

A Distributed Algorithm for Virus Spread Minimization

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Abstract—This paper proposes a discrete-time distributed algorithm based on a local replicator dynamics that allows a group of nodes to achieve virus mitigation over a connected graph when subject to limited resources. The algorithm is distributed in the sense that it can be implemented by the network nodes via local and anonymous interactions. By employing a discrete-time LaSalle invariance principle, we find a bound on the algorithm step size that guarantees asymptotic convergence for agents subject to time-varying interactions. Several simulations illustrate the algorithm performance.

I. INTRODUCTION

Virus spread in computer and human networks is a subject of public concern, as it threatens the security of critical infrastructure and the well-being of the general population. Highly-connected, dynamic networks makes the implementation of strategies to stop epidemics a challenge in scenarios involving multiple operators. First, a collective decision must be made about what the best responses are for the rapid vaccination and/or isolation of infected individuals, possibly under scarce resources, restricted communications, and partial network knowledge. Secondly, a distributed and robust implementation of these best responses over networks calls for the use of distributed algorithms that the multiple operators can employ for this purpose. In this paper, we precisely aim to study such issues for particular classes of network graphs.

Literature review. A main approach to model virus spreading and contagion over networks is given by the SIS (susceptible-infected-susceptible) model and its variations; see [1], [2], [3], [4], which validate such models for virus propagation over computer graphs. Based on this, two main strategies have been proposed to handle infections 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. In this way, [5] and [6] 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 [7], 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 [7] 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.

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A recent formulation of the optimal vaccination for the case of continuous time dynamics is given in [8]. In [8] the authors propose a convex optimization framework to find the optimal allocation of resources under local constraints, nonetheless, this solution is not distributed neither decentralized. Ideas of distributed control have been commonly applied to distributed consensus algorithms [9], [10], where the central focus 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 [11], 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.

Statement of contributions. In this paper, we study a virus mitigation problem based on a general contagion dynamics model. The problem objective is posed by the minimization of the spectral radius of the contagion-dynamics matrix subject to operational constraints. By employing the Perron-Frobenius theorem, 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 provide bounds for the solution in terms of the associated symmetrized problem. After this, we propose a distributed algorithm that implements the desired resource allocation for symmetric matrices. In contrast with previous work, our algorithm can be implemented 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. By means of 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.

Organization. The remainder of this article is organized as follows. Section II presents the mathematical background including some graph theory concepts, as well as some definitions that are used throughout the paper. The problem statement is presented in Section III, where we include a characterization of the solution for weight-balanced matrices as well as a bound for the general case. Next, in Section IV, we introduce some notions on the replicator dynamics as well as the proposed algorithm. In Section V, we present a stability analysis of the algorithm and show bounds for the step size that guarantees asymptotic convergence under time-varying graphs. Section VII presents some simulation results, followed by a discussion of the advantages of using the proposed algorithm.

II. PRELIMINARIES

This section presents notation and basic notions from graph and matrix theory.

A. Notation

In what follows, we denote by $\mathbb{R}_{\geq 0}^d$ the positive orthant of \mathbb{R}^d , for some $d \in \mathbb{N}$, I_N the identity matrix of size $N \times N$, $\text{diag}(a_1, \dots, a_N)$ the $N \times N$ matrix with entries a_i along the diagonal, 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 $\lambda_i(A) \in \text{spec}(A)$, and its *spectral radius* by $\rho(A) = \max_i |\lambda_i(A)|$. When we use inequalities for vectors, we refer to componentwise inequalities.

B. Matrix and graph-theoretic notions

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} .

III. PROBLEM STATEMENT AND SOLUTION APPROACH

In this section, we first revise the contact network dynamics proposed in [4] and the problem statement proposed in [7], which we adopt here. We then extend a theorem in [7] for symmetric, irreducible matrices to weight-balanced, and irreducible matrices. The main motivation for this extension is given by the possibility of having an asymmetric placement of edge firewalls making the interaction graph directed. Our proof relies on the Perron-Frobenius theorem and the Lagrange multiplier approach, instead of using a sensitivity formula. Notice that all proofs of this paper will be found in a forthcoming publication.

