



# Output-Feedback Control of Virus Spreading in Complex Networks With Quarantine

### Luis A. Alarcón-Ramos<sup>1</sup>, Roberto Bernal Jaquez<sup>2\*</sup> and Alexander Schaum<sup>3</sup>

<sup>1</sup> Posgrado en Ciencias Naturales e Ingeniería, Universidad Autónoma Metropolitana-Cuajimalpa, Mexico City, Mexico, <sup>2</sup> Departamento de Matemáticas Aplicadas y Sistemas, Universidad Autónoma Metropolitana-Cuajimalpa, Mexico City, Mexico, <sup>3</sup> Chair of Automatic Control, Kiel-University, Kiel, Germany

OPEN ACCESS

### Edited by:

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Songting Li, New York University, United States Shao-Bo Lin, Wenzhou University, China

### \*Correspondence:

Roberto Bernal Jaquez rbernal@correo.cua.uam.mx

#### Specialty section:

This article was submitted to Mathematics of Computation and Data Science, a section of the journal Frontiers in Applied Mathematics and Statistics

> Received: 06 April 2018 Accepted: 12 July 2018 Published: 08 August 2018

#### Citation:

Alarcón-Ramos LA, Bernal Jaquez R and Schaum A (2018) Output-Feedback Control of Virus Spreading in Complex Networks With Quarantine. Front. Appl. Math. Stat. 4:34. doi: 10.3389/fams.2018.00034 In this paper the problem of designing an output-feedback control for the stabilization of the extinction steady-state in a virus spreading process over a complex network with quarantine is considered. Sufficient conditions are established for the choice of those nodes for which sensor information is necessary and those which should be controlled using notions from constructive control theory. A simple output-feedback control is proposed which exponentially stabilizes the extinction state. Numerical simulation results are provided to illustrate the functioning of the proposed control scheme for a scale-free network of  $N = 10^6$  nodes.

Keywords: complex networks, virus spreading, feedback control, quarantine, sensor location

# **1. INTRODUCTION**

Studies on the propagation and control of viruses and infectious diseases in human and animal populations [1-8] have gained a great importance in the last years. Understanding and controlling spreading processes is a problem of interdisciplinary nature [9-12]. The use of mathematical and physical inspired models that give account of the dynamics of propagation of infections have gained acceptance since the London cholera epidemics in September 1853 when John Snow divided a map of London into sectors (in a way, nowadays, equiparable to a Voronoi diagram) to calculate who was most likely to use each water pump in the city and in this way, discovered that the 40 Broad Street pump was the main focus of the cholera infection.

Some decades later, McKendrick [13] and Kermack and McKendrick [14] proposed the SIR model that divides the population in three different compartments or groups of individuals: Susceptible, Infective, and Recovered (or Removed) that had the disease and become immune or died. This pioneering work gave birth to the SIS (Susceptible-Infected-Susceptible) model mainly because many diseases do not confer any immunity. Extensions such as the SIQ (Susceptible-Infected-Quarantine) model (see e.g., [15–17]) appeared in order to account for the dynamics of the spreading of infectious disease. Accordingly, a new class of quarantined individuals is included. These individuals are removed, with some probability from the class of infected individuals.

Although these models were proposed for modeling spreading in populations with no structure, nowadays the SIS and SIQ models have been extended to model the spreading process in a population mapped on a complex network.

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In recent years, Markov-chain based models for a Susceptible-Infected-Susceptible (SIS) dynamics over complex networks have been used [4–8, 18] to describe spreading processes in networks. Using these models, it is possible to determine the macroscopic properties of the system as well as the description of the dynamics of individual nodes. One interesting result is that the calculated infection threshold depends on the value of the spectral radius of the adjacency matrix, thus relating the network structure with spreading behavior.

