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Efficiency of quarantine and self-protection processes in epidemic spreading control on scale-free networks

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One of the most effective mechanisms to contain the spread of an infectious disease through a population is the implementation of quarantine policies. However, its efficiency is affected by different aspects, for example, the structure of the underlining social network where highly connected individuals as the more likely to become infected, therefore the speed of the transmission of the decease is directly determine by degree distribution of the network. Another, aspect that influences the effectiveness of the quarantine is the self-protection processes of the individuals in the population, that is, they try to avoid contact with potentially infected individuals. In this paper we investigate the efficiency of quarantine and self-protection processes in preventing the spreading of infectious diseases over complex networks with a power-law degree distribution ($P(k) \sim k^{-\nu}$) for different ν values. We propose two alternative scale-free models that result in power-law degree distributions above and below the exponent $\nu = 3$ associated with the conventional Barabási-Albert model. Our results show that the exponent ν determines the effectiveness of these policies on controlling the spreading process. More precisely, we show that for ν exponent below three, the quarantine mechanism loses effectiveness. However, the efficiency is improved if the quarantine is jointly implemented with a self-protection process driving the number of infected individual significantly lower.

Keywords: Complex networks, spread of diseases, quarantine, scale-free networks

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Infectious diseases are by far one of the leading causes of death worldwide. In this sense, one of the most effective mechanisms to contain the spread of an infectious disease in a population is the implementation of quarantine policies. However, other aspects must be considered, for example, degree distribution of the underlining social network points towards the most connected individuals as the more likely to become infected and determine the speed of the transmission of the decease. Additionally, self-protection processes influence the individuals in the population resulting on alterations in their behavior, in particular they try to avoid contact with potentially infected individuals. In this paper, we investigates the efficiency of quarantine and self-protection processes as controllers of the spreading of infections in power-law networks with degree distribution below and above the exponent of the classic Barabási-Albert model. Our results show that the efficiency of these control processes does depend directly on the exponent of the degree distribution with the quarantine being less effective in controlling the infection on networks with low degree distributions exponents. However, the inclusion of the self-protection process compensates this effect and further increases the effectiveness of the control process. These results imply that a good strategy to avoid the emergence of epidemics is the awareness of the population of its presence through social communication programs to activate a self-protection process along with the quarantine protocol.

I. INTRODUCTION

In recent years, evolutionary dynamics in complex networks have attracted the attention of researchers of different areas. In particular, with regards to their effect on the resulting dynamical features of their collective behaviors, such as synchronization or consensus[1–3]. In this sense, epidemic spreading can be modeled as a process occurring on top of a contact network with a given structure, be it fixed, time-varying, having stochastic or even multi-network features[4–7]. As such, major contributions have been made in the mathematical description of how a computer virus spreads in a network of computers, or how a rumor becomes entrenched within a social network; which in turn have impacted the way we model the spread of diseases in our population[8,10]. Moreover, the use of mathematical models better informs the determination of the control measures that need to be taken to stop a disease from spreading. A considerable number of epidemic models have been proposed, the majority of them use the concept of population compartments[11]. That is, the population is partition into different compartments accordingly to health status[4,12], for example: Susceptible (S, the group of individual that can contract the disease), Exposed (E, made of individuals that have been infected but are not infectious, that is, they are in a latent period of the disease), Infected (I, individuals that can infect susceptible individuals), and Removed (R, the part of the population that have recovered from the disease and can not become infected again or individuals that have died). The mathematical models describe the evolution of the concentrations of these compartments usually under the assumption of a fixed size population. Additionally, in several epidemic models the use of control mechanisms to contain the spread of a disease is considered. In this sense, the effect of using a vaccination or a quarantine scheme on the evolution of the disease can be evaluated in terms of the number of infected individuals after the infection process has run its course.

Classical epidemic models consider that the population is totally homogeneous[11–13]. In other words, all individuals have the same probability of contracting the disease, recover from it, or die. As such a constant average rate of infection and recovery can be use for the entire population. However, in a real scenario individuals who interact with a greater number of individuals are more likely to contract a disease than individuals that are relatively isolated from their neighbors. In short, the distribution of connection within a population has a great influence in the spreading process of a disease. For this reason, it is important to take into account the degree of interaction of each individual in determining its probability of contracting a disease. One way to incorporate the complex topology of social networks in epidemic models is to consider its degree distribution, that is, the number of connections of each node has. Recent investigation have confirm that the degree distribution of a social network is well described by a power-law $P(k) \sim k^{-\nu}$. Therefore, its characteristics can be use to establish the probability of infection for each node in the network. This allows to take into account the existence of a few "hub" individuals that concentrate a greater number and therefore are the main contributors of the spreading of the disease, while the contribution to the spread of the majority of the individuals with a relatively low number of connections is less significant. In this context, a particularly interesting investigation was reported by Liu and Zhang[17], where in order to investigate the influence of heterogeneity of the network on the epidemic spreading of a disease, the underlining social network was modeled as a scale-free network generated with the Barabási-Albert (BA) model[16]. That is, the underlining social network was modeled as a non-directed network with degree distribution that follows a power-law $P(k) \sim k^{-\nu}$ with a fixed exponent $\nu = 3$. In the work by Li *et al.*[15] the quarantine control mechanism was also considered in the epidemic model, the proposed model was called $SIQRS$, to indicate the different compartments of the population, with Q referring to the infected individuals placed in quarantine. The effectiveness of the quarantine strategy in stopping the spread of the disease was measured by the authors in terms of the density of infected nodes in steady state (I^{∞}), they showed that I^{∞} decreases as the quarantine rate increases. However, the effect that different exponents ν have on the density of infected nodes in steady state I^{∞} was not investigated. As the exponent of the degree distribution gives a clear indication of the formation of hub nodes in the network and these are the individuals that promote the spreading of the disease, it stands to reason that the degree distribution exponent is also a determining factor in the efficiency of the quarantine policy in stopping epidemic spreading. Another assumption in[15], is that only infected individuals can be quarantined. However, in a real scenario individuals tend to protect themselves by temporally avoiding contacts with infected individuals that is, individuals can quarantine themselves (*self-quarantine* process) or in other situations, the individuals can permanently disconnect from their infected neighbors (*deleting-infected-links* process).

In order to investigate the quarantine and self-protection processes effectiveness in stopping the epidemic spreading, in this paper we investigate the steady state solutions of the $SIQRS$ model over complex networks with different ν values. Considering three cases. In the first, we define quarantine as the only control action. In the second, we implement the quarantine jointly with a *self-quarantine* process. Finally, the quarantine in joint with *deleting-infected-links* process is implemented. Our results show that as the ν exponent decreases, the density of infected individuals in steady state increases for all the cases. In other words, the control mechanisms lose effectiveness as the ν exponent decreases. This is particularly significant when one consider that social networks do not have a fixed power law distribution exponent, and it definitely is not exactly equal to three[18]. However the best results are obtained when both a quarantine and a *self-protection* processes are implemented.

As mentioned above, in recent years, several works about the spread of diseases in complex networks have been published. For example, in[19], Shang *et.al.* study the effect of changes on the network structure in the spread of disease using the well known SIS model. In particular, they study the effect of the community structure over the spread. They found that, epidemics spread faster on networks with higher level of overlapping communities and degree distributions with power law exponents equals to two and three. In[5–7] the SIS model was also considered, but analyzing the effect of the awareness diffusion in the network, and they found that the awareness diffusion plays an important role in the epidemic transmission. In these published works, the numerical experiments are based in complex networks with a fixed power-law exponent equal to 2.5. In this paper, we consider that the topology is fixed during the spread and the awareness is adopted by the individuals that can be in contact with the infected. Another important difference is that we analyze the effect of different power-law exponents in the spreading dynamics of the disease. To his end, in the following Section two alternative versions of the BA model are presented which will be the basis for our investigation on the efficiency of quarantine and self-protection as control processes of the spreading dynamics

The remainder of this paper is organized as follows. An alternative scale-free network model where the degree distribution exponent can be assign to be larger or smaller that three are described in Section II. While the $SIQRS$ epidemic model along with the analysis of the effect of the underlining degree distribution is presented in Section III. Our results and numerical simulations are shown in Section IV. Finally, our results and conclusions are discussed in Section V.

