Hindawi Publishing Corporation
Discrete Dynamics in Nature and Society
Volume 2013, Article ID 956893, 9 pages
http://dx.doi.org/10.1155/2013/956893

Research Article

A New Model for Capturing the Spread of Computer Viruses on Complex-Networks

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Received 7 September 2013; Revised 31 October 2013; Accepted 1 November 2013

Academic Editor: Jinde Cao

Based on complex network, this paper proposes a novel computer virus propagation model which is motivated by the traditional SEIRQ model. A systematic analysis of this new model shows that the virus-free equilibrium is globally asymptotically stable when its basic reproduction is less than one, and the viral equilibrium is globally attractive when the basic reproduction is greater than one. Some numerical simulations are finally given to illustrate the main results, implying that these results are applicable to depict the dynamics of virus propagation.

1. Introduction

Computer viruses, including the narrowly defined viruses and network worms, are loosely defined as malicious codes that can replicate themselves and spread among computers. Usually, computer viruses attack computer systems directly, while worms mainly attack computers by searching for system or software vulnerabilities. With the rapid popularization of the Internet and mobile wireless networks, network viruses have posed a major threat to our work and life. To thwart the fast spread of computer viruses, it is critical to have a comprehensive understanding of the way that computer viruses propagate. Kephart and White [1] proposed the first epidemiological model of computer viruses. From then on, much effort has been done in developing virus spreading models [1–15]. On the other hand, it was found [16–18] that the Internet topology follows the "scale-free" (SF) networks; that is, the probability that a given node is connected to k other nodes follows a power-law of the form $P(k) \sim k^{-\tau}$, with the remarkable feature that $\tau \leq 3$ for most real-world networks. This finding has greatly stimulated the interest in understanding the impact of network topology on virus spreading [16–29].

Recently, Mishra and Jha [2] investigated a so-called SEIQRS model on a homogeneous network by making the following assumptions.

(H1) The population has a homogeneous degree distribution.

(H2) The total population of computers is divided into five groups: susceptible, exposed, infected, quarantine and recovered computers. Let S, E, I, Q, and R denote the numbers of susceptible, exposed, infected, quarantine, and recovered computers, respectively.

(H3) New computers are attached to the Internet at rate A.

(H4) Computers are disconnected from the Internet naturally at a constant rate d and removed with probability α due to the attack of malicious objects.

(H5) S computers become E with constant rate ρ; R computers become S with constant rate η; E computers become I with constant rate μ; I computers become Q with constant rate δ; I computers become R with constant rate γ; Q computers become R with constant rate ε.

According to the above assumptions, the following model is derived (see Figure 1):

$$S'(t) = A - \rho SI - dS + \eta R,$$

$$E'(t) = \rho SI - (d + \mu) E,$$

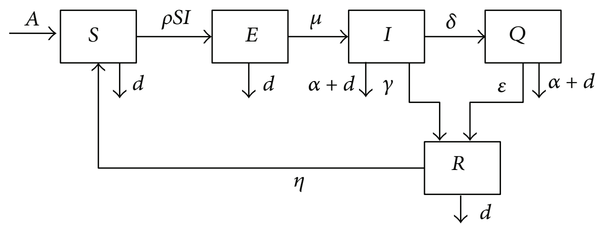

Figure 1: Original model.

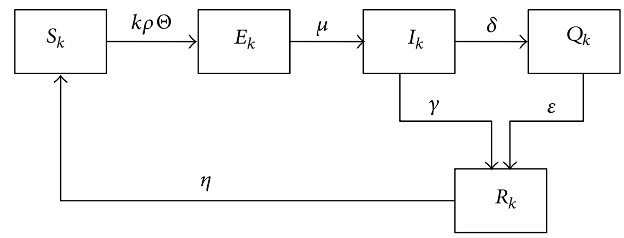

Figure 2: Our model.

$$I'(t) = \mu E - (d + \alpha + \gamma + \delta) I,$$
$$Q'(t) = \delta I - (\alpha + \varepsilon + d) Q,$$
$$R'(t) = \gamma I + \varepsilon Q - (d + \eta) R. \tag{1}$$

In view of the fact that the Internet topology is scale-free rather than exponential in its degree distribution [17, 18, 23], this paper addresses the dynamics of a scale-free network-based SEIQRS model.

For convenience, computers on the Internet are called as nodes in the sequel. For our purpose, the following additional assumptions are imposed on the previous SEIQRS model.

(H6) The node degrees of the network asymptotically follow a power-law distribution, $P(k) \sim k^{-\tau}$, where $P(k)$ stands for the probability that a node chosen randomly from the Internet is of degree k.

(H7) The total number of nodes does not change or, equivalently, $A = 0$, $d = 0$, and $\alpha = 0$.