In the present work we will study the spreading of diseases using a Markov-chain based model for a Susceptible-Infected-Quarentine (SIQ) dynamics over a complex network that has been used in a simplified version for the determination of stability tresholds in recent studies by the authors [15, 17]. We will show that, even when the built-in control strategy of quarantine is not able to ensure virus extinction, it is always possible to solve the problem of epidemic spreading extinction. In order to accomplish this task, we determine sufficient conditions for stabilizing the extinction state in a complex network of arbitrary topology. One remarkable point is that, these conditions give a clue to identify the nodes that do not need any control to reach the extinction state and distinguish them from the nodes that need to be controlled. Inspired on the ideas of control theory, the set of nodes that do not need to be controlled (in order to reach the extinction state) will be associated with the zero dynamics of the system [19, 20]. At the same time, the set of nodes to be monitored and controlled will be identified and a decentralized feedback control will be applied in order to stabilize the extinction state. Accordingly, it is proven that the extinction state is an exponentially stable fixed point for the zero dynamics.

We have performed numerical simulations using a scalefree complex network with 1 million nodes constructed as proposed by Barabasi [21] and found a complete agreement of the numerical results with our theoretical findings.

The paper is organized as follows: section Methods presents the problem statement for the SIQ model mapped on a complex network of arbitrary topology and the control problem we want to solve together with some definitions. In section Results, sufficient conditions for the stabilization of the extinction state are derived. Using these conditions we establish a selection criterion that allows to identify the set of nodes that need to be controlled in order to reach the extinction state. Afterwards, we design a simple stabilizing output-feedback control and present our simulation results. In section Discussion and Conclusions we summarize our main results and present our main conclusions.

## 2. METHODS

As pointed out in the introduction, the SIQ model belongs to a class of models that are used to capture possible human interactions employed to impede the spreading of an infection process and it is essentially an extension of the SIS model in which the model and control strategies are co-developed to yield a kind of closed-loop control model [22]. In order to reveal the dynamics and essential mechanisms of this model, we proceed to (i) formulate the SIQ model in a complex network (ii) introduce the specific control problem.

## 2.1. The SIQ Model in a Complex Network

Consider a network of *N* nodes described by an undirected graph G(V, E) of any topology. Let  $V = \{v_1, v_2, ..., v_N\}$  being the set of nodes and  $E = \{e_{i,j}\}$  the set of connecting edges. The adjacency matrix associated to G(V, E) is given by  $A = \{a_{ij}\}$ , where  $a_{ij} = 1$  if  $e_{i,j} \in E$  and zero otherwise. The set of neighbor nodes of a node  $v_i \in V$  is defined as

$$V_i = \{ v_j \in V \mid a_{ij} = a_{ji} = 1 \} \subset V, \tag{1}$$

and the number of neighbors or degree of a node  $v_i$  is given by  $N_i = |V_i|$ .

As formulated in Bernal Jaquez et al. [15], the underlying process for every node is depicted in **Figure 1**, as a discrete time Markov process. A node  $v_i$  can be in state I (Infected) with probability  $p_i(t)$ , in state Q (Quarantine) with probability  $q_i(t)$ , or in state S (Susceptible) with probability  $s_i(t) = 1 - p_i(t) - q_i(t)$ . At each time step, the probability functions  $p_i(t)$ ,  $s_i(t)$  are updated due to the fact that every node can transit from state S to state I with probability  $1 - \zeta_i$  or from state I to state Q with probability  $\tau_i$  and from state Q to state S with probability  $\mu_i$  because nodes are interacting.

According to the transition diagram shown in **Figure 1**, we have the following dynamical system:

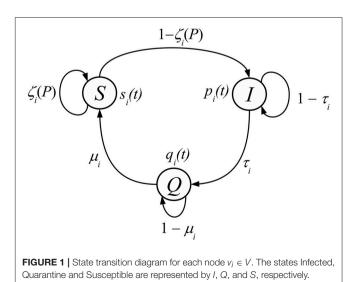
$$p_{i}(t+1) = (1 - \tau_{i})p_{i}(t) + (1 - \zeta_{i}(P(t)))s_{i}(t),$$

$$q_{i}(t+1) = (1 - \mu_{i})q_{i}(t) + \tau_{i}p_{i}(t),$$

$$s_{i}(t+1) = \zeta_{i}(P(t))s_{i}(t) + \mu_{i}q_{i}(t).$$

$$p_{i}(t) + q_{i}(t) + s_{i}(t) = 1, \quad v_{i} \in V,$$
(2)

where, for every node  $v_i \in V$ ,  $\tau_i$  is the internment probability associated to quarantine,  $\mu_i$  is the recovery probability and



 $\zeta_i(P(t))$  is the probability of a node  $v_i$  of not being infected by any neighbor at time *t*, which is given by

$$\zeta_i(P(t)) = \prod_{j=1}^N (1 - \beta_i r_{ij} a_{ij} p_j(t)).$$
(3)

In the above equation, we have defined the vector  $P(t) = [p_1(t), p_2(t), ..., p_N(t)]^T \in [0, 1]^N$  and  $\beta_i$  is the probability of infection during a single contact,  $r_{ij}$  is the probability that the node  $v_i$  performs at least one contact intent with its neighbor  $v_j \in V_i$ . The probability  $r_{ij}$  is also known as the connection probability and depends on the number of contact intents (or interaction rate).

