

A distributed dynamics for virus-spread control [★]

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Abstract

Inspired by a local version of the replicator dynamics, this work proposes a discrete-time and distributed algorithm that allows a connected group of nodes to dynamically achieve virus spreading minimization subject to operational constraints. The proposed algorithm is distributed in the sense that it can be implemented by network nodes via local and anonymous interactions. By employing a discrete-time LaSalle invariance principle, we obtain a bound on the algorithm step size that guarantees asymptotic convergence under time-varying interactions. The performance of the method is illustrated on a simulation example.

Key words: Distributed Control, Spreading Dynamics, Replicator Dynamics

1 Introduction

Virus spreading over computer and human networks is a prevalent concern today, as it poses a threat to the security of interconnected infrastructure and the well-being of the general public. The implementation of strategies to stop epidemics can specially be a challenge when networks are operated by multiple managers who need to preserve the privacy and interest of their constituents. These scenarios would benefit from the development of distributed anonymous coordination algorithms that allow the implementation of best responses in a robust way. Motivated by this, this manuscript proposes a novel algorithm that can serve to resolve these issues for particular classes of network graphs and resource constraints.

Literature review. There are several models of virus spreading and contagion over networks (see e.g., [14, 18] for surveys over virus models and control). One canonical example is given by the SIS (susceptible-infected-susceptible) model and its variations; see [1, 3, 19, 20, 27], which present validation studies of such models for virus propagation over human and computer graphs. Based on this, two main strategies have been proposed to handle such propagation in the literature. One approach considers the detection and isolation capabilities of the infected nodes by means of topology adaptation or quarantine, while another one considers node immunization.

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Along these lines, [6] and [24] propose a distributed strategy to manipulate the topology of the network by disconnecting infected nodes. This solution does not consider the cost of disconnecting the network or constraints on the network connectivity. In [26], the authors propose a decentralized algorithm to control the virus propagation by disconnecting nodes and by applying an antivirus subject to resource constraints. The decentralized algorithm of [26] is based on the use of diagonal matrices in the control input, which are naturally distributed. However, the algorithm that determines these diagonal matrices is not distributed itself. Along the lines of [26], the authors in [25] propose a sparse control allocation of limited resources among a subset of a networks components to minimize the dominant eigenvalue of a linear dynamical process associated with the network. However, as in [26], the proposed algorithm is not distributed itself. A recent formulation of the optimal vaccination for the case of continuous time dynamics is given in [21]. In [21] the authors propose a geometric programming framework to find the optimal allocation of resources under local constraints, nonetheless, this solution is nor distributed neither decentralized. Based on the framework proposed in [21], the authors in [5] propose a distributed resource allocation strategy to control a virus outbreak in a network. The proposed algorithm is based on Distributed Alternating Direction Method of Multipliers (D-ADMM) algorithm, however, the cost on communication is expensive since every operator in the network needs to interchange a local estimation of the variables of the entire network. Ideas of distributed control have been commonly applied to distributed consensus algorithms [2, 15], where the central

idea is to study whether a group of agents in a network using local and anonymous information can reach a global agreement. Similar in spirit to consensus algorithms, the local replicator dynamics has been proposed in [17], where it is applied to dynamic resource allocation. The local replicator dynamics is a model where agents with local communication capabilities tend to reach the same *fitness* using simple interactions, while preserving the simplex invariant.

Statement of contributions. We study a virus spreading minimization problem based on a general contagion dynamics model. We characterize the optimal allocation solution to the virus problem by posing the problem objective as the minimization of the spectral radius of the contagion-dynamics matrix subject to operational constraints. By using the Perron-Frobenius theorem and Lagrange multipliers theory, we obtain a novel characterization of the critical points of the problem that applies to (not necessarily symmetric) weight-balanced matrices. For other matrices, we give bounds for the solution in terms of the associated symmetrized problem. After this, we propose a discrete-time distributed algorithm that implements the desired resource allocation for symmetric matrices. In contrast with previous work, our algorithm can be implemented under partial information by the network nodes by means of local and anonymous interactions. More precisely, our algorithm is based on a discretization of the local replicator dynamics that is further adapted to ensure convergence of the solution to the virus mitigation problem, while satisfying resource constraints. Using a novel discrete-time analysis, we are able to provide a bound on the algorithm step size that guarantees convergence for agents subject to time-varying interactions. Preliminary statements of the results of this paper appeared in [22]. Here, we include the final statements developed in full technical details.

2 Preliminaries and notation

We denote by $\mathbb{R}_{\geq 0}^d$ the positive orthant of \mathbb{R}^d , for some $d \in \mathbb{N}$, $\text{diag}(a_1, \dots, a_N)$ the $N \times N$ matrix with entries a_i along the diagonal, I_N the identity matrix of size $N \times N$, and $\mathbf{1}_N \in \mathbb{R}^N$ the column vector whose elements are all equal to one. The spectrum of A is denoted by $\text{spec}(A)$, an eigenvalue of A is denoted by $\lambda_i(A) \in \text{spec}(A)$, its *spectral radius* by $\rho(A) = \max_i |\lambda_i(A)|$, and the 2-norm of A is denoted by $\|A\|$. When we use inequalities for vectors, we refer to componentwise inequalities.

A real square matrix $A = [a_{ij}]$, $A \in \mathbb{R}_{\geq 0}^{N \times N}$, is called *nonnegative*, if its entries are nonnegative, i.e., $a_{ij} \geq 0$, for all $i, j \in \{1, \dots, N\}$. A directed graph of order N or *digraph* is a pair $\mathcal{G} = (\mathcal{V}, \mathcal{E})$, where \mathcal{V} , the *vertex set*, is a set with N nodes, and $\mathcal{E} \subset \mathcal{V} \times \mathcal{V}$, the *edge set*, is a set of ordered pair of vertices called edges. We denote the graph at time k as $\mathcal{G}^{(k)} = (\mathcal{V}, \mathcal{E}^{(k)})$ with edge set $\mathcal{E}^{(k)} \subset \mathcal{V} \times \mathcal{V}$, $k \in \mathbb{N}$. Given a digraph \mathcal{G} , we define the

unweighted adjacency matrix of \mathcal{G} by $\mathcal{A}(\mathcal{G}) \in \mathbb{R}^{N \times N}$ as $a_{ij} = 1$ if $(i, j) \in \mathcal{E}$, and $a_{ij} = 0$ otherwise. Given a nonnegative matrix $B \in \mathbb{R}^{N \times N}$, its associated *weighted digraph* $\mathcal{G}(B)$ is the graph with $\mathcal{V} = \{1, \dots, N\}$ and edge set defined by the following relationship: $(i, j) \in \mathcal{E}(B)$ if and only if $b_{ij} > 0$. The associated weight of the edge (i, j) is given by the entry b_{ij} . The graph $\mathcal{G}(B)$ is said to be *weight-balanced* if $\sum_{j=1}^N b_{ij} = \sum_{j=1}^N b_{ji}$ for all $i \in \mathcal{V}$, in particular, $\mathcal{G}(B)$ is *undirected* if $b_{ij} = b_{ji}$ for all $(i, j) \in \mathcal{E}$. A pair of indices $i, j \in \mathcal{V}$ of an undirected graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ are called *neighbors* if $(i, j) \in \mathcal{E}$. We let $\mathcal{N}_i(\mathcal{G})$ denote the set of neighbors of i in the digraph \mathcal{G} . A *path* in a graph is an ordered sequence of vertices such that any pair of consecutive vertices in the sequence is an edge of the graph. A graph is *connected* if there exists a path between any two vertices. If a graph is not connected, then it is composed of multiple *connected components*, that is, multiple connected subgraphs. In a connected graph \mathcal{G} , the distance from vertex i to vertex j , denoted as $\text{dist}(i, j)$, is the length (number of edges) of a shortest i - j path in \mathcal{G} .

