

# Stability analysis for virus spreading in complex networks with quarantine and non-homogeneous transition rates

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**Abstract.** Virus propagations in complex networks have been studied in the framework of discrete time Markov process dynamical systems. These studies have been carried out under the assumption of homogeneous transition rates, yielding conditions for virus extinction in terms of the transition probabilities and the largest eigenvalue of the connectivity matrix. Nevertheless the assumption of homogeneous rates is rather restrictive. In the present study we consider non-homogeneous transition rates, assigned according to a uniform distribution, with susceptible, infected and quarantine states, thus generalizing the previous studies. A remarkable result of this analysis is that the extinction depends on the weakest element in the network. Simulation results are presented for large free-scale networks, that corroborate our theoretical findings.

## 1. Introduction

The virus or disease propagation models are important because it is possible to extend their use in other areas, for example, the spreading of rumors or data in computers networks [3, 5, 6], and the analysis of these models allow us to apply certain policies or mechanisms, in order to control the spread of a disease.

A common method to combat the spread of a disease is the isolation of individuals who are infected, by placing them in a state of Q-Quarantine, which is added to the well-know models SI or SIS [1, 2]. For example SIQS, SIQR and SEIQR models are presented in [6, 8, 7], where every individual in the population is classified according to the disease status with homogeneous transition parameters, and where system's thresholds, equilibrium points and their stability are discussed. However, in this paper we consider the model SIQS, where individual states are modeled by a discrete-time Markov chain, but with non-homogeneous transition probabilities. As long as complex networks theory allows exploring the dynamics of propagation in structures generated by relationship established between individuals, we will follow this approach studying any kind of network but taking, in the simulations, the particular case of a network in which nodes' degree follows a Power-Law distribution according to the algorithm proposed in [4]. Besides our theoretical work, simulations are performed in order to corroborate our findings.

The paper is organized as follows: In Section 2, the mathematical model SIQS process is introduced. In Section 3 global extinction conditions are derived. In Section 4, numerical



simulations are presented that corroborate our theoretical results. Finally, conclusions are presented in Section 5.

## 2. SIQ Model

Consider the SIQS model for virus spread in complex network of  $N$  individuals or nodes, as described in [8], but adapted for each individual  $i$  in the network ( $i = 1, 2, \dots, N$ ), as shown in the state diagram in Fig. 1. The transitions between states depend of non-homogeneous parameters, which are described below for each individual  $i$  of the network where:  $\mu_i$  is the recovery probability,  $\tau_i$  is the probability that  $i$  enters quarantine, and  $\zeta_i$  is the probability that  $i$  is not being infected by interacting with its neighbors.

The interactions consist that in each time step, the node  $i$  will perform  $\lambda_i$  average attempts to contact with probability  $\gamma_i$  with each of its neighbors. The nodes  $i$  and  $j$  may be in quarantine at time  $t$  with probability  $q_i(t)$  and  $q_j(t)$  respectively, so that the probability of contact on each attempt would be given by  $\eta_{ij}(t) = \gamma_i(1 - q_i(t))(1 - q_j(t))$ . Therefore, the probability of  $i$  performing at least one contact is given, according to a binomial distribution, by

$$r_{ij}(t) = 1 - [1 - \eta_{ij}(t)]^{\lambda_i}. \quad (1)$$

The probability that the node  $i$  is being infected due to contact with  $j$  is given by  $1 - \beta_i r_{ij}(t) p_j(t)$ , where  $p_j(t)$  is the probability that the node  $j$  is infected at time  $t$ . Considering that the interactions between  $i$  and its neighbors are independent, the probability that  $i$  is not infected by its neighbors is

$$\zeta_{ij}(t) = \prod_{i=1}^N [1 - a_{ij} \beta_i r_{ij}(t) p_j(t)], \quad (2)$$

where  $a_{ij}$  are the entries of the adjacency matrix  $A \in \mathbb{R}^{N \times N}$  that represents the existing connections between the  $N$  nodes of the network. According to the transitions diagram (see Fig. 1), the following mathematical model is obtained:

$$\begin{aligned} p_i(t+1) &= (1 - \tau_i) p_i(t) + (1 - \zeta_i(t))(1 - q_i(t) - p_i(t)), \\ q_i(t+1) &= \tau_i p_i(t) + (1 - \mu_i) q_i(t), \quad i = 1, 2, \dots, N, \\ 1 &= s_i(t+1) + p_i(t+1) + q_i(t+1), \end{aligned} \quad (3)$$

where  $s_i(t)$ ,  $p_i(t)$  and  $q_i(t)$  are the probability of being susceptible, infected and in quarantine at time  $t$ , respectively.

