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Research Article

Considering Quarantine in the SIRA Malware Propagation Model

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As the beginning of the 21st century was marked by a strong development in data science and, consequently, in computer networks, models for designing preventive actions against intruding, data stealing, and destruction became mandatory. Following this line, several types of epidemiological models have been developed and improved, considering different operational approaches. The development of the research line using traditional SIR(Susceptible, Infected, Removed) model for data networks started in the 1990s. In 2005, an epidemiological compartmental model containing antidotal nodes, SIRA (Susceptible, Infected, Removed, Antidotal), was introduced to study how the antivirus policies affect the network reliability. The idea here is to study the consequence of quarantine actions in a network by modifying the SIRA model, introducing quarantine nodes generating the SIQRA (Susceptible, Infected, Quarantine, Removed, Antidotal) model. Analytical and numerical approaches result in parameter conditions for the existence and stability of disease-free and endemic equilibrium points for two different cases: saturation and nonsaturation of the quarantine population block. Based on these results, operational actions can be planned to improve the network reliability.

1. Introduction

A substantial development occurred in data network technology, providing accurate and fast public and private facilities. This has changed the way of data transfer in society, creating a strong dependence on the communication services at all levels of relations. Computers, laptops, and smart phones are an integral part of human life, with a large universe of different types of connections emerging, facilitating daily tasks and improving personal relations.

Unfortunately, there are people and groups using their intelligence to develop hate and bad intentions, creating programs, such as viruses and worms, to invade and to destroy processes, causing collective and individual harmful effects. The power of destruction and the capacity of propagation of the viruses and malwares have increased over the years representing important threats to society and to corporative networks [1–3].

Consequently, there are two main concerns related to the propagation of computer virus and malwares: estimating the economic losses [4–8] and developing security and safety strategies [9]. Thus, a new important branch of computer science has been developed, cybernetic security, having as one of its approaches to build mathematical models, related to the dynamic operation of the systems [10].

This mathematical approach to computer virus propagation was inspired by biology and was divided into two levels: microscopic and macroscopic [1, 11]. The microscopic level is related to the development of antivirus software. Antivirus software is a program capable of detecting threats and preventing damages in the machine. Besides, the spread of virus through the network is avoided as a consequence of the antivirus action [12, 13].

The macroscopic level is based on the classical model of disease propagation [14–16], whose dynamics can indicate the possible infection process and show how to establish policies and strategies to reduce risk, combining parameters as strategies of control [17, 18]. The classical epidemiological macroscopic model SIR, proposed by Kermack and McKendrick, is the basis for the development of

macroscopic models, providing a dynamic model dividing the individuals of a population into three compartments containing the susceptible individuals (S), the infected (I), and the removed (R) ones [14, 15, 19].

Adapting the SIR model to computer populations, two different strategies were developed: deterministic [11, 13, 20–23] or stochastic [12, 24–26]. Regarding the mathematical treatment of time, discrete [27] and continuous [28, 29] models appeared.

Based on the classical SIR model, the deterministic SIRA model was developed, considering constant population [2, 18, 30]. In this case, robust conditions for disease-free equilibrium stability, depending on the node recovery rate, were derived, considering that antidotal nodes are part of the network. Improving the SIRA model, mortality and variable population were considered in the descriptions, allowing new robust parameter relations for disease-free equilibrium that seem to be useful to design data networks [31].

Models taking delays and quarantine into account in the classical SIR model [32] show interesting operational actions to be taken to improve reliability, with bifurcation diagrams indicating parameters values to be avoided [33, 34]. Recently, models including quarantine compartments seem to avoid virus and malware propagation in data networks [35, 36] and to prevent attacks in sensor networks [22, 23, 37, 38].

The main idea to control the virus spread is to keep the nodes isolated for some time [38, 39]. The word "quarantine" means this interaction is interrupted. When a node is found to be infected, it can be quarantined by the detection virus program. It is then monitored for an interval corresponding to the inappropriate behavior indicated by the process. If during this action no wrong behavior is observed, it is released.

In this work, quarantine concept is applied as an additional improvement of the SIRA model and the SIQRA (Susceptible, Infected, Quarantine, Removed, Antidotal) model is developed. Two different cases are studied: with and without interaction between infected and quarantine compartments allowing robust relations between parameters for disease-free equilibrium, providing ideas to improve the reliability of networks.