(H8) $S_k(t)$: the relative density of k-degree S-nodes; $E_k(t)$: the relative density of k-degree E-nodes; $I_k(t)$: the relative density of k-degree I-nodes; $Q_k(t)$: the relative density of k-degree Q-nodes; $R_k(t)$: the relative density of k-degree R-nodes; $S_k(t) + E_k(t) + I_k(t) + Q_k(t) + R_k(t) = 1$.

(H9) The probability that a link has an I-node as one endpoint does not depend on the degree of the other endpoint of the link and, hence, is only a function of $I(t) := (I_1(t), I_2(t), \dots, I_n(t))$. Let $\Theta(I(t))$ denote the probability, $\Theta(I(t)) = (1/\langle k\rangle)\sum_k kP(k)I_k$, where, $\langle k\rangle := \sum_k kP(k)$.

By applying the mean-field technique to the above assumptions, we get a new epidemic model of computer virus, which is formulated as (see Figure 2)

$$\begin{aligned} S_k'(t) &= -k\rho\Theta(t) S_k(t) + \eta R_k(t), \\ E_k'(t) &= k\rho\Theta(t) S_k(t) - \mu E_k(t), \\ I_k'(t) &= \mu E_k(t) - (\gamma + \delta) I_k(t), \\ Q_k'(t) &= \delta I_k(t) - \varepsilon Q_k(t), \\ R_k'(t) &= \gamma I_k(t) + \varepsilon Q_k(t) - \eta R_k(t), \\ & k = 1, \dots, n, \end{aligned} \tag{2}$$

with initial conditions $S_k(0)$, $E_k(0)$, $I_k(0)$, $Q_k(0)$, and $R_k(0) \geq 0$, $1 \leq k \leq n$.

Note that, for every k, we have $S_k(t)+E_k(t)+I_k(t)+Q_k(t)+R_k(t) = 1$; thus, the first set of equations in system (2) can be removed, yielding the following system,

$$\begin{aligned} E_k'(t) &= k\rho\Theta(t)\left(1 - E_k(t) - I_k(t) - Q_k(t) - R_k(t)\right) - \mu E_k(t), \\ I_k'(t) &= \mu E_k(t) - (\gamma + \delta) I_k(t), \\ Q_k'(t) &= \delta I_k(t) - \varepsilon Q_k(t), \\ R_k'(t) &= \gamma I_k(t) + \varepsilon Q_k(t) - \eta R_k(t), \\ & k = 1, \dots, n, \end{aligned} \tag{3}$$

with initial conditions $E_k(0)$, $I_k(0)$, $Q_k(0)$, $R_k(0) \geq 0$ and $E_k(0) + I_k(0) + Q_k(0) + R_k(0) \leq 1$.

The organization of this paper is as follows. Section 2 determines the equilibria of system (3) and the basic reproduction number R_0. Sections 3 and 4 address the global stability of the virus-free equilibrium and the global attractivity of the viral equilibrium, respectively. Numerical examples are provided in Section 5 to support our theoretical results. In the final section, a brief conclusion is given and some future research topics are also pointed out.

2. Basic Reproduction Number and Equilibria

The basic reproduction number R_0, which can be explained as the average number of secondary infections produced by a single infected node during its infection time, is calculated as

$$R_0 = \frac{\langle k^2\rangle}{\langle k\rangle}\frac{\rho}{\gamma + \delta}, \tag{4}$$

where $\langle k^2\rangle$ stands for the second origin moment of the node degree, $\langle k^2\rangle := \sum_k k^2 P(k)$. Then, we have the following theorem.

Theorem 1. *Consider system* (3). *The following assertions hold.*

(1) *There always exists a virus-free equilibrium* $P_0 = (\overbrace{0, 0, \dots, 0}^{4n})^T$.

(2) *There is no viral equilibrium if* $R_0 \leq 1$.

(3) *There exists a unique viral equilibrium*

$$P^* = (E^*, I^*, Q^*, R^*) = (E_1^*, \ldots, E_n^*, I_1^*, \ldots, I_n^*, Q_1^*, \ldots, Q_n^*, R_1^*, \ldots, R_n^*)^T, \quad (5)$$

if $R_0 \le 1$, *where*

$$\begin{aligned} E_k^* &= \frac{\gamma+\delta}{\mu}\frac{kx}{1+(k-1)x\Delta}, \\ I_k^* &= \frac{kx}{1+(k-1)x\Delta}, \\ Q_k^* &= \frac{\delta}{\varepsilon}\frac{kx}{1+(k-1)x\Delta}, \\ R_k^* &= \frac{\gamma+\delta}{\eta}\frac{kx}{1+(k-1)x\Delta}, \\ \Delta &= \frac{\gamma+\delta}{\mu}+\frac{\delta}{\varepsilon}+\frac{\gamma+\delta}{\eta}+1, \end{aligned} \quad (6)$$

x is the unique positive root of the equation

$$f(x) = \rho\sum_k \left[\frac{k^2P(k)}{1+(k-1)x\Delta}\right][1-\Delta x] - \gamma - \delta = 0. \quad (7)$$