II. PROPOSED NETWORK MODELS WITH A PRESCRIBED DEGREE DISTRIBUTION

In order to investigate the efficiency of the quarantine policy to contain the spread of disease on scale free networks, we propose two network models with power law degree distributions where the exponents is in the range $1 < \nu < 6$. These models are described bellow:

A. Model I. Network with an exponent less than three

In a similar way as the classical BA model, our proposed model consists of two steps:

1. **Growth:** Starting from a set of three fully connected nodes at each subsequent time step one node is added, and

2. **Preferential attachment:** In our model the links between the new node and those already existing in the network are added according to the following rules:

   a. With probability p the new node n_{new} is connected with $m = 3$ links, and with the complementary probability $1 - p$ the number of links of the new node n_{new} is taken to be the node degree of a randomly selected node in the network;

   b. The number of links determine in the previous step connect n_{new} node to different nodes already existing in the network with a probability given by

$$\Pi(n_i) = \frac{k_i}{\sum_j k_j}, \tag{1}$$

   where k_i is the degree of the node n_i and $\Pi(n_i)$ describes the probability that node n_i gets a new link.

It is work noting that (1) is similar to the attachment probability proposed in the original BA model[16]. However, by changing the number of connections our proposed model produces networks with degree distribution that follows a power-law with an exponent $\nu \leq 3$.

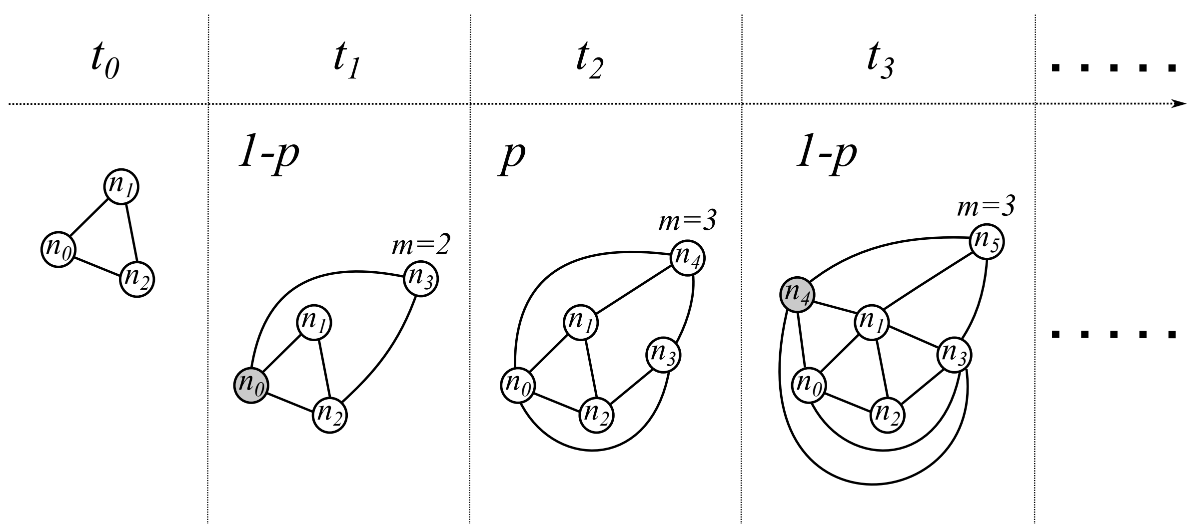

FIG. 1. Growth (from t_0 to t_3) of a network using the Model I. In the Figure the circles represent nodes of the network, the solid lines links and filled circles nodes that have been randomly selected to copy their degree for the new node.

The growth process of a network using the proposed Model 1 is shown in Figure 1. In the first time step t_0, the network consists of three nodes n_0, n_1 and n_2. In the next time step t_1, the node n_3 is added to the network lets assumed that it copies the degree from the node n_0 which is selected randomly. Then, node n_3 is connected randomly to $m = 2$ of the existing nodes in the network with probability 1. In the figure it is assumed that the node n_3 connects to nodes n_0 and n_2. In time step t_2, the node n_4 is added to the network and in this case se assume that $m = 3$, then is connected randomly to the nodes n_0, n_1 and n_3. In t_3, the node n_5 is added to the network and it is assumed that it copies the degree from the node n_4 and connects to the nodes n_1, n_3 and n_4. This process is continued for all the following time steps until the number of nodes in the network is sufficiently large and the structural properties of the network become fixed.

I order to get the behavior of the mean degree $\bar{k}$ as the network growth in the proposed model, we propose the following differential equation,

$$\frac{d\bar{k}(N)}{dN} = p\frac{2m - \bar{k}}{N} + (1-p)p\frac{2\bar{k} - \bar{k}}{N}. \tag{2}$$

with the initial condition $\bar{k}(3) = 2$, which describes the initial network of three nodes fully connected; one gets,

$$\bar{k}(N) = 2mp[\frac{1}{2p-1} - \frac{p+1}{(2p-1)p3^{2(1-p)}}N^{1-2p}]. \tag{3}$$

In Figure 2 we show the degree distribution $P(k)$ and the average degree $\langle k \rangle$ obtained from two different realizations of Model I. For each one, the network was growth to $N = 10000$ nodes. In the first realization the probability of having $m = 3$ links for each new node is set at $p = 0.3$, for the second realization the probability was $p = 0.7$. As shown in Figures 2a and 2b, the degree distribution of the generated network follows a power law with exponents $\nu \sim 1.4$ for $p = 0.3$ and $\nu \sim 2.3$ for $p = 0.7$. It is also important to mention that for $p = 0.3$ the average degree grows more rapidly than for $p = 0.7$ (see Figures 2c and 2d), this indicates that as the value of p decreases the network becomes to be more densely connected.

B. Model II: Network with an exponent larger than three

As before the network model consist of two steps. The network growths one node each time step beginning with three fully connected nodes. However, in this model each new

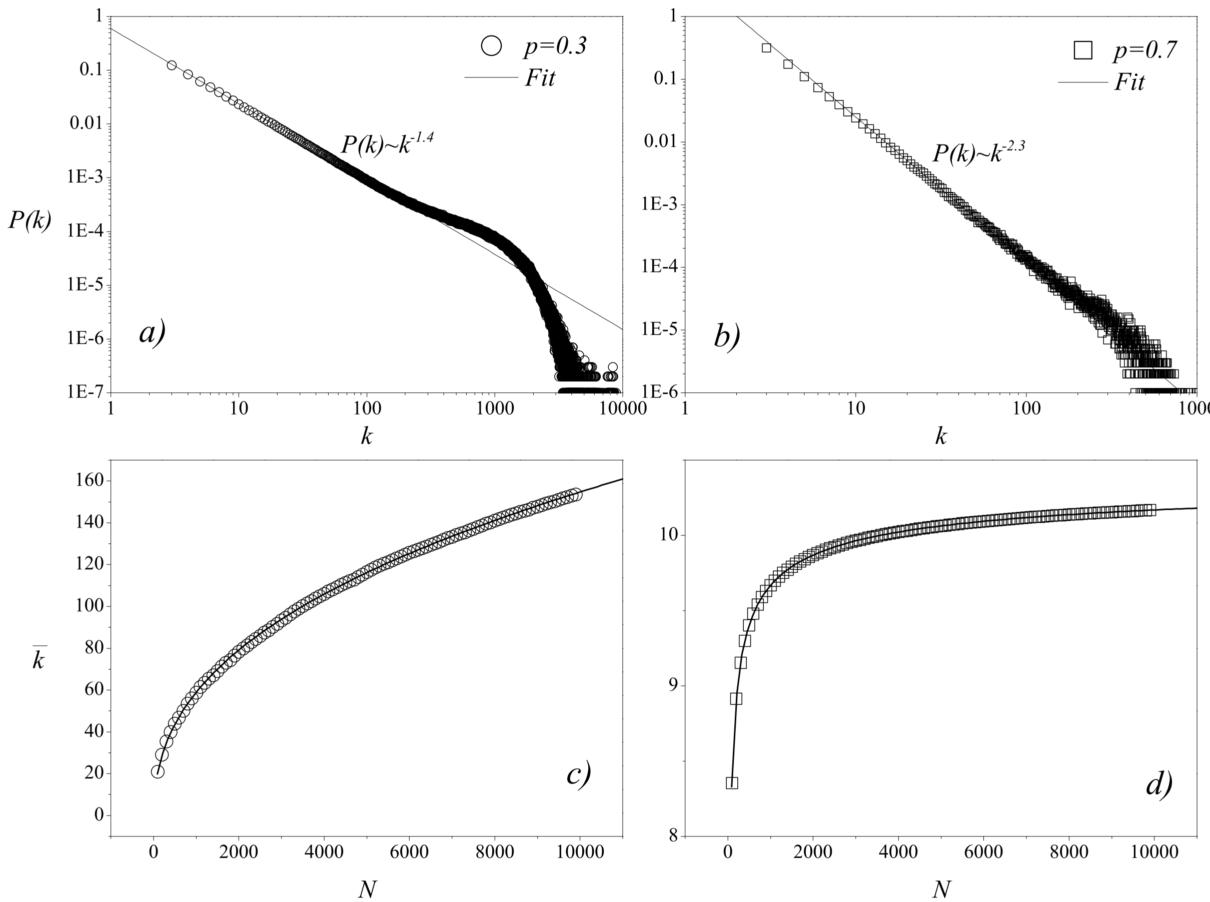

FIG. 2. a) Degree distribution and c) Average degree. Both measured at different sizes of the generated network using Model I with $p = 0.3$. b) Degree distribution and d) Average degree. Measured at different sizes of the generated network using Model I with $p = 0.7$.

