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A Discrete-time Networked Competitive Bivirus SIS Model

Sebin Gracy, Ji Liu, Tamer Başar, and César A. Uribe

Abstract— **The paper deals with the analysis of a discrete-time networked competitive bivirus susceptible-infected-susceptible (SIS) model. More specifically, we suppose that virus 1 and virus 2 are circulating in the population and are in competition with each other. We show that the model is strongly monotone, and that, under certain assumptions, it does not admit any periodic orbit. We identify a sufficient condition for exponential convergence to the disease-free equilibrium (DFE). Assuming only virus 1 (resp. virus 2) is alive, we establish a condition for global asymptotic convergence to the single-virus endemic equilibrium of virus 1 (resp. virus 2) - our proof does not rely on the construction of a Lyapunov function. Assuming both virus 1 and virus 2 are alive, we establish a condition which ensures local exponential convergence to the single-virus equilibrium of virus 1 (resp. virus 2). Finally, we provide a sufficient (resp. necessary) condition for the existence of a coexistence equilibrium.**

I. Introduction

Over the last several decades, modeling and analysis of spreading processes has attracted the attention of researchers across a wide spectrum ranging from mathematical epidemiology [1] and physics [2] to the social sciences [3]. Various models have been studied in the literature; see [4] for a recent overview. This paper focuses on susceptible-infected-susceptible (SIS) models.

While the (networked) SIS model has been studied in detail (see, for instance, [5], [6]), it is not suitable for studying scenarios where there are multiple competing, viruses circulating in the population - a scenario that has been witnessed in the context of spread of gonorrhea and tuberculosis. In the competitive spreading regime, two viruses, say virus 1 and virus 2, simultaneously circulate in the same population - an individual can either be infected with virus 1 or with virus 2 or with neither, but not with both. Competitive bivirus SIS models have been proposed since [7], [8] and more recently in, to cite a few, [9]–[13]. The bulk of the literature on networked competitive bivirus SIS models are focused on the continuous-time case; with the notable exception of [12] (whose analysis of endemic behavior is restricted to providing a lower bound on the number of equilibria) not much attention has been given to the discrete-time networked competitive bivirus SIS model. The present paper aims to address this gap, specifically by addressing what kinds of behavior the aforementioned model exhibits and also by shedding more light on the endemic behavior of the same. Our contributions are as follows.

i) We show that the model is strongly monotone, and that, under certain assumptions, it does not admit any periodic orbit; see Proposition 1 and Theorem 1, respectively.
ii) We provide a condition which guarantees exponential convergence to the disease-free equilibrium (DFE); see Theorem 2.
iii) Assuming that only virus 1 (resp. virus 2) is alive, we secure a condition guaranteeing that for any non-zero initial infection levels the dynamics would converge to the single-virus endemic equilibrium of virus 1 (resp. virus 2); see Theorem 3. The proof of Theorem 3, unlike that of the single-virus case in [14], does not rely on the construction of an appropriate Lyapunov function.
iv) Assuming that both virus 1 and virus 2 are alive, we identify a condition for local exponential convergence to the single-virus endemic equilibrium of virus 1 (resp. virus 2); see Theorem 4.
v) We provide a sufficient condition for the existence (resp. nonexistence) of a coexistence equilibrium, i.e., an equilibrium where both viruses are present in a population node; see Theorem 5 (resp. Theorem 6).

Paper Outline

The paper is organized as follows. The notations are listed immediately after the present subsection. The model, technical preliminaries, and formal statements of problems that this paper will investigate are presented in Section II. A condition for global exponential convergence to the DFE is provided in Section IV, while that for global asymptotic (resp. local exponential) convergence to the single-virus endemic equilibrium of virus 1 (resp. virus 2) is given in Section V. Results on existence (resp. nonexistence) of coexistence equilibirum are provided in Section VI. Numerical examples illustrating our results are provided in Section VII, and finally concluding remarks are given in Section VIII.

