Global dynamics of a novel multi-group model for computer worms*

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In this paper, we study worm dynamics in computer networks composed of many autonomous systems. A novel multi-group SIQR (susceptible-infected-quarantined-removed) model is proposed for computer worms by explicitly considering anti-virus measures and the network infrastructure. Then, the basic reproduction number of worm R_0 is derived and the global dynamics of the model are established. It is shown that if R_0 is less than or equal to 1, the disease-free equilibrium is globally asymptotically stable and the worm dies out eventually, whereas, if R_0 is greater than 1, one unique endemic equilibrium exists and it is globally asymptotically stable, thus the worm persists in the network. Finally, numerical simulations are given to illustrate the theoretical results.

Keywords: computer worm, multi-group model, Lyapunov function, global dynamics

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1. Introduction

Computer worms are a major security threat on computer networks. The propagation of computer worms can lead to distributed denial of service attack, damage the security of classified information, and even cause financial losses.[1] For example, the Code Red worm once infected 3.6×10^5 hosts and caused 2.6 billion dollars of financial losses in 2001.[2] Then, the Slammer worm brought about more than 90% of vulnerable computers in the Internet to shut down within 10 minutes and the Blaster worm attacked 1.88×10^5 hosts running Microsoft operating systems in 2003.[3,4] The recent Conficker worm infected over 13 million IP address throughout the world-wide network.[1] Therefore, controlling worm propagation is of great importance. Working towards this goal, it is necessary for us to model and analyze the dynamic behavior of computer worms.

In view of the similarity between biological viruses and computer worms,[5] epidemiological models such as the SIS (susceptible-infected-susceptible) model and the SIR (susceptible-infected-removed) model have been applied in computer worm studies.[1,2,5–7] In the SIS model, a node is infected and cured repeatedly, while in the SIR model, once the infected nodes are cured, they will never be infected again. Obviously, the basic SIS and SIR models cannot accurately describe worm propagation in the real network environment in which the anti-virus measures are taken.

Recently, some extended models have been suggested which include anti-virus measures.[8–11] Mishra *et al.*[8] assumed that the infected nodes get temporary immunity after running anti-malicious software. So they proposed a SIRS (susceptible-infected-removed-susceptible) model with a fixed period of temporary immunity. Ren *et al.*[9] considered that the anti-virus ability of a network is limited due to the limited software cost. They expressed the removed rate as a piecewise function, and presented a novel SIR model. Zou *et al.*[10] suggested a dynamic quarantine model for worm propagation based on the principle of assumed guilt before proven innocence. Wang *et al.*[11] considered both vaccination and quarantine measures, introducing a more general mitigation epidemic model for a rapid spreading worm.

It is noticed that the models mentioned above are all based on the assumption of a homogenous network. This means that the infected host infects any of the susceptible hosts by the same probability. In fact, a large computer network (e.g., the Internet) is generally non-homogenous in the structure of topology. The different routing tables and ACLs (Access Control Lists) of routers lead to different connectivity in local networks. Some studies have shown that the network topology can also affect the worm propagation. For example, Liljenstam *et al.*[12] thought that the routing can change the connectivity and thus may cut off parts of the population. Thus, they proposed a stratified SIR epidemic model for worm propagation at the level of autonomous systems (ASes). Kim *et al.*[4] evaluated the impact of topological constraints on worm propagation by simulation, showing that a worm may only infect a small number of susceptible nodes corresponding to network

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topological criteria.

Although previous studies have formulated various worm models including different factors to study computer worm propagation behaviors, none tackles the combined effects of both anti-virus measures and network infrastructure on worm propagation in the real computer network environment. Motivated by this, we focus on the following key issues: i) Explicitly considering both anti-virus measures and network infrastructure, we propose a novel multi-group SIQR (susceptible-infected-quarantined-removed) worm model by adopting the multi-group epidemiological model;[13–15] ii) In particular, the global dynamics of the proposed model are established to understand the global behavior of a computer worm.

The rest of this paper is organized as follows. Section 2 formulates the multi-group SIQR epidemic model. The global stability of the model is examined by using the Lyapunov function and LaSalle's invariant set theorem in Section 3. Numerical simulations are carried out to validate the theoretical results in Section 4. Finally, we conclude and discuss the paper in Section 5.