It will be shown that, if the quarantine compartment is introduced with its population not saturated by the number of infected nodes, i.e., the antivirus detection rate is greater than the infection rate, the model does not contain nonlinear terms given by IQ. In this case, the network presents a very satisfactory behavior, with stable disease equilibrium point and no endemic possibility. If the saturation term IQ is present, i.e., the infection rate is greater than the virus detection capacity, in spite of the benefits given by the presence of the quarantine population, an endemic equilibrium appears.

In the next section, hypothesis and equations are presented, followed by a section deriving equilibrium conditions and the parameters relations for the several equilibrium situations. Numerical results are shown next, simulating the network dynamics for some relevant real cases, followed by the conclusion section giving hints about the model improvements.

2. SIQRA Model: Hypothesis and Equations

The model to be studied is a modification to the compartmental SIRA [2, 18, 30], improved in [31], adding a quarantine computer compartment (Q), representing possible infected machines, which are separated to be evaluated concerning infection or recovery (Figure 1). Once entering in the quarantine compartment, after the evaluation, the machine can either return to the network or be removed. If a machine returns, it can become either susceptible or antidotal.

In Figure 1, α_{IA} represents the interaction coefficient between compartments I and A, related to the vaccination rate of the network; β, the interaction between S and I, i.e., measuring how the infected nodes change the operational systems of the susceptible ones; σ, the rate of transformation from R to S, i.e., the recovering capacity of the nodes; and ω, the rate of transformation from Q to S, giving the rate of quarantine liberation.

Parameters α_{SA} and α_{QA} represent how the antidotal nodes actuates over susceptible and quarantine operational systems, respectively; α is the interaction coefficient between compartments Q and R, giving an idea of the rate of nonrecovered nodes subjected to quarantine.

Two different quarantine strategies are presented: one without nonlinear interaction between blocks I and Q, i.e., without a saturation term, and other considering that blocks I and Q interact nonlinearly allowing the onset of endemic situations. Parameter δ represents either the rate of transformation from I to Q in the model without nonlinear interaction or the interaction between compartments Q and I in the model with nonlinear IQ term.

2.1. Model without Nonlinear IQ Term. In this case, examining Figure 1, the state equation representing the model is given by

$$\begin{aligned}
\dot{S} &= -\alpha_{SA}SA - \beta SI + \sigma R + \omega Q,\\
\dot{I} &= \beta SI - \alpha_{IA}AI - \delta I,\\
\dot{Q} &= \delta I - \omega Q - \alpha_{QA}Q - \alpha Q,\\
\dot{R} &= \alpha Q - \sigma R,\\
\dot{A} &= \alpha_{SA}SA + \alpha_{IA}AI + \alpha_{QA}Q.
\end{aligned} \tag{1}$$

The initial conditions are assumed to be $S(0) \geq 0$, $I(0) \geq 0$, $Q(0) \geq 0$, $R(0) \geq 0$, and $A(0) \geq 0$. It can be verified that, for equation (1), the total population $T = S + I + Q + R + A$ is constant.

As a consequence, the state space is 4-dimensional, and examining the dynamic equation for $\dot{I}$, no endemic equilibrium point is verified, i.e., there is no equilibrium point with $I \neq 0$. However, two disease-free equilibrium points ($I = 0$) are possible, described by using the following expressions:

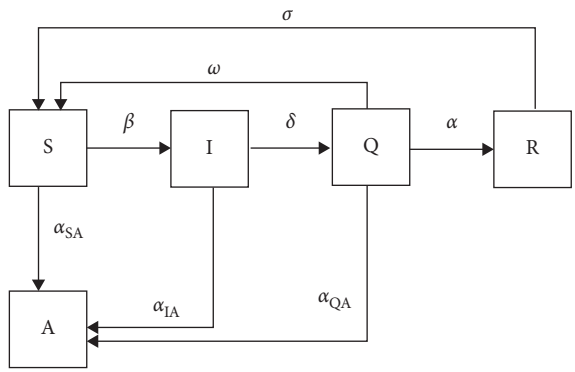

Figure 1: SIQRA model.