To determine the fixed points of the system of equations (3) for each node  $i$ , substitute  $p_i(t+1) = p_i(t) = p_i$ ,  $q_i(t+1) = q_i(t) = q_i$ ,  $s_i(t+1) = s_i(t) = s_i$ , and obtain after some algebra

$$[p_i, q_i, s_i]^T = \left( \frac{1}{1 + (1/\tau_i + 1/\mu_i)\omega_i} \right) \left[ \frac{\omega_i}{\tau_i}, \frac{\omega_i}{\mu_i}, 1 \right]^T, \quad \omega_i = 1 - \zeta_i. \quad (4)$$

From equation (4), we identified two solutions: the parameter independent extinction state  $[0, 0, 1]^T$  given by  $\omega_i = 0$ , and the parameter dependent endemic state  $0 < \omega_i \leq 1$ .

## 3. System dynamics

We are interested in determining the conditions for which the extinction state  $[p_i, q_i, s_i]^T = [0, 0, 1]^T$  is a global attractor for any node  $i$ . First, we consider the following bound

$$1 - \zeta_{ij}(t) \leq \sum_{j=1}^N a_{ij} \beta_i r_{ij}(t) p_j(t). \quad (5)$$

proved in [9, 10] and then determine a linear dynamics that bounds the nonlinear dynamics given by (3). Doing so leads take following result

**Theorem 1.** The extinction state of the SIQS model (3), is a global attractor for any node  $i$  of network, if the following condition holds

$$\sigma(S) \in \{\lambda \in \mathbb{C} : |\lambda| < 1\}, \quad \mu_i > 0, \quad (6)$$

where  $S = I_N - T + BA$ ,  $T = \text{diag}(\tau_i)$ ,  $B = \text{diag}(\beta_i)$ , and  $\sigma$  denotes the spectrum of a matrix.

**Proof:** Substitute (5) and (1) into the first equation of (3)

$$\begin{aligned} p_i(t+1) &\leq (1 - \tau_i)p_i(t) + \sum_{j=1}^N a_{ij}\beta_j p_j(t) \left(1 - [1 - \eta_{ij}(t)]^{\lambda_i}\right) \left(1 - p_i(t) - q_i(t)\right) \\ &= (1 - \tau_i)p_i(t) + \sum_{j=1}^N a_{ij}\beta_j p_j(t) \left(1 - p_i(t) - q_i(t) - [1 - \eta_{ij}(t)]^{\lambda_i} (1 - p_i(t) - q_i(t))\right) \\ &\leq (1 - \tau_i)p_i(t) + \beta_i \sum_{j=1}^N a_{ij}p_j(t). \end{aligned}$$

Accordingly the solutions of (3) are bounded by the solutions of the linear dynamics

$$\begin{bmatrix} p(t+1) \\ q(t+1) \end{bmatrix} \leq \begin{bmatrix} S & 0 \\ T & M \end{bmatrix} \begin{bmatrix} p(t) \\ q(t) \end{bmatrix} = \mathbf{A} \begin{bmatrix} p(t) \\ q(t) \end{bmatrix}, \quad (7)$$

where  $M = \text{diag}(1 - \mu_i)$ ,  $p(t) = [p_1(t), \dots, p_N(t)]^T$  and  $q(t) = [q_1(t), \dots, q_N(t)]^T$ . The linear dynamics given by the matrix  $\mathbf{A}$  are asymptotically stable if and only if  $\sigma(\mathbf{A}) \in \{\lambda \in \mathbb{C} : |\lambda| < 1\}$ , but due to the triangular form of the matrix  $\mathbf{A}$ , it is sufficient that

$$\sigma(S) \in \{\lambda \in \mathbb{C} : |\lambda| < 1\}, \quad \text{QED.}$$

For our purposes, we suppose that  $\tau$  and  $\beta$  are distributed uniformly in the complex network, such that  $\tau_i \in [\tau_{\min}, \tau_{\max}]$  and  $\beta_i \in [\beta_{\min}, \beta_{\max}]$ ,  $i = 1, 2, \dots, N$ . Then, for any vector  $p = [p_1, p_2, \dots, p_N]^T$ , the  $i$ th entry of the product  $Sp$  is given by

$$[Sp]_i = (1 - \tau_i)p_i + \beta_i \sum_{j=1}^N a_{ij}p_j \leq (1 - \tau_{\min})p_i + \beta_i \sum_{j=1}^N a_{ij}p_j \leq (1 - \tau_{\min})p_i + \beta_{\max} \sum_{j=1}^N a_{ij}p_j. \quad (8)$$

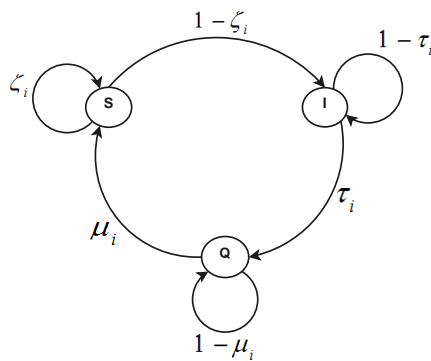
Note that we have bounded (7) more strictly. Taking the second term and according to the Theorem 1, it is sufficient to consider  $\sigma(S)$  for  $T = \tau_{\min}I_N$ , and therefore  $\tau_{\min} > \rho(BA)$ , where  $\rho(\cdot)$  is the spectral radius. Finally, doing the same for the third term in the inequality, it is sufficient to consider  $\sigma(S)$  for  $T = \tau_{\min}I_N$  and  $B = \beta_{\max}I_N$ , and therefore  $\tau_{\min} > \beta_{\max}\rho(A)$ .