2. Model formulation

First, it is necessary to point out that most real-world computer networks are dynamic networks whose topologies are time-varying.[16–18] But, here we assume the network topology is fixed. One reason is that, compared with the worm spreading speed by which worm propagation can reach steady states quickly, the change of network topology is generally relatively slow. Another reason is that considering this change can make theoretical analysis very complicated and difficult. We will consider the time-varying characteristic of network topology in future work. Furthermore, we assume the computer network is composed of n $(n \geq 2)$ ASes. Each AS is equivalent to a group of multi-group models. Each host in the network has one of four possible states: susceptible (S), infected (I), quarantined (Q), and removed (R). The hosts with state S are healthy but vulnerable to worm infection. The hosts with state I mean that they have been infected by a worm and can transmit the worm to the susceptible hosts. The hosts with state Q denote that they have been quarantined (i.e. temporarily disconnected networks) due to exhibiting suspicious behavior of susceptible hosts or failure to clear the worms from the infected hosts in time. The hosts with state R indicate that they have gained immunity to the worm infection by installing an anti-virus program or personal firewall. At the same time, the total number of hosts in k-th $(1 \leq k \leq n)$ AS is partitioned into compartments $S_k(t)$, $I_k(t)$, $Q_k(t)$, and $R_k(t)$ according to hosts' states, denoting the number of susceptible, infected, quarantined, and removed hosts at time t, respectively.

A schematic diagram of hosts' state transition and corresponding parameters are shown in Fig. 1. The susceptible hosts will move to a infected state if they are infected by a worm from their own AS or other associated ASes. In addition, they will go directly to state Q if they exhibit suspicious behavior, or go to state R if they obtain immunity via installing anti-virus software. The infected hosts will become state R given that the worm is cleared and the anti-virus software is setup, otherwise they become Q if the worm cannot be cleared in time. The quarantined hosts become state R due to reinstalling the operation system as well as anti-virus software, or return to the susceptible compartment if they are the susceptible hosts quarantined by mistake before. The explanation for each parameter in Fig. 1 is summarized in Table 1. All the parameters are assumed to be nonnegative. It is worth noting that the transmission rate β_{kj} denotes the inside infection rate in the same AS if $k = j$, otherwise, it denotes the cross infection rate between different ASes.

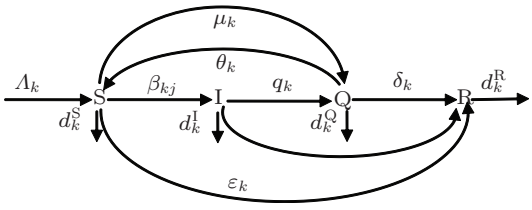


Fig. 1. Schematic diagram of the multi-group SIQR model.

Table 1. Parameters and explanations used in this paper.

Parameter	Explanation
β_{kj}	Transmission rate between compartments S_k and I_j
$d_k^{\mathrm{S}}, d_k^{\mathrm{I}}, d_k^{\mathrm{Q}}, d_k^{\mathrm{R}}$	Natural death rate of S, I, Q, R compartments in the k-th AS, respectively
Λ_k	Influx of new hosts into the k-th AS
ε_k	Removed rate of susceptible hosts in the k-th AS
q_k	Quarantined rate of infected hosts in the k-th AS
μ_k	Quarantined rate of susceptible host in the k-th AS
r_k	Removed rate of infected hosts in the k-th AS
δ_k	Removed rate of quarantined hosts in the k-th AS
θ_k	Released rate of quarantined hosts to susceptible compartment in the k-th AS

Based on the analyses and assumptions mentioned above, the multi-group SIQR model can be constructed by the following differential equations

$$\begin{cases} \dot{S}_k = \Lambda_k + \theta_k Q_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) S_k, \\ \dot{I}_k = \sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^{\mathrm{I}} + q_k + r_k) I_k, \\ \dot{Q}_k = q_k I_k + \mu_k S_k - (d_k^{\mathrm{Q}} + \delta_k + \theta_k) Q_k, \\ \dot{R}_k = \varepsilon_k S_k + r_k I_k + \delta_k Q_k - d_k^{\mathrm{R}} R_k, \quad k = 1, 2, \ldots, n. \end{cases} \tag{1}$$

For each k, summing the four sub-equations in Eq. (1), we have

$$\dot{N}_k = \Lambda_k - d_k^{\mathrm{S}} S_k - d_k^{\mathrm{I}} I_k - d_k^{\mathrm{Q}} Q_k - d_k^{\mathrm{R}} R_k \le \Lambda_k - d_k^* N_k, \tag{2}$$

where $N_k = S_k + I_k + Q_k + R_k$, $d_k^* = \min\{d_k^{\mathrm{S}}, d_k^{\mathrm{I}}, d_k^{\mathrm{Q}}, d_k^{\mathrm{R}}\} > 0$. Hence,

$$\limsup_{t\to\infty} (N_k = S_k + I_k + Q_k + R_k) \le \Lambda_k / d_k^*. \tag{3}$$

Similarly, from the first three sub-equations in Eq. (1), we also easily have

$$\limsup_{t\to\infty} S_k \le \frac{\Lambda_k}{(d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) - \mu_k \theta_k / (d_k^{\mathrm{Q}} + \delta_k + \theta_k)}. \tag{4}$$

Since the variable R_k does not appear in the first three sub-equations of Eq. (1), we can consider the following reduced system

$$\begin{cases} \dot{S}_k = \Lambda_k + \theta_k Q_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) S_k, \\ \dot{I}_k = \sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^{\mathrm{I}} + q_k + r_k) I_k, \\ \dot{Q}_k = q_k I_k + \mu_k S_k - (d_k^{\mathrm{Q}} + \delta_k + \theta_k) Q_k, \\ k = 1, 2, \ldots, n \end{cases} \tag{5}$$

for S_k, I_k, and Q_k, to discuss the dynamic behavior.