node is born with the maximum number of links possible $m = 3$ and with an attractiveness factor $A \geq 0$, which is equal for all the nodes in the network. In the second step, the links of each new node are connected to different nodes already in the network using the attachment probability given by

$$\Pi(n_i) = \frac{k_i + A}{\Sigma_j (k_j + A)}, \tag{4}$$

where k_i is the degree of a node n_i and A is the initial attractiveness of the nodes in the network. Due to the addition of links is constant at each time step, the last equation can be written as:

$$\Pi(n_i) = \frac{k_i + A}{(2m + A)N}. \tag{5}$$

This version of the scale-free model is inspired by the model proposed by Dorogovtsev and Mendez[20], using the attractiveness factor A the resulting scale-free network can be make to have a degree distribution exponent $\nu \geq 3$. In order to obtain the analytical solution for $P(k)$ in this model, it is necessary to know the number Q_i of nodes with i links with respect to the total number N of nodes in the network, that is,

$$P(k) = \frac{Q_i(N)}{N} \tag{6}$$

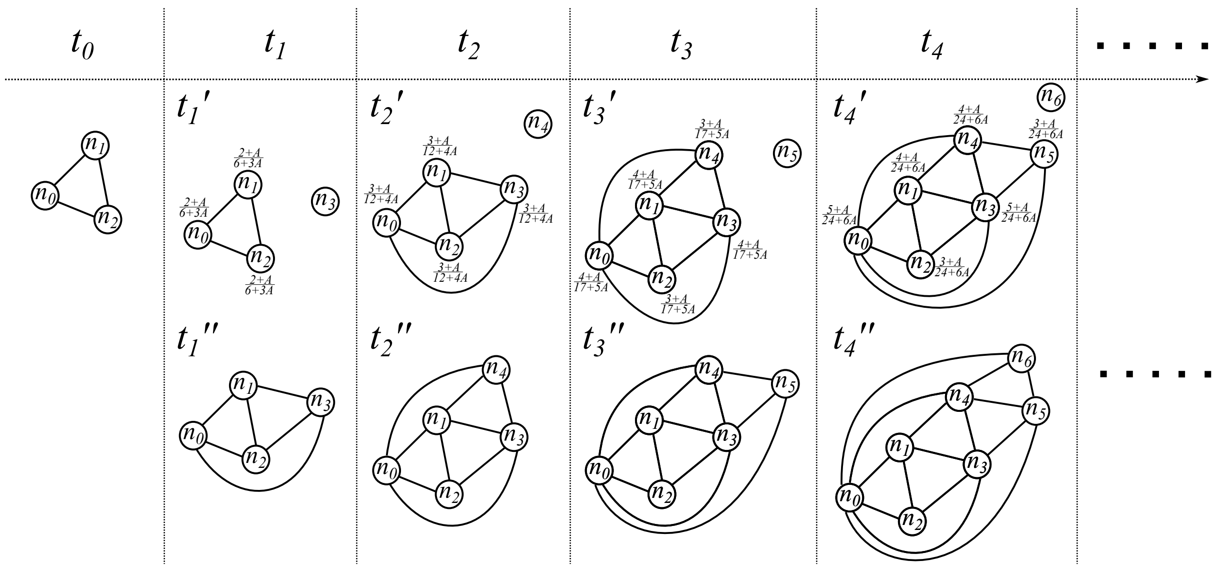

FIG. 3. Growth of a network using the Model II from t_0 to t_4. In the Figure the circles represent to the nodes of the network and the solid lines to the links. It also shows the probability Π for each node.

To get an expression for $Q_i(N)$, the continuum method[21] was employed using the following differential equation:

$$\begin{aligned}\frac{dQ_i(N)}{dN} =& m\,\frac{\overbrace{(i-1+A)Q_{i-1}(N)}^{g_1}}{(2m+A)N}\\ &-m\,\overbrace{(i-1)\frac{(i+A)Q_i(N)}{(2m+A)N}}^{g_2} + \overbrace{\delta_{i,m}}^{g_3}.\end{aligned} \tag{7}$$

The variation of the number Q_i of nodes with i links with respect to the number N of nodes in the network is described by (7). The term g_1 represents how the number of nodes with i links increases and the term g_2 describes how the number of nodes with i links decreases. Finally, the term g_3 models the effect of adding a new node with m links.

In order to obtain $Q_i(N)$, Eq. 7 is solved for $i = m$, $i = m + 1$, and so on. For $i = m$, (7) takes the form,

$$\frac{dQ_m(N)}{dN} = -\frac{m(m + A)}{(2m + A)N}Q_m + 1. \tag{8}$$

Solving (8), we obtain

$$Q_m(N) = \frac{2m + A}{m(m + A) + (2m + A)}N. \tag{9}$$

For the following i value produces:

$$\begin{aligned}
&Q_{m+1} \approx \\
&\frac{m(m + A)(2m + A)}{[m(m + A) + (2m + A)][m(m + 1 + A) + (2m + A)]}N \\
&Q_{m+2}(N) \approx \\
&\frac{m(m + A)m(m + 1 + A)(2m + A)}{[m(m + A) + (2m + A)][m(m + 1 + A) + (2m + A)]} \\
&\frac{1}{[m(m + 2 + A) + (2m + A)]}N,
\end{aligned} \tag{10}$$

with the last results we can deduce,

$$\begin{aligned}
Q_i(N) \approx& (2m + A)\frac{\prod_{x=m}^{i-1}[m(x + A)]N}{\prod_{x=m}^{i}[m(x + A) + 2m + A]} \\
\approx& \frac{(2m + A)\Gamma(2 + A + \frac{A}{m} + m)N}{m\Gamma(m + A)}(i + A)^{-(3+\frac{A}{m})}.
\end{aligned} \tag{11}$$

Then, the degree distribution $P(k)$ obtained with the proposed model has the form

$$P(k) \sim i^{-(3+\frac{A}{m})}$$

decaying as a power law with exponent $\nu \geq 3$. Another important characteristic of a growth model is to know the mean degree $\bar{k}$ as the network growth. For the model, $\bar{k}$ can be obtained solving the following differential equation,

$$\frac{d\bar{k}(N)}{dN} = \frac{2m - \bar{k}}{N}. \tag{12}$$

with the initial condition $\bar{k}(3) = 2$ that describes the initial network consisting of three nodes fully connected. Which yields,

$$\bar{k}(N) = 2m + \frac{3(2 - 2m)}{N}. \tag{13}$$

Figure 3 shows the growth of a network with the Model II. As can be seen, in the first time