2.1 On the replicator dynamics

Replicator dynamics [11, 23, 28] models the interaction of an homogeneous population, where fractions of individuals play a symmetric game. From the biological point of view, it can be seen as mechanism to model the behavior of a population whose individuals seek habitats with different conditions to feed or reproduce. This dynamics is represented by a first-order differential equation, which is composed by the *replicator*, its *fitness*, and the proportion in the population. The replicator represents one individual in the entire population. The fitness is the payoff that the individual gets during the game. Finally, the proportion in the population corresponds to the fraction of individuals in the population that changes as a result of their mutual interactions and fitnesses. A particular choice of replicator dynamics is given by

$$\dot{p}_i(t) = p_i(t)(f_i - \bar{f}), \quad (1)$$

where p_i denotes the proportion of population that play one strategy $i \in \{1, \dots, N\}$, $f_i : \mathbb{R} \rightarrow \mathbb{R}$ is the fitness, and \bar{f} is the average fitness described by $\bar{f} = \sum_{j=1}^N p_j f_j$. The choice of \bar{f} in (1) imposes a useful restriction to the dynamics, as evolutions will belong to the simplex $\Delta_p = \{p \in \mathbb{R}_{> 0}^N \mid \sum_{i=1}^N p_i(t) = 1\}$. When the equilibrium point $p_i^* > 0$ for all i , then the steady state of (1) is achieved when $f_i(p_i^*) = \bar{f}(p^*)$, where $p^* = [p_1^*, \dots, p_N^*]$. The properties of (1) make it useful to solve distributed optimization problems subject to constraints like the virus problem we state in Section 3.

A local version of the original replicator dynamics in (1) is proposed in [17] to account for local interactions of fractions of the population over a graph \mathcal{G} . The local

replicator dynamics is given by

$$\dot{p}_i(t) = p_i \left(f_i \sum_{j \in \mathcal{N}_i} p_j - \sum_{j \in \mathcal{N}_i} p_j f_j \right), \quad (2)$$

where \mathcal{N}_i is the set of neighbors of i in the graph \mathcal{G} . If the choice of the fitness f_i only depends on information of the neighbors and itself, then the algorithm described in (2) is distributed. Moreover, since (2) does not require the exchange of identities, it is said that it accounts for anonymous interactions. The authors in [17] show that this algorithm conserves the most important characteristics of (1), i.e., i) the simplex is invariant, and ii) the equilibrium point is asymptotically stable in Δ_p .

3 Problem statement and solution approach

In this section, we first introduce the contact network dynamics proposed in [19] and the problem statement proposed in [26]. Next, we extend a theorem in [26] for symmetric, irreducible matrices to weight-balanced and irreducible matrices. This extension is motivated by the possibility of having an asymmetric placement of edge isolation (e.g., quarantine or firewalls) making the interaction graph directed. Our proof relies on the Lagrange multiplier approach and the Perron-Frobenius theorem, instead of using a sensitivity formula. Finally, we propose a strategy for the minimization of the virus spread over a network such that minimizes the Perron eigenvalue of the symmetrized counterpart for any non-negative matrix, and we characterize the goodness of this approximation.

3.1 Problem statement

The virus dynamics over a network proposed in [19] is given by

$$x_i^{(k+1)} = \left(1 - \prod_{j=1}^N (1 - a_{ji} x_j^{(k)}) \right), \quad (3)$$

where $x_i^{(k)} \in \mathbb{R}$ is the probability that node i is infected at time k , $i \in \{1, \dots, N\}$ and a_{ji} is defined as

$$a_{ji} = \begin{cases} \beta_{ji}, & \text{for } j \neq i, \\ 1 - \delta_i, & \text{for } j = i. \end{cases}$$

Here, $\beta_{ji} \in [0, 1]$ is the probability that the virus from node i infects node j , and $\delta_i \in [0, 1]$ is the probability of an infected node i to be recovered. Using the Weierstrass product inequality, valid for $a_{ji} x_j^{(k)} \in [0, 1]$, we obtain the following upper bound

$$x_i^{(k+1)} \leq \sum_{j=1}^N a_{ji} x_j^{(k)}, \quad \forall i \in \{1, \dots, N\}.$$

The previous inequality reads in vector notation as

$$x^{(k+1)} \leq A(\delta) x^{(k)}, \quad (4)$$

where $x^{(k)} = [x_1^{(k)}, \dots, x_N^{(k)}]^T$, $\delta = (\delta_1, \dots, \delta_N) \in [0, 1]^N$, and $A(\delta) \in \mathbb{R}^{N \times N}$ is given by

$$A(\delta) = \begin{bmatrix} 1 - \delta_1 & \beta_{21} & \dots & \beta_{N1} \\ \beta_{12} & 1 - \delta_2 & \dots & \beta_{N2} \\ \vdots & \vdots & \ddots & \vdots \\ \beta_{1N} & \beta_{2N} & \dots & 1 - \delta_N \end{bmatrix}.$$

Let $G \triangleq A(\delta) - I_N + D \equiv A(\mathbf{1}_N)$, where $D = \text{diag}(\delta)$, and $\mathcal{G}(I_N + A(\mathbf{1}_N)) = \mathcal{G}(I_N + G)$ be the graph associated with the contact dynamics matrix. We define the *topology matrix* of the network as the matrix $I_N + G$. When there is no confusion, we will denote $\mathcal{G}(I_N + G)$ by \mathcal{G} and \mathcal{A} for the associated unweighted adjacency matrix. In [19], authors prove next proposition,

Proposition 1 ([19]) *An epidemic described by (3) becomes extinct if and only if $\rho(A(\delta)) < 1$.*

We consider the following problems to minimize the effects of virus contagion. The VIRUS MITIGATION problem is given by

$$\begin{aligned} & \min_{\delta \in [0, 1]^N} \rho(A(\delta)), \\ & \text{subject to} \\ & \sum_{i=1}^N \delta_i = \Gamma, \\ & \rho(A(\delta)) < 1. \end{aligned} \quad (5)$$

Depending on the value of Γ , the VIRUS MITIGATION problem is not feasible and we can only solve the relaxed VIRUS SPREAD MINIMIZATION problem:

$$\begin{aligned} & \min_{\delta \in [0, 1]^N} \rho(A(\delta)), \\ & \text{subject to} \\ & \sum_{i=1}^N \delta_i = \Gamma. \end{aligned} \quad (6)$$

Here, we only consider a partial vaccination strategy since we only consider as decision variable δ , while β is fixed. We further assume that there are enough resources in terms of isolation/quarantine capabilities (i.e., β), which make possible to balance the network interaction according to a finite-time distributed algorithm presented in [9].

Remark 1 *When there are not enough resources to balance the network, we can use a similarity transformation $B = XAX^{-1}$, where B is weight-balanced and X*

is a square diagonal matrix that can be found by the algorithm given in [8]. The similarity transformation for balancing the network for irreducible matrices is proven to be unique in [10]. The algorithm in [8] requires information of the in- and out-neighbors. What prevents this algorithm to be computed in a distributed way, is the fact that at every step it is normalized using 1-norm, however, all results of this algorithm hold when it is used ∞ -norm for normalizing. By this modification in the algorithm, we can implement it in a distributed way. Since the algorithm converges asymptotically to the diagonal X , the result provided by this algorithm is only an approximation. The effect of such approximation is out of scope of this paper.

Remark 2 The linear constraint in (5) and (6) serves to model that the combined effort of operators to implement δ_i should be upper bounded by a total resource value of Γ . That is, $\sum_i \delta_i \leq \Gamma$. However, it is easy to see that the solution of this problem is always at the boundary of the constraint if $A(\delta)$ is irreducible and nonnegative; that is, $\sum_i \delta_i = \Gamma$, is satisfied by the optimal solution.

3.2 Solution characterization for balanced matrices

We present a characterization of the solution to a relaxed problem for weight-balanced matrices in Theorem 2 to provide sufficient conditions for feasibility for the VIRUS MITIGATION and VIRUS SPREAD MINIMIZATION problems. Previous to this, the next theorem recalls that the function $\rho(A(\delta))$ is a convex function of δ and, hence, the problems introduced in Section 3.1 are convex. Proofs for all results in this paper can be found in the Appendix.

Theorem 1 ([4]) *Let B be a nonnegative matrix and $D = \text{diag}(\delta_1, \dots, \delta_N)$. Then, the Perron eigenvalue of $B + D$, $\rho(B + D)$, is a convex function of D .*

In particular, the VIRUS MITIGATION problem is feasible when the set of δ satisfying $\delta \in [0, 1]^N$, $\rho(A(\delta)) < 1$ and $\sum_{i=1}^N \delta_i = \Gamma$ is non empty. On the other hand, the VIRUS SPREAD MINIMIZATION is feasible when the set of δ satisfying $\delta \in [0, 1]^N$ and $\sum_{i=1}^N \delta_i = \Gamma$ is non empty.