Obviously, the omega limit sets of Eq. (5) are contained in the following bounded region in the non-negative cone of $\mathbb{R}^{3n}$:

$$\Gamma = \left\{ (S_1, I_1, Q_1, \ldots, S_n, I_n, Q_n) \in \mathbb{R}_+^{3n} \;\middle|\; \begin{array}{l} S_k \le \dfrac{\Lambda_k}{(d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) - \mu_k \theta_k / (d_k^{\mathrm{Q}} + \delta_k + \theta_k)} \\ S_k + I_k + Q_k \le \dfrac{\Lambda_k}{d_k^*} \\ k = 1, 2, \ldots, n \end{array} \right\}. \tag{6}$$

It can be verified that the region Γ is positively invariant. In addition, the behavior of R_k is determined by the last sub-equation in Eq. (1).

3. Stability analysis

The global stability of a system is one of the most important topics related to global dynamic behavior.[19–23] In the following, we will prove the global stability of the proposed model (Eq. (5)) by using a graph-theoretic approach to the method of global Lyapunov functions (see Refs. [24] and [25]). It is easily found that equation (5) has the disease-free equilibrium $P_0 = (S_1^0, 0, Q_1^0, \ldots, S_n^0, 0, Q_n^0)$, where $S_k^0 = \Lambda_k / ((d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) - \mu_k \theta_k / (d_k^{\mathrm{Q}} + \delta_k + \theta_k))$ and $Q_k^0 = \mu_k \Lambda_k / ((d_k^{\mathrm{S}} + \varepsilon_k + \mu_k)(d_k^{\mathrm{Q}} + \delta_k + \theta_k) - \mu_k \theta_k)$ $(k = 1, 2, \ldots, n)$. By using the next generation matrix method,[26] the basic reproduction number of a worm is given by

$$\boldsymbol{R}_0 = \rho(\boldsymbol{F}\boldsymbol{V}^{-1}), \quad k = 1, 2, \ldots, n, \tag{7}$$

where ρ denotes the spectral radius, and

$$F = \begin{bmatrix} S_1^0 \beta_{11} & \cdots & S_1^0 \beta_{1n} \\ \vdots & \ddots & \vdots \\ S_n^0 \beta_{n1} & \cdots & S_n^0 \beta_{nn} \end{bmatrix}_{n\times n}, \tag{8}$$

$$V = \mathrm{diag}[d_k^{\mathrm{I}} + q_k + r_k], \quad (1 \le k \le n). \tag{9}$$

It can be verified that $\rho(\boldsymbol{F}\boldsymbol{V}^{-1}) = \rho(\boldsymbol{V}^{-1}\boldsymbol{F})$, so R_0 can also be rewritten by

$$\begin{aligned} \boldsymbol{R}_0 &= \rho(\boldsymbol{V}^{-1}\boldsymbol{F}) \\ &= \rho\left(\begin{bmatrix} \frac{S_1^0 \beta_{11}}{d_1^{\mathrm{I}} + q_1 + r_1} & \cdots & \frac{S_1^0 \beta_{1n}}{d_1^{\mathrm{I}} + q_1 + r_1} \\ \vdots & \ddots & \vdots \\ \frac{S_n^0 \beta_{n1}}{d_n^{\mathrm{I}} + q_n + r_n} & \cdots & \frac{S_n^0 \beta_{nn}}{d_n^{\mathrm{I}} + q_n + r_n} \end{bmatrix}_{n\times n} \right) \\ &= \rho(M(S_1^0, S_2^0, \ldots, S_n^0)) = \rho(M_0). \end{aligned} \tag{10}$$

Theorem 1 Assume that $B = (\beta_{kj})_{n\times n}$ is irreducible. If $R_0 \le 1$, then P_0 is the unique equilibrium of Eq. (5) and it is globally asymptotically stable in Γ; while if $R_0 > 1$, then P_0 is unstable and equation (5) is uniformly persistent in $\overset{\circ}{\Gamma}$ (interior of Γ).