Next, for any nonnegative matrix we propose a strategy for virus spread minimization that minimizes the Perron eigenvalue of the symmetrized counterpart, and we characterize the goodness of this approximation.

A. Problem Statement

The virus dynamics proposed in [4] is given by

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

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

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

where $x^{(k)} = [x_1^{(k)}, \dots, x_N^{(k)}]^T$. The previous inequality reads in vector notation as

$$x^{(k+1)} \leq A(\delta)x^{(k)}, \quad (2)$$

where $\delta = (\delta_1, \dots, \delta_N) \in [0, 1]^N$, and $A(\delta)$ is defined as

$$A(\delta) = \begin{bmatrix} 1 - \delta_1 & \beta_{21} & \dots & \beta_{n1} \\ \beta_{12} & 1 - \delta_2 & \dots & \beta_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ \beta_{1n} & \beta_{2n} & \dots & 1 - \delta_N \end{bmatrix} = I_N - D + G.$$

Here, $A(\delta) \in \mathbb{R}^{N \times N}$, $D = \text{diag}(\delta)$, and $G = A(\delta) - I_N + D \equiv A(\mathbf{1}_N)$. Let $\mathcal{G}(I_N + A(\mathbf{1}_N)) = \mathcal{G}(I_N + G)$ be the graph associated to the virus 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 [4], authors prove next proposition,

Proposition 1 ([4]): An epidemic described by (1) 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

$$\begin{aligned} & \min_{\delta \in [0, 1]^N} \rho(A(\delta)), \\ & \text{subject to} \\ & \sum_{i=1}^N \delta_i = \Gamma, \\ & \rho(A(\delta)) < 1. \end{aligned} \quad (3)$$

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

$$\begin{aligned} & \min_{\delta \in [0, 1]^N} \rho(A(\delta)), \\ & \text{subject to} \\ & \sum_{i=1}^N \delta_i = \Gamma. \end{aligned} \quad (4)$$

Note that we only consider a partial vaccination strategy, i.e., we only consider as decision variable δ , while β is fixed. We further assume that for the initial condition of the network 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 [12].

B. Solution Characterization for Balanced Matrices

In order to provide sufficient conditions for feasibility for the VIRUS MITIGATION and VIRUS SPREAD MINIMIZATION problems, we present a characterization of the solution to a relaxed problem for weight-balanced matrices in Theorem 2. Previous to this, we recall the next theorem that shows the function $\rho(A(\delta))$ is a convex function of δ and, thus, the problems introduced in Section III-A are convex.

Theorem 1 ([13]): Let A be nonnegative, and $D = \text{diag}(\delta_1, \dots, \delta_N)$. Then, the Perron eigenvalue of $A + D$, $\rho(A + D)$, 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 $I_N + G$, respectively.

Theorem 2: For a weight-balanced, nonnegative, and irreducible matrix $I_N + G$ 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 $i \neq j$. More precisely, the solution is characterized by

$$\rho^*(A(\delta^*)) = \frac{\sum_{j=1}^N r_j - \Gamma}{N}, \quad (5)$$

$$\delta_i^* = \frac{Nr_i - \sum_{j=1}^N r_j + \Gamma}{N}. \quad (6)$$

Corollary 1 (Sufficient conditions for problem feasibility): When $I_N + G$ is weight-balanced, nonnegative, and irreducible, then a feasible solution to the VIRUS SPREAD MINIMIZATION problem is given by (6) if

$$\begin{aligned} \max_i \left(\sum_{k,j=1, j \neq k}^N \beta_{jk} - N \sum_{j=1, j \neq i}^N \beta_{ji} \right) &\leq \Gamma \\ &\leq \sum_{i,j=1, j \neq i}^N \beta_{ji} + N(1 - \max_i \sum_{j=1, j \neq i}^N \beta_{ji}). \end{aligned} \quad (7)$$