Proof. After imposing the stationarity condition, we have

$$\begin{aligned} k\rho\Theta(t)\left(1-E_k(t)-I_k(t)-Q_k(t)-R_k(t)\right)-\mu E_k(t) &= 0, \\ \mu E_k(t)-(\gamma+\delta)I_k(t) &= 0, \\ \delta I_k(t)-\varepsilon Q_k(t) &= 0, \\ \gamma I_k(t)+\varepsilon Q_k(t)-\eta R_k(t) &= 0. \end{aligned} \quad (8)$$

It is easily verified that $P_0 = (\overbrace{0,0,\ldots,0}^{4n})^T$ is always a root of this system. Solving the system, we get

$$\begin{aligned} E_k^* &= \frac{\gamma+\delta}{\mu}\frac{kx}{1+(k-1)x\Delta}, \\ I_k^* &= \frac{kx}{1+(k-1)x\Delta}, \\ Q_k^* &= \frac{\delta}{\varepsilon}\frac{kx}{1+(k-1)x\Delta}, \\ R_k^* &= \frac{\gamma+\delta}{\eta}\frac{kx}{1+(k-1)x\Delta}, \end{aligned} \quad (9)$$

where x is the unique positive root of the equation

$$f(x) = \rho\sum_k \left[\frac{k^2P(k)}{1+(k-1)x\Delta}\right][1-\Delta x] - \gamma - \delta = 0. \quad (10)$$

If $R_0 \le 1$, we have $E^* = I^* = Q^* = R^* = 0$, implying that $f(x) = 0$ and, thus, (10) has no positive roots. Hence, assertion (3) holds. Now, assume $R_0 > 1$. The observations that (a) $f(0) > 0$, (b) $f'(x) < 0$ for $x \ge 0$, and (c) $f(+\infty) > 0$ imply that (10) has a unique positive root. Hence, assertion (8) also holds. □

Remark 2. It can be seen from Theorem 1 that $E_1^* < E_2^* < \cdots < E_n^*$, $I_1^* < I_2^* < \cdots < I_n^*$, $Q_1^* < Q_2^* < \cdots < Q_n^*$ and $R_1^* < R_2^* < \cdots < R_n^*$. This shows that, when in the steady state P^*, the infection density for a higher node degree is higher than that for a lower node degree.

3. Stability of the Virus-Free Equilbrium

It is clear that $P_0 = (\overbrace{0,0,\ldots,0}^{4n})$ is the virus-free equilibrium of system (3). In this section, we will prove that virus-free equilibrium is globally asymptotically stable when $R_0 < 1$.

For convenience, let

$$\Omega = \{x = (x_1, x_2, \ldots, x_{4n}) \mid x_i \ge 0\ \forall 1 \le i \le 4n, \; x_i + x_{i+n} + x_{i+2n} + x_{i+3n} \le 1\ \forall 1 \le i \le n\}. \quad (11)$$

Let $x(t) = (E(t), I(t), Q(t), R(t))^T$ and rewrite system (3) in matrix-vector notation as

$$x(t) = Ax(t) + H(x(t)), \quad (12)$$

with initial condition $x(0) \in \Omega$, where

$$A = \begin{bmatrix} A_{11} & 0 \\ A_{21} & A_{22} \end{bmatrix}_{(4n\times 4n)},$$

$$A_{11} = \begin{bmatrix} -\mu & 0 & \cdots & 0 & \frac{p(1)\rho}{\langle k\rangle} & \frac{2p(2)\rho}{\langle k\rangle} & \cdots & \frac{np(n)\rho}{\langle k\rangle} \\ 0 & -\mu & \cdots & 0 & \frac{2p(1)\rho}{\langle k\rangle} & \frac{4p(2)\rho}{\langle k\rangle} & \cdots & \frac{2np(n)\rho}{\langle k\rangle} \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & -\mu & \frac{np(1)\rho}{\langle k\rangle} & \frac{2np(2)\rho}{\langle k\rangle} & \cdots & \frac{n^2 p(n)\rho}{\langle k\rangle} \\ \mu & 0 & \cdots & 0 & -(\gamma+\delta) & 0 & \cdots & 0 \\ 0 & \mu & \cdots & 0 & 0 & -(\gamma+\delta) & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & \mu & 0 & 0 & \cdots & -(\gamma+\delta) \end{bmatrix}_{(2n\times 2n)},$$

$$A_{21} = \begin{bmatrix} 0 & 0 & \cdots & 0 & \delta & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 0 & \delta & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & 0 & 0 & 0 & \cdots & \delta \\ 0 & 0 & \cdots & 0 & \gamma & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 0 & \gamma & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & 0 & 0 & 0 & \cdots & \gamma \end{bmatrix}_{(2n\times 2n)},$$

