{12}\\ Q_2 & -(\eta+\mu_h) & 0 & 0 & Q_6 & 0 & Q_{10} & Q_{12}\\ 0 & \eta & -(\gamma+\mu_h) & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & -Q_4 & 0 & 0 & -Q_{11} & -Q_{13}\\ 0 & 0 & 0 & Q_5 & -(\mu_p+\delta_p) & 0 & Q_{11} & Q_{13}\\ 0 & -Q_3 & 0 & 0 & -Q_7 & -Q_8 & 0 & 0\\ 0 & Q_3 & 0 & 0 & Q_7 & Q_9 & -\mu_v & 0\\ 0 & 0 & 0 & 0 & \alpha_E & 0 & \alpha_v & -\mu_E\end{bmatrix}$$

where,

$$Q_1=\beta_hI_v^*+\beta_pI_p^*+\alpha_h\ E^*+\mu_h\ ,\ Q_2=\beta_hI_v^*+\beta_pI_p^*+\alpha_h\ E^*\ ,\ Q_3=\beta_hS_v^*,$$

$$Q_4=\beta_pI_v^*+\alpha_p\ E^*+\mu_p\qquad,\ Q_5=\beta_pI_v^*+\alpha_p\ E^*\qquad,\ Q_6=\beta_pS_h^*,$$

$$Q_7=\beta_vS_v^*\qquad,\ Q_8=\beta_vI_p^*+\beta_hI_h^*+\mu_v\qquad,\ Q_9=\beta_vI_p^*+\beta_hI_h^*,$$

$$Q_{10} = \beta_h S_h^* \qquad , Q_{11} = \beta_p S_p^* \qquad , Q_{12} = \alpha_h S_h^* \qquad , Q_{13} = \alpha_p S_p^*$$

The characteristics equation of $J(\varepsilon_1)$ is

$$\lambda^8 + k_1\lambda^7 + k_2\lambda^6 + k_3\lambda^5 + k_4\lambda^4 + k_5\lambda^3 + k_6\lambda^2 + k_7\lambda + k_8 = 0$$

If and only if $R_0 > 1$, the model's endemic equilibrium is locally asymptotically stable. However, because of the nature of the transmission model, it is very difficult to deal with the stability of the endemic equilibrium analytically. Therefore, it was an excellent opportunity to discuss it numerically.

Then $k_1 = 18.7057914$, $k_2 = 769.0026435,$

$k_3 = 6846.3356876$, $k_4 = 30939.2899134,$

$k_5 = -2055455.276191,$ $k_6 = -342258.28868,$

$k_7 = -201370.7669887,$ $k_8 = 24604.5523005$

It is obvious that not all $k_i > 0$, therefore the system is unstable in case of disease.

5. Numerical Results

We use the parameter values, which are briefly defined in Table 1, to illustrate the outcomes of the numerical solution of the suggested model. For all numerical results, we take into account the time unit in a day. Certain parameter values are assumed for this exercise for the sake of illustration. **Matlab** and **Python** were used to simulate the model (1) numerically. Analysis of how model parameters affected the disease's transmission dynamics was done. Since, most of the parametric values are not readily available it is needed to assume some values. However, some are available at [(Jin-Qiang et al.2021), (Khan et al. 2021), (Bonyah et al. 2016), (Nyabadza and Bonyah 2015), (Marsollier al. 2002), (Hayman and Hibble 2001) and (Bollinger et al. 1950)]. The initial conditions were taken at initial time of zero and the final time was 120 considered as S_h, I_h, R_h,S_p, I_p,S_v, I_v and E as 400, 40, 100, 100, 10, 100, 20 and 10. The simulation study's findings are displayed in Figures (2,3,4,5,6,7,8,9)