Proof Let $S = (S_1, S_2, \ldots, S_n)$ and $S^0 = (S_1^0, S_2^0, \ldots, S_n^0)$, then $M(S^0) = M_0$. Since $0 \le S_k \le S_k^0$ $(1 \le k \le n)$, then we further have $0 \le M(S) \le M(S_0) = M_0$. On the other hand, M_0 is irreducible from the irreducibility of $\boldsymbol{B} = (\beta_{kj})_{n\times n}$. According to the well-known Perron–Frobenius Theorem, M_0 has a positive eigenvector $\omega(\omega_1, \omega_2, \ldots, \omega_n)$ with respect to $\rho(M_0)$, i.e., the following equation holds

$$\omega \cdot \rho(M_0) = \omega \cdot M_0. \tag{11}$$

We choose the following Lyapunov function

$$L=\sum_{k=1}^{n}\frac{\omega_k}{(d_k^{\mathrm{I}}+q_k+r_k)}I_k. \tag{12}$$

Then

$$\begin{aligned}\dot{L} &= \sum_{k=1}^{n}\frac{\omega_k}{(d_k^{\mathrm{I}}+q_k+r_k)}\dot{I}_k\\ &= \sum_{k=1}^{n}\frac{\omega_k}{(d_k^{\mathrm{I}}+q_k+r_k)}\left[\sum_{j=1}^{n}\beta_{kj}S_kI_j-(d_k^{\mathrm{I}}+q_k+r_k)I_k\right]\\ &= \omega\cdot(M(S)I-I)\\ &\le \omega\cdot(M_0I-I)\\ &= [\rho(M_0)-1]\omega\cdot I\le 0 \ \text{ if } \ R_0\le 1.\end{aligned} \tag{13}$$

If $R_0=\rho(M_0)<1$, then $\dot{L}=0$ if and only if $I=0$. If $R_0=1$, then $\dot{L}=0$, which implies

$$\omega\cdot M(S)I=\omega\cdot I. \tag{14}$$

Furthermore, if $S\neq S^0$, then $\omega\cdot M(S)<\omega\cdot M(S^0)=\omega$, thus equation (14) has only the trivial solution $I=0$. Therefore, we have $\dot{L}=0$ if and only if $I=0$ or $S=S^0$ when $R_0\le 1$. We can prove that the only compact invariant subset of the set Γ (where $\dot{L}=0$) is the singleton $\{P_0\}$. By using LaSalle's Invariance Principle, P_0 is globally asymptotically stable in Γ.

If $R_0=\rho(M_0)>1$ and $I\neq 0$, we know that $\omega\cdot M_0-\omega=[\rho(M_0)-1]\omega>0$. From the continuity property, we have $\dot{L}=\omega\cdot(M(S)I-I)>0$ in the neighborhood of P_0 in $\overset{\circ}{\Gamma}$. This implies that P_0 is unstable. Using a uniform persistent result from Ref. [27] and similar way in the proof of Proposition 3.3 of Ref. [28], we can draw the conclusion that when $R_0>1$, the instability of P_0 implies the uniform persistence of Eq. (5). This completes the proof of Theorem 1.

From Theorem 1, we know that if $R_0>1$, equation (5) is uniformly persistent and its solutions in $\overset{\circ}{\Gamma}$ are uniform bounded, which implies the existence of an equilibrium of Eq. (5) in $\overset{\circ}{\Gamma}$.[29] Let $P^*=(S_1^*,I_1^*,Q_1^*,\ldots,S_n^*,I_n^*,Q_n^*)$ be an endemic equilibrium, then we have the following equilibrium equations

$$\Lambda_k+\theta_kQ_k^*=\sum_{j=1}^{n}\beta_{kj}S_k^*I_j^*+(d_k^{\mathrm{S}}+\varepsilon_k+\mu_k)S_k^*, \tag{15}$$

$$\sum_{j=1}^{n}\beta_{kj}S_k^*I_j^*=(d_k^{\mathrm{I}}+q_k+r_k)I_k^*, \tag{16}$$

$$q_kI_k^*+\mu_kS_k^*=(d_k^{\mathrm{Q}}+\delta_k+\theta_k)Q_k^*. \tag{17}$$

Theorem 2 Assume that $\boldsymbol{B}=(\beta_{kj})_{n\times n}$ is irreducible and equation (18) is satisfied

$$(S_k^*-S_k)(Q_k^*-Q_k)<0 \ \text{ for } \ S_k^*\neq S_k \ \text{ and } \ Q_k^*\neq Q_k. \tag{18}$$

If $R_0>1$, there exists a unique endemic equilibrium P^*, and P^* is globally asymptotically stable in $\overset{\circ}{\Gamma}$.