$$P_1 = (S, I, Q, R, A) = (0, 0, 0, 0, A) = (0, 0, 0, 0, T),$$
$$P_2 = (S, I, Q, R, A) = (S, 0, 0, 0, 0) = (T, 0, 0, 0, 0). \quad (2)$$

To study the local stability of these equilibrium points, the Jacobian matrix, (J), must be calculated [40]:

$$J = \begin{bmatrix} -\alpha_{SA}A - \beta I & -\beta S & \omega & \sigma & -\alpha_{SA}S \\ \beta I & \beta S - \alpha_{IA}A - \delta & 0 & 0 & -\alpha_{IA}I \\ 0 & \delta & -\omega - \alpha_{QA} - \alpha & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ \alpha_{SA}A & \alpha_{IA}A & \alpha_{QA} & 0 & \alpha_{SA}S + \alpha_{IA}I \end{bmatrix}. \quad (3)$$

Considering the P_1 equilibrium point, the Jacobian matrix, J_{P_1}, is given by

$$J_{P_1} = \begin{bmatrix} -\alpha_{SA}T & 0 & \omega & \sigma & 0 \\ 0 & -(\alpha_{IA}T + \delta) & 0 & 0 & 0 \\ 0 & \delta & -(\omega + \alpha_{QA} + \alpha) & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ \alpha_{SA}T & \alpha_{IA}T & \alpha_{QA} & 0 & 0 \end{bmatrix}. \quad (4)$$

By using MATLAB R2013a [41], the eigenvalues of J_{P_1} are $\lambda_1 = 0$, $\lambda_2 = -(\alpha_{IA}T + \delta)$, $\lambda_3 = -\sigma$, $\lambda_4 = -\alpha_{SA}T$, and $\lambda_5 = -(\alpha + \omega + \alpha_{QA})$. The zero eigenvalue only indicates that the state space dimension is 4 in spite of the 5-equation model. The other eigenvalues are real and negative, for any parameter combination with physical meaning, implying that P_1 is asymptotically stable.

Repeating the procedure for the equilibrium point P_2, the Jacobian matrix, J_{P_2}, is given by

$$J_{P_2} = \begin{bmatrix} 0 & -\beta T & \omega & \sigma & -\alpha_{SA}T \\ 0 & (\beta T - \delta) & 0 & 0 & 0 \\ 0 & \delta & -(\omega + \alpha_{QA} + \alpha) & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ 0 & 0 & \alpha_{QA} & 0 & \alpha_{SA}T \end{bmatrix}, \quad (5)$$

whose eigenvalues are $\lambda_1 = 0$, $\lambda_2 = (\alpha_{SA}T + \delta)$, $\lambda_3 = \beta T - \delta$, $\lambda_4 = -\sigma$, and $\lambda_5 = -(\alpha + \omega + \alpha_{QA})$.

Again, the zero eigenvalue only indicates that the state space dimension is 4 in spite of the 5-equation model. For any parameter combination with physical meaning, one of the eigenvalues, λ_2, is real and positive, indicating that P_2 is unstable.

2.2. Model with Nonlinear IQ Term. Including the possibility of saturation for the IQ term is important mainly for small networks, where the increase of this product could provoke a time-out situation for the whose system.

In this case, examining Figure 1, the state equation representing the model is given by

$$\begin{aligned} \dot{S} &= -\alpha_{SA}SA - \beta SI + \sigma R + \omega Q, \\ \dot{I} &= \beta SI - \alpha_{IA}AI - \delta QI, \\ \dot{Q} &= \delta QI - \omega Q - \alpha_{QA}Q - \alpha Q, \\ \dot{R} &= \alpha Q - \sigma R, \\ \dot{A} &= \alpha_{SA}SA + \alpha_{IA}AI + \alpha_{QA}Q. \end{aligned} \quad (6)$$

The initial conditions are assumed to be $S(0) \geq 0$, $I(0) \geq 0$, $Q(0) \geq 0$, $R(0) \geq 0$, and $A(0) \geq 0$. It can be verified that, for equation (6), the total population $T = S + I + Q + R + A$ is constant. As a consequence, the state space is 4-dimensional.