The inequality (8) says that  $\tau_{\min}$  and  $\beta_{\max}$  play an important role for the conditions of (3), bounded by linear dynamics (7). These conditions are summarized as follows: *i*)  $\rho(\mathbf{A}) > 1$ , *ii*)  $\tau_{\min} > \rho(BA)$  and *iii*)  $\tau_{\min} > \beta_{\max}\rho(A)$ . The first one is a necessary condition, while the others are sufficient conditions to assure the extinction state of the system (3) be a global attractor.

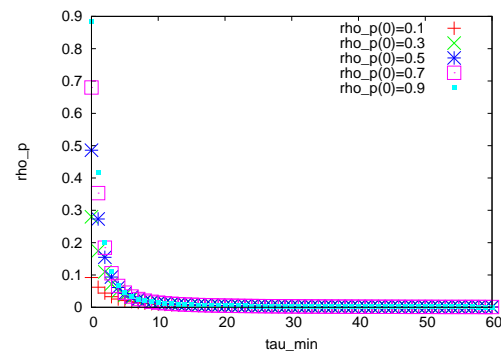
#### 4. Experiments

We performed a set of simulations of (3) on a complex network generated according to [4], with  $m_o = 5$  and  $m = 2$ . As it been above, it seems that the recovery probability  $\mu_i$  and the average number of attempts to contact a neighbor don't play an important role in the dynamics of (3), so we considered  $\mu_i = 0.5$ ,  $\lambda_i = 10000$  (simulating *reactive process*), and  $\beta_i \in (0.055, 0.065)$  distributed uniformly. For our matrix  $A$ ,  $\rho(A) = 8.3439$ , therefore  $\tau_{\min} > 0.542$ . However  $\rho(BA) = 0.508$ , so that  $\tau_{\min} > 0.508$ , as it is shown in figures 2 and 3 for several initial conditions. In all figures, we used  $\rho_p(t)$  and  $\rho_q(t)$  that represent the average probability of finding an individual infected or in quarantine respectively. To be more precise, consider  $\rho_p(t) = \frac{1}{N} \sum_{i=1}^N p_i(t)$ .

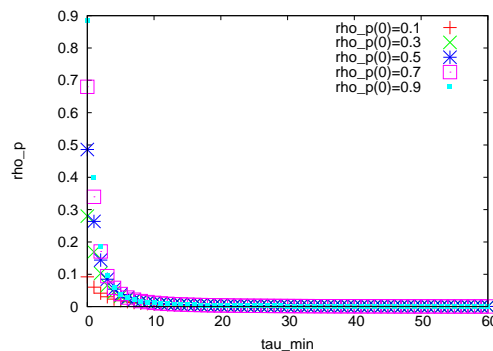
Although Fig. 2 and 3 show that the system given by (3) reaches the extinction state, if we take a value of  $\tau_{\min} < 0.508$ , for example  $\tau_{\min} = 0.480$ , the system also reaches the extinction state. To illustrate this case in Fig. 4, the response for several values of  $\tau_{\min}$  are shown. Note that  $\tau_{\min}$  is a bifurcation parameter with threshold  $\tau_{\min_c} \approx 0.43$ , as it can see from Fig. 4.



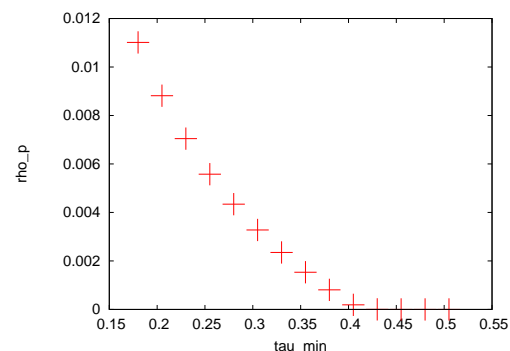
**Figure 1.** State transition diagram associated to the SIQS model.



**Figure 2.** For all curves,  $\rho_q(0) = 0.1$ ,  $\tau_{min} > 0.542$  and  $\tau_{max} < 0.570$ .



**Figure 3.** For all curves,  $\rho_q(0) = 0.1$ ,  $\tau_{min} > 0.508$  and  $\tau_{max} < 0.570$ .



**Figure 4.**  $\rho_p$  vs  $\tau_{min}$  for large values of  $t$ .

## 5. Conclusions

We analyzed the stability of the extinction state of virus spreading in a complex network with Power-Law connectivity, quarantine mechanism, and non-homogeneous state transition probabilities. Sufficient conditions for the stability of the extinction state are obtained, in terms of the weakest individuals given by their probability putting in quarantine ( $\tau_{min}$ ) and the probability of infection ( $\beta_{max}$ ). However, the necessary condition provides a greater margin, being  $\tau$  the only bifurcation parameter in our analysis, from which the system reaches the extinction state or endemic state.

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