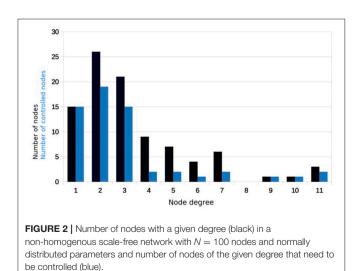
Note that in system (2)

$$0 \leq \mu_i, \tau_i, r_{ij}, \beta_i, \zeta_i(P(t)), p_i(t), q_i(t), s_i(t) \leq 1$$

From the model (2) we point out that

- Unlike the model proposed in Bernal Jaquez et al. [15] the system (2) considers non-homogeneous properties given by μ<sub>i</sub>, τ<sub>i</sub>, β<sub>i</sub> and r<sub>ij</sub>.
- Quarantine is a control mechanism which is introduced in order to prevent virus spreading, however it could probably not be sufficient for achieving the extinction state, depending on the stability conditions (to be determined below). We can consider, instead, the objective of this work to design a controller to stabilize the extinction state, e.g., by adapting inherent propagation parameters like the propability of infection  $\beta_i$  of some nodes to be specified.

We consider that each node has a manipulable variable  $u_i(t)$ , which is amenable for control. For the system 2, this manipulable variable can be  $\beta_i$  or  $r_{ij}$ , i.e., we consider that, for each node  $v_i$ , it is possible to improve its health or avoid to perform several contact attempts with its neighbor nodes, the control will adapt one of these parameters, that will be selected according to our mathematical analysis.



### 2.2. Control Problem

Quarantine is an heuristic control mechanism or strategy that intents to reduce a virus propagation in a population. As stated in the last subsection, these kind of models probably are not sufficient to ensure the system to reach the extinction state. This is due to the fact that no adaptation of the network parameters is implemented in dependence of the actual system state. Such a mechanism is proposed in the sequel including decisions on (i) the subset of nodes  $V_M \subset V$  which should be monitored, i.e., whose actual state must be known at each time instant, (ii) the subset of nodes  $V_C \subset V$  which have to be controlled, i.e., whose interaction parameters ( $u_i = \beta_i$  or  $u_i = r_{ij}$ ) should be subject to *on-line* adaptation, and (iii) the specific control law  $u_i(t) = \varphi_i(P(t))$  which should be used for this adaptation.

The chosen approach follows the constructive (i.e., passivity-based) control idea, and consist in two steps:

- a) Assigning the necessary outputs so that the associated zero dynamics is asymptotically stable.
- b) Designing controllers  $u_i(t) = \varphi_i(Y_i(t))$  so that for some  $0 \le \gamma < 1$  it holds that

$$p_i(t) \leq p_{io}\gamma^t$$
,  $p_i(t=0) = p_{io}$ .

# **3. RESULTS**

In this section the main results are presented. In particular sufficient conditions for the stabilization of the extinction state are derived including (i) a selection criterion for the nodes to be monitored in terms of the connectivity parameters, the infection probability and the graph topology and (ii) the design of a simple stabilizing output-feedback control scheme. Simulation results illustrate the functioning of the proposed control scheme for a scale-free network with  $N = 10^6$  nodes.