$$A_{22} = \begin{bmatrix} -\varepsilon & 0 & \cdots & 0 & 0 & 0 & \cdots & 0 \\ 0 & -\varepsilon & \cdots & 0 & 0 & 0 & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & -\varepsilon & 0 & 0 & \cdots & 0 \\ \varepsilon & 0 & \cdots & 0 & -\eta & 0 & \cdots & 0 \\ 0 & \varepsilon & \cdots & 0 & 0 & -\eta & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & \cdots & \varepsilon & 0 & 0 & \cdots & -\eta \end{bmatrix}_{(2n\times 2n)},$$

$$H(x(t)) = -\rho\Theta\Big(E_1(t) + I_1(t) + Q_1(t) + R_1(t), \ldots, n\left(E_n(t) + I_n(t) + Q_n(t) + R_n(t)\right), \overbrace{0, \ldots, 0}^{3n}\Big). \tag{13}$$

Theorem 3. *Consider system* (12); $P_0 = (\overbrace{0, 0, \ldots, 0}^{4n})$ *is locally asymptotically stable if* $R_0 < 1$*, whereas* P_0 *is a saddle point if* $R_0 < 1$.

Proof. The characteristic equation with respect to P_0 is

$$\begin{aligned} \det(\lambda E_{4n} - A) &= \det\begin{pmatrix} \lambda E_{2n} - A_{11} & 0 \\ -A_{21} & \lambda E_{2n} - A_{22} \end{pmatrix} \\ &= \det(\lambda E_{2n} - A_{11})(\lambda E_{2n} - A_{22}) = 0. \end{aligned} \tag{14}$$

We obtain

$$\begin{aligned} &\det(\lambda E_{4n} - A) \\ &\quad = (\lambda+\eta)^n (\lambda+\varepsilon)^n (\lambda+\mu)^{n-1} \\ &\quad\quad \times (\lambda+\delta+\gamma)^{n-1} \begin{bmatrix} -\lambda-\mu & \rho\frac{\langle k^2\rangle}{\langle k\rangle} \\ \mu & -\lambda-\gamma-\delta \end{bmatrix} \\ &\quad = (\lambda+\eta)^n (\lambda+\varepsilon)^n (\lambda+\mu)^{n-1} (\lambda+\delta+\gamma)^{n-1} \\ &\quad\quad \times \left((\lambda+\mu)(\lambda+\gamma+\delta) - \mu\rho\frac{\langle k^2\rangle}{\langle k\rangle}\right) \\ &\quad = (\lambda+\eta)^n (\lambda+\varepsilon)^n (\lambda+\mu)^{n-1} (\lambda+\delta+\gamma)^{n-1} \\ &\quad\quad \times \left(\lambda^2 + (\gamma+\delta+\mu)\lambda + \mu(\gamma+\delta) - \mu\rho\frac{\langle k^2\rangle}{\langle k\rangle}\right) = 0. \end{aligned} \tag{15}$$

This equation has negative roots $-\eta$ and $-\varepsilon$ with multiplicity n and negative roots $-\mu$, $-\delta$, and $-\gamma$ with multiplicity $n-1$. Now let

$$g(\lambda)=\lambda^2+(\gamma+\delta+\mu)\lambda+\mu(\gamma+\delta)-\mu\rho\frac{\langle k^2\rangle}{\langle k\rangle}=0. \quad (16)$$

Suppose $R_0<1$. Then, $(\gamma+\delta)-\rho(\langle k^2\rangle/\langle k\rangle)>0$ and it follows from the Hurwitz criterion that all roots of the characteristic equation have negative real parts, implying that P_0 is locally asymptotically stable. Now, assume $R_0>1$. Then, $(\gamma+\delta)-\rho(\langle k^2\rangle/\langle k\rangle)<0$ and the characteristic equation has exactly one positive root, implying that P_0 is a saddle point. □

Lemma 4 (see [16]). *Consider a system $dx/dt=f(x)$ defined at least in a compact set C. Then, C is invariant if, for every point y on ∂C, the vector $f(y)$ is tangent to or pointing into C.*

Lemma 5. *The set Ω is positively invariant for system* (12). *That is, $x(0)\in\Omega$ implies $x(t)\in\Omega$ for all $t>0$.*

Proof. $\partial\Omega$ consists of the following 5Δ sets:

$$S_i=\{x\in\Omega\mid x_i=0\},\qquad T_i=\{x\in\Omega\mid x_{i+n}=0\},$$
$$U_i=\{x\in\Omega\mid x_{i+2n}=0\},\qquad V_i=\{x\in\Omega\mid x_{i+3n}=0\},$$
$$W_i=\{x\in\Omega\mid x_i+x_{i+n}+x_{i+2n}+x_{i+3n}=1\}, \quad (17)$$