Denote by $r_i = 1 + \sum_{j=1, j \neq i}^N \beta_{ji}$ and $c_i = 1 + \sum_{j=1, j \neq i}^N \beta_{ij}$, the sum of row and column entries of $I_N + A(\mathbf{1}_N)$, respectively.

Theorem 2 *For a weight-balanced, nonnegative, and irreducible matrix $A(\delta)$ the solution to the VIRUS SPREAD MINIMIZATION problem without the restrictions $\delta_i \in [0, 1]$, $i \in \{1, \dots, N\}$, is given by making the sums of each row of $A(\delta)$ equal to each other, i.e., $-\delta_i + r_i = -\delta_j + r_j$ for $i \neq j$. Precisely, the solution is*

characterized by

$$\rho^*(A(\delta^*)) = \frac{\sum_{j=1}^N r_j - \Gamma}{N}, \quad (7)$$

$$\delta_i^* = \frac{Nr_i - \sum_{j=1}^N r_j + \Gamma}{N}. \quad (8)$$

Corollary 1 (Sufficient conditions for problem feasibility): *When $A(\delta)$ is weight-balanced, nonnegative, and irreducible, then a feasible solution to the VIRUS SPREAD MINIMIZATION problem is given by (8) if*

$$\begin{aligned} \max_i \left(\sum_{k,j=1, j \neq k}^N \beta_{jk} - N \sum_{j=1, j \neq i}^N \beta_{ji} \right) &\leq \Gamma \quad (9) \\ &\leq \sum_{i,j=1, j \neq i}^N \beta_{ji} + N(1 - \max_i \sum_{j=1, j \neq i}^N \beta_{ji}). \end{aligned}$$

Moreover, a feasible solution to the VIRUS MITIGATION problem is given by (8) if

$$\sum_{i,j=1, j \neq i}^N \beta_{ji} < \Gamma \leq \sum_{i,j=1, j \neq i}^N \beta_{ji} + N(1 - \max_i \sum_{j=1, j \neq i}^N \beta_{ji}). \quad (10)$$

3.3 Solution bound for unbalanced matrices

When the topology matrix $I_N + A(\mathbf{1}_N)$ is not weight-balanced and there are not enough resources to make it so as in [9], Theorem 2 is not applicable. Nonetheless, the VIRUS SPREAD MINIMIZATION problem can be relaxed to minimizing $\rho(\bar{A}(\delta))$, where $\bar{A}(\delta) = I_N - D + \frac{1}{2}(A(\mathbf{1}_N) + A(\mathbf{1}_N)^T)$. The next lemma shows that this upper bound to the solution $\rho^*(A(\delta^*))$, is at the same time upper bounded by $\min_{\delta} \|A(\delta)\|$.

Lemma 1 *Let $\bar{A}(\delta) = I_N - D + \frac{1}{2}(A(\mathbf{1}_N) + A(\mathbf{1}_N)^T)$ be the symmetrization of $A(\delta) = I_N - D + A(\mathbf{1}_N)$. Then $\min_{\delta} \rho(\bar{A}(\delta)) \leq \min_{\delta} \|A(\delta)\|$ and $\min_{\delta} \rho(\bar{A}(\delta)) \geq \rho^*(A(\delta^*))$.*

Since it holds that $\|A(\delta)\| \geq \rho(\bar{A}(\delta)) \geq \rho(A(\delta))$ as shown in Lemma 1, an upper bound for a feasible solution of the VIRUS MITIGATION problem is given by solving the following problem:

$$\begin{aligned} \min_{\delta \in [0, 1]^N} \rho(\bar{A}(\delta)) \\ \text{subject to} \\ \sum_{i=1}^N \delta_i = \Gamma, \\ \rho(\bar{A}(\delta)) < 1. \end{aligned} \quad (11)$$

This is based on the following lemma.

Lemma 2 *The VIRUS MITIGATION problem is feasible if Problem (11) is feasible. In that case, an upper bound to the solution of the VIRUS MITIGATION problem is given by a solution to Problem (11).*

In the next lemma, we describe explicitly the upper bound given by solving problem (11).

Lemma 3 *Consider a virus dynamics with associated nonnegative and irreducible $A(\mathbf{1}_N)$. Let Γ satisfy the sufficient condition (9) for the topology $I_N + \frac{A(\mathbf{1}_N) + A(\mathbf{1}_N)^T}{2}$. Then, an upper bound for the solution of the VIRUS SPREAD MINIMIZATION problem for $I_N + A(\mathbf{1}_N)$ is given by $\rho^*(A(\delta^*)) \leq \frac{\sum_{j=1}^N (r_j + c_j) - \Gamma}{2N}$.*

Finally, we characterize the distance of these bounds to the solution of the VIRUS SPREAD MINIMIZATION problem.

Lemma 4 *Consider a virus dynamics with associated nonnegative and irreducible $A(\mathbf{1}_N)$. Let Γ satisfy (9) for the topology $I_N + \frac{A(\mathbf{1}_N) + A(\mathbf{1}_N)^T}{2}$. Let δ^{*1} , δ^{*2} and δ^{*3} be the vector solutions given in (8) for the topology matrices $I_N + A(\mathbf{1}_N)$, $I_N + A(\mathbf{1}_N)^T$ and $I_N + \frac{1}{2}(A(\mathbf{1}_N) + A(\mathbf{1}_N)^T)$, respectively. Let δ^* be the solution to the VIRUS SPREAD MINIMIZATION problem and $e_i \triangleq |\delta_i^* - \delta_i^{*3}|$, for $i \in \{1, \dots, N\}$, be the errors between the solution given by Lemma 3 and the optimal solution δ^* . Then, $e_i \leq \frac{1}{2}|\delta_i^{*1} - \delta_i^{*2}|$, $i \in \{1, \dots, N\}$.*

4 The constrained Euler replicator algorithm

This section describes the CONSTRAINED EULER REPLICATOR algorithm proposed to solve the VIRUS SPREAD MINIMIZATION problem. This algorithm is based on the replicator dynamics and a local version of it, see Section 2.1, which allows for the automatic satisfaction of the linear resource constraint.

Consider the probabilities of recovery $\delta \in [0, 1]^N$ and the network graph \mathcal{G} , which are defined in the VIRUS SPREAD MINIMIZATION problem. In what follows, we assume that the topology matrix $I_N + A(\mathbf{1}_N)$ is symmetric, nonnegative, and the graph associated with it is connected. Recall that Theorem 2 shows that the solution to a relaxed version of the VIRUS SPREAD MINIMIZATION problem is given by a δ that makes the sum of the rows in matrix $A(\delta)$ to be equal. Motivated by the fact that

at the equilibrium of the continuous-time replicator dynamics all fitnesses are equal and other constraints are also naturally satisfied, we want solve the VIRUS SPREAD MINIMIZATION problem by employing a discretization of these dynamics and by defining local fitness as the i^{th} row sum of matrix $A(\delta)$.

Using Euler first-order differences, we discretize the continuous-time local replicator dynamics (2),

$$p_i^{(k+1)} = p_i^{(k)} + \epsilon^{(k)} p_i^{(k)} \left(f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} - \bar{f}_i^{(k)} \right), \quad (12)$$

where $k \in \mathbb{N}$, $\bar{f}_i^{(k)} = \sum_{j \in \mathcal{N}_i} p_j^{(k)} f_j^{(k)}$, and $\epsilon^{(k)} > 0$. Define $p = [\delta_1/\Gamma, \dots, \delta_N/\Gamma]^T \in [0, 1]^N$ and $f_i(p_i) = r_i - \Gamma p_i = r_i - \delta_i$, $i \in \{1, \dots, N\}$, where recall that r_i is the i^{th} row sum of $I_N + A(\mathbf{1}_N)$. Then $f_i(\Gamma p_i) \equiv f_i(\delta_i)$ is the i^{th} row sum of $A(\delta)$. In compact form, the dynamics in (12) read as:

$$p^{(k+1)} = p^{(k)} + \epsilon^{(k)} \text{diag}(p^{(k)}) (\text{diag}(f^{(k)}) \mathcal{A} p^{(k)} - \mathcal{A} \bar{f}^{(k)}), \quad (13)$$