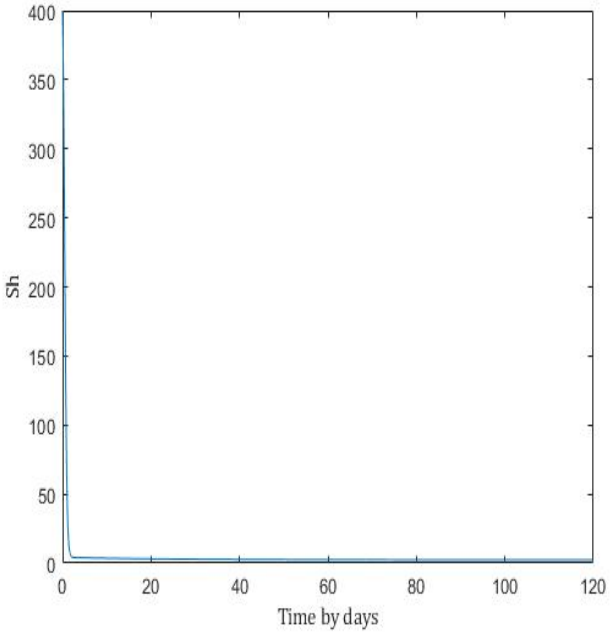

Figure 2

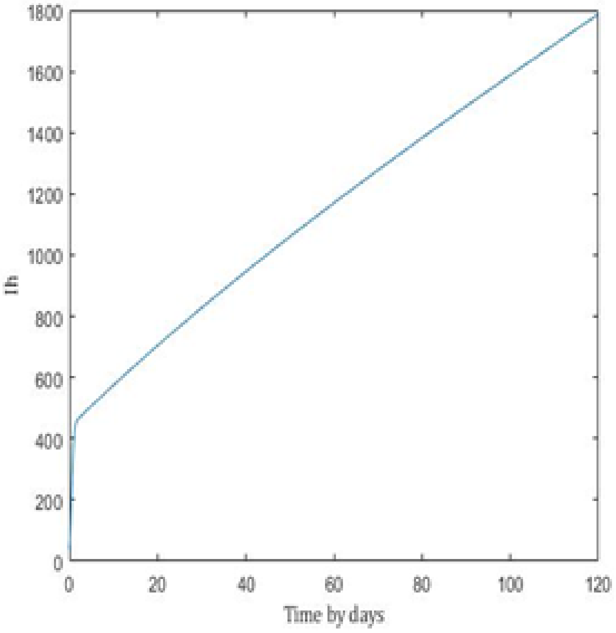

Figure 3

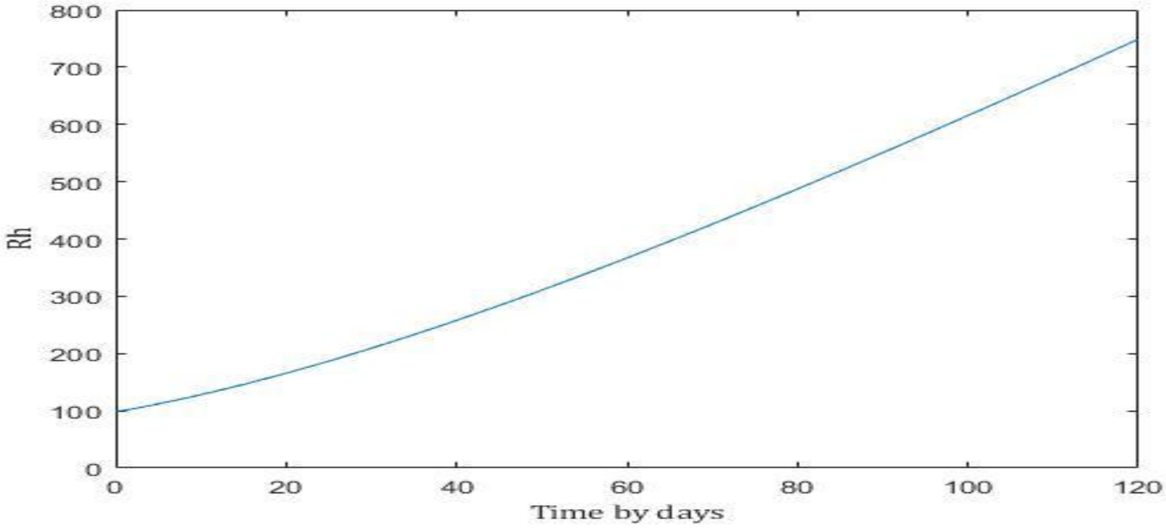

Figure 4

In figures 2,3 and 4 we can illustrate Human variables in model (1) S_h, I_h and R_h numerically.