# 3.1. Selection of Monitored and Controlled Nodes

Taking into account that  $p_i(t) + q_i(t) + s_i(t) = 1$  for each  $v_i \in V$  and to be consistent with the control idea, we consider that  $\zeta_i(P) = \zeta_i(P, U)$ , where the vector  $U(t) = [u_{c1}(t), u_{c2}(t), \dots, u_{cK}(t)]^T$ ,  $v_{ci} \in V_C$  represent the manipulable set of parameters associated with  $\beta_i$  or  $r_{ij}$ . So, we can rewrite system (2) as follows

$$p_{i}(t+1) = (1 - \tau_{i})p_{i}(t) + (1 - \zeta_{i}(P(t), U(t)))(1 - p_{i}(t) - q_{i}(t)),$$

$$q_{i}(t+1) = (1 - \mu_{i})q_{i}(t) + \tau_{i}p_{i}(t),$$

$$(4)$$

$$\zeta_{i}(P, U) = \prod_{j=1}^{N} (1 - \beta_{i}r_{ij}a_{ij}p_{j}(t)).$$

The fixed points associated with the dynamics (4) for some constant  $U^*$  (i.e.,  $\beta_i$  and  $r_{ij}$  are set to some constant value) can be determined by substituting the relations  $p_i(t + 1) =$ 

 $p_i(t) = p_i^*$  and  $q_i(t + 1) = q_i(t) = q_i^*$ . After some algebra it follows that

$$p_{i}^{*} = \frac{1 - \zeta_{i}(P^{*}, U^{*})}{\tau_{i} + \left(1 + \frac{\tau_{i}}{\mu_{i}}\right)\left(1 - \zeta_{i}(P^{*}, U^{*})\right)},$$

$$q_{i}^{*} = \frac{\tau_{i}}{\mu_{i}} \frac{1 - \zeta_{i}(P^{*}, U^{*})}{\tau_{i} + \left(1 + \frac{\tau_{i}}{\mu_{i}}\right)\left(1 - \zeta_{i}(P^{*}, U^{*})\right)},$$

$$s_{i}^{*} = \frac{\tau_{i}}{\tau_{i} + \left(1 + \frac{\tau_{i}}{\mu_{i}}\right)\left(1 - \zeta_{i}(P^{*}, U^{*})\right)}.$$
(5)

Note that the extinction state  $(p_i^* = 0, q_i^* = 0, s_i^* = 1)$  in (2), for  $v_i \in V$  is a fixed point when  $\zeta_i(0, U^*) = 1$ . However, up to this point, it is not clear if the extinction state or any other fixed point given by (5) are stable. The extinction state means that no viruses are propagated over the network and, as we will see in the following Lemma, knowledge of the conditions under which this state is reached, will give us a clue of how viruses are propagated.

The approach followed subsequently exploits ideas from Wang et al. [4], and Bernal Jaquez et al. [15] by establishing a linear bounding dynamics for (4) that has the origin (P, Q) = (0, 0) as exponentially stable fixed point.

Lemma 1. Consider the dynamics (4) on a complex network with graph G(V, E) and adjacency matrix **A**. The extinction state (P, Q) = (0, 0) is globally exponentially stable if the constant vector  $U^*$  (i.e., for some constant values of  $\beta_i$  and  $r_{ij}$ ) is such that

$$\sigma(\mathbf{H}) < 1, \quad U^* = [u_1^*, \dots, u_N^*],$$
 (6)

where  $\sigma(\cdot)$  is the spectral radius of the matrix **H** defined as

$$\mathbf{H} = \begin{bmatrix} \mathbf{I} - \mathbf{T} + \mathbf{BR} & \mathbf{0} \\ \mathbf{T} & \mathbf{I} - \mathbf{M} \end{bmatrix},\tag{7}$$

where

$$\mathbf{T} = diag(\tau_i), \quad \mathbf{B} = diag(\beta_i), \quad \mathbf{R} = [r_{ij}a_{ij}], \quad \mathbf{M} = diag(\mu_i).$$
(8)

and I being the identity matrix.

*Proof:* As it is proved in Wang et al. [4], and Bernal Jaquez et al. [15],  $\zeta_i(P, U^*)$  can be bounded as follows

$$1 - \zeta_i(P(t), U^*) \le \sum_{j=1}^N \beta_i r_{ij} a_{ij} p_j(t).$$
(9)