where \mathcal{A} is the unweighted adjacency matrix of \mathcal{G} , $f^{(k)} = [f_1^{(k)}, \dots, f_N^{(k)}]^T$, and $\bar{f}^{(k)} = [p_1^{(k)} f_1^{(k)}, \dots, p_N^{(k)} f_N^{(k)}]^T$. To solve the problems of interest, we want to keep $\delta \in [0, 1]^N$. Notice that (12) does not constraint its states as $p_i \leq \frac{h_i}{\Gamma}$ for certain desired constraints $h_i > 0$ for $i \in \{1, \dots, N\}$ (in our particular virus problem $h_i = 1$ for $i \in \{1, \dots, N\}$). Because of this, we propose a variation of (12) called the CONSTRAINED EULER REPLICATOR algorithm, whose convergence is analyzed in Section 5. A short description of the CONSTRAINED EULER REPLICATOR algorithm is given as follows. Each node computes its own state $\delta_i^{(k+1)} = \Gamma p_i^{(k+1)}$, $i \in \{1, \dots, N\}$. If all trajectories are inside $\Omega \triangleq \{\delta^{(k)} \in \mathbb{R}_{>0}^N \mid \mathbf{1}_N^T \delta^{(k)} = \Gamma, \delta^{(k)} \leq h_i\}$, then the algorithm reduces to (12). Otherwise, if node i violates the constraint $\delta_i \leq h_i$, then it stores the difference in $\alpha_i \in \mathbb{R}_{\geq 0}$ and puts $\delta_i^{(k+1)} = h_i$ (lines 4 to 6). Note that line 9 restores $\frac{\alpha_i}{\Gamma}$ to $p^{(k+1)}$. i.e., the evolution of $p^{(k)}$ in line 9 is equivalent to the evolution of (12) in any case.

The computation of the step size for the CONSTRAINED EULER REPLICATOR algorithm and the algorithm in (13) are discussed in the next section.

5 Stability analysis

In this section, we analyse the properties of the discrete-time algorithm (13) and provide a sufficient condition on $\epsilon^{(k)}$ that guarantees its stability. The algorithm can be used to solve a relaxed version of the VIRUS SPREAD

Algorithm 1 CONSTRAINED EULER REPLICATOR

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1: for  $k > 0$  do
2:   Compute  $p_i^{(k+1)}$  as in (12)
3:    $\delta_i^{(k+1)} = \Gamma p_i^{(k+1)}$ 
4:   if  $\delta_i^{(k+1)} > h_i$  then
5:      $\alpha_i^{(k+1)} = \delta_i^{(k+1)} - h_i$ 
6:      $\delta_i^{(k+1)} = h_i$ 
7:   else  $\alpha_i^{(k+1)} = 0$ 
8:   end if
9:    $p_i^{(k+1)} = \frac{\delta_i^{(k+1)} + \alpha_i^{(k+1)}}{\Gamma}$ 
10:   $k = k + 1$ 
11: end for
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MINIMIZATION problem, where the constraint $\delta_i \leq 1$ is omitted. Finally, we analyze the effects of the CONSTRAINED EULER REPLICATOR algorithm when $h_i = 1$, for all $i \in \{1, \dots, N\}$.

Next, we show that the algorithm in (13) conserves the most important characteristics of (1), i.e., i) the simplex is invariant for small enough step size as shown in Lemma 5, ii) all individuals get the same fitness at the equilibrium with the choice of an adequate fitness as shown in Lemma 6, and iii) the equilibrium point is asymptotically stable in Δ_p as shown in Theorem 3.

Lemma 5 (Invariance of Δ_p under (13)): *The dynamics in (13) leaves Δ_p invariant for a sequence $\epsilon^{(k)} < \frac{1}{\max_{i,j}(f_i^{(k)} - f_j^{(k)})}$, $k \geq 0$.*

Lemma 6 (Equilibria of (13)): *Assume that Γ satisfies (9) and consider the dynamics (13) with initial condition $p^{(0)} \in \Delta_p$. Then the equilibrium points p^* of (13) such that $p^* > 0$ coincide with those of the continuous-time replicator dynamics.*

As a consequence of Lemma 6, each connected component of a disconnected graph arrives at a common equilibrium fitness, i.e., the set of nodes of each component agrees on the same average fitness. These equilibrium fitnesses can differ from one connected component to another.

Lemma 7 (Equilibrium point characterization under (10)): *Let \mathcal{G} be a (not necessarily connected) graph, let Γ satisfy (9), and consider the dynamics (13) with initial condition $p^{(0)} \in \Delta_p$. Then, the equilibrium point $p^* > 0$ of (13) is given by*

$$p_i^* = \frac{|\mathcal{X}|r_i + \Gamma \sum_{j \in \mathcal{X}} p_j^{(0)} - \sum_{j \in \mathcal{X}} r_j}{|\mathcal{X}|\Gamma}, \quad (14)$$

where $i \in \mathcal{X}$ and $(\mathcal{X}, \mathcal{E}_{\mathcal{X}}) \subset \mathcal{G}$ represents a connected component of \mathcal{G} .

Theorem 3 (Sufficient conditions for the stability of the algorithm in (13)): *Suppose Γ satisfies (10), the set of neighbors in (12) are time-variant satisfying $\bigcup_{k \geq k_0} \mathcal{A}(\mathbf{1}_{\mathcal{N}})^{(k)}$ is connected for all $k_0 \in \mathbb{Z}_{\geq 0}$.*

Then, the algorithm (13) converges to the solution of the VIRUS MITIGATION problem, and is asymptotically stable to this solution in Δ_p for a sequence $\epsilon^{(k)} < \min\{\frac{1}{\max_{i,j}(f_i^{(k)} - f_j^{(k)})}, \frac{1}{\Gamma \max_i p_i^{(k)}}\}$, $k \geq 0$.

Remark 3 *In order to compute the $\epsilon^{(k)}$ given in Theorem 3 in a distributed way, agents can employ a min consensus algorithm. It means that every node takes the minimum of the messages of neighbors and their own. This algorithm has time complexity $\text{diam}(\mathcal{G})$ for fixed graphs \mathcal{G} . Therefore, to implement a new iteration of the dynamic equation (12), each node first implements a min consensus algorithm during $\text{diam}(\mathcal{G})$ rounds to obtain the new $\epsilon^{(k)}$.*

Remark 4 *To have a time-invariant (and more conservative) ϵ given in Theorem 3, we can use the fact that $\max_{i,j}(f_i^{(k)} - f_j^{(k)}) \leq 2 \max_i |f_i^{(k)}| \leq 2 \max_i r_i + \Gamma$ provided $p^{(k)} \in (0, 1)^N$ by Lemma 5. Then, ϵ can be chosen as $\epsilon < \frac{1}{2 \max_i r_i + \Gamma}$. This time-invariant step size can be determined by using a min consensus algorithm before running the CONSTRAINED EULER REPLICATOR algorithm.*

Remark 5 *The evolution of $p^{(k)}$ in the CONSTRAINED EULER REPLICATOR algorithm is equivalent to the evolution of (13), then the equilibrium point, properties and the stability analysis already done for (13) hold for the CONSTRAINED EULER REPLICATOR algorithm. However, notice when some $\alpha_i^{(k)} > 0$ in the CONSTRAINED EULER REPLICATOR algorithm, then $\mathbf{1}_N^T \delta^{(k)} \leq \Gamma$, but this can only happen for some finite time since $p^{(k)} \rightarrow p^*$ asymptotically as shown in Theorem 3, and for $k > K$ (i.e., when trajectories are close to the equilibrium) we know that $\mathbf{1}_N^T \delta^{(k)} = \Gamma$.*

Remark 6 *The reader may infer that the result in Theorem 3 can be obtained by the consensus algorithm of [16] instead of using the proposed algorithm (13). However, consensus algorithms consider linear multiagent interactions and, thus, it employs linear systems tools. Our algorithm is nonlinear and requires nonlinear tools to prove stability. The extent of this generalization is analogous to what happens with respect to linear versus nonlinear system stability analysis. Moreover, by means of our proposed algorithm, we solve a constrained optimization problem that cannot be solved by the consensus algorithm of [16]. One simple fact to see why the algorithms are not comparable is that the simplex is invariant to our*

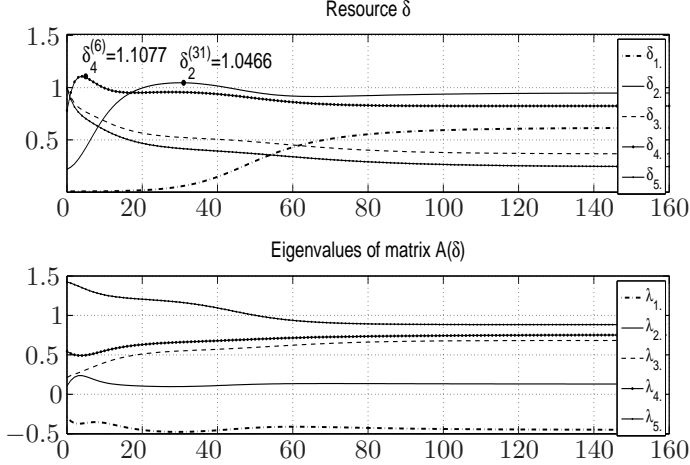


Fig. 1. Trajectories of the example given in (15) for the algorithm in (13).

algorithm, which does not happen with the consensus algorithm.