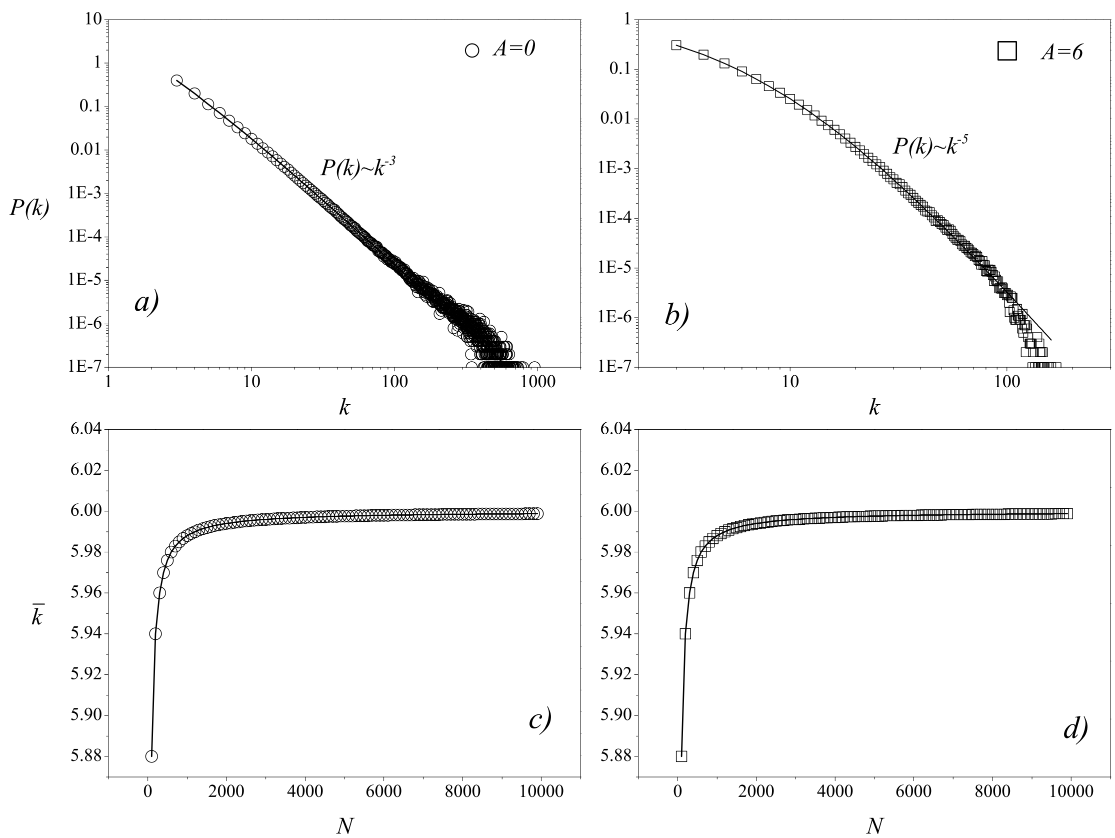

FIG. 4. a) Degree distribution and c) Average degree measured at different sizes of the generated network using Model II with $A = 0$. b) Degree distribution and d) Average degree measured at different sizes of the generated network using Model II with $A = 6$.

step t_0, the network consists of three nodes n_0, n_1 and n_2. In the next time step t_1, the node n_3 is added to the network and the probabilities from nodes in the network to get a new link from n_3 are showed in t'_1, in this case all nodes have the same probability and it is assumed that n_3 connects to all (t''). A similar process occur in t_2 and t_3. However, in t'_4 it is possible to see that difference in the probabilities of nodes n_0 to n_5 depend of the A value. That is, as the value of A becomes to be greater the probabilities for the nodes tends to be more uniform and as the network grows the emergence of hub nodes is less frequent. In Figure 4 are showed the degree distribution $P(k)$ and the average degree $\bar{k}$ obtained from two different realization of the model. Each realization of the network was grown to $N = 10000$ nodes for the first realization $A = 0$, while for the second the attractiveness value was set to $A = 6$. As shown in Figures 4a and 4b, the degree distribution of the generated network follows a power law with exponent $\nu \sim 3$ for $A = 0$ and $\nu \sim 5$ for $A = 6$. Also, it is important to mention that the average degree has the same behavior in both cases (see Figs. 4c and 4d), that is $\langle k \rangle \sim 6$ as $N \gg 1$ in both cases.

III. QUARANTINE AND *SELF-PROTECTION* PROCESSES

In this section we investigate the quarantine and *self-protection* processes efficiency to stop the epidemic spreading in networks with the structure given by Models I and II. We study three cases:

A. Quarantine as the only control action

In order to contain the spread of infectious diseases, one of the most effective control actions is the quarantine policy, that consists in isolate several infected individuals to impaired the contagion process and reduce the emergence of new infected individuals. In this section is considered an epidemic model that implements the quarantine as a control action. In particular, we focus in a *SIQRS* model and analyze its efficiency in scale-free networks with different degree distributions. In the model, it is assumed that the network consist in N nodes and each node of the network can only exist in one of the four discrete states, namely, susceptible, infected, quarantined or removed, and the infection spreads over the links of the network. Another assumption is that the population is fixed, that is, births and deaths of nodes are not considered, and thus

$$S(t) + I(t) + Q(t) + R(t) = 1, \tag{14}$$

where $S(t)$ describes the density of susceptible nodes, $I(t)$ the density of infected nodes, $Q(t)$ the density of quarantine nodes, and $R(t)$ the density of recovered nodes at time t, respectively.

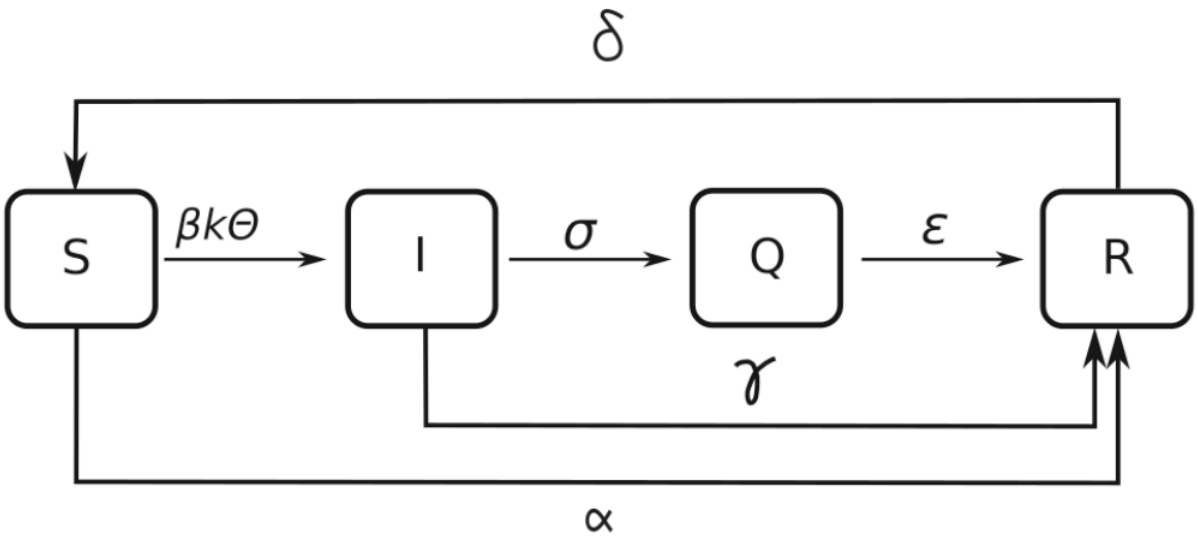

FIG. 5. Flow diagram of the *SIQRS* epidemic model.

In Figure 5 the flow diagram of the *SIQRS* epidemic model is described and the transitions between the different states are explained bellow:

S $\rightarrow$ **I** : A susceptible node is infected with probability $\beta k \theta$. In which β is the infective probability of the disease, k is the degree of the node and θ is the fraction of links over which the infection can spread. In other words, the fraction of links pointing to infected nodes. As such, a node is more likely to contract the disease as its node degree is larger.

S $\rightarrow$ **R**: Susceptible nodes become recovered (removed) with probability α. In this model we considered that several susceptible nodes have temporary immunity, ether because of vaccination or natural immunity, in either case, the immunity is only temporary.

I $\rightarrow$ **Q**: To contain the spreading of the infection, infected nodes are quarantined with probability σ.

I $\rightarrow$ **R**: Infected nodes recover spontaneously with probability γ.

Q $\rightarrow$ **R**: As a result of antiviral treatment or other mechanisms some of the quarantine nodes become recovered with probability ϵ and this gives them a temporary immunity.

R $\rightarrow$ **S**: With probability δ, nodes in the recovered state lose their temporary immunity and become again susceptible nodes.

In analyzing the dynamics of the epidemic model we consider that the probability for a node to become infected depends directly on its node degree. Additionally, since the network connectivity is heterogeneous the presence of nodes with different degrees needs to be taken into consideration. As such, it is convenient to assume that the population is organized in classes. In particular, we will consider that within each class all nodes have the same node degree k, with $k \in [m : k_{max}]$ where k_{max} is the highest node degree value for the entire network. Also, within each class, the nodes can be in only one of four different compartments, $S_k(t)$, $I_k(t)$, $Q_k(t)$ and $R_k(t)$ which represent the densities of susceptible, infected, quarantined and removed nodes with degree k at time t, respectively. Furthermore the density of susceptible, infected, quarantined and recovered nodes in the entire network is defined as:

$$S(t) = \textstyle\sum_k S_k(t)P(k), \quad I(t) = \sum_k I_k(t)P(k),$$

$$Q(t) = \textstyle\sum_k Q_k(t)P(k), \; R(t) = \sum_k R_k(t)P(k).$$

Under the assumptions described above, the mean-field reaction rate dynamical equations for class k, can be written as:

$$\begin{aligned}
\tfrac{dS_k(t)}{dt} &= -\beta k S_k(t)\theta(t) - \alpha S_k(t) + \delta R_k(t) \\
\tfrac{dI_k(t)}{dt} &= \beta k S_k(t)\theta(t) - \gamma I_k(t) - \sigma I_k(t) \\
\tfrac{dQ_k(t)}{dt} &= \sigma I_k(t) - \epsilon Q_k(t) \\
\tfrac{dR_k(t)}{dt} &= \gamma I_k(t) + \epsilon Q_k(t) + \alpha S_k(t) - \delta R_k(t)
\end{aligned} \tag{15}$$

where the fraction $\theta(t)$ of links pointing to infected nodes is given by

$$\theta(t) = \frac{\Sigma_k k P(k) I_k(t)}{\Sigma_s P(s)} = \frac{1}{\bar{k}} \Sigma_k k P(k) I_k(t). \tag{16}$$

in which $P(k)$ is the degree distribution and $\bar{k}$ is the average degree within the network and denotes the normalization factor.