Substituting this bound into the first equation in (4) and after some algebra one obtains

$$p_i(t+1) \le (1-\tau_i)p_i(t) + (1-p_i(t)-q_i(t))\sum_{j=1}^N \beta_i r_{ij} a_{ij} p_j(t),$$
  
$$\le (1-\tau_i)p_i(t) + \sum_{j=1}^N \beta_i r_{ij} a_{ij} p_j(t).$$

This can be written in matrix form as

$$\begin{bmatrix} P(t+1) \\ Q(t+1) \end{bmatrix} \leq \begin{bmatrix} \mathbf{I} - \mathbf{T} + \mathbf{BR} & \mathbf{0} \\ \mathbf{T} & \mathbf{I} - \mathbf{M} \end{bmatrix} \begin{bmatrix} P(t) \\ Q(t) \end{bmatrix},$$

where  $P(t) = [p_1(t), ..., p_N(t)]^T$  and  $Q(t) = [q_1(t), ..., q_N(t)]^T$ , and the inequality being interpreted as element-wise. Therefore, the solutions of  $p_i(t)$  are bounded by the linear dynamics

$$x_{i}(t+1) = (1 - \tau_{i})x_{i}(t) + \sum_{j=1}^{N} \beta_{i}r_{ij}a_{ij}x_{j}(t),$$

$$w_{i}(t+1) = \tau_{i}x_{i}(t) + (1 - \mu_{i})w_{i}(t), \quad v_{i} \in V$$
(10)

i,e., for all  $t \ge 0$  it holds that

$$0 \le p_i(t) \le x_i(t), \quad q_i(t) = w_i(t)$$
 (11)

if p(0) = x(0), q(0) = w(0). The linear dynamics can be expressed in matrix form as

$$\begin{bmatrix} X(t+1) \\ W(t+1) \end{bmatrix} = \begin{bmatrix} \mathbf{I} - \mathbf{T} + \mathbf{BR} & \mathbf{0} \\ \mathbf{T} & \mathbf{I} - \mathbf{M} \end{bmatrix} \begin{bmatrix} X(t) \\ W(t) \end{bmatrix} = :\mathbf{H} \begin{bmatrix} X(t) \\ W(t) \end{bmatrix},$$
(12)

where  $X(t) = [x_1(t), \dots, x_N(t)]^T$  and  $W(t) = [w_1(t), \dots, w_N(t)]^T$ . It holds that  $(X^T, W^T)^T = (0^T, 0^T)^T$  is exponentially stable if and only if the eigenvalues of the associated matrix **H** are contained in the open unit circle  $\mathbb{C}_1 = \{\lambda \in \mathbb{C} \mid |\lambda| < 1\}$ . Taking into account (11) it follows that a necessary and sufficient condition for global exponential stability of  $(P^T, Q^T)^T = 0$  is given by (6).

The expontial stability condition (6) is very general and does not provide any idea on how to select nodes to be controlled or monitored in order to reach the extinction state. However, using this result as a point of departure, we can get insight into the condition that every node  $v_i \in V$  has to fulfill in order to ensure that P(t) converges to  $P^* = 0$  as shown in the following Lemma.

Lemma 2. For a constant  $U^*$  (i.e., for some constant value for  $\beta_i$  and  $r_{ij}$ ), the state vector  $(P^T(t), Q^T(t))^T$  globally exponentially converges to the extinction state  $(P^T, Q^T)^T = 0$  if for every node  $v_i \in V$  it holds that

$$\beta_i < \frac{\tau_i}{\sum_{j=1}^N r_{ij} a_{ij}}.$$
(13)

*Proof:* In virtue of Lemma 1 it is sufficient to show that if the condition (13) holds, the matrix **H** defined in (6) has only eigenvalues within the open unit circle  $\mathbb{C}_1 \subset \mathbb{C}$ , or equivalently, that its spectral radius  $\sigma(\mathbf{H}) < 1$ . Note that due to the block-diagonal structure of the matrix **H** its eigenvalues are given by the eigenvalues of the two matrices on its diagonal, i.e., in terms of the matrix spectra

$$\mathcal{S}(\mathbf{H}) = \mathcal{S}(\mathbf{I} - \mathbf{T} + \mathbf{BR}) \cap \mathcal{S}(\mathbf{I} - \mathbf{M}),$$