Furthermore, a feasible solution to the VIRUS MITIGATION problem is given by (6) if

$$\sum_{i,j=1, j \neq i}^N \beta_{ji} < \Gamma \leq \sum_{i,j=1, j \neq i}^N \beta_{ji} + N(1 - \max_i \sum_{j=1, j \neq i}^N \beta_{ji}). \quad (8)$$

C. Solution Bound for Unbalanced Matrices

When the topology matrix $I_N + G$ is not weight-balanced and there are not enough resources to make it so as in [12], Theorem 2 is not applicable. However, the VIRUS SPREAD MINIMIZATION problem can be relaxed to minimizing $\rho(\bar{A}(\delta))$, where $\bar{A}(\delta) = I_N - D + \frac{1}{2}(G + G^T)$. 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 $\bar{A}(\delta) = I_N - D + \frac{1}{2}(G + G^T)$ be the symmetrization of $A(\delta) = I_N - D + G$. 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:

$$\begin{aligned} \min_{\delta \in [0, 1]^N} \rho(\bar{A}(\delta)) \\ \text{subject to} \\ \sum_{i=1}^N \delta_i = \Gamma, \\ \rho(\bar{A}(\delta)) < 1. \end{aligned} \quad (9)$$

This is based on the two following lemmas.

Lemma 2: An epidemic characterized by (2) will become extinct if only if $\|A(\delta)\| < 1$.

Lemma 3: The VIRUS MITIGATION problem is feasible and only if Problem (9) is feasible. In that case, an upper bound to the solution of the VIRUS MITIGATION problem is given by a solution to Problem (9).

In the next lemma, we describe explicitly the upper bound given by solving problem (9).

Lemma 4: Consider a virus dynamics with associated nonnegative and irreducible G . Let Γ satisfy the sufficient condition (7) for the topology $I_N + \frac{G+G^T}{2}$. Then, an upper bound for the solution of the VIRUS SPREAD MINIMIZATION problem for $I_N + G$ 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 5: Consider a virus dynamics with associated nonnegative and irreducible G . Let Γ satisfy (7) for the topology $I_N + \frac{G+G^T}{2}$. Let δ^{*1} , δ^{*2} and δ^{*3} be the vector solutions given in (6) for the topology matrices $I_N + G$, $I_N + G^T$ and $I_N + \frac{1}{2}(G + G^T)$, respectively. Let δ^* be the solution to the VIRUS MITIGATION 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 4 and the optimal solution δ^* . Then, $e_i \leq \frac{1}{2}|\delta_i^{*1} - \delta_i^{*2}|$, $i \in \{1, \dots, N\}$.

IV. THE CONSTRAINED EULER REPLICATOR ALGORITHM

This section presents the proposed CONSTRAINED EULER REPLICATOR algorithm with which we aim to solve the VIRUS SPREAD MINIMIZATION problem. The algorithm is shown in Section IV-B based on the replicator dynamics and a local version of it. The latter are briefly reviewed in Section IV-A.

A. On the Replicator Dynamics

Replicator dynamics [14], [15], [16] models the interaction of an homogeneous population, where fractions of individuals play a symmetric game. The replicator dynamics is represented by a first-order differential equation that is composed by the *replicator*, its *fitness*, and the proportion in the population. The replicator corresponds to one individual in the population. The fitness, usually positive, is the utility that the individual obtains during the game. Finally, the proportion in the population represents 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

$$\dot{p}_i(t) = p_i(t)(f_i - \bar{f}), \quad (10)$$

where p_i denotes the proportion of individuals that play one strategy $i \in \{1, \dots, N\}$, f_i 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 (10) imposes a useful restriction to the dynamics, as evolutions will belong to the simplex $\Delta_p = \{p \in \mathbb{R}_{>0}^N \mid \sum_{i=1}^N p_i(t) = 1\}$. This motivates the choice of the replicator dynamics to solve the VIRUS MITIGATION and the VIRUS SPREAD MINIMIZATION problems.