Examining the model equations, it can be concluded that the system presents three equilibrium points: two disease-free ($I = 0$), given by P_1 and P_2, and one endemic ($I \neq 0$), given by P_3, with

$$P_1 = (S, I, Q, R, A) = (0, 0, 0, 0, A) = (0, 0, 0, 0, T),$$
$$P_2 = (S, I, Q, R, A) = (S, 0, 0, 0, 0) = (T, 0, 0, 0, 0), \quad (7)$$
$$P_3 = (S, I, Q, R, A) = (0, I, 0, 0, 0) = (0, T, 0, 0, 0).$$

To study the local stability of these equilibrium points, the Jacobian matrix, (J), must be calculated [40]:

$$J = \begin{bmatrix} -\alpha_{SA}A - \beta I & -\beta S & \omega & \sigma & -\alpha_{SA}S \\ \beta I & \beta S - \alpha_{IA}A - \delta Q & \delta I & 0 & -\alpha_{IA}I \\ 0 & \delta Q & \delta I - \omega - \alpha_{QA} - \alpha & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ \alpha_{SA}A & \alpha_{IA}A & \alpha_{QA} & 0 & \alpha_{SA}S + \alpha_{IA}I \end{bmatrix}. \quad (8)$$

Considering the P_1 equilibrium point, the Jacobian matrix, J_{P_1}, is given by

$$J_{P_1} = \begin{bmatrix} -\alpha_{SA}T & 0 & \omega & \sigma & 0 \\ 0 & -\alpha_{IA}T & 0 & 0 & 0 \\ 0 & 0 & -\omega - \alpha_{QA} - \alpha & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ \alpha_{SA}T & \alpha_{IA}T & \alpha_{QA} & 0 & 0 \end{bmatrix}. \quad (9)$$

By using MATLAB R2013a [41], the eigenvalues of J_{P_1} are $\lambda_1 = 0$, $\lambda_2 = -\sigma$, $\lambda_3 = -\alpha_{IA}T$, $\lambda_4 = -\alpha_{SA}T$, and $\lambda_5 = -(\alpha + \omega + \alpha_{QA})$.

The zero eigenvalue only indicates that the state space dimension is 4 in spite of the 5-equation model. The other eigenvalues are real and negative, for any parameter combination with physical meaning, implying that P_1 is asymptotically stable.

Repeating the procedure for the equilibrium point P_2, the Jacobian matrix, J_{P_2}, is given by

$$J_{P_2} = \begin{bmatrix} 0 & -\beta T & \omega & \sigma & -\alpha_{SA}T \\ 0 & \beta T & 0 & 0 & 0 \\ 0 & 0 & -\omega - \alpha_{QA} - \alpha & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ 0 & 0 & \alpha_{QA} & 0 & \alpha_{SA}T \end{bmatrix}, \quad (10)$$

whose eigenvalues are $\lambda_1 = 0$, $\lambda_2 = \alpha_{SA}T$, $\lambda_3 = \beta T$, $\lambda_4 = -\sigma$, and $\lambda_5 = -(\alpha + \omega + \alpha_{QA})$.

Again, the zero eigenvalue only indicates that the state space dimension is 4, in spite of the 5-equation model. For any parameter combination with physical meaning, one of the eigenvalues, λ_2, is real and positive, indicating that P_2 is unstable.

The endemic equilibrium point, P_3, is characterized by the presence of infected individuals ($I \neq 0$) and to perform calculations, it is supposed that there is no antidotal node in the network ($A = 0$).

For P_3, the Jacobian matrix, J_{P_3}, is given as follows:

$$J_{P_3} = \begin{bmatrix} -\beta T & 0 & \omega & \sigma & 0 \\ \beta T & 0 & \delta T & 0 & -\alpha_{IA}T \\ 0 & 0 & \delta T - \omega - \alpha_{QA} - \alpha & 0 & 0 \\ 0 & 0 & \alpha & -\sigma & 0 \\ 0 & 0 & \alpha_{QA} & 0 & \alpha_{IA}T \end{bmatrix}, \quad (11)$$

whose eigenvalues are $\lambda_1 = -\beta T$, $\lambda_2 = 0$, $\lambda_3 = \delta T - \alpha - \omega - \alpha_{QA}$, $\lambda_4 = -\sigma$, and $\lambda_5 = \alpha_{IA}T$.