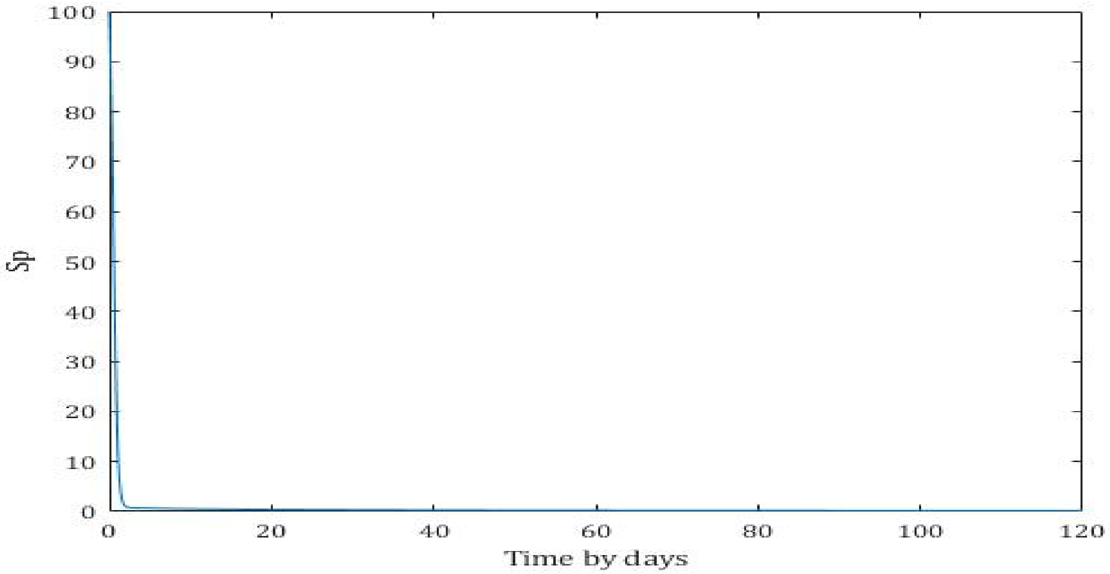

Figure 5

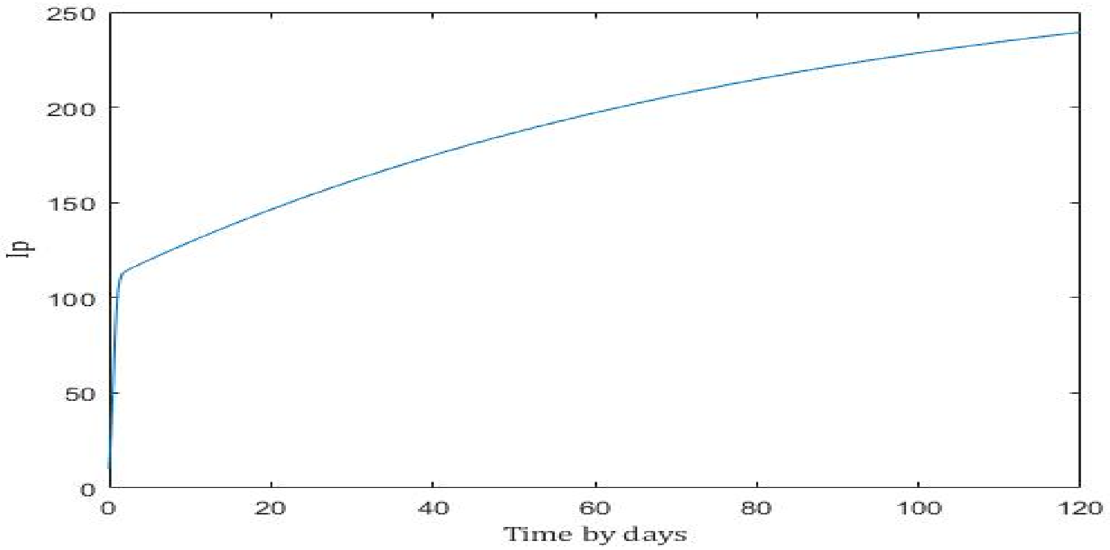

Figure 6

Figure 5 and Figure 6 show Possum Variables S_p and I_p in model (1) numerically.