A local version of the original replicator dynamics in (10) is proposed in [11] to account for local interactions of fractions of the population over a graph \mathcal{G} :

$$\dot{p}_i(t) = p_i \left(f_i \sum_{j \in \mathcal{N}_i} p_j - \sum_{j \in \mathcal{N}_i} p_j f_j \right), \quad (11)$$

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 local information, then the algorithm described in (11) is distributed. In [11], the authors show that this algorithm conserves the most important characteristics of (10), i.e., i) the simplex is invariant, and ii) the equilibrium point is asymptotically stable in Δ_p .

B. The CONSTRAINED EULER REPLICATOR Algorithm

Consider the network graph \mathcal{G} and the probabilities of transmission $\delta \in [0, 1]^N$. In what follows, assume that the topology matrix $I_N + G$ is nonnegative, symmetric and the graph associated to it is connected. As shown in Theorem 2, the solution to a relaxed version of the VIRUS SPREAD MINIMIZATION problem is given when the sum of the rows in matrix $A(\delta)$ are equal. Because at equilibrium of replicator dynamics all fitnesses are equal and other constraints are naturally satisfied, we aim to solve VIRUS SPREAD MINIMIZATION problem by employing a discretization of (11) and defining the fitness as the i^{th} row sum of matrix $A(\delta)$.

By discretizing the continuous-time local replicator dynamics (11) using Euler first-order differences, we obtain

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

where $k \in \mathbb{N}$, $\bar{f}^{(k)} = \sum_{j \in \mathcal{N}_i} p_j^{(k)} f_j^{(k)}$, 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 $I_N + G$. 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 $\bar{f}^{(k)} = [p_1^{(k)} f_1^{(k)}, \dots, p_N^{(k)} f_N^{(k)}]^T$. Notice that (12) does not constraint its states as $p_i \leq \frac{h_i}{\Gamma}$ for certain desired constraints $h_i > 0$, for $i \in \{1, \dots, N\}$, something required in order to solve the problems of interest. Because of this, we propose a variation of (12) called the CONSTRAINED EULER REPLICATOR algorithm, whose convergence is analyzed in the next section. 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 $\Omega = \{\delta^{(k)} \in \mathbb{R}_{>0}^N \mid \mathbf{1}_N^T \delta^{(k)} = \Gamma, \delta^{(k)} \leq h_i\}$, 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 5 to 7). Note that line 11 restores $\frac{\alpha_i}{\Gamma}$ to $p^{(k+1)}$, i.e., the evolution of $p^{(k)}$ in line 11 is equivalent to the evolution of (12) in any case. The distributed computation of the step size

Algorithm 1: CONSTRAINED EULER REPLICATOR

Input: $h_i, p_i^{(0)}, \Gamma$
1 Initialize $\alpha_i = 0$;
2 for $k > 0$ **do**
3 Compute $p_i^{(k+1)}$ as in (12);
4 $\delta_i^{(k+1)} = \Gamma p_i^{(k+1)}$;
5 **if** $\delta_i^{(k+1)} > h_i$ **then**
6 $\alpha_i^{(k+1)} = \delta_i^{(k+1)} - h_i$;
7 $\delta_i^{(k+1)} = h_i$;
8 **else**
9 $\alpha_i^{(k+1)} = 0$;
10 **end**
11 $p_i^{(k+1)} = \frac{\delta_i^{(k+1)} + \alpha_i^{(k+1)}}{\Gamma}$;
12 $k = k + 1$;
13 end

for the CONSTRAINED EULER REPLICATOR algorithm, and algorithm in (13) is discussed in the next section.