As in the other cases, the zero eigenvalue only indicates that the state space dimension is 4, in spite of the 5-equation model. For any parameter combination with physical meaning, one of the eigenvalues, λ_5, is real and positive, indicating that P_3 is unstable.

3. Numerical Experiments

By using the Simulink tool from MATLAB R2013a [41], model simulations were performed to confirm the analytical results, showing the possible behaviors of the dynamical system when quarantine and antidotal compartments are present. The total population $T = (S + I + Q + R + A)$ is set equal to $N = 100$, to express the results in percentage, and the time unit is normalized, according to the normalized rates of interactions.

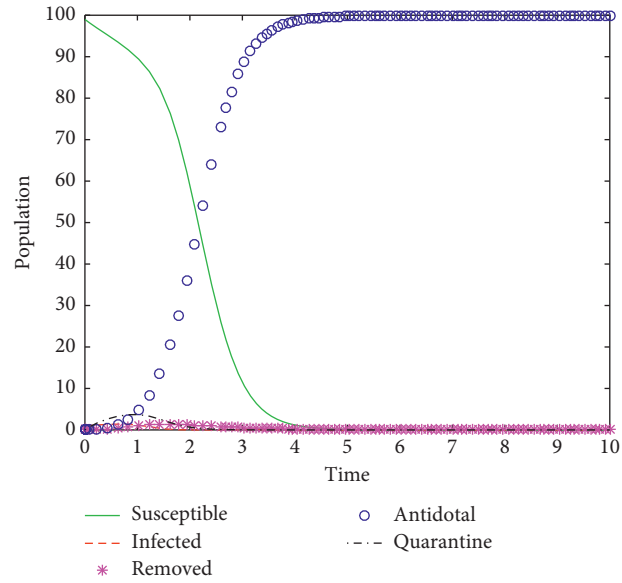

Figure 2: SIQRA without the IQ term: time evolution reaching P_1.

3.1. Numerical Experiments: Model without the IQ Saturation Term. To simulate this situation, the parameters and population were chosen to show the stability of the equilibrium points. Considering $\alpha_{SA} = 0.025$, $\beta = 0.1$, $\omega = 2$, $\sigma = 0.8$, $\alpha_{IA} = 0.25$, $\delta = 9$, $\alpha_{QA} = 0.5$, and $\alpha = 0.5$ for all simulations.

If an infected node is introduced into the network, the asymptotically stable equilibrium, P_1, is reached, as Figure 2 shows, with initial conditions $S = 99$, $I = 1$, $A = 0$, $R = 0$, and $Q = 0$.

If the infected population is high, the introduction of either an antidotal node (Figure 3(a)) or a quarantine node (Figure 3(b)) drives the populations to stable equilibrium.

When the network consists only of susceptible and removed computers, it is possible to verify that even the disease-free unstable equilibrium point, P_2, is reachable for any parameter combination, because the unstable eigenvector direction I has been avoided. Figure 4 shows this situation starting with $S = 90$ and $R = 10$ and reaching P_2.

3.2. Numerical Experiments: Model with the IQ Saturation Term. As analytically shown, depending on the initial condition, the temporal evolution of network ends at three different points: stable disease-free, unstable disease-free, and unstable endemic. To show these three cases, the parameters are set at $\alpha_{SA} = 0.025$, $\beta = 0.1$, $\omega = 2$, $\sigma = 0.8$, $\alpha_{IA} = 0.25$, $\delta = 9$, $\alpha_{QA} = 0.5$, and $\alpha = 0.5$.

If the network starts with only one antidotal machine, the stable disease-free P_1 is always reached, as Figure 5 shows for the initial condition $(S, I, Q, R, A) = (85, 9, 0, 5, 1)$.