Proof Denote

$$\bar{\beta}_{kj}=\beta_{kj}S_k^*I_j^*, \quad 1\le k,j\le n, n\ge 2, \tag{19}$$

and matrix

$$\bar{\boldsymbol{B}}=\begin{bmatrix}\sum_{l\neq 1}\bar{\beta}_{1l} & -\bar{\beta}_{21} & \cdots & -\bar{\beta}_{n1}\\ -\bar{\beta}_{12} & \sum_{l\neq 2}\bar{\beta}_{2l} & \cdots & -\bar{\beta}_{n2}\\ \vdots & \vdots & \ddots & \vdots\\ -\bar{\beta}_{1n} & -\bar{\beta}_{2n} & \cdots & \sum_{l\neq n}\bar{\beta}_{nl}\end{bmatrix}. \tag{20}$$

Since $\boldsymbol{B}=(\beta_{kj})_{n\times n}$ is irreducible, then matrix $(\bar{\beta}_{kj})_{n\times n}$ is also irreducible. By using Lemma 2.1 in Refs. [24] and [25], a basis for the solution space of the linear system

$$\bar{\boldsymbol{B}}v=0 \tag{21}$$

can be expressed as $v=(v_1,v_2\ldots,v_n)=(c_{11},c_{22},\ldots,c_{nn})$, where c_{kk} denotes the cofactor of the k-th diagonal entry of $\bar{\boldsymbol{B}}$, and $v_k=c_{kk}>0$, $1\le k\le n$.

Choose the Lyapunov function as

$$\begin{aligned}V &= \sum_{k=1}^{n}v_k\left[\left(S_k-S_k^*-S_k^*\ln\frac{S_k}{S_k^*}\right)+\left(I_k-I_k^*-I_k^*\ln\frac{I_k}{I_k^*}\right)\right.\\ &\quad \left.+\left(Q_k-Q_k^*-Q_k^*\ln\frac{Q_k}{Q_k^*}\right)\right].\end{aligned} \tag{22}$$

Differentiating V along solutions to Eq. (5) and combining Eq. (15) to Eq. (17), we have

$$\begin{aligned}\dot{V} &= \sum_{k=1}^{n}v_k\left[\left(\dot{S}_k-\frac{S_k^*}{S_k}\dot{S}_k\right)+\left(\dot{I}_k-\frac{I_k^*}{I_k}\dot{I}_k\right)+\left(\dot{Q}_k-\frac{Q_k^*}{Q_k}\dot{Q}_k\right)\right]\\ &= \sum_{k=1}^{n}v_k\left[\Lambda_k+\theta_kQ_k-(d_k^{\mathrm{S}}+\varepsilon_k+\mu_k)S_k\right.\\ &\quad -\frac{S_k^*}{S_k}\Lambda_k-\frac{S_k^*}{S_k}\theta_kQ_k+\sum_{j=1}^{n}\beta_{kj}S_k^*I_j+(d_k^{\mathrm{S}}+\varepsilon_k+\mu_k)S_k^*\\ &\quad -(d_k^{\mathrm{I}}+q_k+r_k)I_k-\sum_{j=1}^{n}\beta_{kj}S_kI_j\frac{I_k^*}{I_k}+(d_k^{\mathrm{I}}+q_k+r_k)I_k^*\\ &\quad +q_kI_k+\mu_kS_k-(d_k^{\mathrm{Q}}+\delta_k+\theta_k)Q_k\\ &\quad \left.-\frac{Q_k^*q_k}{Q_k}I_k-\frac{Q_k^*\mu_k}{Q_k}S_k+(d_k^{\mathrm{Q}}+\delta_k+\theta_k)Q_k^*\right]\\ &= \sum_{k=1}^{n}v_k\left[(d_k^{\mathrm{S}}+\varepsilon_k+\mu_k)S_k^*\left(2-\frac{S_k}{S_k^*}-\frac{S_k^*}{S_k}\right)\right.\\ &\quad \left.+\left(\sum_{j=1}^{n}\beta_{kj}S_k^*I_j-(d_k^{\mathrm{I}}+q_k+r_k)I_k\right)\right)\\ &\quad +\left(2\sum_{j=1}^{n}\beta_{kj}S_k^*I_j^*-\sum_{j=1}^{n}\beta_{kj}\frac{(S_k^*)^2I_j^*}{S_k}-\sum_{j=1}^{n}\beta_{kj}S_kI_j\frac{I_k^*}{I_k}\right)\\ &\quad +\left(q_kI_k+\mu_kS_k-\left(d_k^{\mathrm{Q}}+\delta_k+\theta_k\frac{S_k^*}{S_k}\right)Q_k\right)\\ &\quad \left.\times\left(1-\frac{Q_k^*}{Q_k}\right)\right].\end{aligned} \tag{23}$$