V. STABILITY ANALYSIS

In this section, we study 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 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 $i \in \{1, \dots, N\}$.

We show next that the algorithm in (13) conserves the most important characteristics of (10), i.e., i) the simplex is invariant for small enough step size as shown in Lemma 6,

ii) all individuals get the same fitness at the equilibrium with the choice of an adequate fitness as shown in Lemma 7, and iii) the equilibrium point is asymptotically stable in Δ_p as shown in Theorem 3.

Lemma 6 (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 7 (Equilibria of (13)): Assume that Γ satisfies (7), 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 7, 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 8 (Equilibrium point characterization under (8)): Let \mathcal{G} be a (not necessarily connected) graph, let Γ satisfy (7), 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 (8), the set of neighbors in (12) are time-variant satisfying $\bigcup_{k \geq k_0} \mathcal{G}^{(k)}$ is connected for all $k_0 \in \mathbb{Z}_{\geq 0}$. Then, the equilibrium point is asymptotically stable 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 1: To compute the $\epsilon^{(k)}$ of Theorem 3 in a distributed way, agents can employ a min consensus algorithm. By means of this, 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, in order 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 2: In order 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 6. Then ϵ can be chosen as $\epsilon < \frac{1}{2 \max_i r_i + \Gamma}$. This time-invariant step size can be determined using a min consensus algorithm before running the CONSTRAINED EULER REPLICATOR algorithm.

Remark 3: 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

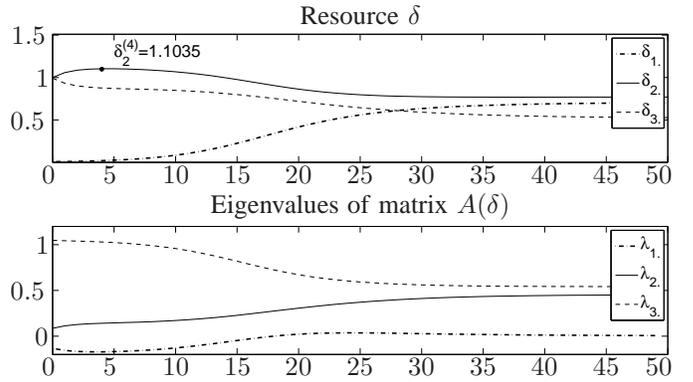


Fig. 1. Trajectories of the example given in (15) for the algorithm in (13) using $\Gamma = 2$, and $\delta^{(0)} = \Gamma[1/256, 1/2, 127/256]$.

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 $\mathbf{1}_N^T \delta^{(k)} = \Gamma$.

VI. SIMULATIONS AND DISCUSSION

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

$$A(\delta) = \begin{bmatrix} 1 - \delta_1 & 1/4 & 0 \\ 1/4 & 1 - \delta_2 & 1/16 \\ 0 & 1/16 & 1 - \delta_3 \end{bmatrix}, \quad (15)$$

subject to $\Gamma = 2$. 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 $\delta^{(0)} = \Gamma[1/256, 1/2, 127/256]$. The optimal value is $\delta^* = \Gamma[0.3542, 0.3854, 0.2604]$. 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 $\delta_2^{(0)} = 1$ and $\delta_2^{(4)} = 1.1035$. This is solved by the CONSTRAINED EULER REPLICATOR algorithm, which performance is shown in Figure 2 for the same 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 $\delta_2^{(k)} \leq 1$ for $k \geq 0$, which shows that the algorithm constrains its states as expected. Figure 3 shows the performance of the CONSTRAINED EULER REPLICATOR algorithm for the same initial condition as in Figure 1, $\Gamma = 2$, and the following unbalanced topology matrix

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

In Figure 3 we use $\bar{A}(\delta)$ as shown in Lemma 5 to approximate the solution given by the CONSTRAINED EULER REPLICATOR algorithm to the optimal one. In this case, we employ the same notation of the variables as defined in Lemma 5. For that, we have $\delta^{*3} = [0.70415, 0.70415, 0.5917]$,