where  $S(\mathbf{A})$  denotes the spectrum of a matrix  $\mathbf{A}$ , i.e., the union of all its eigenvalues. The eigenvalues of the matrix  $\mathbf{I} - \mathbf{M}$  are contained in  $\mathbb{C}_1$ , given that  $\mathbf{M}$  is diagonal with entries  $0 < \mu_i < 1$ . Thus ,it remains to show that  $S(\mathbf{I} - \mathbf{T} + \mathbf{BR}) \subset \mathbb{C}_1$ . This can be analyzed by applying Gerschgorin's Theorem [23], which provides an upper-bound estimate for the spectral radius of a given matrix. In the following, let  $\lambda$  represent an arbitrary eigenvalue of the matrix  $\mathbf{I} - \mathbf{T} + \mathbf{BR}$ . The application of this theorem to the matrix  $\mathbf{I} - \mathbf{T} + \mathbf{BR}$  provides the following inequality

$$|\lambda| \le |1 - \tau_i + \beta_i \sum r_{ij} a_{ij}| = 1 - \tau_i + \beta_i \sum r_{ij} a_{ij}$$
(14a)

 $i = 1, \ldots, N$ . Thus,  $|\lambda| < 1$  is satisfied if

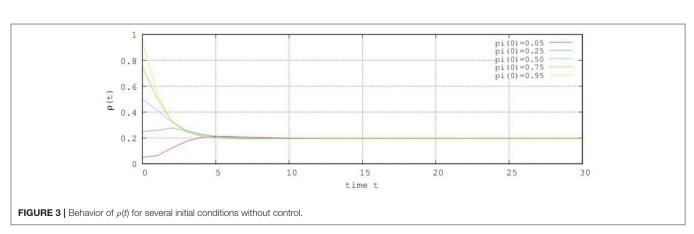
$$\sum_{j=1}^{N} \beta_i r_{ij} a_{ij} < \tau_i, \quad \forall v_i \in V$$

or equivalently if (13) holds true. This complete the proof.  $\Box$ 

Note that, as stated in the proof the convergence to zero of X (and thus P) is independent of the behavior of W (or accordingly Q). This resides in the fact that the dynamics represent a cascade structure. Accordingly, for the purpose of stabilizing the extinction state it is sufficient to ensure that less nodes get infected than pass into quarantine. This intuitively clear condition is exactly what is formally stated in Lemma 2.

The condition (13) gives a criterion on how to choose the nodes to be monitored. If condition (13) does not hold for some set of nodes, then it is appropriate to consider this collection as the set of nodes to be monitored  $V_M$ . Additionally, according to (13), the set of controlling nodes can be set as  $V_C = V_M$ . That is, we can consider that all controlled nodes are monitored. In this way, we can select  $\beta_i$  (or  $r_{ij}$ ) as the parameter amenable for control purposes for those nodes that do not satisfy (13).

Further note that in case that the network parameters are homogenous, i.e., all nodes have the same parameter values  $\mu, \beta, \tau, r_{ij} = r$ , the selection criterion for a node to be controlled is directly related to its degree  $\mathcal{N}_i = \sum_{i=1}^N a_{ij}$  (i.e., here simply the number of neighboring nodes) and can be expressed as



 $v_i \in V_C \,\forall \, i \colon \mathcal{N}_i > \frac{\tau}{r\beta}$ 

Nevertheless, when the parameter distribution is nonhomogenous, it is possible that nodes with high degree do not have to be controlled and nodes with small degree have to be, given the particular constellation between  $\tau_i$ ,  $\beta_i$  and  $r_{ij}$ according to condition (13). This is illustrated in **Figure 2** for a scale-free network with N = 100 nodes and normally distributed parameters.

Note that in the notion of constructive control theory (see e.g., [19, 24]), the dynamics of the nodes that are not controlled establishes the zero dynamics (i.e., the dynamics resulting from the restriction that  $p_i = 0$  for all *i* such that  $v_i \in V_c$ ) and by construction this dynamics is asymptotically stable. Therefore, the zero dynamics correspond to a spreading process over a reduced network, from which the monitored (and thus controlled) nodes have been withdrawn, given that for  $p_i(t) \equiv 0$  the node  $v_i$  does no longer interact with its neighbors.