Notations and Preliminaries

We denote the set of real numbers by $\mathbb{R}$, and the set of nonnegative real numbers by $\mathbb{R}_+$. For any positive integer n, we use $[n]$ to denote the set $\{1, 2, ..., n\}$. We use $\mathbf{0}$ and $\mathbf{1}$ to denote the vectors whose entries all equal 0 and 1, respectively, and use I to denote the identity matrix, the sizes of the vectors and matrices are specified only if they

Sebin Gracy is with the Department of Electrical Engineering and Computer Science, South Dakota School of Mines and Technology, Rapid City, SD, USA (sebin.gracy@sdsmt.edu). Ji Liu is with the Department of Electrical and Computer Engineering, Stony Brook University, Stony Brook, NY, USA (ji.liu@stonybrook.edu). Tamer Başar is with the Coordinated Science Laboratory, University of Illinois Urbana-Champaign (basar1@illinois.edu). César A. Uribe is with the Department of Electrical and Computer Engineering, Rice University, Houston, TX, USA (sebin.gracy@rice.edu, cauribe@rice.edu). The works of SG and CAU were partially supported by the National Science Foundation under grants No. 2211815 and No. 2213568; SG was also supported by a grant from the Rice Academy of Fellows. Research of TB was supported in part by the National Science Foundation under Grant No. ECCS 20-32321.

are not clear from the context. For a vector x we denote the square matrix with x along the diagonal by $\mathrm{diag}(x)$. For any two real vectors $a, b \in \mathbb{R}^n$ we write $a \geq b$ if $a_i \geq b_i$ for all $i \in [n]$, $a > b$ if $a \geq b$ and $a \neq b$, and $a \gg b$ if $a_i > b_i$ for all $i \in [n]$. Likewise, for any two real matrices $A, B \in \mathbb{R}^{n\times m}$, we write $A \geq B$ if $A_{ij} \geq B_{ij}$ for all $i \in [n]$, $j \in [m]$, and $A > B$ if $A \geq B$ and $A \neq B$. For a square matrix M, we use $\sigma(M)$ to denote the spectrum of M, $\rho(M)$ to denote the spectral radius of M, and $s(M)$ to denote the largest real part among the eigenvalues of M, i.e., $s(M) = \max\{\mathrm{Re}(\lambda) : \lambda \in \sigma(\mathrm{M})\}$. For a set $\mathcal{M}$ with boundary, we denote the boundary as $\partial\mathcal{M}$, and the interior as $\mathrm{Int}(\mathcal{M}) := \mathcal{M} \setminus \partial\mathcal{M}$. Given a matrix A, $A \prec 0$ (resp. $A \preccurlyeq 0$) indicates that A is negative definite (resp. negative semidefinite), whereas $A \succ 0$ (resp. $A \succcurlyeq 0$) indicates that A is positive definite (resp. positive semidefinite). A real square matrix A is called Metzler if all its off-diagonal entries are nonnegative. If $A(= [a_{ij}]_{n\times n})$ is a nonnegative matrix, then $\rho(A)$ decreases monotonically with a decrease in a_{ij} for any $i, j \in [n]$.

II. Problem Formulation

In this section, we first introduce the discrete-time networked competitive bivirus SIS model, which is followed by assumptions that are either needed for ensuring that the model is well-defined and/or for paving the way for the main theoretical findings of the present paper. Finally, we provide formal statements of problems that the present paper will focus on.

A. Model

We consider two competing viruses, say virus 1 and virus 2, spreading over a network of n population nodes. Each node is a collection of individuals, and has its own healing (resp. infection) rates with respect to virus ℓ, δ_i^ℓ (resp. β_i^ℓ), for $\ell = 1, 2$. All individuals within a node have the same infection (resp. healing) rates; individuals across different nodes possibly have different infection (resp. healing) rates - that is, homogeneity within a population and heterogeneity across the meta-population. The spread of the two viruses can be represented by a 2-layer graph, say $\mathcal{G}$. The vertex set of $\mathcal{G}$ is the set of population nodes; for $\ell = 1, 2$, the edge set E^ℓ captures the interconnection between the various nodes in the context of the spread of virus ℓ. We denote by $A^\ell = [a_{ij}^\ell]_{n\times n}$ (where $a_{ij}^\ell \geq 0$) the weighted adjacency matrix for layer ℓ. Note that $(i, j) \in E^\ell$ if, and only if, $a_{ij}^\ell > 0$.

We use $x_i^\ell(t)$ to denote the fraction of the population in node i that is infected with virus ℓ at time t. The evolution of this fraction is represented by the following scalar differential equation:

$$\dot{x}_i^\ell(t) = -\delta_i^\ell x_i^\ell(t) + \big(1 - \textstyle\sum_{r=1}^m x_i^r(t)\big) \sum_{j=1}^n \beta_{ij}^\ell x_j^\ell(t), \quad (1)$$

where $\beta_{ij}^\ell = \beta_i^\ell a_{ij}^\ell$, and $\ell = 1, 2$. In vector form, equation (1) can be written as

$$\begin{aligned} \dot{x}^1(t) &= \Big(\big(I - (X^1 + X^2)\big)B^1 - D^1\Big)x^1(t), \\ \dot{x}^2(t) &= \Big(\big(I - (X^1 + X^2)\big)B^2 - D^2\Big)x^2(t), \end{aligned} \quad (2)$$

where $x^1, x^2 \in \mathbb{R}^n$; D^ℓ, B^ℓ for $\ell = 1, 2$ are of appropriate dimensions, and $X^\ell = \mathrm{diag}\,(x^\ell)$ for $\ell = 1, 2$.

