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GLOBAL STABILITY ANALYSIS OF A VEISV MODEL FOR NETWORK WORM ATTACK

Mahmood Parsamanesh[1]

In this paper, a VEISV network worm attack model is investigated. It is established that the worm-free equilibrium is locally as well as globally asymptotically stable when $\mathcal{R}_0 < 1$. When $\mathcal{R}_0 > 1$, the local and global asymptotic stability of the worm-epidemic equilibrium are derived employing the second additive compound matrix approach and the direct Lyapunov method, respectively.

Keywords: Worm attack, Next generation matrix, Second additive compound matrix, Global stability, Lyapunov function.

MSC2010: 34D23, 37B25.

1. Introduction

Toutonji et al. in [15] established the following VEISV model for network worm attack:

$$\begin{cases} V' = -fEV - \psi_1 V + \varphi S, \\ E' = fEV - (\alpha + \psi_2)E, \\ I' = \alpha E - (\gamma + \theta)I, \\ S' = \mu N + \psi_1 V + \psi_2 E + \gamma I - \varphi S \end{cases} \tag{1}$$

The parameters and notations in the model are summarized in Table 1. In procedure of building the model it has been assumed that the number of replaced hosts is equal to the number of dysfunctional hosts as $\mu N = \theta I$ [15]. Then by summarizing the equations of system (1) we find that $N' = 0$ and thus total number of hosts $N = V(t) + E(t) + I(t) + S(t)$ is fixed. obviously, the region $\Gamma = \{(V, E, I, S) \in \mathbb{R}^4_+ : V + E + I + S = N\}$ is the positively invariant set of (1). Also $f = \frac{\alpha\beta}{N}$ represents the force of incident where β is contact rate. Omitting the variable $S = N - V - E - I$ from system (1) the following system is obtained:

$$\begin{cases} V' = \varphi N - fEV - (\psi_1 + \varphi)V - \varphi E - \varphi I, \\ E' = fEV - (\alpha + \psi_2)E, \\ I' = \alpha E - (\gamma + \theta)I. \end{cases} \tag{2}$$

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[1] Department of mathematics, Faculty of Sciences, University of Zabol, Zabol, Iran, e-mail: m.parsamanesh@uoz.ac.ir

Table 1. Notations and parameters in the VEISV model (1).

Parameter	Explanation
$V(t)$	Number of vulnerable hosts at time t
$E(t)$	Number of exposed hosts at time t
$I(t)$	Number of infectious hosts at time t
$S(t)$	Number of secured hosts at timet
N	Total number of hosts
β	Contact rate
α	State transition rate from E to I
ψ_1	State transition rate from V to S
ψ_2	State transition rate from E to S
γ	State transition rate from I to S
φ	State transition rate from S to V
θ	Dysfunctional rate
μ	Replacement rate

Two equilibria of system (2) are: the worm-free equilibrium when $E = 0$

$$EQ_{wf} = (V^0, E^0, I^0) = \left(\frac{\varphi N}{\psi_1 + \varphi}, 0, 0 \right),$$

and the worm-epidemic equilibrium for $E > 0$

$$\begin{aligned} EQ_{we} &= (V^*, E^*, I^*) \\ &= \left(\frac{(\alpha + \psi_2)N}{\alpha\beta}, \frac{\alpha\beta\varphi - (\psi_1 + \varphi)(\psi_2 + \alpha)}{\alpha\beta\left(\alpha + \psi_2 + \varphi(1 + \frac{\alpha}{\gamma+\theta})\right)} N, \frac{\alpha}{\gamma + \theta} E^* \right). \end{aligned}$$

To find the basic reproduction number of the model, we use the next generation matrix method developed in [16]. Suppose the vector $\mathbf{y}$ indicates all infected states such as exposed and infectious individuals. Thus let $\mathbf{y} = (E, I)$, then from system (2) it can be seen that

$$\frac{d\mathbf{y}}{dt} = \mathcal{F} - \mathcal{W},$$

with $\mathcal{F} = \begin{pmatrix} fEV \\ 0 \end{pmatrix}$ and $\mathcal{W} = \begin{pmatrix} -(\alpha + \psi_2)E \\ \alpha E - (\gamma + \theta)I \end{pmatrix}$.