It is well known that the arithmetic mean is greater than or equal to the geometric mean, so $S_k/S_k^*+S_k^*/S_k\ge 2$, with

equality holding if and only if $S_k = S_k^*$, then

$$(d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) S_k^* (2 - \frac{S_k}{S_k^*} - \frac{S_k^*}{S_k}) \le 0. \tag{24}$$

Since $\bar{B}v = 0$, thus $\sum_j^n \bar{\beta}_{jk} v_j = \sum_{i=1}^n \bar{\beta}_{ki} v_k$ is satisfied. In addition, combining with Eqs. (16) and (19), we have

$$\sum_j^n \beta_{jk} S_j^* I_k^* v_j = \sum_{i=1}^n \beta_{ki} S_k^* I_i^* v_k = (d_k^{\mathrm{I}} + q_k + r_k) I_k^* v_k, \quad 1 \le k \le n. \tag{25}$$

This implies that

$$\begin{aligned} \sum_{k=1}^n v_k \sum_{j=1}^n \beta_{kj} S_k^* I_j &= \sum_{k=1}^n I_k \sum_{j=1}^n \beta_{jk} S_j^* v_j \\ &= \sum_{k=1}^n (d_k^{\mathrm{I}} + q_k + r_k) I_k v_k. \end{aligned} \tag{26}$$

From Eq. (18), and the third sub-equation in Eq. (5), it can be derived that

$$\left(q_k I_k + \mu_k S_k - \left(d_k^{\mathrm{Q}} + \delta_k + \theta_k \frac{S_k^*}{S_k} \right) Q_k \right) \left(1 - \frac{Q_k^*}{Q_k} \right) \le 0, \tag{27}$$

with equality holding $S_k = S_k^*$ and $Q_k^* = Q_k$.

Using Eqs. (24), (26), (27), and $\bar{\beta}_{jk}$ in Eq. (19), we have

$$\begin{aligned} \dot{V} &\le \sum_{k=1}^n v_k \left(2 \sum_{j=1}^n \bar{\beta}_{kj} - \sum_{j=1}^n \bar{\beta}_{kj} \frac{S_k^*}{S_k} - \sum_{j=1}^n \bar{\beta}_{kj} \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right) \\ &= \sum_{k,j=1}^n v_k \bar{\beta}_{kj} \left(2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right) : \\ &= H_n(S_1, I_1, S_2, I_2, \ldots, S_n, I_n). \end{aligned} \tag{28}$$

In the following discussion, we will point out that $H_n(S_1, I_1, S_2, I_2, \ldots, S_n, I_n) \le 0$ for all $(S_1, I_1, S_2, I_2, \ldots, S_n, I_n) \in \overset{\circ}{\Gamma}$. It is noticed that such a result has been proved for a multi-group SIR model.[24] Here, for the completeness of this paper, we will prove it again by using a more simple method in Ref. [25] for the proposed model Eq. (5). Let $L = G(B)$ denote the directed graph associated with matrix B, T a directed spanning subtree of L, U an unicyclic of L which is a disjoint union of rooted trees whose roots form a directed cycle, C_U a cycle of U, $l = l(U)$ the number of arcs in C_U, and $E(U)$ the set of directed arcs in U. Then

$$H_n = \sum_U H_{n,U}, \tag{29}$$

with

$$H_{n,U} = \prod_{(r,m) \in E(U)} \bar{\beta}_{rm} \left(2l - \sum_{(k,j) \in E(U)} \left(\frac{S_k^*}{S_k} + \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right) \right). \tag{30}$$

Note that for each unicycle graph U,

$$\prod_{(k,j) \in E(U)} \frac{S_k^*}{S_k} \times \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} = \prod_{(k,j) \in E(U)} \frac{I_j I_k^*}{I_k I_j^*} = 1. \tag{31}$$

Thus,

$$\sum_{(k,j) \in E(U)} \left(\frac{S_k^*}{S_k} + \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} \right) \ge 2l, \tag{32}$$

then $H_{n,U} \le 0$ for each U, and $H_{n,U} = 0$ if and only if

$$\frac{S_k^*}{S_k} = \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*}, \quad (k,j) \in E(U). \tag{33}$$

Therefore,

$$H_n = \sum_U H_{n,U} \le 0. \tag{34}$$

We have proved that $\dot{V} \le 0$ with $\dot{V} = 0$ if and only if $S_k = S_k^*$, $Q_k^* = Q_k$, and $H_n = 0$. Note that if $S_k = S_k^*$, $1 \le k \le n$, then $H_n = 0$ if and only if $I_k = aI_k^*$, $k = 1, 2, \ldots, n$, where a is an arbitrary positive number. Substituting $S_k = S_k^*$, $Q_k^* = Q_k$, and $I_k = aI_k^*$ into the first sub-equation of Eq. (1), we have

$$0 = \Lambda_k + \theta_k Q_k^* - a \sum_{j=1}^n \beta_{kj} S_k^* I_j^* - (d_k^{\mathrm{S}} + \varepsilon_k + \mu_k) S_k^*. \tag{35}$$