In order to get the equilibrium solution in steady state, $E_+(S_k^\infty, I_k^\infty, Q_k^\infty, R_k^\infty)$, is needed make the right side of equation (7) equals to zero,

$$\begin{aligned} -\beta k S_k^\infty \theta^\infty - \alpha S_k^\infty + \delta R_k^\infty = & \; 0 \\ \beta k S_k^\infty \theta^\infty - \gamma I_k^\infty - \sigma I_k^\infty = & \; 0 \\ \sigma I_k^\infty - \epsilon Q_k^\infty = & \; 0 \\ \gamma I_k^\infty + \epsilon Q_k^\infty + \alpha S_k^\infty - \delta R_k^\infty = & \; 0 \end{aligned} \tag{17}$$

with,

$$\theta^\infty = \frac{\Sigma_k k P(k) I_k^\infty}{\bar{k}}. \tag{18}$$

Solving for S_k^∞, Q_k^∞ and R_k^∞ we obtain,

$$\begin{aligned} S_k^\infty =& \frac{\gamma + \sigma}{\beta k \theta^\infty} I_k^\infty \\ Q_k^\infty =& \frac{\sigma}{\epsilon} I_k^\infty \\ R_k^\infty =& \frac{\beta k \theta^\infty + \alpha}{\delta} S_k^\infty \\ =& \frac{(\beta k \theta^\infty + \alpha)(\gamma + \sigma)}{\delta \beta k \theta^\infty} I_k^\infty. \end{aligned} \tag{19}$$

Taking into account the normalization condition

$$S_k^\infty + I_k^\infty + Q_k^\infty + R_k^\infty = 1, \tag{20}$$

and substituting equation (19) in equation (20), we obtain for I_k^∞

$$I_k^\infty \left[\frac{\gamma + \sigma}{\beta k \theta^\infty} + \frac{\sigma}{\epsilon} + \frac{(\beta k \theta^\infty + \alpha)(\gamma + \sigma)}{\delta \beta k \theta^\infty + 1} \right] = 1, \tag{21}$$

$$I_k^\infty = \frac{\delta \beta k \theta^\infty}{\beta k \theta^\infty \left[\delta (1 + \frac{\sigma}{\epsilon}) + (\gamma + \sigma) \right] + (\gamma + \sigma)(\delta + \alpha)}. \tag{22}$$

Then, inserting equation (22) in equation (18), one gets

$$\begin{aligned} \theta^\infty =& \frac{1}{\bar{k}} \sum_k \frac{\delta \beta k^2 P(k) \theta^\infty}{\beta k \theta^\infty \left[\delta (1 + \frac{\sigma}{\epsilon}) + (\gamma + \sigma) \right] + (\gamma + \sigma)(\delta + \alpha)} \\ \triangleq& f(\theta^\infty). \end{aligned} \tag{23}$$

Obviously, the last equation has a trivial solution $\theta^{\infty} = 0$. To ensure that equation (23) has a non trivial solution, that is $0 < \theta^{\infty} \leq 1$. The following conditions must be both satisfied

$$\left[\frac{df(\theta^{\infty})}{d\theta^{\infty}}\right]_{\theta^{\infty}=0} > 1, \qquad f(1) \leq 1,$$

so, we have

$$\frac{\delta\beta}{(\alpha+\delta)(\gamma+\sigma)}\frac{\overline{k^2}}{\bar{k}} > 1$$

We can obtain the epidemic threshold β_c using the last equation as,

$$\frac{\delta\beta}{(\alpha+\delta)(\gamma+\sigma)}\frac{\overline{k^2}}{\bar{k}} > 1,$$

$$\beta > \underbrace{(1+\frac{\alpha}{\delta})(\gamma+\sigma)\frac{\bar{k}}{\overline{k^2}}}_{\beta_c}.$$

as it can be seen, the epidemic threshold β_c depends on the fluctuations in the degree distribution and mean degree of the network. And, if $\beta < \beta_c$ the epidemic disappears, in otherwise an epidemic outbreak occurs.

B. Quarantine jointly with *self-quarantine* process

In the epidemic model described before, is considered that only infected individuals can be quarantined. However, in a real scenario individuals tend to protect themselves by avoiding contacts with infected individuals temporally, we call this process *self-quarantine*. In this sense, the flow diagram of the SIQRS model is shown in Fig. 6, where η describes the probability that a susceptible individual is quarantined. Then, the mean-field reaction rate dynamical equations for class k (Eq. 15), takes the form:

$$\begin{array}{rcl} \frac{dS_k(t)}{dt} & = & -\beta k S_k(t)\theta(t) - (\alpha+\eta)S_k(t) + \delta R_k(t) \\ \frac{dI_k(t)}{dt} & = & \beta k S_k(t)\theta(t) - \gamma I_k(t) - \sigma I_k(t) \\ \frac{dQ_k(t)}{dt} & = & \sigma I_k(t) - \epsilon Q_k(t) \\ \frac{dR_k(t)}{dt} & = & \gamma I_k(t) + \epsilon Q_k(t) + (\alpha+\eta)S_k(t) - \delta R_k(t) \end{array}, \tag{24}$$

the density I_k^{∞} and the epidemic threshold, take the form:

$$I_k^{\infty} = \frac{\delta\beta k\theta^{\infty}}{\beta k\theta^{\infty}\left[\delta(1+\frac{\sigma}{\epsilon}) + (\gamma+\sigma)\right] + (\gamma+\sigma)(\delta+(\alpha+\eta))}. \tag{25}$$

$$\beta > \underbrace{(1+\frac{(\alpha+\eta)}{\delta})(\gamma+\sigma)\frac{\bar{k}}{\bar{k^2}}}_{\beta_c},$$

respectively.

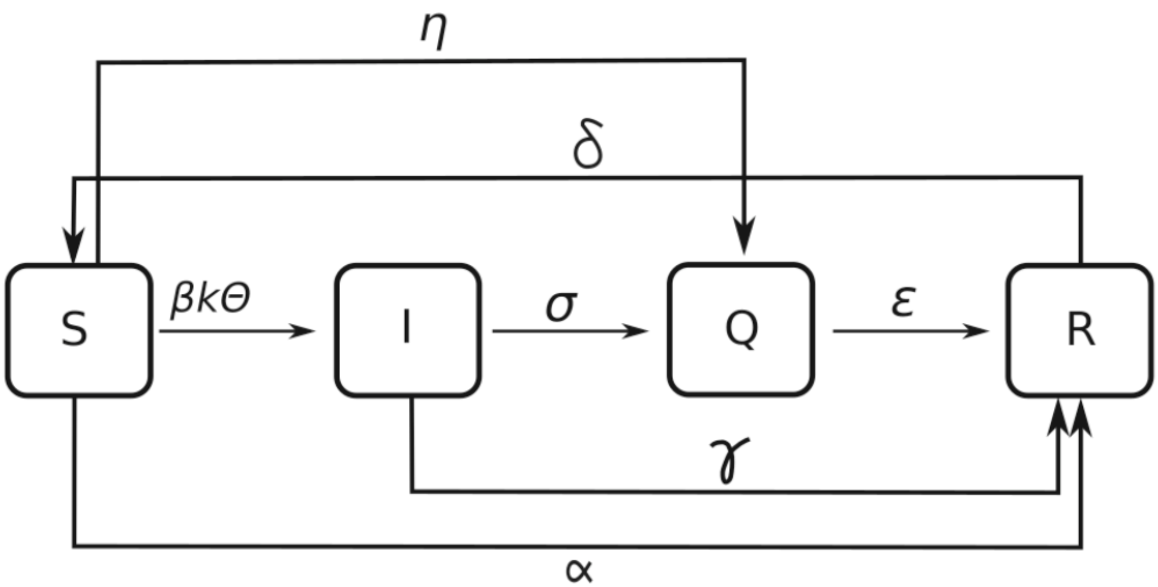

FIG. 6. Flow diagram of the *SIQRS* epidemic model including the *self-quarantine* process.