From an application point of view, the discrete-time version of (2) is more appealing than the continuous-time model, since a) it possibly enables an easier comparison of experimental data with the predictions of a model, and b) the numerical exploration of discrete-time epidemic models is fairly straightforward and consequently can be immediately implemented by non-mathematicians. The latter is of immense importance in the context of public health [15].

The goal of this paper is to consider a discretized version of (2); comment on its limiting behavior above the epidemic threshold; and analyze its various equilibria, viz. existence, uniqueness and stability. With respect to the former aspect, the present paper aims to develop and gather a series of results that could be viewed as the discrete-time counterparts of (possibly a subset of) the findings in [11], [16].

The discrete-time competitive networked bivirus SIS model that the present paper focuses on is inspired from [12]. Specifically, by applying Euler's forward discretization [17] to (2), we obtain the following:

$$\begin{aligned} x^1(k+1) &= x^1(k) + h\Big(\big(I - (X^1 + X^2)\big)B^1 - D^1\Big)x^1(k), \\ x^2(k+1) &= x^2(k) + h\Big(\big(I - (X^1 + X^2)\big)B^2 - D^2\Big)x^2(k). \end{aligned} \quad (3)$$

B. Assumptions

We need the following assumptions so as to ensure that our model is well-defined.

Assumption 1: For all $i \in [n]$, and $\ell \in [2]$, $x_i^\ell(0)$, $(1 - x_i^1(0) - x_i^2(0)) \in [0, 1]$.

Assumption 2: For all $i \in [n]$, and $\ell \in [2]$, we have $\delta_i^\ell > 0$ and $\beta_{ij}^\ell \geq 0$.

Assumption 3: For all $i \in [n]$, and $\ell \in [2]$, $h\delta_i^\ell < 1$ and $h\sum_{\ell=1}^2 \sum_{j=1}^n \beta_{ij}^\ell \leq 1$.

We define the set $\mathcal{D}$ as follows:

$$\mathcal{D} := \{(x^1, x^2) \mid x^\ell \geq \mathbf{0}, \ell = 1, 2, \textstyle\sum_{\ell=1}^2 x^\ell \leq \mathbf{1}\}. \quad (4)$$

With Assumptions 1-3 in place, we recall the following.

Lemma 1: [12, Lemma 1] Consider system (3) under Assumptions 1-3. For all $i \in [n]$, and $\ell \in [2]$, $x_i^\ell(k)$, $(1 - x_i^1(k) - x_i^2(k)) \in [0, 1]$ for all $k \geq 0$.

Lemma 1 implies that the set $\mathcal{D}$ is positively invariant. That is, supposing an initial state is in $\mathcal{D}$, then the forward orbits generated by said initial condition will lie in $\mathcal{D}$. In other words, Lemma 1 ensures that the model in system 3 is well-defined, in the sense that the state values stay in the interval $[0, 1]$ for all time instants; otherwise, since the states represent fractions or approximations of probability, the state values will not correspond to physical reality. Throughout this paper, the term "global" will mean: for all initial conditions in the set $\mathcal{D}$.

We need the following assumptions for aiding the development of the main results of the present paper.

Assumption 4: We have $B^\ell \neq 0$, for each $\ell \in [2]$, $h \neq 0$, and $n > 1$.

Assumption 4 ensures that we are considering group models, and that there is at least one pair of nodes that share an edge in layer ℓ for $\ell = 1, 2$; otherwise, $B^\ell = 0$ for at least one $\ell \in [2]$. Consequently, we are assured that, assuming virus 1 (resp. virus 2) is present in node i (resp. j) for some i(resp. j) $\in [n]$, the spread is non-trivial, i.e., the disease can spread across the network, and not be localized to just one node.

Assumption 5: The matrix B^ℓ is irreducible, for $\ell = 1, 2$. Assumption 5 is equivalent to insisting that each layer of the spread graph be strongly connected.

We need a slightly restrictive version of Assumption 3, presented below.