Also let

$F = \frac{\partial \mathcal{F}}{\partial \mathbf{y}}\Big|_{EQ_{wf}} = \begin{pmatrix} fV^0 & 0 \\ 0 & 0 \end{pmatrix}$ and $W = \frac{\partial \mathcal{W}}{\partial \mathbf{y}}\Big|_{EQ_{wf}} = \begin{pmatrix} \alpha + \psi_2 & 0 \\ -\alpha & \gamma + \theta \end{pmatrix}$.

Therefore we obtain

$$\mathcal{R}_0 = \rho(FW^{-1}) = \frac{\alpha\beta\varphi}{(\psi_1 + \varphi)(\psi_2 + \alpha)}, \tag{3}$$

where, $\mathcal{R}_0$ is called the basic reproduction number of model (2) and it is defined as the number of secondary infectious hosts in a completely vulnerable network[3]. Note that

$$E^* = \frac{(\psi_1+\varphi)(\psi_2+\alpha)(\mathcal{R}_0-1)}{\alpha\beta\left(\alpha+\psi_2+\varphi(1+\frac{\alpha}{\gamma+\theta})\right)}N,$$

and thus the worm-epidemic equilibrium EQ_{we} exists if $\mathcal{R}_0 > 1$.
By above discussion we have the following:

Lemma 1.1. *System (2) has ONLY the worm-free equilibrium* EQ_{wf} *when* $\mathcal{R}_0 \leq 1$*. If* $\mathcal{R}_0 > 1$ *the system also has a UNIQUE worm-epidemic equilibrium* EQ_{we}*.*

2. **Stability of the worm-free equilibrium**

It can be seen easily that the eigenvalues of the Jacobian matrix of system (2) at the worm-free equilibrium EQ_{wf} are real and negative provided that $\mathcal{R}_0 < 1$. from this or Theorem 2 in [16] we have the following:

Lemma 2.1. *The worm-free equilibrium* EQ_{wf} *is locally asymptotically stable for* $\mathcal{R}_0 < 1$ *and unstable for* $\mathcal{R}_0 > 1$*.*

The global asymptotic stability of the disease-free equilibrium has been studied separately by many authors[2, 5, 6, 10]. We use the approach introduced in [2] to derive the global asymptotic stability of EQ_{wf}. We first describe briefly this procedure.
Assume the system can be written in the following form:

$$\begin{aligned} \frac{d\mathbf{x}}{dt} &= h(\mathbf{x},\mathbf{y}), \\ \frac{d\mathbf{y}}{dt} &= g(\mathbf{x},\mathbf{y}), \quad g(\mathbf{x},0)=0, \end{aligned} \tag{4}$$

where $\mathbf{x}$ and $\mathbf{y}$ denote uninfected states (such as susceptible, vaccinated and quarantined individuals) and infected states (such as exposed and infectious individuals), respectively. Also, denote $U_0 = (\mathbf{x}^0, 0)$ as the disease-free equilibrium of the system and assume that two below conditions hold:
$(\mathcal{H}_1)$ $\mathbf{x}^0$ is globally asymptotically stable for $\frac{d\mathbf{x}}{dt} = h(\mathbf{x},0)$,
$(\mathcal{H}_2)$ $g(\mathbf{x},\mathbf{y}) = A\mathbf{y} - \hat{g}(\mathbf{x},\mathbf{y}), \hat{g}(\mathbf{x},\mathbf{y}) \geq 0 \in \Gamma$,
where $A = \frac{\partial g}{\partial \mathbf{y}}\Big|_{U_0}$ is a Metzler matrix (the off-diagonal elements of A are non-negative) and Γ is the positive invariant region in which the system is considered. Then the following lemma holds[2].