6 Simulations

In this section, we illustrate the response of the discrete local replicator dynamics in (13) and the CONSTRAINED EULER REPLICATOR algorithm for the symmetric matrix

$$A(\delta) = \begin{bmatrix} 1 - \delta_1 & 1/2 & 0 & 0 & 0 \\ 1/2 & 1 - \delta_2 & 0 & 1/3 & 0 \\ 0 & 0 & 1 - \delta_3 & 1/4 & 0 \\ 0 & 1/3 & 1/4 & 1 - \delta_4 & 1/8 \\ 0 & 0 & 0 & 1/8 & 1 - \delta_5 \end{bmatrix}, \quad (15)$$

subject to $\Gamma = 3$. In order to exemplify a switching topology, we use a pseudorandom number $0 - 1$ given by a uniform distribution for every edge of the associated adjacency matrix of $A(\delta)$ during the evolution $\delta^{(k)}$. In Figure 1, we show the behavior of (13) for $\epsilon = 1/2$ and the initial condition $\delta^{(0)} = \Gamma[2/768, 56/768, 2/6, 200/768, 254/768]$ and $\lambda_1(A(\delta^{(0)})) = 1.424$. Since $\lambda_1(A(\delta^{(0)})) > 1$, then the virus is spreading over the network. The optimal value is $\delta^* = \Gamma[0.2056, 0.3167, 0.1222, 0.2750, 0.0806]$ and the minimizer is $\lambda_1(A(\delta^*)) = .8833$. Since $\lambda_1(A(\delta^*)) < 1$, we achieve the main objective that is to give an optimal response to stop the epidemics by our dynamic algorithm. Notice that, the discrete local replicator dynamics in (13) does not satisfy $\delta^{(k)} \leq 1$ for $k > 0$ in general. This fact is exemplified in Figure 1, where $\delta_3^{(0)} = 1$, $\delta_2^{(24)} = 1.0466$, and $\delta_4^{(6)} = 1.1077$. This issue is solved by the CONSTRAINED EULER REPLICATOR algorithm, which performance is shown in Figure 2 for the same

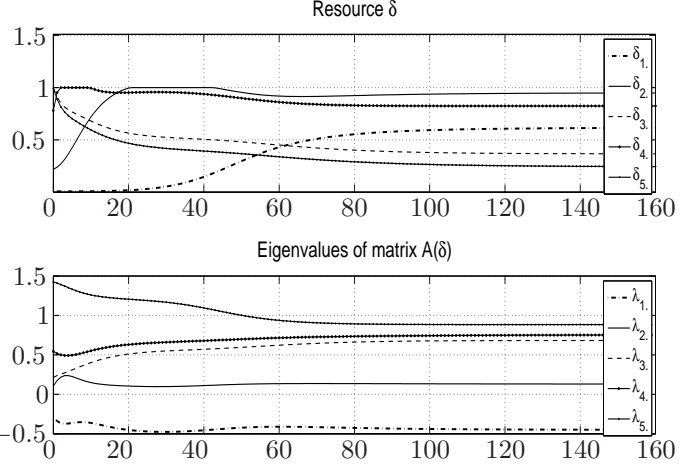


Fig. 2. Trajectories of the example given in (15) for the CONSTRAINED EULER REPLICATOR algorithm.

conditions as for Figure 1. Figure 2 shows that the CONSTRAINED EULER REPLICATOR algorithm converges to the desired equilibrium point of (13). Also, note that $\delta_i^{(k)} \leq 1$ for $k \geq 0$ and $i \in \{1, \dots, 5\}$, which shows that the algorithm constraints its states as expected. Figure 3 shows the performance of the CONSTRAINED EULER REPLICATOR algorithm for initial conditions $\delta^{(0)} = \Gamma[1/256, 1/2, 127/256]$, $\Gamma = 2$, and the following unbalanced topology matrix

$$A(\delta) = \begin{bmatrix} 1 - \delta_1 & 1/10 & 0 \\ 1/4 & 1 - \delta_2 & 1/16 \\ 1/8 & 1/16 & 1 - \delta_3 \end{bmatrix}. \quad (16)$$

The trajectories for this example are shown in Figure 3, where we use $\hat{A}(\delta)$ as shown in Lemma 4 to approximate the solution given by the CONSTRAINED EULER REPLICATOR algorithm to the optimal one. Using the same notation of the variables as defined in Lemma 4, we get $\delta^{*3} = [0.70415, 0.70415, 0.5917]$, $\rho(A(\delta^{*3})) = 0.5010$, $\delta^{*1} = [17/30, 187/240, 157/240]$, $\delta^{*2} = [101/120, 151/240, 127/240]$, $\rho(A(\delta^{*1})) = \rho(A(\delta^{*2})) = 0.5333$. The optimal value is $\rho^*(A(\delta^*)) = 0.5002$ for $\delta^* = [0.6884, 0.7199, 0.5917]$. This example shows that the expected error is achieved.

The following example is based on the e-mail communication network from the Enron corporation, constructed by taking the first 600 nodes from the dataset available in [13]. We fix the probabilities of transmission to be proportional to the in-degree of each node on the network. Figure 4 shows the performance of the CONSTRAINED EULER REPLICATOR algorithm for this example. The initial conditions for this example are $\delta^{(0)} = \frac{\Gamma}{N} \mathbf{1}_N$, $\Gamma = 40$. Figure 4 shows that starting from $\rho(A(\delta^{(0)})) > 1$ we get $\rho(A(\delta^*)) = .9588$ by using the CONSTRAINED EULER

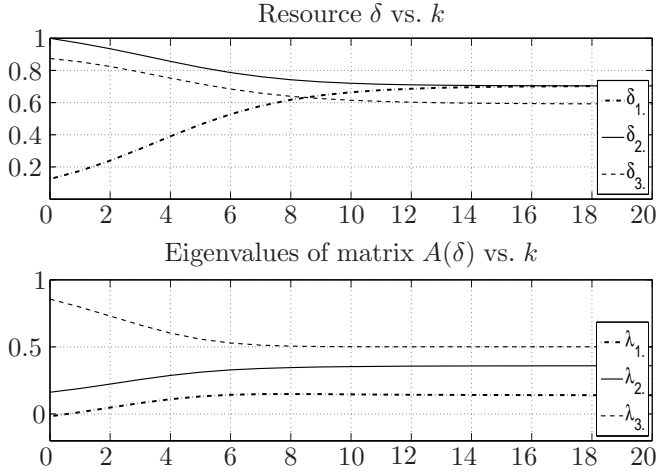


Fig. 3. Trajectories of the CONSTRAINED EULER REPLICATOR algorithm for the approximation to the optimum given by Lemma 4

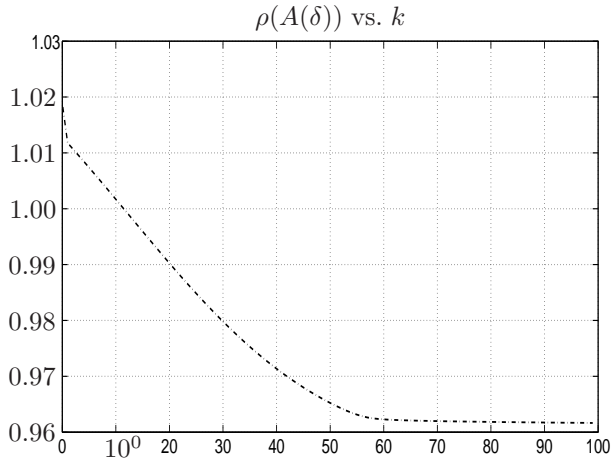


Fig. 4. Trajectories of the CONSTRAINED EULER REPLICATOR algorithm for the Enron network example.