Assumption 6: For all $i \in [n]$, and $\ell \in [2]$, $h\delta_i^\ell + h\sum_{\ell=1}^{2}\sum_{j=1}^{n}\beta_{ij}^\ell \leq 1$.

It is immediate that Assumption 6 implies Assumption 3; the converse is not necessarily true.

System (3) has three kinds of equilibria, viz. healthy state or disease-free equilibrium (DFE), $(\mathbf{0}, \mathbf{0})$; the single-virus endemic equilibrium corresponding to virus ℓ (for each $\ell \in [2]$), $(\bar{x}^\ell, \mathbf{0})$, where $\mathbf{0} \ll \bar{x}^\ell \ll \mathbf{1}$ for $\ell = 1, 2$; and coexistence equilibria, $(\bar{x}^1, \bar{x}^2)$, where $\mathbf{0} \ll \bar{x}^1, \bar{x}^2 \ll \mathbf{1}$, and, furthermore, $\bar{x}^1 + \bar{x}^2 \ll \mathbf{1}$. The Jacobian associated with system (3), evaluated at an arbitrary point (x^1, x^2) in the state space, is as given in (5).

C. Technical preliminaries

We will be needing the following technical details in the sequel [18], [19]. A continuous map $T : X \to X$ on the subset $X \subset Y$ is

i) monotone if, for any $x, y \in X$, $x \leq y \implies Tx \leq Ty$
ii) strongly monotone if $x < y \implies Tx \ll Ty$
iii) strongly order-preserving (SOP) if T is monotone, and when $x < y$ there exist respective neighborhoods U, V of x, y and $n_0 \geq 1$ such that $n \geq n_0 \implies T^n U \leq T^n V$.
iv) type-K monotone if $\forall x, y \in \mathbb{R}^n_{\geq 0}$ and $x < y$, it follows that for each $i \in [n]$
   a) $x_i = y_i \implies f(x_i) \leq f(y_i)$; and
   b) $x_i < y_i \implies f(x_i) < f(y_i)$.

Consider the system

$$x(k+1) = f(x(k)). \tag{6}$$

Throughout, we will assume that $f \in \mathcal{C}^1$, where $\mathcal{C}^1$ denotes the class of continuously differentiable functions. Let $J(.)$ denote the Jacobian associated with system (6). We say that system (6) is *monotone* if the matrix $J(.)$ has only nonnegative entries irrespective of the argument [20, page 141]; if the matrix $J(.)$ is also irreducible, then we say that system (6) is *strongly monotone*.

We will also require the notion of sub-homogeneous systems, introduced in [19]. We say that a positive map $f : \mathbb{R}^n \to \mathbb{R}^n$ is sub-homogeneous if

$$\alpha f(x) \leq f(\alpha x), \ \ \forall x \in \mathbb{R}^n_{\geq 0} \text{ and } \alpha \in [0, 1].$$

D. Problem Statements

With respect to system (3), we ask the following questions:

i) What kinds of behavior does this system exhibit?
ii) What is a sufficient condition for global exponential convergence to the DFE?
iii) What is a sufficient condition for global asymptotic convergence to a single-virus endemic equilibrium?
iv) Can we identify a sufficient condition for the local exponential stability of the boundary equilibrium?
v) Can we identify a sufficient condition for the existence of a coexistence equilibrium?
vi) Can we identify a sufficient condition for the nonexistence of a coexistence equilibrium?

III. System (3) is strongly monotone and does not admit periodic orbits

In this section, we first investigate whether (or not) system (3) is monotone, and subsequently leverage the answer to said question to draw overarching conclusions about the typical behavior of the system. We have the following result.

Proposition 1: Under Assumptions 1,2, 4-6, system (3) is strongly monotone.

Proof: See proof of [21, Proposition 1]. □

Proposition 1 can be viewed as not just the discrete-time counterpart of [11, Lemma 3.3] but also a stronger version of the same, since Proposition 1 establishes that the map which governs the dynamics of system (3) is strongly monotone, whereas [11, Lemma 3.3] only assures that the flow is monotone.

Proposition 1 should be understood as follows: suppose that $(x_A^1(0), x_A^2(0))$ and $(x_B^1(0), x_B^2(0))$ are two initial conditions in int(D) satisfying i) $x_A^1(0) > x_B^1(0)$ and ii) $x_A^2(0) < x_B^2(0)$. Since system (3) monotone, it follows that, for all $k \in \mathbb{Z}_{\geq 0}$, i) $x_A^1(k) \gg x_B^1(k)$ and ii) $x_A^2(k) \ll x_B^2(k)$.