Lemma 2.2. *The disease-free equilibrium* $U_0 = (\mathbf{x}^0, 0)$ *of system (4) is globally asymptotically stable provided that* $\mathcal{R}_0 < 1$ *and assumptions* $(\mathcal{H}_1)$ *and* $(\mathcal{H}_2)$ *are satisfied.*

Now we state the following theorem:

Theorem 2.1. *The worm-free equilibrium EQ_{wf} of system (2) is globally asymptotically stable if $\mathcal{R}_0 < 1$.*

Proof. Let $\mathbf{x} = V$ and $\mathbf{y} = (E, I)$. Thus

$$h(\mathbf{x}, \mathbf{y}) = \varphi N - fEV - (\psi_1 + \varphi)V - \varphi E - \varphi I,$$

which is a linear system that is globally asymptotically stable at $\mathbf{x}^0 = V^0$. On the other hand

$$g(\mathbf{x}, \mathbf{y}) = \begin{pmatrix} fEV - (\alpha + \psi_2)E \\ \alpha E - (\gamma + \theta)I \end{pmatrix},$$

and this follows that

$$A = \frac{\partial g}{\partial \mathbf{y}}\Big|_{U_0} = \begin{pmatrix} fV^0 - (\alpha + \psi_2) & 0 \\ \alpha & -(\gamma + \theta) \end{pmatrix},$$

and

$$\hat{g} = A\mathbf{y} - g = \begin{pmatrix} fE(V^0 - V) \\ 0 \end{pmatrix}.$$

From first equation of system (1) we have

$$\begin{aligned} V' &= -fEV - \psi_1 V + \varphi S \\ &\le -\psi_1 V + \varphi(N - V - I - E) \\ &\le -(\psi_1 + \varphi)V + \varphi N. \end{aligned}$$

Therefore we always have $V \le V^0 = \frac{\varphi N}{\psi_1 + \varphi}$ and thus $\hat{g} \ge 0$. Hence conditions $(\mathcal{H}_1)$ and $(\mathcal{H}_2)$ of the Lemma 2.2 hold and this completes the global asymptotic stability of EQ_{wf}.

Remark 2.1. The stability of EQ_{wf} also has been derived by Toutonji et al. in [15]. They defined the Lyapunov function $L(t) = E(t)$ for global stability and showed that

$$L'(t) \le (\alpha + \psi_2)(\mathcal{R}_0 - 1)E(t).$$

3. **Stability of the worm-epidemic equilibrium**

In this section we focus on the stability of the worm-epidemic equilibrium EQ_{we}. First we consider the local asymptotic stability of EQ_{we} by applying the following lemma[12].

Lemma 3.1. *Any matrix $M \in \mathcal{M}_n(\mathbb{R})$ is stable if and only if*
(1) The second additive compound matrix $M^{[2]}$ is stable,
(2)$(-1)^n det(M) > 0$.

A survey on definitions and properties of compound matrices and their connections to differential equations can be found in [13]. The second additive compound matrix of a $n \times n$ matrix $A = \left(a_{ij}\right)$ is an $\binom{n}{2} \times \binom{n}{2}$ matrix and it is denoted by $A^{[2]}$. For $n = 3$, it is as follows:

$$A^{[2]} = \begin{pmatrix} a_{11} + a_{22} & a_{23} & -a_{13} \\ a_{32} & a_{11} + a_{33} & a_{12} \\ -a_{31} & a_{21} & a_{22} + a_{33} \end{pmatrix}.$$

The following theorem considers the local asymptotic stability of the worm-epidemic state.