REPLICATOR algorithm.

7 Conclusions

We have studied a virus minimization problem for a general SIS model, characterizing an explicit solution to the problem for weight-balanced contagion-dynamics matrices. We have given a strategy that stabilizes the spread for general network topologies when there are enough network resources. Based on that characterization, we have proposed a novel discrete-time distributed algorithm to stop infection spreading under time varying topologies. Our approach solves the optimization problem by allocating limited immunization resources under the system constraints. As future work we would like to consider more sophisticated constraints in the problems

we have stated. For example we could consider a constraint of the form $\sum c(\delta_i) \leq \Gamma$ (where c is the cost of modifying the rate δ_i) instead of the original one $\delta_i = \Gamma$.

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A Proofs

PROOF. [Theorem 2] Since $A(\delta)$ is nonnegative and irreducible for all δ , by the Perron-Frobenius theorem we have that $\rho(A) \leq \max_i \{-\delta_i + r_i\}$. In order to obtain an upper bound for $\rho^*(A(\delta^*))$, we minimize the maximum row sum of $A(\delta)$, i.e,

$$\begin{aligned} & \min_{\delta} (\max_i -\delta_i + r_i) \\ & \text{subject to} \\ & \sum_{i=1}^N \delta_i = \Gamma. \end{aligned} \tag{A.1}$$

The problem stated in (A.1) can be reformulated as

$$\begin{aligned} & \min_{z, \delta} z \\ & \text{subject to} \\ & z \geq \max_i (-\delta_i + r_i), \\ & \sum_{i=1}^N \delta_i = \Gamma, \end{aligned} \tag{A.2}$$

where $z \in \mathbb{R}$ is a new variable. It holds that $z \geq \max_i (-\delta_i + r_i)$ if and only if $z \geq -\delta_i + r_i$ for all $i \in \{1, \dots, N\}$. Then, the Lagrangian of (A.2) is given by

$$\mathcal{L}(z, \delta, \nu, \mu) = z + \nu \left(\sum_{i=1}^N \delta_i - \Gamma \right) + \sum_{i=1}^N \mu_i (-z - \delta_i + r_i),$$

where ν , and $\mu = [\mu_1, \dots, \mu_N]$ are the KKT multipliers for the equality and inequality constraints, respectively. Suppose that $\bar{y}^* = (\bar{\mu}^*, \bar{z}^*, \bar{\delta}^*, \bar{\nu}^*)$ is a solution to (A.2). From complementary slackness, we have $\bar{\mu}_i^* (-\bar{z}^* - \bar{\delta}_i^* + r_i) = 0$ for all $i \in \{1, \dots, N\}$. Moreover, $\frac{\partial \mathcal{L}}{\partial z} \Big|_{\bar{y}^*} = 1 - \sum_{i=1}^N \bar{\mu}_i^* = 0$, $\frac{\partial \mathcal{L}}{\partial \delta_i} \Big|_{\bar{y}^*} = \bar{\nu}^* - \bar{\mu}_i^* = 0$, and $\bar{\nu}^* = \bar{\mu}_i^* = \frac{1}{N}$. A critical point is given when $\bar{z}^* = -\bar{\delta}_i^* + r_i, \forall i \in \{1, \dots, N\}$. Note that all $\bar{\mu}_i^*$ are active (i.e, $\bar{\mu}_i^* > 0$). From the fact that problem (A.2) gives an upper bound to the solution of the VIRUS SPREAD MINIMIZATION problem without the $\delta \in [0, 1]^N$ restriction, it follows that $\rho^*(A(\delta^*)) \leq \bar{z}^* = \max_i \{-\bar{\delta}_i^* + r_i\}$. Since $\bar{z}^* = \max_i \{-\bar{\delta}_i^* + r_i\} = \min_i \{-\bar{\delta}_i^* + r_i\} = -\bar{\delta}_i^* + r_i, \forall i$, so $\bar{z}^* = -\bar{\delta}_i^* + r_i, \forall i$. Similarly, an analogous condition holds when we consider $\rho(A(\delta)^T) \geq \min_i \{-\delta_i + c_i\}$, which follows from the Perron-Frobenius theorem. The analogous problem to (A.1) with the alternative objective $\max_{\delta} \min_i (-\delta_i + c_i)$ leads to a solution $\underline{z}^* = -\underline{\delta}_i^* + c_i, \forall i$, which satisfies $\underline{z}^* \leq \rho^*(A(\delta^*)^T)$.

From $\rho(A(\delta)) = \rho(A(\delta)^T)$ for any δ , we obtain the relation $\underline{z}^* \leq \rho^*(A(\delta^*)) \leq \bar{z}^*$. Using that $\sum_i \delta_i = \Gamma$, and that $\bar{z}^* = -\bar{\delta}_i^* + r_i$ (resp. $\underline{z}^* = -\underline{\delta}_i^* + c_i$) for

all $i \in \{1, \dots, N\}$, we obtain (7) (resp. the analogous equation to (7) with c_i replacing r_i). From the weight-balanced property of $I_N + G$, we have that $r_i = c_i$ for all $i \in \{1, \dots, N\}$, and thus $\bar{\delta}_i^* = \underline{\delta}_i^*$ for all $i \in \{1, \dots, N\}$. Thus, $\underline{z}^* = \bar{z}^* = \rho^*(A(\delta^*))$.

Finally, (8) is obtained by replacing (7) into the expression $\rho^*(A(\delta^*)) = -\delta_i^* + r_i$. \square

PROOF. [Corollary 1] For the left-hand side of the inequality (9), assume $\delta_i^* \geq 0$. It follows that $Nr_i - \sum_{j=1}^N r_j + \Gamma \geq 0$, which is equivalent to $\Gamma \geq \max_i (\sum_{k,j=1, j \neq k}^N \beta_{jk} - N \sum_{j=1, j \neq i}^N \beta_{ji})$. The right-hand side of inequalities (9) and inequality (10) follows from imposing $1 - \delta_i^* \geq 0$, $i \in \{1, \dots, N\}$. By replacing δ_i^* in $N - N\delta_i^* \geq 0$ from (8), we have that

$$\begin{aligned} \Gamma &\leq \sum_{j=1}^N r_j - Nr_i + N \iff \\ \Gamma &\leq N + \sum_{i,j=1, j \neq i}^N \beta_{ji} - N(1 + \sum_{j=1, j \neq i}^N \beta_{ji}) + N. \end{aligned}$$

It holds that $\Gamma \leq N + \sum_{i,j=1, j \neq i}^N \beta_{ji} - N \sum_{j=1, j \neq i}^N \beta_{ji}$ if and only if $\Gamma \leq \sum_{i,j=1, j \neq i}^N \beta_{ji} + N(1 - \max_i \sum_{j=1, j \neq i}^N \beta_{ji})$. For the left-hand side of the inequality (10), assume $\rho^*(A(\delta^*)) < 1$. By replacing (7) in the previous inequality, we obtain $\Gamma > \sum_{j=1}^N r_j - N$. The result follows after replacing the definition of r_j , $j \in \{1, \dots, N\}$. Notice that $\sum_{i,j=1, j \neq i}^N \beta_{ji} \geq \max_i (\sum_{k,j=1, j \neq k}^N \beta_{jk} - N \sum_{j=1}^N \beta_{ji})$, then the left side of the inequality (10) implies that $\delta_i^* \geq 0$. \square

PROOF. [Lemma 1] For the first inequality we use the fact that $\rho(A) \leq \|A\|$ holds for any matrix A , [12]. Notice that $\bar{A}(\delta)$ can be expressed as $\bar{A}(\delta) = \frac{1}{2}(A(\delta) + A^T(\delta))$. Then, $\|\bar{A}(\delta)\| = \frac{1}{2}\|A(\delta) + A^T(\delta)\| \leq \frac{1}{2}(\|A(\delta)\| + \|A^T(\delta)\|) = \|A(\delta)\|$, it follows that $\min_\delta \rho(\bar{A}(\delta)) \leq \min_\delta \|A(\delta)\| \leq \min_\delta \|A(\delta)\|$. For the second inequality, we refer the reader to [7], where it is proven that $\rho(A) \leq \rho(\frac{1}{2}(A + A^T))$ for any nonnegative matrix A , so the result follows. \square