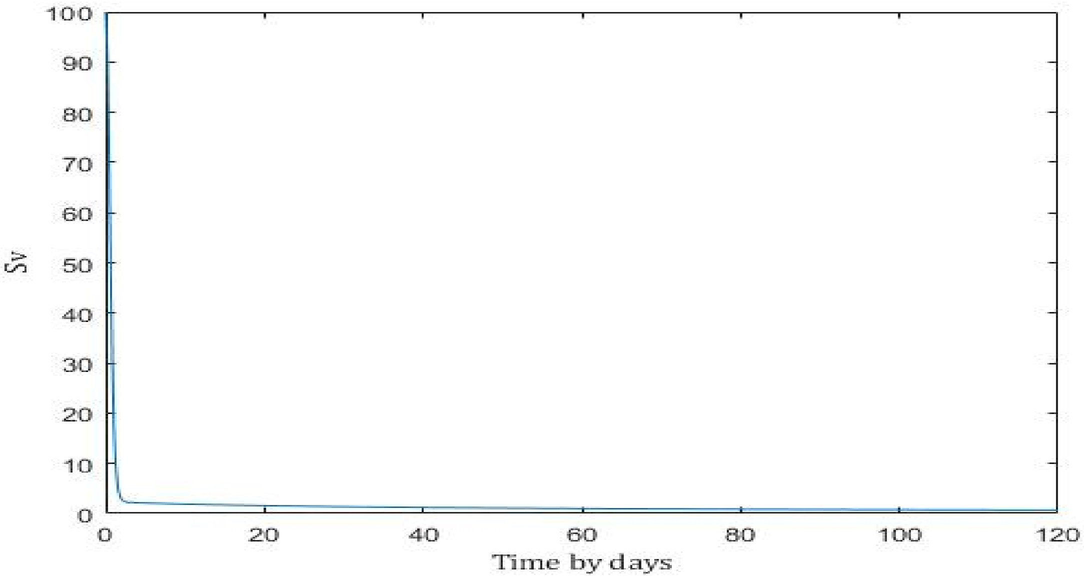

Figure 7

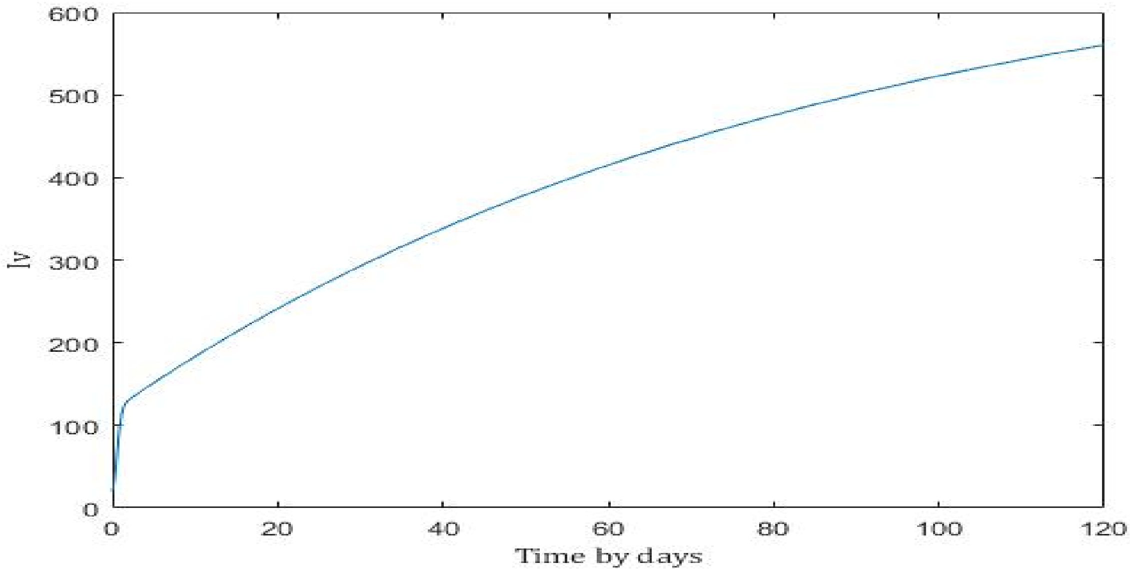

Figure 8

We can illustrate vector variables S_v and I_v numerically in model (1) by figure 7 and figure 8.

Adding Figure 9 to show environment variable E in model (1) numerically.

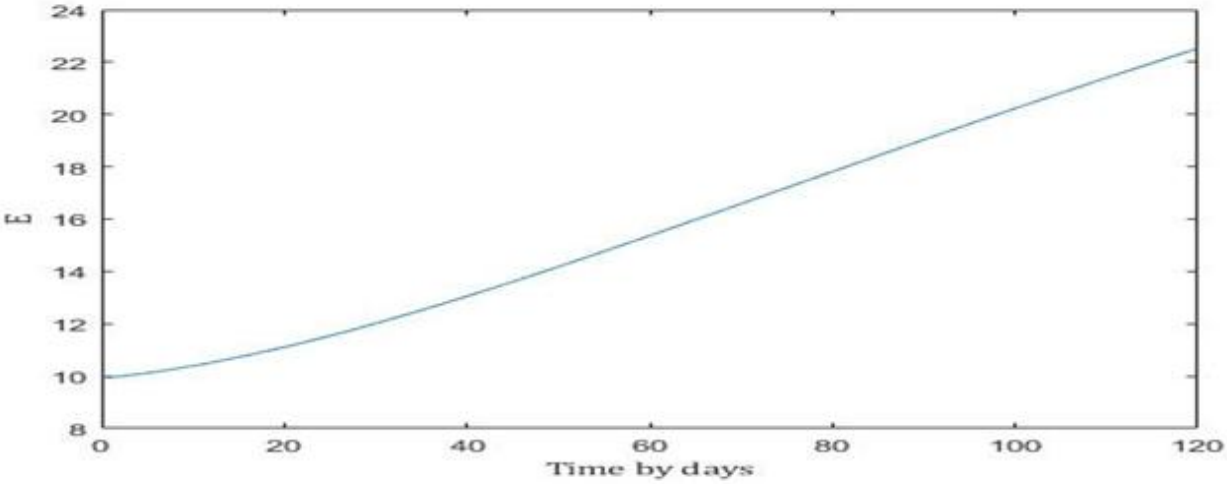

Figure 9

We will show in the following figures the effect of certain elements with certain variables.

Population infected human(I_h) in our model is very sensitive to η, β_h

The recovery rate of infected humans(η) as shown in figure10 : increasing in η indicates a decreasing in infected humans. The contact rate between $S_h$and I_p (β_h) as shown in figure11.As shown in figures 10&11 the curve behavior I_h changes on time depends on the value of η, β_h.