Theorem 3.1. *The worm-epidemic equilibrium EQ_{we} is locally asymptotically stable if $\mathcal{R}_0 > 1$.*

Proof. Note that EQ_{we} is stable if and only if the corresponding Jacobian matrix $J(EQ_{we})$ is stable. The Jacobian matrix at EQ_{we} and its second additive compound matrix are

$$J(EQ_{we}) = \begin{pmatrix} -(fE^* + \psi_1 + \varphi) & -(\alpha + \psi_2 + \varphi) & -\varphi \\ fE^* & 0 & 0 \\ 0 & \alpha & -(\gamma + \theta) \end{pmatrix}.$$

and

$$J^{[2]}(EQ_{we}) = \begin{pmatrix} -fE^* - (\psi_1 + \varphi) & 0 & \varphi \\ \alpha & -fE^* - (\psi_1 + \varphi + \gamma + \theta) & -(\alpha + \psi_2 + \varphi) \\ 0 & fE^* & -(\gamma + \theta) \end{pmatrix}.$$

Then we have

$$det(J(EQ_{we})) = -fE^*[(\alpha + \psi_2 + \varphi)(\gamma + \theta) + \alpha\varphi] < 0,$$

hence condition (2) of Lemma 3.1 holds. This also implies that $\lambda_1\lambda_2\lambda_3 < 0$, where $\lambda_j, j = 1, 2, 3$ is an eigenvalue of the Jacobian matrix $J(EQ_{we})$. Thus either $\mathfrak{R}(\lambda_j) < 0$ for $j = 1, 2, 3$ or $\mathfrak{R}(\lambda_1) < 0 \leq \mathfrak{R}(\lambda_2) \leq \mathfrak{R}(\lambda_3)$, in which $\mathfrak{R}(\lambda)$ indicates real part of λ.

Besides, it easily can be seen that $tr(J(EQ_{we})) < 0$. This means that $\lambda_1 + \lambda_2 + \lambda_3 < 0$ and thus we have $\mathfrak{R}(\lambda_1 + \lambda_2) < 0$ and $\mathfrak{R}(\lambda_1 + \lambda_3) < 0$.

Now note that eigenvalues of matrix $J^{[2]}(EQ_{we})$ are $\lambda_1+\lambda_2$, $\lambda_1+\lambda_3$ and $\lambda_2+\lambda_3$. In addition we have

$$\begin{aligned} -1 &= sgn\left(J^{[2]}(EQ_{we})\right) \\ &= sgn\left(\mathfrak{R}(\lambda_1 + \lambda_2)\mathfrak{R}(\lambda_1 + \lambda_3)\mathfrak{R}(\lambda_2 + \lambda_3)\right) \\ &= sgn\left(\mathfrak{R}(\lambda_2 + \lambda_3)\right). \end{aligned}$$

Therefore all eigenvalues of $J^{[2]}(EQ_{we})$ have negative real parts and this shows that part (1) of Lemma 3.1 is also satisfied.

As the next object, we turn to establish the global stability of the worm-epidemic equilibrium EQ_{we} of system (1). Yang employed a geometric approach developed by Li and Muldowney[11] and proved that EQ_{we} is globally asymptotically stable under some conditions[18]. To accomplish this task, we use the Direct Lyapunov Method[9], one of the most powerful techniques for qualitative analysis of a dynamical system. This method has been used widely to global analysis of epidemic models[1, 4, 7, 8, 14, 17]. However, efficiency of this method depends on finding an auxiliary function, called the Lyapunov function which usually is not straightforward.

Theorem 3.2. *The worm-epidemic equilibrium EQ_{we} of system (1) is globally asymptotically stable if $\mathcal{R}_0 > 1$.*

Proof. System (1) can be written in the form

$$\begin{cases} E' = fEV - (\alpha + \psi_2)E, \\ I' = \alpha E - (\gamma + \theta)I, \\ S' = (\mu + \psi_1)N + (\psi_2 - \psi_1)E + (\gamma - \psi_1)I - (\varphi + \psi_1)S. \end{cases} \tag{5}$$