which have

$$\begin{aligned}\varphi_i&=\Big(0,\dots,0,\overset{i}{-1},0,\dots,0\Big),\\ \varsigma_i&=\Big(0,\dots,0,\overset{i+n}{-1},0,\dots,0\Big),\\ \xi_i&=\Big(0,\dots,0,\overset{i+2n}{-1},0,\dots,0\Big),\\ \psi_i&=\Big(0,\dots,0,\overset{i+3n}{-1},0,\dots,0\Big),\\ \zeta_i&=\Big(0,\dots,0,\overset{i}{1},0,\dots,0,\overset{i+n}{1},0,\dots,\\ &\qquad 0,\overset{i+2n}{1},0,\dots,0,\overset{i+3n}{1},0,\dots,0\Big)\end{aligned} \quad (18)$$

as their respective outer normal vectors. For $1\le i\le n$, we have

$$\begin{aligned}&\left(\frac{dx}{dt}\Big|_{x\in S_i}\cdot\varphi_i\right)\\ &\quad=-i\rho\frac{\sum_k kp(k)}{\langle k\rangle}\left(1-x_{i+n}-x_{i+2n}-x_{i+3n}\right)\le 0,\\ &\left(\frac{dx}{dt}\Big|_{x\in T_i}\cdot\varsigma_i\right)=-\mu x_i\le 0,\\ &\left(\frac{dx}{dt}\Big|_{x\in U_i}\cdot\xi_i\right)=-\delta x_{i+n}\le 0,\\ &\left(\frac{dx}{dt}\Big|_{x\in V_i}\cdot\psi_i\right)=-\left(\gamma x_{i+n}+\varepsilon x_{i+2n}\right)\le 0,\\ &\left(\frac{dx}{dt}\Big|_{x\in W_i}\cdot\zeta_i\right)=-\eta x_{i+3n}\le 0.\end{aligned} \quad (19)$$

Thus, the claimed result follows from Lemma 4. □

Lemma 6 (see [16]). *Consider an n-dimensional autonomous system*

$$\frac{dx(t)}{dt}=Ax(t)+H(x(t)),\quad x\in D, \quad (20)$$

where A is an irreducible $n\times n$ matrix, D is a region containing the origin, $H(x)\in C^1(D)$, and $\lim_{x\to 0}\|H(x)\|/\|x\|=0$. Assume there exist, a positively invariant compact convex set $C\subset D$ containing the origin, a positive number r, and a real eigenvector ω of A^T, such that

(C1) $(x,\omega)\ge r\|x\|$ *for all* $x\in C$,

(C2) $(H(x),\omega)\le 0$ *for all* $x\in C$,

(C3) *the origin forms the largest positively invariant set included in* $N=\{x\in C\mid (H(x),\omega)=0\}$.

Then, one has that

(1) $s(A^T)<0$ *implies that the origin is globally asymptotically stable in C, and*

(2) $s(A^T)>0$ *implies that there exists $m>0$ such that, for each $x_0\in C-\{0\}$, the solution $\phi(t,x_0)$ to system* (12) *satisfies* $\lim_{t\to\infty}\inf\|\phi(t,0)\|\ge m$.

We are ready to prove.

Theorem 7. *Consider system* (12). *Then, P_0 is globally asymptotically stable in Ω, if $R_0<1$.*

Proof. Let $C=\Omega$ and look at (12). As matrix A^T is irreducible and all of its nondiagonal entries are nonnegative, it follows from [13] that A^T has a positive eigenvector $\omega=(\omega_1,\dots,\omega_{4n})$ corresponding to its eigenvalue $s(A^T)$. Let $\omega_0=\min_i\omega_i>0$. Then, for all $x\in\Omega$, we have

$$\begin{aligned}(x,\omega)&\ge\omega_0\sum_{i=1}^{4n}x_i\ge\omega_0\left(\sum_{i=1}^{4n}x_i^2\right)^{1/2}=\omega_0\|x\|,\\ (H(x),\omega)&=-\rho\Theta\sum_{i=1}^{n}i\omega_i\left(x_i+x_{i+n}+x_{i+2n}+x_{i+3n}\right)\le 0.\end{aligned} \quad (21)$$

Moreover, $(H(x),\omega)=0$ implies that $x=0$. Hence, the claimed result follows from assertion (2) of Lemma 6. □

4. Global Attractivity of the Viral Equilibrium

We will ascertain the global attractivity of the viral equilibrium.

Theorem 8. *If $R_0 > 1$, then the infection solution of* (12) $P^* = (\overbrace{P_1^*, P_2^*, \ldots, P_{4n}^*}^{4n})$ *is globally attractive in* $\Omega - \{0\}$.