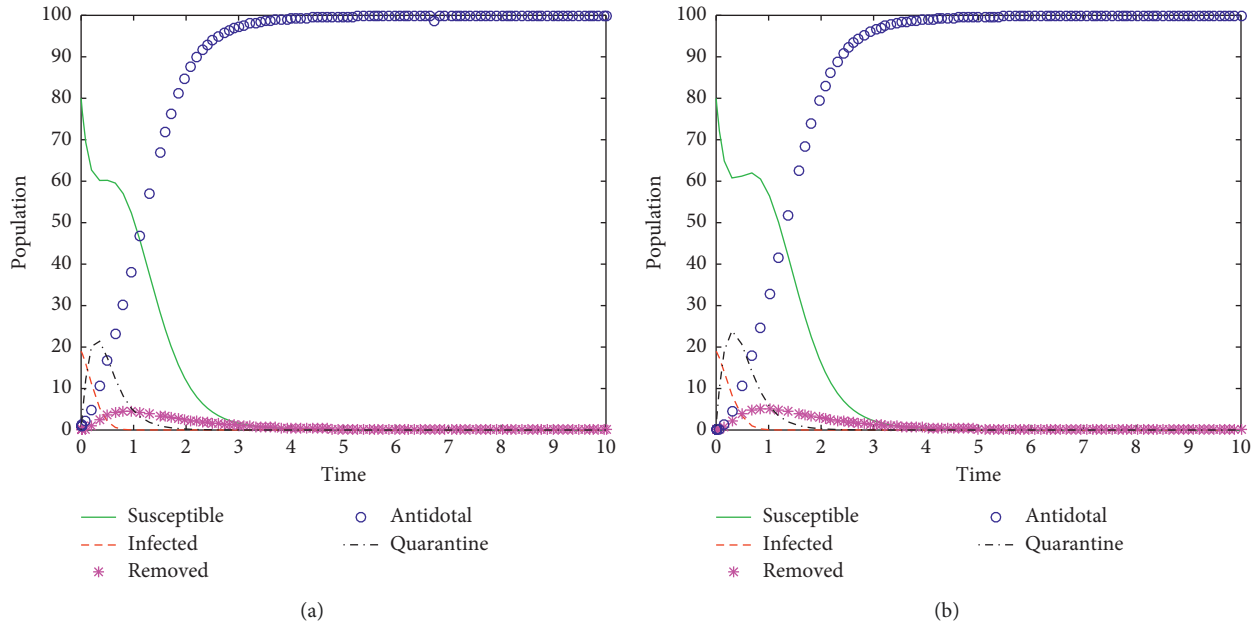

Figure 3: SIQRA without the IQ term: time evolution reaching P_1, starting with high I: (a) Introducing one antidotal, (b) Introducing one quarantine.

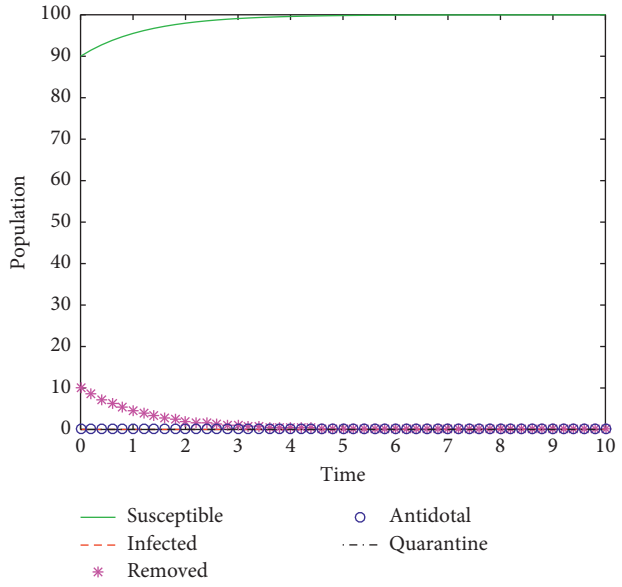

Figure 4: SIQRA without the IQ term: time evolution reaching P_2.