For positive constants m, n and c, consider the function

$$W = W(V, E, I) = m\left(E - E^* - E^* \ln \frac{E}{E^*}\right) + \frac{n}{2}(I - I^*)^2 + \frac{c}{2}(S - S^*)^2,$$

thus we have

$$\begin{aligned} W' &= m\frac{E'}{E}(E - E^*) + nI'(I - I^*) + cS'(S - S^*) \\ &= m[fV - (\alpha + \psi_2)](E - E^*) + n[\alpha E - (\gamma + \theta)I](I - I^*) \\ &\quad + c[(\mu + \psi_1)N + (\psi_2 - \psi_1)E + (\gamma - \psi_1)I - (\varphi + \psi_1)S](S - S^*) \end{aligned}$$

At EQ_{we} we have from (5)

$$\begin{aligned} &\alpha + \psi_2 = fV^*, \\ &\alpha E^* - (\gamma + \theta)I^* = 0, \\ &(\mu + \psi_1)N = (\psi_1 - \psi_2)E^* + (\psi_1 - \gamma)I^* + (\varphi + \psi_1)S^*. \end{aligned} \tag{6}$$

Hence we get

$$\begin{aligned} W' = {} & m[f(V - V^*)](E - E^*) + n[\alpha(E - E^*) - (\gamma + \theta)(I - I^*)](I - I^*) \\ & + c[(\psi_2 - \psi_1)(E - E^*) + (\gamma - \psi_1)(I - I^*) - (\varphi + \psi_1)(S - S^*)](S - S^*). \end{aligned}$$

We see

$$(V - V^*)(E - E^*) = -(E - E^*)^2 - (I - I^*)(E - E^*) - (S - S^*)(E - E^*),$$

then we have

$$\begin{aligned} W' &= -mf(E - E^*)^2 - n(\gamma + \theta)(I - I^*)^2 - c(\varphi + \psi_1)(S - S^*)^2 \\ &\quad + [-mf + n\alpha](E - E^*)(I - I^*) \\ &\quad + [-mf + c(\psi_2 - \psi_1)](E - E^*)(S - S^*) \\ &\quad - c(\psi_1 - \gamma)(I - I^*)(S - S^*) \\ &= -UMU^\top, \end{aligned} \tag{7}$$

where $U = (E - E^*, I - I^*, S - S^*)$ and

$$M = \begin{pmatrix} mf & \frac{mf-n\alpha}{2} & \frac{mf+c(\psi_1-\psi_2)}{2} \\ \frac{mf-n\alpha}{2} & n(\gamma+\theta) & \frac{c(\psi_1-\gamma)}{2} \\ \frac{mf+c(\psi_1-\psi_2)}{2} & \frac{c(\psi_1-\gamma)}{2} & c(\varphi+\psi_1) \end{pmatrix}.$$

We claim that there exists m, n and c such that matrix M is negative definite for suitably chosen parameters and then EQ_{we} is globally asymptotically stable. For instance, choosing

$$m = 1, \quad n = \frac{\beta}{N}, \quad \text{and} \quad c = \frac{\alpha\beta}{N(\psi_2 - \psi_1)},$$

we can easily seen that for $\psi_1 = \gamma$, the matrix M is negative definite.

4. **Simulations and numerical examples**

In this section the numerical solutions of the model are given and theoretical results obtained in previous sections are studied via some examples.

Example 4.1. Assume that the units of time and host size suggest one hour and one thousand hosts, respectively. Let the value of the parameters in model (5) are $\beta = 15$, $\alpha = 0.15$, $\theta = 0$, $\psi_1 = 0.02$, $\psi_2 = 0.8$, $\gamma = 0.5$, $\varphi = 0.005$. Also suppose that the initial number of hosts are $E(0) = 0.01$, $I(0) = 0.001$ and $S(0) = 0$ with a total number $N = 1500$ of hosts. Then the basic reproduction number $\mathcal{R}_0 = 0.474$ is less than one and thus the worm-free equilibrium $EQ_{wf} = (300, 0, 0)^\top$ is globally stable. The solution of system (2) until the end time $T = 500$ is shown in Figure 1 together with the equilibrium EQ_{wf} as exact solution. The error value of the approximated numerical solution is evaluated as norm two of difference between the numerical solution and the theoretical solution of worm-free equilibrium:

$$\text{error} = \| X_{T=1000} - EQ_{wf} \|_2 = 2.576 \times 10^{-4}$$

Example 4.2. Assume that the units of time and host size, and initial values of hosts are as Example 4.1. Choose parameters in the model as $\beta = 45$, $\alpha = 0.3$, $\theta = 0$, $\psi_1 = 0.003$, $\psi_2 = 0.8$, $\gamma = 0.5$, $\varphi = 0.005$. With these values $\mathcal{R}_0 = 7.671$ is greater than one and therefore the worm-epidemic equilibrium $EQ_{we} = (122.222, 5.887, 3.5312)^\top$ is globally stable. The system (1) has been solved with these parameter values until time $T = 1000$. Figure 2 shows trajectories of V and S components while Figure 3 displays this for E and I. Also, The corresponding component of the worm-epidemic equilibrium as the exact solution has been shown in each figure. The error value of the approximation for these parameter values is obtained as error $= 7.7616 \times 10^{-5}$. Moreover the phase portraits of the numerical solution are given in Figure 4 to illustrate the behavior of the model.

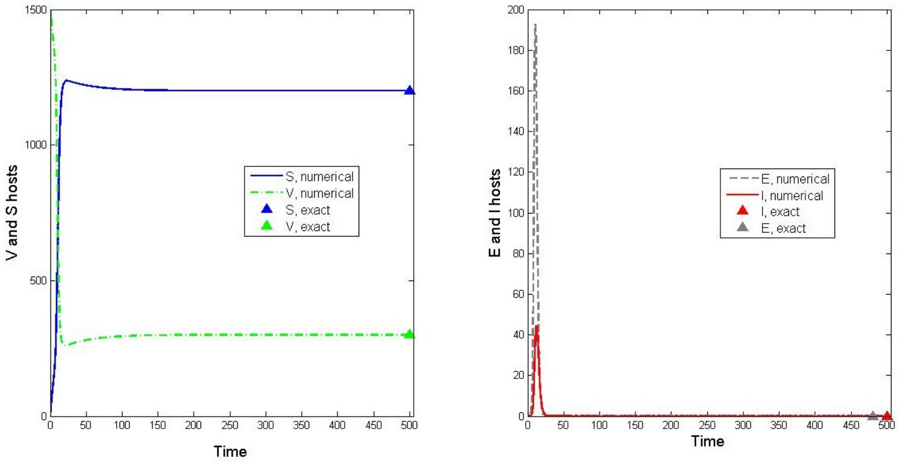

FIGURE 1. Solutions of the model for values in Example 4.1 together with their exact solution.

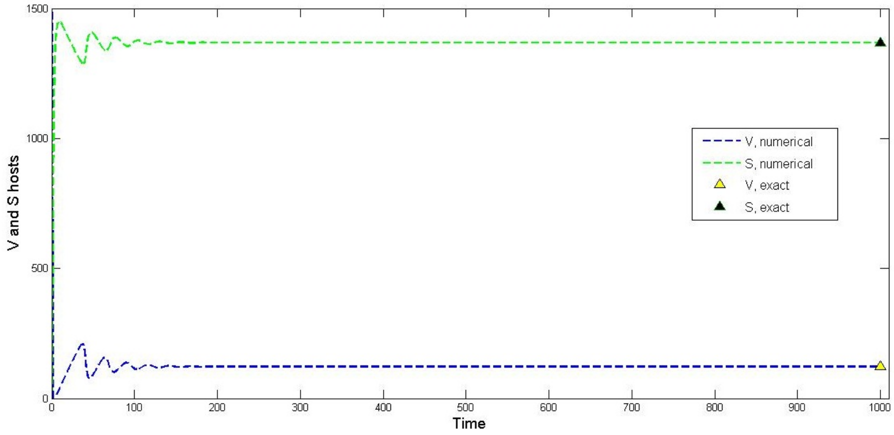

FIGURE 2. Solutions for components V and S until time $T = 1000$ for values in Example 4.2 together with their exact solution.