C. Quarantine in joint with ***deleting-infected-links*** process

Another process present in a real scenario is that several susceptible individuals can disconnect permanently of its neighbor infected individuals. In order to investigate the impact of this process, we include the probability ψ that one susceptible individual disconnects from its neighbor infected individuals. In this case, the flow diagram is the same of Fig. 6, but due to the fluctuation of the degree in the network, the θ probability also depends on ψ.

IV. NUMERICAL RESULTS

In order to investigate the effect of network topology on the steady state behavior of the proposed *SIQRS* epidemic models we chose the parameter set $\alpha = 0.1$, $\delta = 0.4$, $\gamma = 0.5$, and $\epsilon = 0.6$ and let the influence of the node degree and the probability of quarantine vary between $\sigma = 0, 0.2, 0.4$ and $\beta = 0.01, 0.02, ..., 0.5$, respectively. As a point of comparison, we first investigate the case with the quarantine as the only control process and using a scale-free network with degree distribution following a power-law exponent $\nu = 3$. That is, the underlining network is a realization of the classical BA model. The simulations were for networks of 10000 nodes with $m = 3$ and three values for $\sigma = 0, 0.2$ and 0.4. The dynamics of the spreading process were started with an initial infection of $I_0 = 100$ nodes, the infected nodes were selected randomly. It is important to mention that, each simulation was repeated 1000 times and averaged the results obtained are presented in Figure 7.

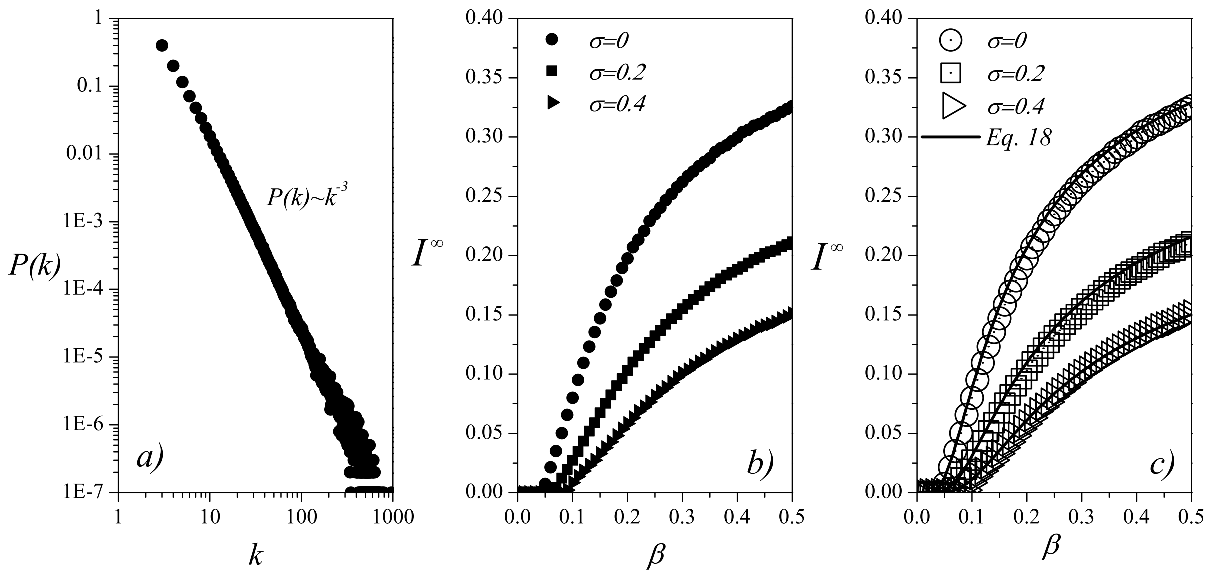

FIG. 7. a) Degree distribution of the network. b) Relation between I^{∞} and β with $\sigma = 0, 0.2$ and 0.4. c) Comparison between numerical simulations and the analytical solution given by equation (31).

In particular, Figure 7a) shows the degree distribution of the network considered in the simulations, as can be seen the degree distribution $P(k) \sim k^{-3}$ as expected for a realization of the BA model. Figure 7b) shows the relation between I^{∞} and β for three different values of $\sigma = 0, 0.2$ and 0.4. As it can be seen, as the quarantine rate σ increases, the density of infected nodes decreases for all values of β.

In order to validate the results indicated by the numerical simulations, an analytical solution is derived for $I^{\infty} = \sum_k I_k^{\infty}(t)P(k)$ using equations (22), (23) and the values of the degree distribution $P(k)$ and the average degree $\bar{k}$ of the network. For the networks generated using the BA model[16] we have:

$$P(k) \sim 2m^2k^{-3}, \qquad \bar{k} = \int_m^\infty kP(k) = 2m. \tag{26}$$

Substituting equation (26) in equation (23) we get,

$$\theta^\infty = m\theta^\infty \sum_k \frac{\delta\beta}{k\left[\beta k\theta^\infty\left[\delta(1+\frac{\sigma}{\epsilon}) + (\gamma+\sigma)\right] + (\gamma+\sigma)(\delta+\alpha)\right]}. \tag{27}$$

Integrating over all k values, results in

$$\frac{1}{m} = \beta\delta \lim_{b\to\infty} \int_m^b \frac{1}{k\left[\beta k\theta^\infty\left[\delta(1+\frac{\sigma}{\epsilon}) + (\gamma+\sigma)\right] + (\gamma+\sigma)(\delta+\alpha)\right]} dk, \tag{28}$$

and solving for θ^∞, we obtain

$$\theta^\infty = \frac{(\gamma+\sigma)(\delta+\alpha)}{m\beta\left[\delta(1+\frac{\sigma}{\epsilon}) + (\gamma+\sigma)\right]\left[e^{\frac{(\gamma+\sigma)(\delta+\alpha)}{m\beta\delta}} - 1\right]}. \tag{29}$$

Using equation (29) and (22) and integrating for all k values, we obtain for I^∞ as,

$$I^\infty = \frac{2m^2\beta\delta}{\delta(1+\frac{\sigma}{\epsilon}) + (\gamma+\sigma)} \lim_{b\to\infty} \int_m^b \frac{dk}{k^2\left[k + m\left(e^{\frac{(\gamma+\sigma)(\delta+\alpha)}{m\beta\delta}} - 1\right)\right]} dk, \tag{30}$$

$$I^\infty = \frac{2\left[m\beta\delta\left(e^{\frac{(\gamma+\sigma)(\delta+\alpha)}{m\beta\delta}} - 1\right) - (\gamma+\sigma)(\delta+\alpha)\right]}{m\beta\left(e^{\frac{(\gamma+\sigma)(\delta+\alpha)}{m\beta\delta}} - 1\right)^2\left[\delta(1+\frac{\sigma}{\epsilon}) + (\gamma+\sigma)\right]} \tag{31}$$

Figure 7c) shows that the analytical predictions 31 and the numerical simulations fit appropriately.

With the aim of analyze the effect of the network topology on the quarantine efficiency, we repeat the previous simulations but using scale-free networks with power-law exponents $\nu = 1.4, 2.3$ and 5. For the growth of these networks, we use the Model I with $p = 0.3$ and $p = 0.7$ and the Model II with $A = 6$ respectively.