By leveraging the fact that system (3) is monotone, we can draw overarching conclusions on the kinds of behavior that system (3) exhibits. Roughly speaking, we are able to say what happens to the trajectories of system (3) (corresponding to almost all initial conditions) as time goes to infinity. The formal details are in the next theorem, prior to which we define the following map associated with system (3). Define

$$f(x(t)) := \begin{bmatrix} f^1(x(t)) & \mathbf{0} \\ \mathbf{0} & f^1(x(t)) \end{bmatrix} \times x(t), \tag{7}$$

where $f^1(x(t)) = I + h(I - (x^1 + X^2)B^1$ and $f^2(x(t)) = I + h(I - (x^1 + X^2)B^2 - D^2)$.

Theorem 1: Consider system (3) under Assumptions 1,2, 4-6. Suppose that there exists a fixed point in int $\mathcal{D}$. Then all periodic points of system (3) are fixed points. Furthermore, $\lim_{x\to\infty} f^k(x) = \bar{\bar{x}}$ for all $x(0) \in \mathcal{D}$, where $\bar{\bar{x}}$ is a fixed point of $f(.)$ in int $\mathcal{D}$.

Proof: See proof of [21, Theorem 1]. □

Note that Theorem 1 excludes the possibility of existence of limit cycles. Also, note that given that system (3) is monotone, no other complex behavior is allowed; see [22, page 70].

Remark 1: Theorem 1 is the discrete-time counterpart of [11, Theorem 3.6]. The crucial difference is that Theorem 1 relies on the assumption that there exists an equilibrium of

$$J(x^1,x^2)=\begin{bmatrix} I-hD^1+h(I-X^1-X^2)B^1-h\,\mathrm{diag}(B^1x^1) & -h\,\mathrm{diag}(B^1x^1) \\ -h\,\mathrm{diag}(B^2x^2) & I-hD^2+h(I-X^1-X^2)B^2-h\,\mathrm{diag}(B^2x^2)\end{bmatrix} \tag{5}$$

system (3) in the interior of $\mathcal{D}$, while [11, Theorem 3.6] does not need such an assumption.

The result in Theorem 1, as mentioned previously, relies on the assumption that there exists a fixed point in int $\mathcal{D}$. Indeed, system (3) admits an equilibrium in int $\mathcal{D}$. A parameter-based condition which ensures the admittance of such an eequilibrium has been provided in [23, Theorem 12], while another condition will be provided in Theorem 5 of the present paper.

IV. Analysis of the DFE

By looking at equation (3), and by invoking the definition of fixed point of a discrete map, it is immediate that the DFE is always an equilibrium point of system (3); this is independent of any conditions that the system parameters may (or may not) fulfil. We recall the following result.

Proposition 2: [12, Theorem 1] Consider system (3) under Assumptions 1-5. Suppose that $\rho(I-hD^\ell+hB^\ell)\leq 1$ for $\ell=1,2$. Then, the DFE is asymptotically stable with a domain of attraction $\mathcal{D}$, where $\mathcal{D}$ is as defined in (4).

It turns out that if the inequalities in Proposition 2 are tightened, then, one obtains exponential convergence to the DFE, as we detail in the following theorem.

Theorem 2: Consider system (3) under Assumptions 1-3. Suppose that $\rho(I-hD^\ell+hB^\ell)<1$ for $\ell=1,2$. Then, the DFE is exponentially stable with a domain of attraction $\mathcal{D}$, where $\mathcal{D}$ is as defined in (4).

The proof is similar to that of [24, Theorem 1].

Proof: See proof of [21, Theorem 2]. □

V. Analysis of the single-virus endemic equilibrium

It is known that the conditions in Proposition 2 guarantees that the DFE is the unique equilibrium of system (3); see [12, Theorem 2]. If one of these two spectral radii condition are violated, i.e., , if $\rho(I-hD^\ell+hB^\ell)>1$ for some $\ell\in[2]$, then it turns out that there exists, besides the DFE, the single-virus endemic equilibrium (also interchangeably referred to as boundary equilibrium) corresponding to virus ℓ, namely $(\bar{x}^\ell,\mathbf{0})$; see [12, Proposition 2]. Furthermore, $(\bar{x}^\ell,\mathbf{0})$ is locally asymptotically stable; see [12, Corollary 1]. However, [12] makes no comment on the global asymptotic stability of $(\bar{x}^\ell,\mathbf{0})$. In this section, we first strengthen [12, Corollary 1] by establishing global asymptotic stability of $(\bar{x}^\ell,\mathbf{0})$. Second, we allow for $\rho(I-hD^\ell+hB^\ell)>1$ for each $\ell\in[2]$, and establish local exponential convergence to $(\bar{x}^\ell,\mathbf{0})$.