Proof. Theorem 3 ensures the existence of the viral equilibrium. We need to prove that if $R_0 > 1$, there is a unique constant equilibrium P^* in $\Omega - \{0\}$. Let $x^* = P^*$, Assume that $x = x^* > 0$ and $y = y^* > 0$ are two constant solutions of (12) in $\Omega - \{0\}$. If $x^* \neq y^*$, then there exists i_0, $i_0 = 1, 2, \ldots, 4n$, such that $x_{i0}^* \neq y_{i0}^*$, where x_{i0}^* is the i_0th component of the vector x^*. Without loss of generality, assume $x_{i0}^* > y_{i0}^*$, and $x_{i0}^*/y_{i0}^* > x_i^*/y_i^*$ for all $i = 1, \ldots, 4n$. Since x^* and y^* are constant solutions of (12), we substitute them into (12). And if $1 \le i_0 \le n$, we obtain,

$$\begin{aligned} &k\rho\Theta(x^*)(1 - x_{i0}^* - x_{i0+n}^* - x_{i0+2n}^* - x_{i0+3n}^*) - \mu x_{i0}^* \\ &\quad = k\rho\Theta(y^*)(1 - y_{i0}^* - y_{i0+n}^* - y_{i0+2n}^* - y_{i0+3n}^*) - \mu y_{i0}^* \\ &\quad = 0, \end{aligned} \tag{22}$$

where $\Theta(x^*) = (1/\langle k\rangle)\sum_k kP(k)x_i^*$.

After equivalent deformation, it follows that

$$\begin{aligned} &k\rho\Theta(x^*)(1 - x_{i0}^* - x_{i0+n}^* - x_{i0+2n}^* - x_{i0+3n}^*)\frac{y_{i0}^*}{x_{i0}^*} - \mu y_{i0}^* \\ &\quad = k\rho\Theta(y^*)(1 - y_{i0}^* - y_{i0+n}^* - y_{i0+2n}^* - y_{i0+3n}^*) - \mu y_{i0}^* \\ &\quad = 0. \end{aligned} \tag{23}$$

But $x_{i0}^*/y_{i0}^* > x_i^*/y_i^*$ for all i and

$$\begin{aligned} &(1 - x_{i0}^* - x_{i0+n}^* - x_{i0+2n}^* - x_{i0+3n}^*)\frac{y_{i0}^*}{x_{i0}^*} \\ &\quad < (1 - y_{i0}^* - y_{i0+n}^* - y_{i0+2n}^* - y_{i0+3n}^*). \end{aligned} \tag{24}$$

Thus, from the above inequality, we get

$$\begin{aligned} &k\rho\Theta(x^*)(1 - x_{i0}^* - x_{i0+n}^* - x_{i0+2n}^* - x_{i0+3n}^*)\frac{y_{i0}^*}{x_{i0}^*} \\ &\quad < k\rho\Theta(y^*)(1 - y_{i0}^* - y_{i0+n}^* - y_{i0+2n}^* - y_{i0+3n}^*). \end{aligned} \tag{25}$$

This is a contradiction. Similarly, we can also get contradictions when $n + 1 \le i_0 \le 2n$, $2n + 1 \le i_0 \le 3n$, and $3n + 1 \le i_0 \le 4n$. Therefore, there exists a unique constant solution $P^* = (P_1^*, P_2^*, \ldots, P_{4n}^*)$ of (3) in $\Omega - \{0\}$. Now, we shall prove that x^* is globally attractive in $\Omega - \{0\}$. To find the asymptotic behavior of the solutions of (12) in Ω, we define the following functions, $F : \Omega \to R$ and $f : \Omega \to R$ for $P \in \Omega$, where $F(x) = \max_i(x_i/x_i^*)$, $f(x) = \min_i(x_i/x_i^*)$, $F(x)$ and $f(x)$ are continuous and the right-hand derivative exists along solutions of (12). Let $x = x(t)$ be a solution of (12), we may assume that $F(x(t)) = x_{i0}(t)/x_{i0}^*$, $1 \le i_0 \le 4n$, $t \in [t_0, t_0 + \varepsilon]$ for a given t_0 and a sufficiently small $\varepsilon > 0$. Then,

$$F'(x(t_0)) = \frac{x_{i_0}'(t_0)}{x_{i_0}^*}, \quad t \in [t_0, t_0 + \varepsilon], \tag{26}$$

where F' is defined as

$$F' = \lim_{h\to 0^+} \sup \frac{F(x(t+h)) - F(x(t))}{h}. \tag{27}$$

If $1 \le i_0 \le n$, from (12) we have

$$\begin{aligned} &x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} \\ &\quad = \frac{x_{i_0}^*}{x_{i_0}(t_0)} k\rho\Theta(x_{i_0+n}(t_0)) \\ &\qquad \times (1 - x_{i_0}(t_0) - x_{i_0+n}(t_0) - x_{i_0+2n}(t_0) - x_{i_0+3n}(t_0)) - \mu x_{i_0}^*. \end{aligned} \tag{28}$$