Clearly, the right-hand side of Eq. (35) is strictly decreasing in a. According to Eq. (15), we know that equation (35) holds if and only if $a = 1$, namely at P^*. So, the largest invariant subset where $\dot{V} = 0$ is the singleton $\{P^*\}$. By LaSalle's Invariance Principle, P^* is globally asymptotically stable in $\overset{\circ}{\Gamma}$. Here, it is necessary to point out that the global stability of P^* implies that the endemic equilibrium is unique in $\overset{\circ}{\Gamma}$. This completes the proof of Theorem 2.

4. Numerical simulation

In this section, in order to validate the theoretical analysis, we do several numerical simulations. To make the simulations easy, the network of two ASes is considered here (i.e. $N = 2$), so we have the following two-group epidemic model

$$\begin{cases} \dot{S}_1 = \Lambda_1 + \theta_1 Q_1 - (\beta_{11} S_1 I_1 + \beta_{12} S_1 I_2) \\ \qquad - (d_1^{\mathrm{S}} + \varepsilon_1 + \mu_1) S_1, \\ \dot{I}_1 = (\beta_{11} S_1 I_1 + \beta_{12} S_1 I_2) - (d_1^{\mathrm{I}} + q_1 + r_1) I_1, \\ \dot{Q}_1 = q_1 I_1 + \mu_1 S_1 - (d_1^{\mathrm{Q}} + \delta_1 + \theta_1) Q_1, \\ \dot{S}_2 = \Lambda_2 + \theta_2 Q_2 - (\beta_{21} S_2 I_1 + \beta_{22} S_2 I_2) \\ \qquad - (d_2^{\mathrm{S}} + \varepsilon_2 + \mu_2) S_2, \\ \dot{I}_2 = (\beta_{21} S_2 I_1 + \beta_{22} S_2 I_2) - (d_2^{\mathrm{I}} + q_2 + r_2) I_2, \\ \dot{Q}_2 = q_2 I_2 + \mu_2 S_2 - (d_2^{\mathrm{Q}} + \delta_2 + \theta_2) Q_2. \end{cases} \tag{36}$$

Here, we assume that $\beta_{12} > 0$ and $\beta_{21} > 0$, showing that the worm can propagate cross two ASes each other. If $\beta_{11} > 0$ and $\beta_{22} > 0$, then it implies that worm spreading also occurs inside the first AS and the second one respectively. The other values of parameters are set as follows: $\Lambda_1 = 1$, $\theta_1 = 1/5$, $d_1^{\mathrm{S}} = 1/20$, $\varepsilon_1 = 1/50$, $\mu_1 = 1/20$, $d_1^{\mathrm{I}} = 1/10$, $q_1 = 1/20$, $r_1 = 3/10$, $d_1^{\mathrm{Q}} = 1/20$, $\delta_1 = 1/4$; $\Lambda_2 = 1.5$, $\theta_2 = 5/12$, $d_2^{\mathrm{S}} = 1/25$, $\varepsilon_2 = 3/100$, $\mu_2 = 2/25$, $d_2^{\mathrm{I}} = 1/15$, $q_2 = 1/10$, $r_2 = 2/5$, $d_2^{\mathrm{Q}} = 1/20$, $\delta_2 = 1/5$.