It turns out that one can leverage a result on discrete maps from [18] to guarantee global asymptotic stability of the single-virus endemic equilibrium. Before presenting the result, we recall the notion of ordered fixed points. Consider am arbitrary map $f(.)$, let y_1 and y_2 be its fixed points. We say that y_1 and y_2 are ordered if $y_1\gg y_2$ or if $y_1\ll y_2$. We have the following theorem.

Theorem 3: Consider system (3) under Assumptions 1-2, 4-6. Suppose that $\rho(I-hD^1+hB^1)>1$ and $\rho(I-hD^2+hB^2)\leq 1$. The boundary equilibrium $(\bar{x}^1,\mathbf{0})$ is asymptotically stable, with a domain of attraction $\mathcal{D}\setminus\mathbf{0}$, where $\mathcal{D}$ is as defined in (4).

Proof: See proof of [21, Theorem 3]. □

Theorem 3 guarantees global asymptotic stability of the boundary equilibrium $(\bar{x}^1,\mathbf{0})$. That is, for all non-zero initial conditions, the dynamics of system (3) converge to $(\bar{x}^\ell,\mathbf{0})$. Note that, for the particular case of single virus spread, [14, Theorem 1] also provides a sufficient condition for GAS of the equilibrium point $\bar{x}^1$. The proof of [14, Theorem 1] relies on Lyapunov techniques, whereas that of Theorem 3 uses results on existence of fixed points in discrete maps, and is significantly shorter.

Note that Theorem 3 allows for, without loss of generality, either $\rho(I-hD^1+hB^1)>1$ or $\rho(I-hD^2+hB^2)>1$, but not both. A natural question of interest, then, would be to understand what happens when both $\rho(I-hD^1+hB^1)>1$ and $\rho(I-hD^2+hB^2)>1$. We aim to address the same in the rest of the present paper.

Theorem 4: Consider system (3) under Assumptions 1-2, 4-6. Suppose that $\rho(I-hD^\ell+hB^\ell)>1$ for $\ell=1,2$. The boundary equilibrium $(\bar{x}^1,\mathbf{0})$ is asymptotically stable if $\rho(I-hD^2+(I-\bar{X}^1)B^2)\leq 1$. If $\rho(I-hD^2+(I-\bar{X}^1)B^2)>1$, then the boundary equilibrium $(\bar{x}^1,\mathbf{0})$ is unstable.

The proof is inspired from that of [11, Theorem 3.9].

Proof: See proof of [21, Theorem 4]. □

VI. (Non)Existence of a coexistence equilibrium

The analysis of system (3) has as yet focused on the existence and stability of the single-virus endemic equilibria corresponding to virus ℓ for each $\ell\in[2]$. In this section, we aim to provide conditions for the existence (resp. nonexistence) of a (resp. any) coexistence equilibrium.

A sufficient condition for the existence of a coexistence equilibrium for system (3) has been provided in [23, Theorem 12]. Note that [23, Theorem 12] relies on the assumption that both the boundary equilibria are unstable, i.e., $\rho(I-hD^2+(I-\bar{X}^1)B^2)>1$ and $\rho(I-hD^1+(I-\bar{X}^2)B^1)>1$. We establish existence of a coexistence equilibrium for a different stability configuration of the boundary equilibria, namely $\rho(I-hD^2+(I-\bar{X}^1)B^2)<1$ and $\rho(I-hD^1+(I-\bar{X}^2)B^1)<1$. We have the following result:

Theorem 5: Consider system (3) under Assumptions 1-2, 4-6. Suppose that $\rho(I-hD^\ell+hB^\ell)>1$ for $\ell=1,2$. Let $(\bar{x}^1,\mathbf{0})$ and $(\mathbf{0},\bar{x}^2)$ denote the boundary equilibria corresponding to virus 1 and virus 2, respectively. Suppose that $\rho(I-hD^2+(I-\bar{X}^1)B^2)<1$ and $\rho(I-hD^1+(I-\bar{X}^2)B^1)<1$. Suppose further that $\bar{x}^1<\bar{x}^2$. Then, there exists an unstable coexistence equilibrium $(\hat{x}^1,\hat{x}^2)$, where $\mathbf{0}\ll(\hat{x}^1,\hat{x}^2)\ll\mathbf{1}$.