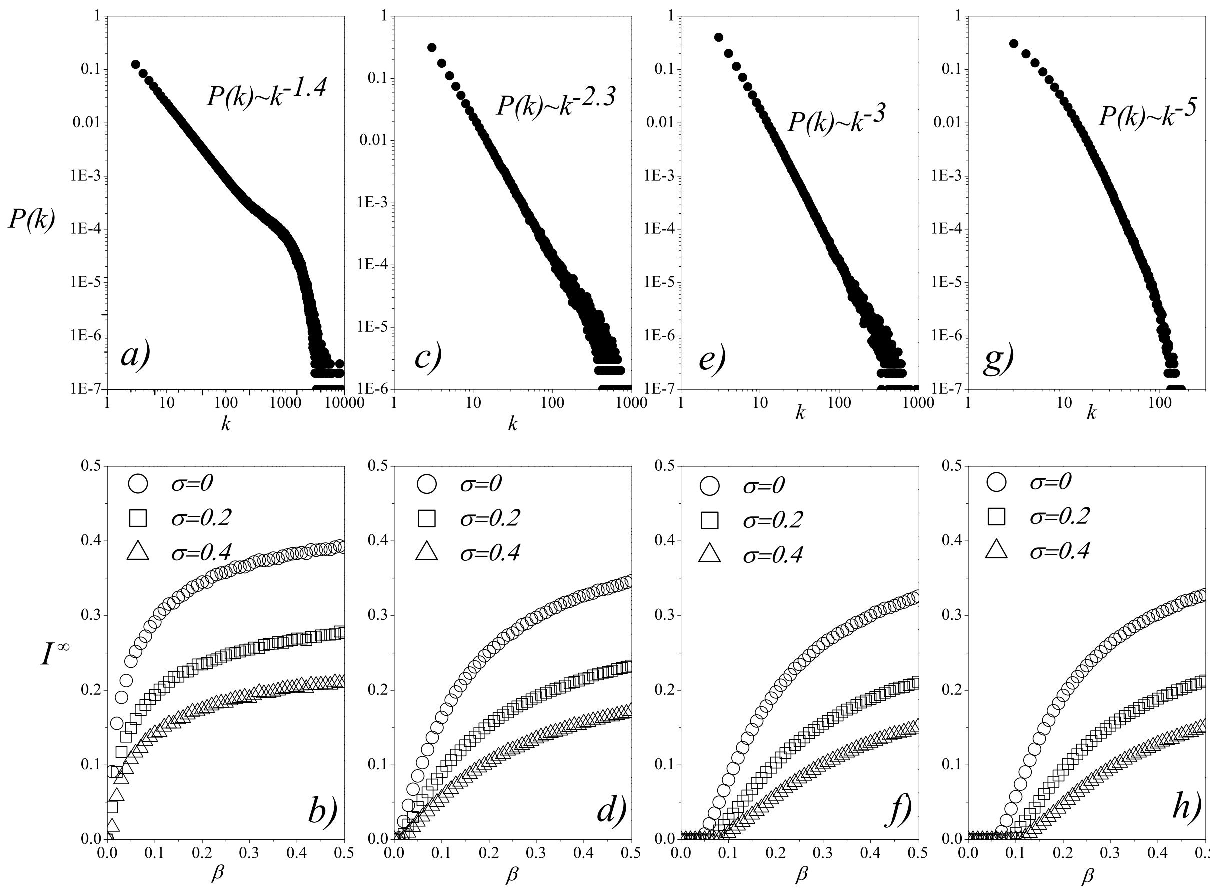

FIG. 8. Comparison of the densities I^{∞} retrieved from the simulations for different values of β, σ and ν.

In Figure 8 are shown the results of the simulations described above. In 8a and 8b are showed the degree distribution of the network with $\nu \sim 1.4$ and the relation between I^{∞} and β obtained from the *SIQRS* model over this network. Similarly, in Figs. 8c and 8d for the network with $\nu \sim 2.3$, Figs. 8e and 8f for the network with $\nu \sim 3$ and Figs. 8g and 8h for the network with $\nu \sim 5$.

As it can be seen in Figs. 8b, 8d, 8f and 8h, as the exponent ν decreases, the density I^{∞} increases significantly for all the σ values. In contrary, for $\nu = 3$ and $\nu = 5$, the density I^{∞} have a similar behavior as β increases. Another interesting phenomenon is that, for

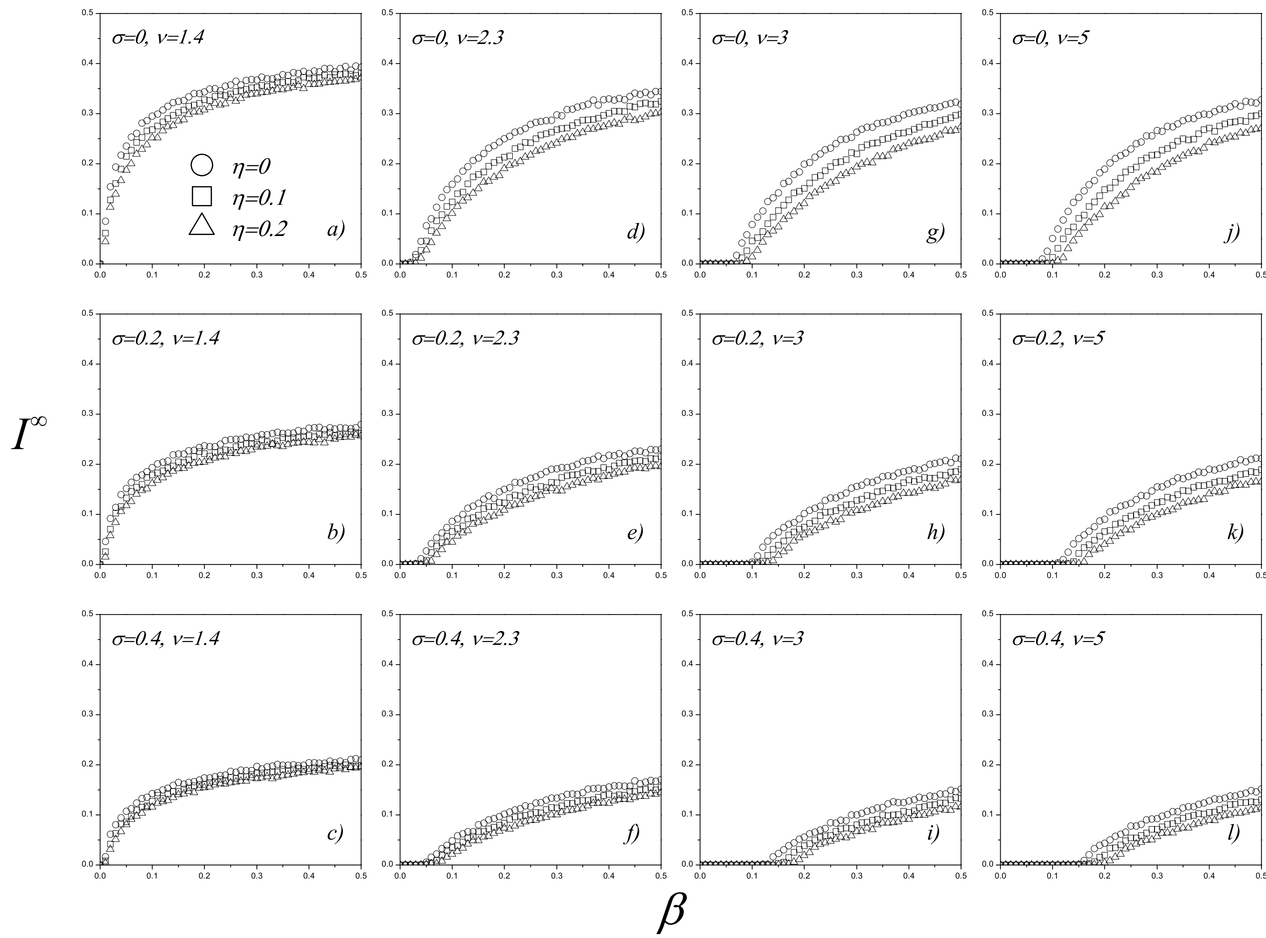

FIG. 9. Comparison of the densities I^{∞} retrieved from the simulations for different values of β, σ, ν and η.

$\nu = 5$, I^{∞} starts to grow later that for $\nu = 3$. A possible cause for this behavior is that, as the exponent ν increases, the quantity of nodes hardly connected decreases and as a consequence, the emergence of super spreader nodes is less likely for $\beta \approx 0$.

In order to investigate the efficiency of quarantine in joint with the *self-quarantine* process we reproduce the numerical simulations of the Fig. 8 including the *self-quarantine* process with $\eta = 0, 0.1, 0.2$. The results of the numerical simulations are showed in Figure 9. In Figure 9a, 9b and 9c is showed the I^{∞} obtained using the complex network with power-law exponent $\nu \sim 1.4$ defining $\sigma = 0$, 0.2 and 0.4 respectively, and with $\eta = 0, 0.1, 0.2$. Similarly for $\nu \sim 2.3$ in Figs. 9d, 9e, 9f, for $\nu \sim 3$ in Figs. 9g, 9h, 9i and for $\nu \sim 5$ in Figs. 9j, 9k, 9l. As can be seen, in all the cases the density of infected individuals decreases as the