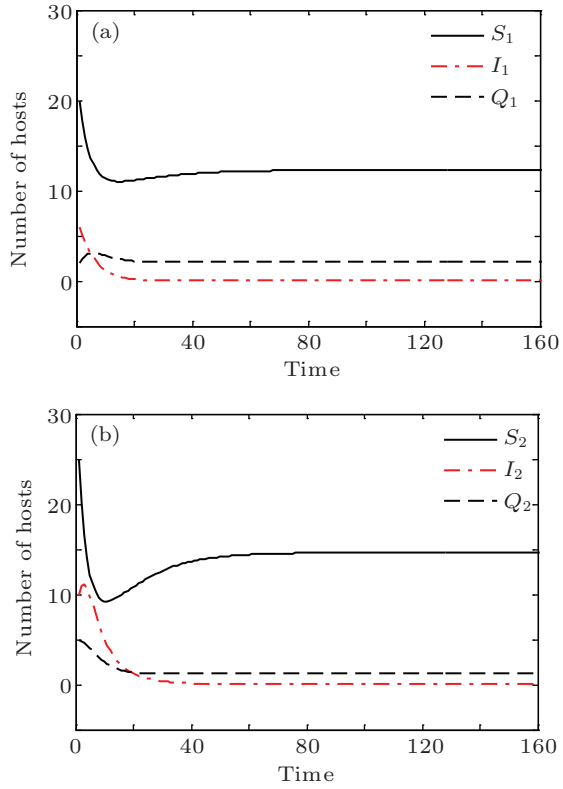


Fig. 2. (color online) When $R_0 \approx 0.77 < 1$, the disease-free equilibrium $P_0 = (12.2807, 0, 2.1930, 14.6368, 0, 1.3208)$ is globally asymptotically stable. Figures 2(a) and 2(b) show that the worm gradually dies out with time evolution in the first and second ASes respectively. Initial values are: $S_1(0) = 20$, $I_1(0) = 6$, $Q_1(0) = 2$, $S_2(0) = 25$, $I_2(0) = 10$, and $Q_2(0) = 5$.

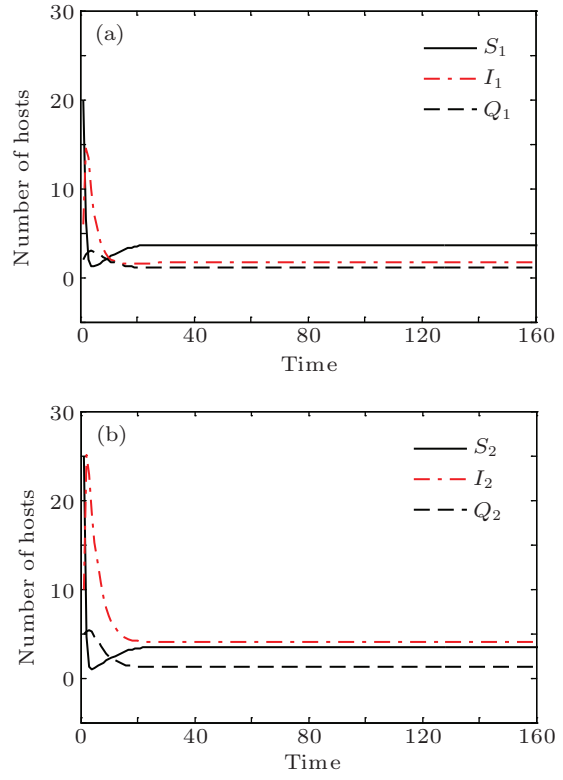


Fig. 3. (color online) When $R_0 \approx 4.19 > 1$, the endemic equilibrium $P^* = (3.5989,\ 1.6358,\ 1.0809,\ 3.4091,\ 4.0919,\ 1.2308)$ is globally asymptotically stable. Figures 3(a) and 3(b) show that the worm persists with time evolution in the first and second ASes respectively. Initial values are: $S_1(0) = 20$, $I_1(0) = 6$, $Q_1(0) = 2$, $S_2(0) = 25$, $I_2(0) = 10$, and $Q_2(0) = 5$.

Since $\beta_{12} > 0$, $\beta_{21} > 0$, the matrix

$$\boldsymbol{B} = \begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{21} & \beta_{22} \end{bmatrix}$$

is irreducible. If

$$\boldsymbol{B} = \begin{bmatrix} 0.01 & 0.003 \\ 0.005 & 0.015 \end{bmatrix},$$

we have $R_0 \approx 0.77 < 1$. In this case, the disease-free equilibrium $P_0 = (12.2807, 0, 2.1930, 14.6368, 0, 1.3208)$ of Eq. (5) is globally asymptotically stable from Theorem 1 (see Fig. 2).

However, if

$$\boldsymbol{B} = \begin{bmatrix} 0.05 & 0.03 \\ 0.02 & 0.08 \end{bmatrix},$$

we have $R_0 \approx 4.19 > 1$. From Theorem 2, equation (5) has a unique endemic equilibrium

$$P^* = (3.5989,\ 1.6358,\ 1.0809,\ 3.4091,\ 4.0919,\ 1.2308)$$

and it is globally asymptotically stable (see Fig. 3).

5. Conclusion and discussion

In this paper, we have presented a multi-group SIQR model at the level of autonomous systems (ASes) for worm propagation in computer networks. The model includes not only anti-virus measures but also the infrastructure of computer network. By using a graph-theoretic approach to the method of global Lyapunov functions, the global dynamics of the model have been analyzed rigorously. The results have shown that the model has a globally stable disease-free equilibrium if the basic reproduction number of the worm is less than or equal to 1, while it has a unique endemic equilibrium which is globally stable if the basic reproduction number is greater than one. Finally, numerical simulations are given to validate the theoretical results. The proposed model, a more accurate worm model, can help us to understand the dynamic behavior of computer worms. Moreover, the theoretical results are able to provide some useful guidance for making effective countermeasures on worm propagation.

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