Proof: See proof of [21, Theorem 5]. □

Remark 2: Theorem 5 ensures not just the existence of a coexistence equilibrium but also guarantees that said coexistence equilibrium is unstable. In the context of system (2) (which is the continuous-time counterpart of system (3)), it is known that the stability configuration of the boundary equilibria as in (the continuous-time version of) Theorem 5 only ensures that the coexistence equilibrium is either neutrally stable (i.e., for the associated Jacobian, there exists an eigenvalue with real part equal to zero) or unstable; see [11, Corollary 3.15]. Thanks to [16], where it is shown that for system (2) the equilibria are hyperbolic, it is known that generically, i.e., for almost all choices of parameter matrices D^1, D^2, B^1, B^2, the coexistence equilibrium is unstable.

Note that given a discrete-time bivirus system with dynamics as in (3), it is straightforward to *verify* whether said system fulfills the conditions of Theorem 5. The converse problem of *designing* bivirus networks such that the conditions in Theorem 5 are fulfilled is more involved; for the continuous-time case, see [25].

We identify a sufficient condition for the nonexistence of a coexistence equilibrium.

Theorem 6: Consider system (3) under Assumptions 1-2, 4-6. Suppose that $\rho(I - hD^\ell + hB^\ell) > 1$ for $\ell = 1, 2$. Let $(\bar{x}^1, \mathbf{0})$ and $(\mathbf{0}, \bar{x}^2)$ denote the boundary equilibria corresponding to virus 1 and virus 2, respectively. If $\bar{x}^1 \ll \bar{x}^2$, then there does not exist any coexistence equilibrium.

Proof: See proof of [21, Theorem 6]. □

For the continuous-time case, if $\bar{x}^2 \gg \bar{x}^1$ then $\bar{x}^2$ is locally exponentially stable, and $\bar{x}^1$ is unstable. while if $B^2 > B^1$ then, in addition to the aforementioned stability configuration for the boundary equilibria, it also turns out that there does not exist a coexistence equilibrium; see [11, Corllary 3.11, statements 1 and 3]. Moreover, it is also known that if $B^2 > B^1$ then $\bar{x}^2 \gg \bar{x}^1$, whereas the converse is not necessarily true [11]; this means that for the continuous-time case it is not known if $\bar{x}^2 \gg \bar{x}^1$ implies that there does not exist any coexistence equilibrium. For the discrete-time case, $B^2 > B^1$ guarantees the nonexistence of any coexistence equilibrium; see [23, Theorem 13], whereas no such result was previously available for the case when $\bar{x}^2 \gg \bar{x}^1$– Theorem 6 closes this gap.

We next identify a condition which ensures that, under the hypothesis of Theorem 5, no orbit of system (3) converges to the boundary of $\mathcal{D}$, $\partial\mathcal{D}$, where $\mathcal{D}$ is as defined in (4). To this end, we need the following Assumption, which is stronger than Assumption 5.

Assumption 7: The matrix B^ℓ is primitive, for $\ell = 1, 2$.

Observe that every primitive matrix is irreducible; see [26, Lemma 2.11]. Therefore, Assumption 7 implies Assumption 5; the converse is false. We have the following result.

Proposition 3: Consider system (3) under Assumptions 1, 2, 4, 6 and 7. Suppose that $\rho(I - hD^\ell + hB^\ell) > 1$ for $\ell = 1, 2$. There are no orbits remaining in $\partial\mathcal{D}$.

Proof: See proof of [21, Proposition 3]. □

VII. Numerical Examples

We illustrate our results on a fully connected network of $(n =)10$ nodes. Each entry in the matrix B^1 (which is the weighted adjacency matrix for the spread of virus 1, scaled by the infection rate of each node with respect to virus 1) is a random scalar drawn from the uniform distribution in the interval $(0, 1)$. We set $B^2 = B^1 + I_{10\times 10}$. We choose $D^1 = 30 \times I$, and $D^2 = 60 \times I$. We set $h = 0.001$. With the aforementioned choice of parameters, it turns out that $\rho(I - hD^1 + hB^1) = 0.975$, and $\rho(I - hD^2 + hB^2) = 0.946$. Therefore, in line with the result in Theorem 2, virus 1 (resp. virus 2) gets eradicated exponentially quickly; see blue (resp. red) line in Figure 1.