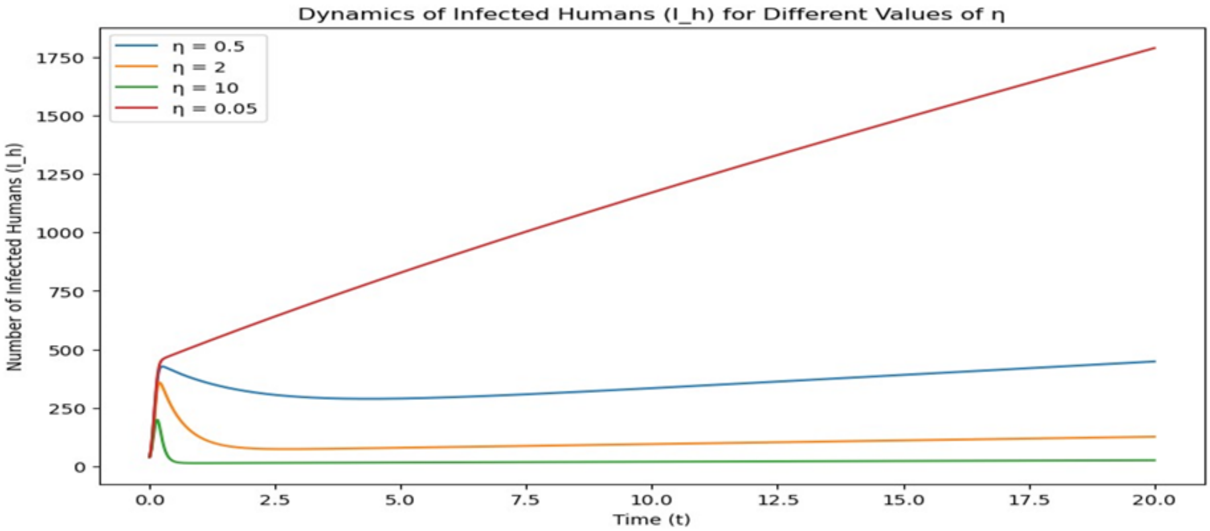

Figure 10

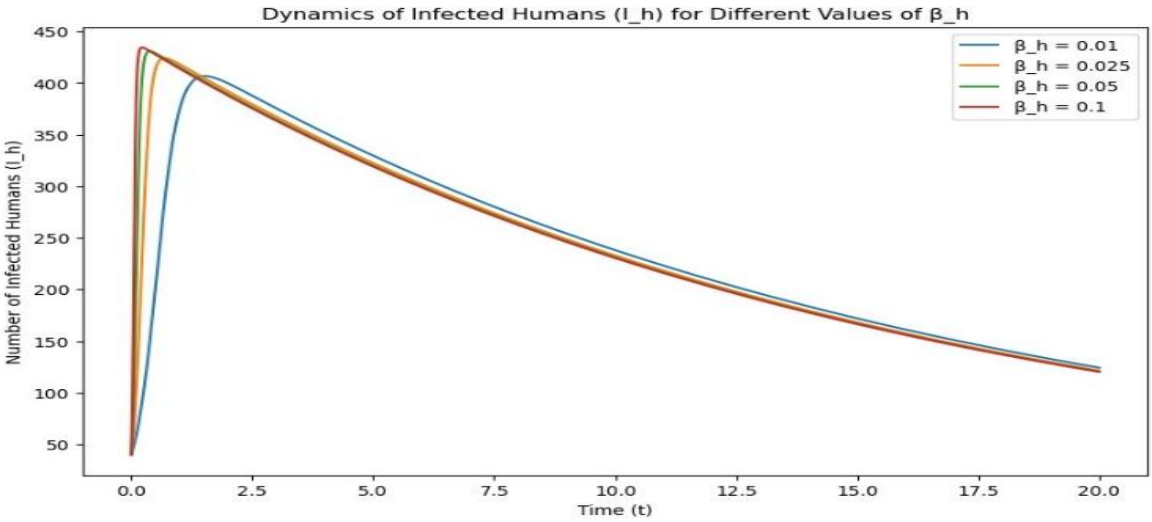

Figure11

Population infected possum (I_p) in our model is very sensitive to δ_p

The death rate due to infection in possum (δ_p) as shown in figure 12.