PROOF. [Lemma 2] We have that $\min_\delta \|A(\delta)\| < 1 \implies \rho^*(A(\delta^*)) < 1$, then it holds that $\min_\delta \rho(\bar{A}(\delta)) < 1 \implies \rho^*(A(\delta^*)) < 1$. Thus, there exists δ satisfying the constraints of the VIRUS MITIGATION problem if there exists δ satisfying the constraints of Problem (11). \square

PROOF. [Lemma 3] Notice that $\bar{A}(\delta) = I_N - D + \frac{1}{2}(G + G^T)$, is symmetric, so we can apply Corollary 1 for

$\rho^*(\bar{A}(\delta^*))$ under the sufficient condition (9) for Γ . The upper bound follows from $\rho^*(A(\delta^*)) \leq \rho^*(\bar{A}(\delta^*))$. \square

PROOF. [Lemma 4] Note that the solution given by Lemma 3 is the middle point between δ^{*1} and δ^{*2} . Also note that $\rho(A(\delta^{*1})) = \rho(A(\delta^{*2}))$. By the convexity of $\rho(A(\delta))$ in Theorem 1, we know that $\min\{\delta_i^{*1}, \delta_i^{*2}\} \leq \delta_i^* \leq \max\{\delta_i^{*1}, \delta_i^{*2}\}$, so the result follows. \square

PROOF. [Lemma 5] We have to show two properties to conclude that Δ_p is invariant under (13). First, it holds that $\mathbf{1}_N^T p^{(k+1)} = \mathbf{1}_N^T p^{(k)}$, and second, $p_i^{(k)} > 0$ for all $i \in \{1, \dots, N\}$, and $k > 0$, for a small enough step size. To show the first property, we multiply by $\mathbf{1}_N^T$ on both sides of (13)

$$\mathbf{1}_N^T p^{(k+1)} = \mathbf{1}_N^T p^{(k)} + \epsilon^{(k)} (\bar{f}^{(k)T} \mathcal{A} p^{(k)} - p^{(k)T} \mathcal{A} \bar{f}^{(k)}),$$

where we use the fact $p^{(k)T} = \mathbf{1}_N^T \text{diag}(p^{(k)})$, and $\bar{f}^{(k)T} = p^{(k)T} \text{diag}(f^{(k)})$. Since the matrix \mathcal{A} is symmetric, then we have the property $p^{(k)T} \mathcal{A} \bar{f}^{(k)} = \bar{f}^{(k)T} \mathcal{A} p^{(k)}$. Therefore, we have that $\mathbf{1}_N^T p^{(k+1)} = \mathbf{1}_N^T p^{(k)}$ for any $\epsilon^{(k)} > 0$. For the second property, we rewrite (12) as $p_i^{(k+1)} = p_i^{(k)}(1 - \Delta_i^{(k)})$, where $\Delta_i^{(k)} \triangleq \epsilon^{(k)} (\bar{f}_i^{(k)} - f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)})$. Then,

$$\begin{aligned} \max_i \Delta_i^{(k)} &= \epsilon^{(k)} \max_i \sum_{j \in \mathcal{N}_i} p_j^{(k)} (f_j^{(k)} - f_i^{(k)}) \\ &\leq \epsilon^{(k)} \max_{i,j} (f_i^{(k)} - f_j^{(k)}). \end{aligned}$$

Then, a sufficient condition for which $\max_i \Delta_i^{(k)} < 1$ is given when $\epsilon^{(k)} < \frac{1}{\max_{i,j} (f_i^{(k)} - f_j^{(k)})}$. \square

PROOF. [Lemma 6] Clearly, an equilibrium point is $p_i^* = 0$ for all $i \in \{1, \dots, N\}$, but by assumption we only consider $p^* > 0$. Now, suppose $p^* > 0$, then it must be that

$$\sum_{j \in \mathcal{N}_i} p_j^* (f_i^* - f_j^*) = 0, \quad (\text{A.3})$$

for all $i \in \{1, \dots, N\}$. By assumption we have that Γ is large enough, or in other words, the size of Γ allows $f_i^* = f_j^*$ for all $i, j \in \{1, \dots, N\}$ and $p^* > 0$. Since \mathcal{G} is connected, then (A.3) holds if $f_i^* = f_j^*$ for all $i, j \in \{1, \dots, N\}$. Now we proceed to show the uniqueness of this solution. For that, we want to show that the set $J = \{p \in \mathbb{R}^N \mid f_i(p_i) = f_j(p_j) \forall i, j \in \{1, \dots, N\}, \mathbf{1}_N^T p = 1\}$

reduces to a single point p^* . By assumption f_i is a strictly decreasing monotone function and its inverse f_i^{-1} always exists. Notice that f_i^{-1} is decreasing since $f_i \circ f_i^{-1} = 1$, and $\frac{\partial f_i^{-1}}{\partial p_i} = \left(\frac{\partial f_i}{\partial p_i}\right)^{-1} < 0$. Assume that there exists $\hat{\alpha} \neq \bar{\alpha}$ for $\hat{\alpha}, \bar{\alpha} \in \mathbb{R}$ such that $\hat{p} = f^{-1}(\hat{\alpha} \mathbf{1}_N)$, and $\bar{p} = f^{-1}(\bar{\alpha} \mathbf{1}_N)$, which satisfies $\mathbf{1}_N^T \hat{p} = \mathbf{1}_N^T \bar{p} = 1$. Write $\hat{p} - \bar{p} = f^{-1}(\hat{\alpha} \mathbf{1}_N) - f^{-1}(\bar{\alpha} \mathbf{1}_N)$. Multiplying last expression by $\mathbf{1}_N^T$, it follows

$$\sum_{j=1}^N (f_j^{-1}(\hat{\alpha}) - f_j^{-1}(\bar{\alpha})) = \mathbf{1}_N^T \hat{p} - \mathbf{1}_N^T \bar{p} = 0. \quad (\text{A.4})$$

Recall that f_i is strictly decreasing monotone function, i.e., for $x, y \in \mathbb{R}$ we have that $f_i(x) < f_i(y)$ iff $x > y$. Using last fact we have that $f_i^{-1}(x) < f_i^{-1}(y)$ iff $x > y$. Without loss of generality assume $\hat{\alpha} > \bar{\alpha}$ (if the opposite inequality is satisfied, simply switch the roles of $\hat{\alpha}$ and $\bar{\alpha}$ in what follows), then $f_i^{-1}(\hat{\alpha}) < f_i^{-1}(\bar{\alpha})$ (Recall $\hat{\alpha} \neq \bar{\alpha}$ by assumption). We have that $f_i^{-1}(\hat{\alpha}) - f_i^{-1}(\bar{\alpha}) < 0$, which implies that $f_i^{-1}(\hat{\alpha})$ and $f_i^{-1}(\bar{\alpha})$ have the same sign. Therefore, the only solution to (A.4) is given when $\hat{\alpha} = \bar{\alpha}$, and the set \mathcal{J} reduces to a single point p^* . \square

PROOF. [Lemma 7] Note that \mathcal{G} is not necessary connected. In order to get (14), we use $\sum_{j \in \mathcal{X}} p_j^{(k)} = \sum_{j \in \mathcal{X}} p_j^{(0)}$ for all $k \geq 0$, which is given by the conservativeness of the states in Lemma 5. We have that $f_i^* = f_j^*$ for all $i, j \in \mathcal{X}$ by Lemma 6. It follows $\Gamma p_i^* \sum_{j \in \mathcal{X}} 1 = \sum_{j \in \mathcal{X}} (r_i - r_j + \Gamma p_j^*)$, and the result follows. Notice that when the graph is connected we have the same expression as in (8). \square