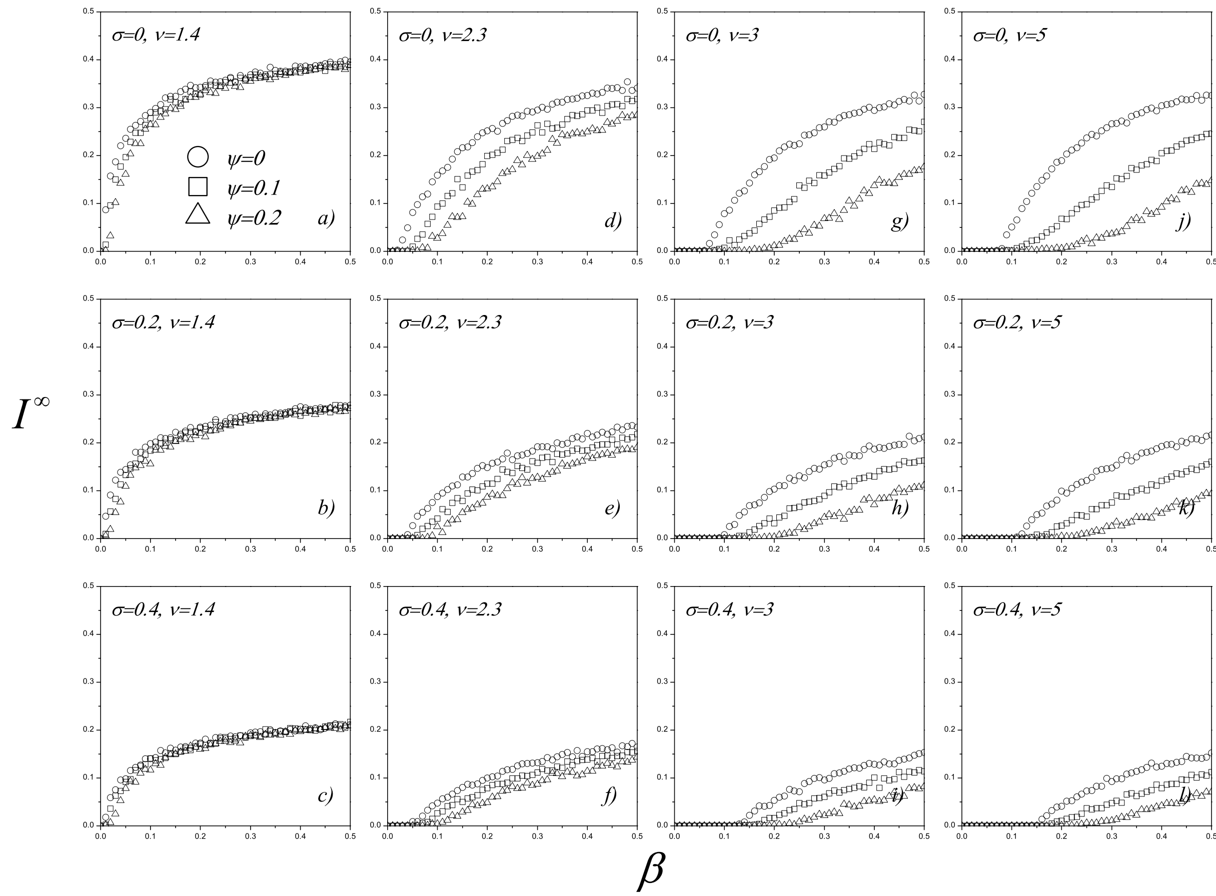

FIG. 10. Comparison of the densities I^{∞} retrieved from the simulations for different values of β, σ, ν and ψ.

η probability increases. However, the best efficiency in the contain the spread is obtained when the *self-quarantine* process and the quarantine as a global process are implemented in joint. Finally, to investigate the efficiency of quarantine in joint with the *deleting-infected-links* process we reproduce the numerical simulations of the Fig. 8 including the probability $\psi = 0, 0.1, 0.2$ in the spreading process. The results of the numerical simulations are showed in Figure 10. In Figure 10a, 10b and 10c is showed the I^{∞} obtained using the complex network with power-law exponent $\nu \sim 1.4$ defining $\sigma = 0$, 0.2 and 0.4 respectively, and with $\psi = 0, 0.1, 0.2$. Similarly for $\nu \sim 2.3$ in Figs. 10d, 10e, 10f, for $\nu \sim 3$ in Figs. 10g, 10h, 10i and for $\nu \sim 5$ in Figs. 10j, 10k, 10l. As can be seen, in all the cases the density of infected individuals decreases as the ψ probability increases. However, the best efficiency in the contain the spread is obtained when the *deleting-infected-links* and the quarantine as a

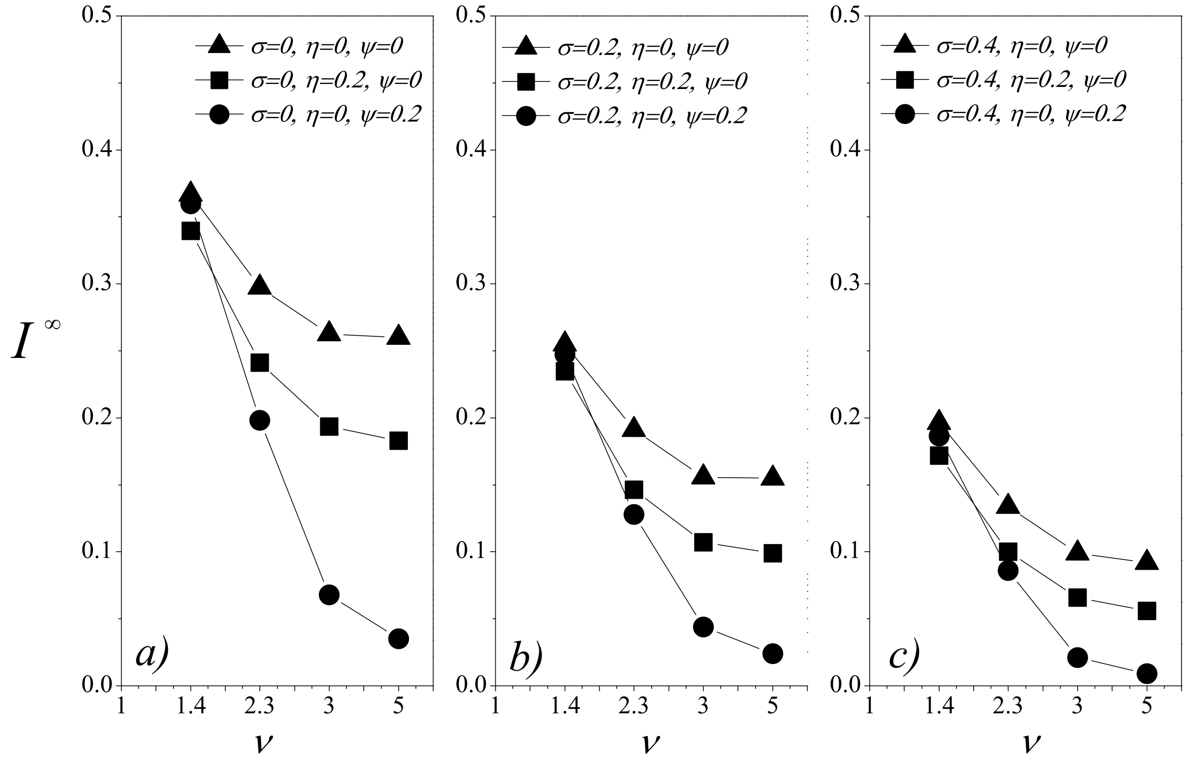

FIG. 11. Relation between the density I^{∞} and the power-law exponent ν for $\beta = 0.3$, and different values for σ, η and ψ.

global processes are implemented together. The previous results indicate that quarantine is an effective measure to contain the spread of a disease, however its effectiveness increases if it is combined with the implementation of some *self-protection* process by the individuals of the population. Figure 11 shows a clearer view of this conclusion. That is, in Fig. 11 is showed the relation between the density I^{∞} and the power-law exponent ν of the degree distribution in the network. From the figure, it is possible to see that the worst efficiency (solid triangles) is obtained when the quarantine is defined as the only control action. However, when it is combined with *self-protection* processes as the *self-quarantine* (solid squares) and *deleting-infected-links* (solid circles) processes the best efficiency is obtained.

V. CONCLUDING REMARKS

In summary, in this paper we have investigated the efficiency of the quarantine policy in networks with different topologies. More precisely, we have proposed a *SIQRS* epidemic model and we measured the density of infected individuals in steady state generated with that model in networks with degree distribution following a power-law $P(k) \sim k^{-\nu}$ with different ν values. We found that the efficiency of the *SIQRS* model is strongly related with the ν value. More exactly, we found that as the exponent ν decreases lower three, the efficiency of the quarantine decreases. Also, in this paper we investigated the efficiency of the quarantine in joint with *self-protection* processes and we found that the addition of self-protection process improves the efficiency in containing the spread of the decease. That is, the density of infected individuals in steady state considerably reduces. This result implies that the awareness of the population through social health programs can be a good strategy to reduce the number of infected individuals during the spread of a disease.

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