And we obtain

$$\begin{aligned} &x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} = \mu \frac{x_{i_0}^*}{x_{i_0}(t_0)} x_{i_0-n}(t_0) - (\gamma + \delta) x_{i_0}^*, \\ &\qquad \text{when } n + 1 \le i_0 \le n; \\ &x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} = \delta \frac{x_{i_0}^*}{x_{i_0}(t_0)} x_{i_0-n}(t_0) - \varepsilon x_{i_0}^*, \\ &\qquad \text{when } 2n + 1 \le i_0 \le 3n; \\ &x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} = \gamma \frac{x_{i_0}^*}{x_{i_0}(t_0)} x_{i_0-2n}(t_0) + \varepsilon \frac{x_{i_0}^*}{x_{i_0}(t_0)} x_{i_0-n}(t_0) - \eta x_{i_0}^*, \\ &\qquad \text{when } 3n + 1 \le i_0 \le 4n. \end{aligned} \tag{29}$$

According to the definition of $F(x(t))$, we have

$$\frac{x_{i_0}(t_0)}{x_{i_0}^*} \ge \frac{x_i(t_0)}{x_i^*}, \quad i = 1, 2, \ldots, 4n. \tag{30}$$

Then if $F(x(t_0)) > 1$, we obtain

$$\begin{aligned} x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} &\le k\rho\Theta\left(x_{i_0+n}^*\right)\left(1 - x_{i_0}^* - x_{i_0+n}^* - x_{i_0+2n}^* - x_{i_0+3n}^*\right) \\ &\quad - \mu x_{i_0}^* = 0, \\ x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} &\le \mu x_{i_0-n}^* - (\gamma + \delta) x_{i_0}^* = 0, \\ x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} &\le \delta x_{i_0-n}^* - \varepsilon x_{i_0}^* = 0, \end{aligned} \tag{31}$$

or

$$x_{i_0}^* \frac{x_{i_0}'(t_0)}{x_{i_0}(t_0)} \le \gamma x_{i_0-2n}^* + \varepsilon x_{i_0-n}^* - \eta x_{i_0}^* = 0. \tag{32}$$

Since $x_{i_0}^* > 0$ and $x_{i_0}(t_0) > 0$, we conclude that $x_{i_0}'(t_0) > 0$. Therefore, if $F(x(t_0)) > 1$, $F'(x(t_0)) < 0$.

Similarly, we can testify that $F(x(t_0)) = 1$ implies $F'(x(t_0)) \le 0$, and $f(x(t_0)) < 1$ implies $f'(x(t_0)) > 0$. If $f(x(t_0)) = 1$, then $f'(x(t_0)) \ge 0$. Denote

$$\begin{aligned} U(x) &= \max\{F(x) - 1, 0\}, \\ V(x) &= \max\{1 - f(x), 0\}. \end{aligned} \tag{33}$$

Both $U(x)$ and $V(x)$ are continuous and non-negative for $x \in \Omega$. Notice that $U'(x(t)) \le 0$, $V'(x(t)) \le 0$. Let

$$H_U = \left\{x \in \Omega \mid U'(x) = 0\right\}, \qquad H_V = \left\{x \in \Omega \mid V'(x) = 0\right\}, \tag{34}$$

then we have

$$H_U = \{x \mid 0 \le x_i \le x_i^*\}, \qquad H_V = \{x \mid x_i^* \le x_i \le 1\} \cup \{0\}. \tag{35}$$

According to the LaSalle invariant set principle, any solution of (12) starting in Ω will approach $H_U \cap H_V$. And $H_U \cap H_V = \{x^*\} \cup \{0\}$. But if $x(t) \ne 0$, by Lemma 6 we know that $\lim_{t\to\infty} \inf \|x(t)\| \ge m > 0$. Then we conclude that any solution $x(t)$ of (12), such that $x(0) \in \Omega - \{0\}$, satisfies $\lim_{t\to\infty} x(t) = x^*$, so $x = P^*$ is globally attractive in $\Omega - \{0\}$. □

Conjecture 9. *Consider system* (12) *and suppose* $R_0 > 1$. *Then the infection equilibrium,* P^*, *is globally asymptotically stable in* $\Omega - \{0\}$.

5. Numerical Examples

In this section, some numerical simulations are given to support our results. To demonstrate the global stability of the infection-free solution of system (3), we take the following set of parameter values: $\rho = 0.04$, $\mu = 0.8$, $\gamma = 0.8$, $\varepsilon = 0.5$, $\delta = 0.2$, $\eta = 0.4$, which runs on a scale-free network with $n = 1000$ and $\tau = 2.4$. In this case, we have $R_0 = 0.8825 < 1$. The time plots of the four relative densities are plotted in Figure 3, from which it can be seen that the virus would die out.