### 3.2. Feedback Control Design

The question addressed in this section is how to design the feedback control for the nodes  $v_j \in V_C$  so that  $\lim_{t\to\infty} |p_j(t) - p_j^*| = 0$ . Up to this point, we have not considered the dependency of  $\zeta(P, U)$  on U, given that U was considered as a set of constant parameters. This dependency will permit to explicitly determine a control law  $u_i(t) = \beta_i(t)$  that steers the nodes  $v_j \in V_C$  to their desired values  $p_j^* = 0$ . With this idea, the following theorem is established

Theorem 1. Consider the dynamics given by (4) and consider the nodes that do not satisfy (13) as the set  $V_C$  of nodes to be controlled. Let  $V_M = V_C$ , that is, all controlled nodes are monitored. If the controls  $u_i(t)$  satisfy

$$0 \le u_i(t) < \bar{\beta}_i = \frac{\tau_i}{\sum_{j=1}^N r_{ij} a_{ij}},$$
 (15)

then  $(P^T, Q^T)^T = 0$  is exponentially stable.

*Proof:* The Theorem can be easily proven as follows. Let  $\bar{\beta}_i$  be given as in (15). It follows that

$$0 \le u_i(t) < \beta_i,$$
  
$$\Leftrightarrow \quad 0 \le u_i(t)r_{ij}a_{ij} < \bar{\beta}_i r_{ij}a_{ij},$$

$$\Leftrightarrow \quad 0 \leq \sum_{j=1}^{N} u_i(t) r_{ij} a_{ij} < \sum_{j=1}^{N} \bar{\beta}_i r_{ij} a_{ij}.$$

Given that for  $\beta_i \leq \overline{\beta}_i$  inequality (13) is satisfied, one obtains

$$0 \leq \sum_{j=1}^N u_i(t)r_{ij}a_{ij} < \sum_{j=1}^N \bar{\beta}_i r_{ij}a_{ij} < \tau_i,$$

or equivalently

$$\sum_{j=1}^N u_i(t)r_{ij}a_{ij} < \tau_i$$

implying that inequality (13) is satisfied. In consequence, the exponential stability of  $(P^T, Q^T)^T = 0$  follows.

Note that following a similar reasoning, a control law can be established for the case that  $u_i(t) = r_{ij}(t)$ . Nevertheless, this approach will not be explicitly elaborated at this place.

From Theorem 1, we have that in order to stabilize the extinction state for the dynamics (4) it is sufficient to design feedback controls  $u_i(t)$  for all nodes  $v_i \in V_C$ , which take values below the upper-bound  $\bar{\beta}_i$  defined in (15). For example, a simple linear feedback control given by

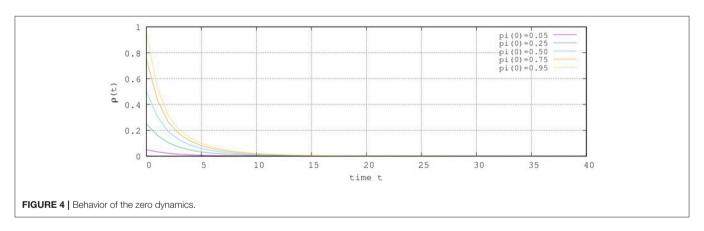
$$u_i(t) = \beta_i(t) = \gamma \bar{\beta}_i(1 - p_i(t)), \quad \gamma \in (0, 1)$$
 (16)

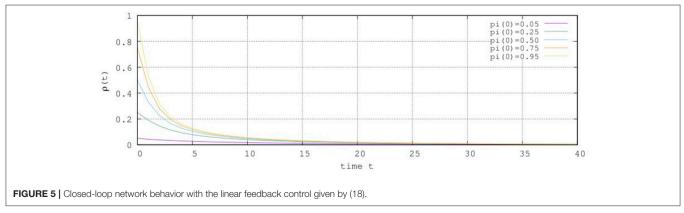
does satisfy this condition. Note that the advantage of using a time varying control law  $\beta_i(t)$  consists in actively adapting the infection probability on the actual needs, i.e., the actual network state. In comparison with imposing a constant value for  $\beta_i$  this possibly enables to optimize the control effort over time, because according to (16)  $\beta_i \rightarrow \gamma \overline{\beta}_i$  with  $p_i \rightarrow 0$ . The performance using this simple output-feedback control is illustrated in the subsequent section.