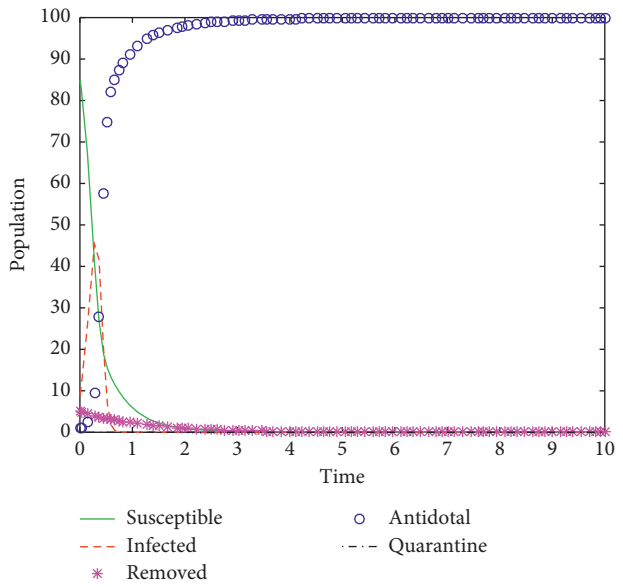

Figure 5: SIQRA with the IQ term: time evolution reaching P_1 starting with an antidotal machine.

Another way to capture the disease-free stable equilibrium P_1 is considering the same parameter values and starting with a condition without antidotal machines but with at least a quarantine one. Figure 6 shows the temporal evolution of the dynamic model for the initial conditions $(S, I, Q, R, A) = (85, 9, 1, 5, 0)$.

When the network consists only of susceptible and removed computers, it is possible to verify that even the disease-free unstable equilibrium point, P_2, is reachable for any parameter combination, because the unstable eigenvector direction (I) has been avoided. Figure 7 shows a temporal evolution starting at $S = 90$ and $R = 10$ and reaching the disease-free equilibrium P_2.

Starting without antidotal or quarantine machines, even one infected node drives the network to collapse at an endemic equilibrium point. Figure 8 shows a temporal evolution initial condition $(S, I, Q, R, A) = (99, 1, 0, 0, 0)$, reaching the endemic equilibrium point P_3.

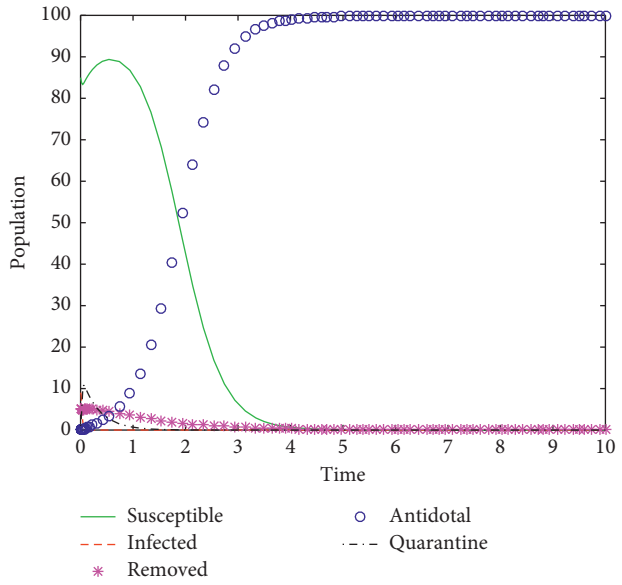

Figure 6: SIQRA with the IQ term: time evolution reaching P_1 starting with a quarantine machine.

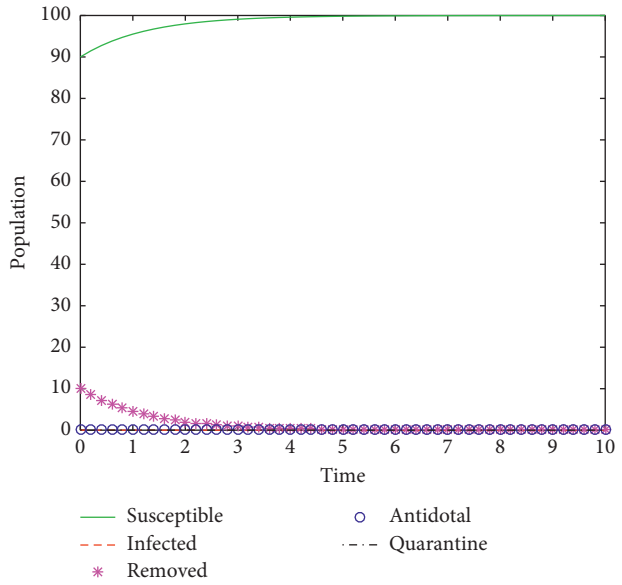

Figure 7: SIQRA with the IQ term: time evolution reaching P_2.