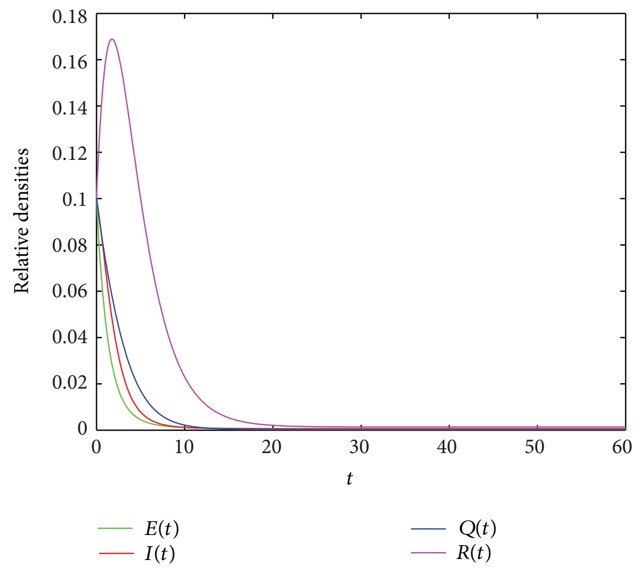

FIGURE 3: Global stability of infection-free solution.

To demonstrate the global attractivity of the viral equilibrium of system (3), we take the following set of parameter values: $\rho = 0.2$, $\mu = 0.8$, $\gamma = 0.8$, $\varepsilon = 0.5$, $\delta = 0.2$, $\eta = 0.4$, which runs on a scale-free network with $n = 1000$ and $\tau = 2.4$. In this case, we have $R_0 = 4.4124 > 1$. The time plots of the four relative densities are plotted in Figure 4, from which it can be seen that the virus would persist.

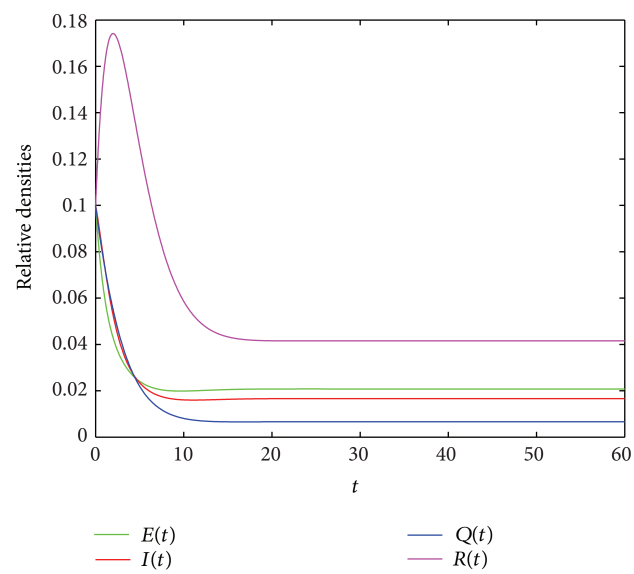

FIGURE 4: Global attractivity of infection solution.

Consider system (12) with $\rho = 0.2$, $\mu = 0.8$, $\gamma = 0.8$, $\varepsilon = 0.5$, $\delta = 0.2$, $\eta = 0.4$ and $n = 1000$. For $\tau \in \{2.0, 2.2, 2.4, 2.6\}$,

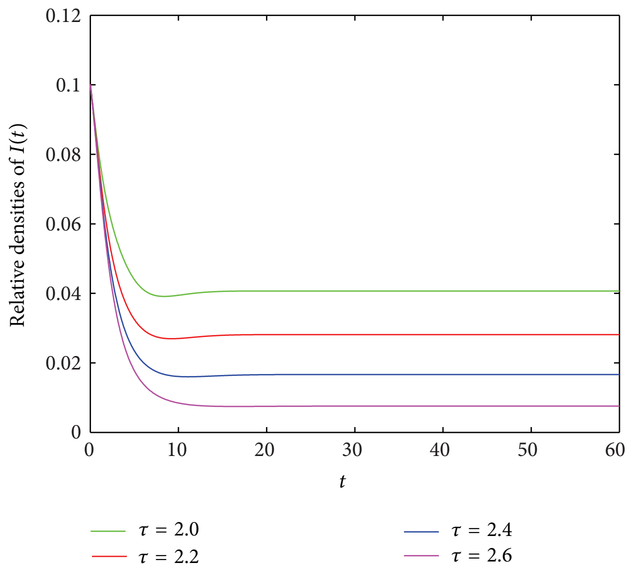

Figure 5: Evolution of $I(t)$ for different τ values.

Figure 5 demonstrates how $I(t)$ evolves with time. It can be seen that smaller exponent τ favors virus spreading.

6. Conclusions

To clearly understand how the Internet topology affects the spread of computer viruses, a new model capturing the epidemics of computer viruses on scale-free networks has been proposed. The basic reproduction number R_0 of the model has been calculated. The global asymptotic stability of the virus-free equilibrium has been shown when R_0 is below one, and the global attractivity of the viral equilibrium has been proved if R_0 is above one. Our future work will focus on establishing impulsive models on complex networks and studying the effect of impulsive immunization on computer virus propagation.

Acknowledgments

The work is supported by the National Natural Science Foundation of China under Grant no. 61304117, the Natural Science Foundation of the Jiangsu Higher Education Institutions of China under Grant no. 13KJB520008, the doctorate teacher support project of JiangSu Normal University under Grant no. 12XLR021.

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