5. Conclusions

In this paper a VEISV propagation model for network worm attack was discussed. After a glance on basic properties of the model including, the basic reproduction number and the equilibria of the model, we turned on the stability of these states. It was proved that the worm-free state is locally as well as globally asymptotically stable when $\mathcal{R}_0 < 1$. Furthermore, the second additive compound matrix approach was used to establish the local asymptotic stability of worm-epidemic state when $\mathcal{R}_0 > 1$. In this case, the global stability of the state was also concluded by the aid of a Lyapunov function. Finally, numerical simulations confirm the theoretical results discussed in the paper.

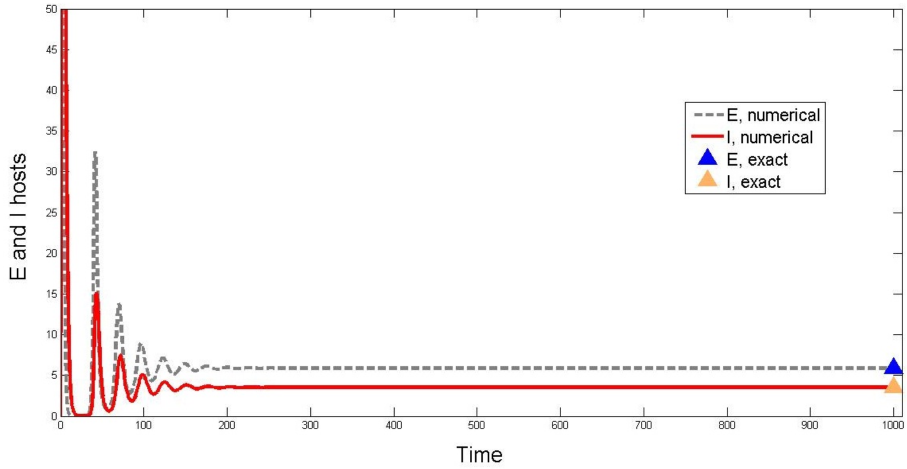

FIGURE 3. Solutions for components E and I until time $T = 1000$ for values in Example 4.2 together with their exact solution.

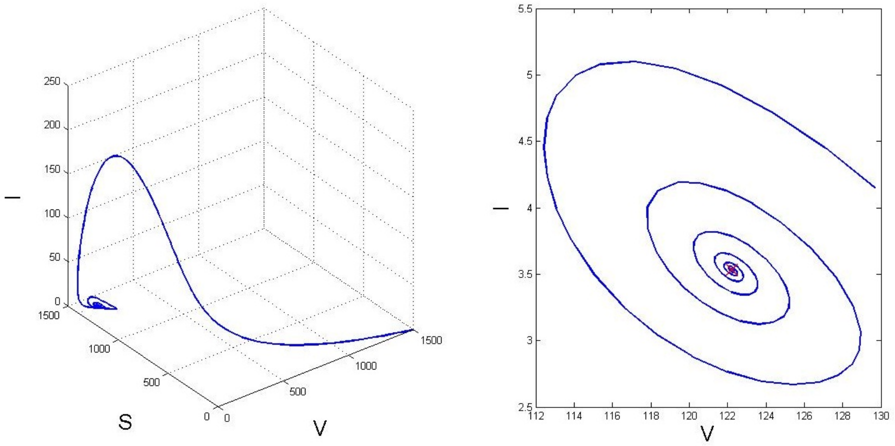

FIGURE 4. Phase portrait for solution of model (1) in three dimensions (left) and two dimension (right) for values in Example 4.2

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