PROOF. [Theorem 3] Let $f(p) = [f_1(p_1), \dots, f_N(p_N)]$ be the vector representation of the fitnesses. Consider the Lyapunov function candidate $V : \mathbb{R}^N \rightarrow \mathbb{R}$, $V(f^{(k)}(p)) = \max_{i \in \mathcal{V}} f_i^{(k)}(p_i)$. Notice that V is a valid Lyapunov function because $f(p^*)$ is a global minimum by Theorem 2, and then $V(f^{(k)}(p)) \geq V(f(p^*))$. Define $\Delta V^{(k)} = V(f^{(k+1)}(p)) - V(f^{(k)}(p))$, for all $k \geq 0$, where $V(f^{(k+1)}(p)) = \max_i f_i^{(k+1)} = \max_i \{r_i - \Gamma p_i^{(k+1)}\}$. Then,

$$\begin{aligned} \Delta V^{(k)} &= \max_{i \in \mathcal{V}} f_i^{(k+1)} - \max_{i \in \mathcal{V}} f_i^{(k)} \\ &= \max_{i \in \mathcal{V}} \left(r_i - \Gamma p_i^{(k)} - \epsilon^{(k)} \Gamma p_i^{(k)} f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} \right. \\ &\quad \left. + \epsilon^{(k)} \Gamma p_i^{(k)} \bar{f}_i^{(k)} \right) - \max_{i \in \mathcal{V}} f_i^{(k)} \end{aligned}$$

$$\begin{aligned} &= \max_{i \in \mathcal{V}} \left(f_i^{(k)} + \epsilon^{(k)} \Gamma p_i^{(k)} \bar{f}_i^{(k)} \right. \\ &\quad \left. - \epsilon^{(k)} \Gamma p_i^{(k)} f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} \right) - \max_{i \in \mathcal{V}} f_i^{(k)} \\ &= \max_{i \in \mathcal{V}} \left(f_i^{(k)} + \epsilon^{(k)} \Gamma p_i^{(k)} (\bar{f}_i^{(k)} - f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)}) \right. \\ &\quad \left. - \max_{l \in \mathcal{V}} f_l^{(k)} \right). \end{aligned}$$

Let $f_{\max}^{(k)} = \max_{i \in \mathcal{V}} f_i^{(k)}$. Then,

$$\begin{aligned} \Delta V^{(k)} &= \max_{i \in \mathcal{V}} \left(f_i^{(k)} + \epsilon^{(k)} \Gamma p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} f_j^{(k)} \right. \\ &\quad \left. - \epsilon^{(k)} \Gamma p_i^{(k)} f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} - f_{\max}^{(k)} \right) \\ &= \max_{i \in \mathcal{V}} \left(f_i^{(k)} - \epsilon^{(k)} \Gamma p_i^{(k)} f_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} - f_{\max}^{(k)} \right. \\ &\quad \left. + \epsilon^{(k)} \Gamma p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} (f_j^{(k)} + f_{\max}^{(k)} - f_{\max}^{(k)}) \right) \\ &= \max_{i \in \mathcal{V}} \left(-\epsilon^{(k)} \Gamma p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} (f_{\max}^{(k)} - f_j^{(k)}) \right. \\ &\quad \left. - (1 - \epsilon^{(k)} \Gamma p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)}) (f_{\max}^{(k)} - f_i^{(k)}) \right). \end{aligned} \quad (\text{A.5})$$

We require $\Delta V^{(k)} \leq 0$, so, it is sufficient to guarantee that $1 - \epsilon^{(k)} \Gamma p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} > 0$ since $(f_{\max}^{(k)} - f_i^{(k)}) \geq 0$. For that we choose $\epsilon^{(k)} < \min \left\{ \frac{1}{\max_{i,j} (f_i^{(k)} - f_j^{(k)})}, \frac{1}{\Gamma \max_i p_i^{(k)}} \right\}$.

Note that if $\max_{i,j} (f_i^{(k)} - f_j^{(k)}) \geq \Gamma \max_i p_i^{(k)}$, then $\epsilon^{(k)} \Gamma p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} < 1$ since $p_i^{(k)} \in \Delta_p$ by Lemma 5. On the other hand, if $\max_{i,j} (f_i^{(k)} - f_j^{(k)}) < \Gamma \max_i p_i^{(k)}$, then $\epsilon^{(k)} < \frac{1}{\Gamma \max_i p_i^{(k)}} \leq \frac{1}{\max_{i,j} (f_i^{(k)} - f_j^{(k)})}$, and $p_i^{(k)} \in \Delta_p$ by Lemma 5. Then, $\Delta V^{(k)} \leq 0$ in any case.

We have just shown that $\Delta V^{(k)}$ is non-positive. We show next that there is not trajectory that can stay identically at points where $\Delta V^{(k)} = 0$ other than the equilibrium. There are three possible scenarios i) at the equilibrium, ii) when $f_i^{(k)} = f_{\max}^{(k)}$ for some $i \in \mathcal{V}$, $f_j^{(k)} = f_{\max}^{(k)}$ for all $j \in \mathcal{N}_i$ and $|\mathcal{V}_{\text{eq}}^{(k)}| < N$, where $\mathcal{V}_{\text{eq}}^{(k)} = \{i \in \mathcal{V} | f_i^{(k)} = f_{\max}^{(k)}\}$, and iii) when $f_i^{(k)} = f_{\max}^{(k)}$ for some $i \in \mathcal{V}$, and $\mathcal{N}_i = \emptyset$.

For case (ii), we have $\mathcal{V}_{\text{eq}}^{(k)} \subset \mathcal{V}$. Let $\gamma \triangleq \max\{\text{dist}(l, j) \mid l \in \mathcal{V} \setminus \mathcal{V}_{\text{eq}}^{(k)}, j \in \mathcal{V}_{\text{eq}}^{(k)}\}$, that is, γ defines the maximum distance between nodes with maximum fitness and nodes with strictly smaller fitness. Next, we characterize γ for time-invariant \mathcal{G} . Assume $\Delta V^{(k)} = 0$ but trajectories are not at the equilibrium. Define $\Delta f_i^{(k)} = f_i^{(k+1)} - f_i^{(k)}$. Pick $i \in \mathcal{V}_{\text{eq}}^{(k)}$ such that there exists some neighbor j satisfying $j \in \mathcal{N}_i \cap (\mathcal{V} \setminus \mathcal{V}_{\text{eq}}^{(k)})$. Note that node i always exists since the assumption that the graph is connected. Using an analogous procedure as the one to show that $\Delta V^{(k)}$ is non-positive, and the fact that at least one node $j \in \mathcal{N}_i$ does not have maximum fitness, it follows that $f_{\max}^{(k)} - f_j^{(k)} < 0$ for some $j \in \mathcal{N}_i$, so that $\Delta f_i^{(k)} = f_i^{(k+1)} - f_{\max}^{(k)} = -p_i^{(k)} \sum_{j \in \mathcal{N}_i} p_j^{(k)} (f_{\max}^{(k)} - f_j^{(k)}) < 0$. Then $|\mathcal{V}_{\text{eq}}^{(k+1)}| < |\mathcal{V}_{\text{eq}}^{(k)}|$. Repeat this process γ times (note that γ is an upper bound for the time that it takes a node with maximum fitness to interact with a neighbor having strictly smaller fitness), then after $m > k + \gamma$ at most the number of agents having $f_{\max}^{(k)}$ is 1 or else $f_i^{(m)} < f_{\max}^{(k)}$, which implies $\Delta V^{(m+k)} < 0$ if trajectories are not at equilibrium. Therefore, $V(f^{(k+\gamma)}(p)) - V(f^{(k)}(p)) < 0$. Note for the time-variant $\mathcal{G}^{(k)}$ the bound γ can increase with respect to the one shown in the time-invariant \mathcal{G} since there exists the possibility that at some instant a vertex in $\mathcal{V}_{\text{eq}}^{(k)}$ does not have a neighbor with fitness less than $f_{\max}^{(k)}$, but γ is finite since the union of graphs is connected as $k \rightarrow \infty$, which implies that trajectories do not get trapped in $\Delta V = 0$.

For case (iii), we have that at least one node $i \in \mathcal{V}_{\text{eq}}^{(k)}$ will have a neighbor $j \in \mathcal{V} \setminus \mathcal{V}_{\text{eq}}^{(k)}$ such that $f_j^{(k)} < f_{\max}^{(k)}$ as $k \rightarrow \infty$, let say that this happens at instant $m + 1 \geq k$, then $\Delta f_i^{(m+1)} = f_i^{(m+1)} - f_{\max}^{(m)} = -p_i^{(m)} \sum_{j \in \mathcal{N}_i} p_j^{(m)} (f_{\max}^{(m)} - f_j^{(m)}) < 0$, then $|\mathcal{V}_{\text{eq}}^{(m+1)}| < |\mathcal{V}_{\text{eq}}^{(m)}|$. The same process occurs for all nodes in $\mathcal{V}_{\text{eq}}^{(k)}$ since the union of graphs is connected as $k \rightarrow \infty$. Therefore, by LaSalle's invariance principle, every trajectory starting in Δ_p approaches f^* as $k \rightarrow \infty$. \square