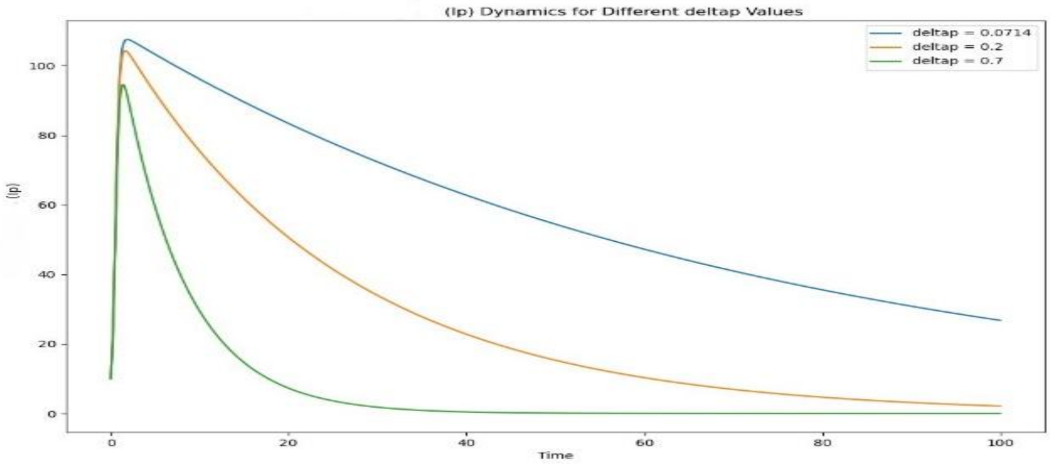

Figure 12

Population infected possum (I_p) in our model is very sensitive to β_v

The contact rate between $I_v$and E (β_v) as shown in figure13.

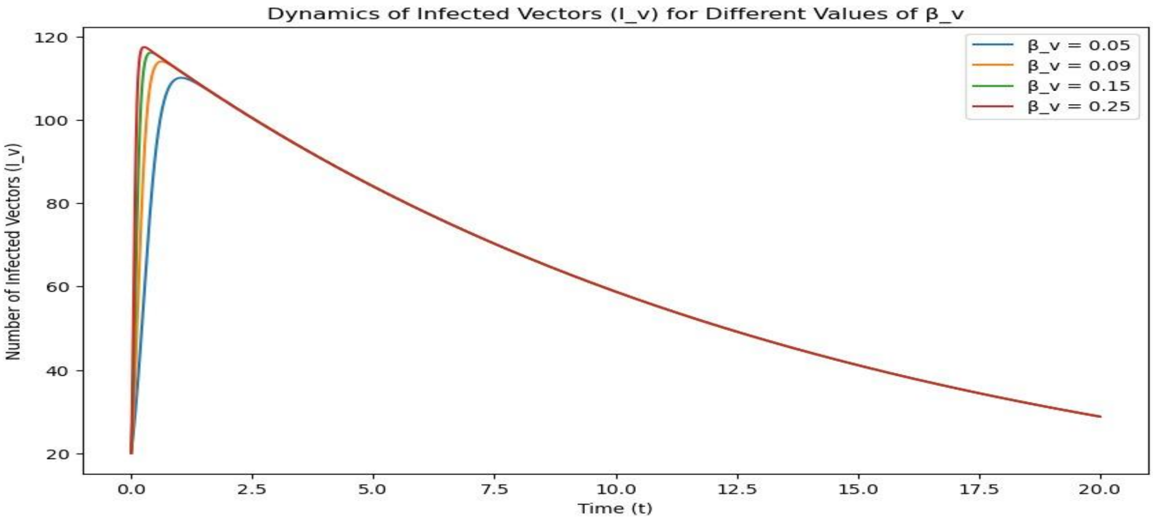

Figure 13

6. Conclusion

In our present work, we employ a mathematical model to thoroughly investigate the dynamics of Buruli ulcer. Evolutionary differential equations provide an efficient model for the Buruli infection. Separate investigations were conducted into the PVE model. The local asymptotic results for the sub-model at free disease and at endemic case were investigated for the case when R_0 less or greater than 1.We observed that the sub-model are found locally for the given fixed points. Further, we investigated the fully infected model (which added the Human model to the earlier model) and presented its stability for the local case when $R_0 < 1$ also at free disease and in endemic case . The mathematical results were obtained and discussed. we noticed the effectiveness of certain values on Infected Items and illustrated it by figures.

In future we look forward to finding a tool which can decrease the infected items in our model (1) and may increase the recovery items.

Funding agency

Not found

Ethics/bioethics

This research did not cause harm to any human or animal.

Declaration of Competing Interest

The authors declare no conflict of interest.

Author Contributions:

The final manuscript was read, approved, and each author made an equal contribution to this work.

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