Brief paper

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 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 simulation examples.

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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 especially 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 scenario, 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., Nowzari, Preciado, & Pappas, 2015; Pastor-Satorras, Castellano, Van Mieghem, & Vespignani, 2014 for surveys over virus models and control). One canonical example is given by the SIS (susceptible–infected–susceptible) model and its variations; see Ahn and Hassibi (2013), Chakrabarti, Wang, Wang, Leskovec, and Faloutsos (2008), Peng, Jin, and Shi (2010), Prakash, Tong, Valler, Faloutsos, and Faloutsos (2010), Wang, Chakrabarti, Wang, and Faloutsos (2003), 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. Along these lines, Enyioha, Preciado, and Pappas (2013) and Tomovski and Kocarev (2012) 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 Wan, Roy, and Saberi (2008), 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 Wan et al. (2008) 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 Wan et al. (2008), the authors in Torres, Roy, and Wan (2015) propose a sparse control allocation of limited resources among a subset of network's components to minimize the dominant eigenvalue of a linear dynamical process associated with the network. However, as in Wan et al. (2008), the proposed algorithm is not distributed itself. A recent formulation of the optimal vaccination for the case of continuous time dynamics is given in Preciado, Zargham, Enyioha, Jadbabaie, and Pappas (2014). In Preciado et al. (2014) the authors propose a geometric programming framework to find the optimal allocation of resources under local constraints, nonetheless, this solution is neither distributed nor decentralized. Ideas of distributed control have been commonly applied to distributed consensus algorithms Bullo, Cortés, and Martínez (2009), Olfati-Saber, Fax, and Murray (2006), 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 Pantoja, Quijano, and Passino (2011), 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 Ramírez and Martínez (2014). 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 $d \in \mathbb{N}$, $\text{diag}(a_1, \ldots, a_N)$ 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 $i, j \in \{1, \ldots, N\}$. 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 $\mathcal{V} = \{1, \ldots, N\}$ 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 (Hofbauer & Sigmund, 1998; Taylor & Jonker, 1978; Weibull, 1997) 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

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

where p_i denotes the proportion of population that play one strategy $i \in \{1, \ldots, N\}$, $f_i : \mathbb{R} \to \mathbb{R}$ 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 $p^* = [p_1^*, \ldots, p_N^*]$. 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 Pantoja et al. (2011) to account for local interactions of fractions of the population over a graph $\mathcal{G}$. The local replicator dynamics is given by

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

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 Pantoja et al. (2011) 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

This section introduces the contact network dynamics proposed in Peng et al. (2010) and the problem statement given in Wan et al. (2008). Next, we extend a theorem in Wan et al. (2008) 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 nonnegative matrix, and we characterize the goodness of this approximation.

3.1. Problem statement

The virus dynamics over a network proposed in Peng et al. (2010) is given by

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