For the next simulation, we use the same network and the sampling rate as for the simulation in Figure 1, with the exception that every entry in both B^1 and B^2 is a random scalar drawn from the uniform distribution in the interval $(0, 1)$. Entries in D^1 and D^2 are also chosen in a similar fashion, except that each element in D^1 is multiplied by 20. We choose $x^1(0) = 0.5 \times \mathbf{1}$, and $x^2(0) = 0.4 \times \mathbf{1}$. With such a choice of parameters, we have that $\rho(I - hD^1 + hB^1) = 0.9989$, and $\rho(I - hD^2 + hB^2) = 1.0045$. Consequently, consistent with the result in Theorem 3, the dynamics of the system converge to the single-virus endemic equilibrium of virus 2 (i.e, $\bar{x}^2 = [\,0.842 \;\; 0.83 \;\; 0.98 \;\; 0.85 \;\; 0.88 \;\; 0.91 \;\; 0.89 \;\; 0.82 \;\; 0.96 \;\; 0.89\,]$); see the red line in Figure 2.

For the next simulation, the setup remains the same as that in the simulation for Figure 2, with the exception that for a randomly generated choice of B^1 and B^2, the healing rates are chosen as follows: $D^1 = \text{diag}([\,9.19\ 0.9\ 2.55\ 4.27\ 5.77\ 8.995\ 2.18\ 9.67\ 4.33\ 7.84\,])$, and $D^2 = \text{diag}([\,0.01\ 0.013\ 0.015\ 0.016\ 0.06\ 0.015\ 0.011\ 0.0015\ 0.005\ 0.003\,])$. We choose $x^1(0) = 0.7 \times \mathbf{1}$, and $x^2(0) = 0.8 \times \mathbf{1}$. It turns out that $\rho(I - hD^1 + hB^1) = 1.0014$, and $\rho(I - hD^2 + hB^2) = 1.005$; hence, $\rho(I - hD^1 + hB^1) > 1$, and $\rho(I - hD^2 + hB^2) > 1$. Furthermore, $\rho(I - hD^1 + (I - \bar{X}^2)hB^1) = 0.9991$, and $\rho(I - hD^2 + (I - \bar{X}^1)hB^2) = 1.005$; hence $\rho(I - hD^1 + (I - \bar{X}^2)hB^1) < 1$, and $\rho(I - hD^2 + (I - \bar{X}^1)hB^2) > 1$. Consequently, in line with our findings in Theorem 4, the single-virus endemic equilibrium corresponding to virus 1 is unstable (see blue line in Figure 3), while the single-virus endemic equilibrium corresponding to virus 2 is asymptotically stable (see the red line in Figure 3).

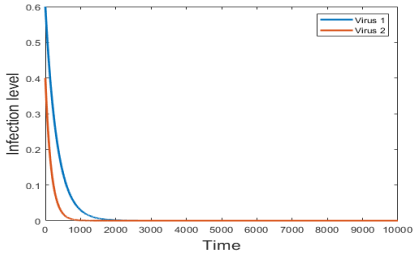

Fig. 1: Simulation with two viruses (red and blue), converging to the DFE.

VIII. Conclusion

The paper dealt with the analysis of the discrete-time networked competitive bivirus SIS model. Specifically, we

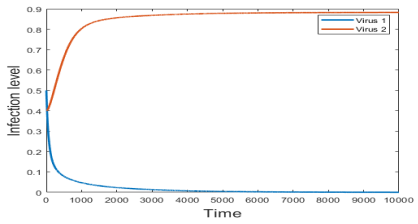

Fig. 2: Virus 1 dies out, while virus 2 becomes endemic.

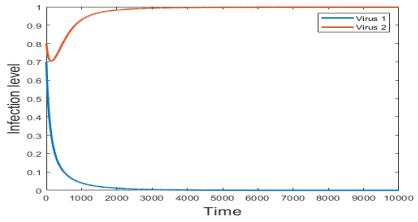

Fig. 3: Simulation with two viruses (red and blue). The single-virus endemic equilibrium of virus 1 is unstable, whereas that of virus 2 is asymptotically stable.

showed that the system is strongly monotone, and that, under certain assumptions, it does not admit any periodic orbit. We identified a sufficient condition for exponential convergence to the DFE. Thereafter, assuming that only one of the viruses is alive, we identified a sufficient condition for global asymptotic convergence to the endemic equilibrium of this virus - the proof does not depend on the construction of Lyapunov functions. Assuming that both the viruses are alive, we secured a sufficient condition for local asymptotic convergence to the boundary equilibrium of one of the viruses. Finally, we provided a sufficient (resp. necessary) condition for the existence of a coexistence equilibrium.

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