3.3. Simulations with Real Data. In [42], an infection control model was developed and tested by using data from cybernetic crimes in Japan networks. The population data S and I given in [42] was taken to test the SIQRA models, identifying β with the infection rate and σ with the recovering rate.

The normalization of these practical data to be compatible with the time and population scales used here gives $S_0 = 23.01$, $I_0 = 76.99$, $A_0 = 0$, $Q_0 = 0$, $R_0 = 0$, $\alpha_{SA} = 0.025$, $\beta = 7.85.10^{-11}$, $\omega = 2$, $\sigma = 8.890729.10^{-4}$, $\alpha_{IA} = 0.25$, $\delta = 9$, $\alpha_{QA} = 0.5$, and $\alpha = 0.5$. Simulating the SIQRA model without the IQ term, the results are shown in Figure 9, with the final state presenting about 10% of removed machines.

To avoid removing machines, the SIQRA model with IQ term can be used but demands at least an initial antidotal machine. Without changing parameters, Figure 10 shows the results adopting $S_0 = 22.01$, $I_0 = 76.99$, $A_0 = 1$, $Q_0 = 0$, and $R_0 = 0$.

Figure 8: SIQRA with the IQ term: time evolution reaching P_3.

Figure 9: SIQRA without the IQ term: simulation with real data.

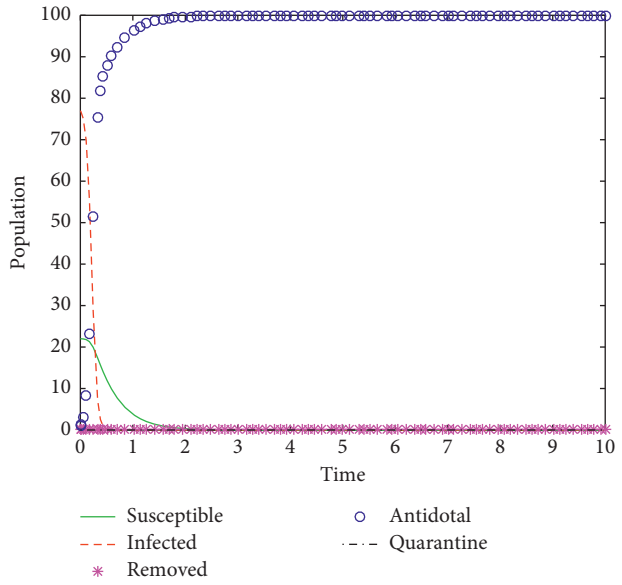

Figure 10: SIQRA with the IQ term: simulation with real data.

4. Conclusions

Classical SIR models applied to data communication systems inspired the first SIRA model, introducing antidotal nodes that supposedly improve the operational network robustness [2]. Bifurcations of equilibrium points and conditions for existence and stability of disease-free equilibrium points for the SIRA model were derived [18, 30], suggesting network design strategies.

Recently, the SIRA model showed improvement related to the practical situation considering variable populations, deriving network robustness conditions [31]. Here, the SIRA model was complemented with a quarantine strategy (SIQRA model), and the simulations indicate that network performance can be increased in the great majority of the cases and hypothesis that must be tested in real situations.

The main results regarding the SIQRA model are divided into two cases: with and without saturation condition. Saturation is about the behavior of the Q term that depends on the antivirus program capacity and the infection rate. If the antivirus detection rate is greater than the infection rate, there is no saturation. If the infection rate surpasses the antivirus detection capacity, saturation occurs.

If the Q compartment is not subjected to the possibility of saturation (no IQ term), the stable disease-free equilibrium point exists and is always reached. However, if there is any possibility of saturation (IQ term present), an initial antidotal or quarantine node is necessary. If there is neither initial antidotal nor quarantine node, even a single infected machine collapses the network.

Testing the models with real data shows that quarantine is effective to combat infection in data networks. The noninclusion of IQ terms, in spite of eliminating infected nodes, implies the removal of a certain number of machines. The inclusion of the term IQ avoids machine removal but demands the inclusion of either a quarantine or an antidotal node.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this article.

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