## 3.3. Simulations

In order to verify our results, we perform several simulations of the dynamical system (4), for different initial conditions, with the following considerations

- We used a scale-free network of  $N = 10^6$  described by G(V, E), that incorporates preferential attachment according to Barabási and Albert [21]. We started with a small number  $m_o = 9$  of vertices, linked randomly, and at every step we add a new node or vertex with m = 3 edges until we reach  $N = 10^6$ . We emphasize that our results are independent of the network's topology.
- To facilitate our simulations, we consider that  $r_{ij} = r_{ji}$ .
- The constant values for the recovery probability  $\mu_i$ , the probability of infection  $\beta_i$ , the internment probability  $\tau_i$ , and the contact probability  $r_i$  were distributed uniformly over the nodes with values in the interval [0.2, 0.7].





• To show and corroborate our results, we calculated the average probability  $\rho(t)$  given by

$$\rho(t) = \frac{1}{N} \sum_{i=1}^{N} p_i(t).$$
(17)

• The sets  $V_C$  and  $V_M$  are chosen according to Lemma 2 as the sets of nodes that do not satisfy (13). For the case considered here 424569 nodes out of  $N = 10^6$  (i.e., about 42.5%) have to monitored and controlled.

Simulation studies have been performed considering the following scenarios:

- I. Absence of control: All parameters of the system (4) have constant values which not necessarily satisfy condition (13).
- II. Zero dynamics: The output was constrained to Y(t) = 0 by setting  $\beta_j = 0$  and  $p_j(0) = 0$  for all  $v_j \in V_M = V_C$ .
- III. Linear feedback control: The linear feedback control given by (16) has been implemented for all  $v_i \in V_M = V_C$ .

## I. Absence of Control

In the absence of control the network reaches an endemic attractor state where about a 20% of the nodes are probably infected after about 20 time units as can be seen in **Figure 3**.

### **II. Zero Dynamics**

To corroborate that the zero dynamics are exponentially stable, we set Y(t) = 0 for those nodes that do not satisfy (13). This is achieved by setting  $\beta_i = 0$  for  $v_i \in V_M$ .

**Figure 4** shows the behavior of the nodes associated with the zero dynamics. Note that the extinction state is reached after 18 time steps.

### **III. Linear Feedback Control**

To show the performance of the proposed simple outputfeedback control scheme (16), it has been implemented for all monitored and controlled nodes with the gain  $\gamma = 0.9$  and the upper bound  $\bar{\beta}_i$  calculated according to (15). This yields the output-feedback controller.

$$\beta_i(t) = \frac{\gamma \tau_i(1 - p_i(t))}{\sum_{j=1}^N r_j a_{ij}}, \quad \text{for} \quad \gamma = 0.9 \quad \text{and} \quad \forall v_i \in V_C = V_M.$$
(18)

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Note that the control (18), depends on the state of the node *i* given by  $p_i(t)$ , and the properties of its neighbors given by  $\bar{\beta}_i$ . **Figure 5** shows the result of the simulation with the applied control (18). As predicted in Theorem 1 the extinction state is a close-loop attractor, and is reached in about 40 time steps.

## 4. DISCUSSIONS AND CONCLUSIONS

The problem of deciding which nodes in a complex network with guarantine should be controlled and how to control them in order to achieve that in the closed-loop system the extinction state becomes a (global) attractor has been studied. Sufficient conditions for virus extinction have been derived using a constructive control approach by suitably identifying the zero dynamics according to a threshold condition for the stability of the extinction state. The associated node selection criterion does depend on the transmission probability between the nodes and their neighbors, the degree of each node and its probability to pass into quarantine. It has been shown that in spite of the strongly nonlinear dynamics of the spreading process the extinction state can be efficiently stabilized using a simple linear bounded output-feedback control if the nodes to be controlled are selected according to the proposed scheme. The performance and behavior of the spreading process without and with control has been illustrated for a scale-free network with  $N = 10^6$ nodes.

# AUTHOR CONTRIBUTIONS

All authors designed and did the research, in particular the stability analysis. LA-R and AS conceived and designed the control and the numerical experiments. LA-R performed the numerical experiments. All authors analyzed the data. LA-R and RB wrote the paper. All authors reviewed the manuscript. All authors have read and approved the final manuscript.

## FUNDING

This work was partially sponsored by Rector office of UAM Cuajimalpa through Programa de Apoyo a Proyectos Interdisciplinarios.

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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