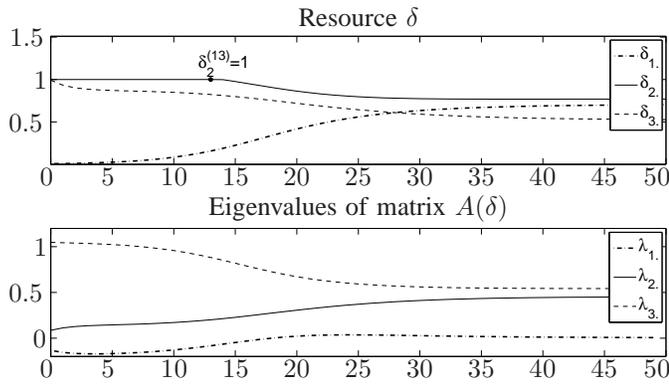


Fig. 2. Trajectories of the example given in (15) for the CONSTRAINED EULER REPLICATOR algorithm using $\Gamma = 2$, and $\delta^{(0)} = \Gamma[1/256, 1/2, 127/256]$.

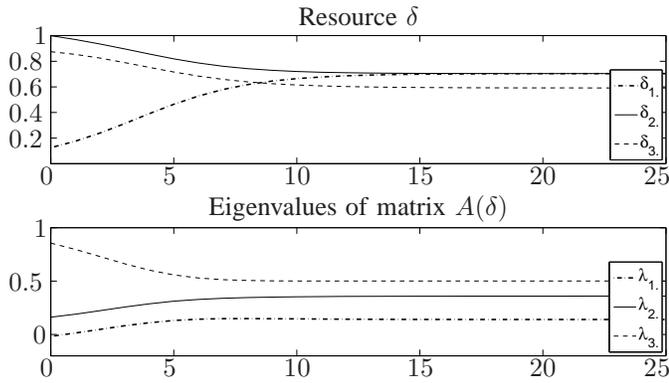


Fig. 3. Trajectories of the CONSTRAINED EULER REPLICATOR algorithm for the approximation to the optimum given by Lemma 5

$\rho(A(\delta^{*3})) = 0.5010$, $\delta^{*1} = [17/30, 187/240, 157/240]$, $\delta^{*2} = [101/120, 151/240, 127/240]$, $\rho(A(\delta^{*1})) = 0.5333$. The optimal value is $\rho^*(A(\delta^*)) = 0.5002$ for $\delta^* = [0.6884, 0.7199, 0.5917]$. These values show that we achieve the expected error. In order to find the optimum $\rho^*(A(\delta^*))$ when the problem is unbalanced, we could exploit the convexity of the cost function $\rho(A(\delta))$ as shown in Theorem 1, and use a line search for every subset of size 2 of the vertex set. That is, for every pair of vertices we could use Lemma 4 to start close to the solution, and then use Lemma 5 for the descent direction for which the Perron eigenvalue is reduced, i.e., starting in δ^{*1} or δ^{*2} , we evaluate δ^{*3} and find if we have to reduce/increase each δ_i for all $i \in \{1, \dots, N\}$. For a small enough step size when reducing/increasing δ and conserving the constraint $\mathbf{1}_N^T \delta = \Gamma$, by convexity on $\rho(A(\delta))$ we know that will converge to the optimal solution. However, the difficulty on following that approach is given by the computation of the Perron eigenvalue in a distributed way, which is out of scope of this paper.

VII. CONCLUSIONS

Here, we have studied a virus mitigation problem for a general SIS model, characterizing an explicit solution to the problem for weight-balanced topology 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 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 study the design of schemes that include the distributed computation of the Perron eigenvector, and the capacity of adapting the topology to minimize the epidemic spread.

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