On a Continuous-Time Multi-Group Bi-Virus Model with Human Awareness

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Abstract—This paper studies the effect of human awareness on a distributed continuous-time bi-virus model in which two competing viruses diffuse over a network comprised of multiple groups of individuals. When contacting infected individuals in their own and neighboring groups, individuals may either be infected by one of the two viruses with a virus-dependent infection rate or become alert. Alert individuals may be infected by either virus but with a smaller virus-dependent infection rate, and the alert state also diffuses over the network. Limiting behaviors of the model are studied by analyzing the equilibria of the system and their stability. Both equilibria and their stability are compared with those of the model without human awareness.

I. INTRODUCTION

The spread of epidemic processes over large populations has been widely studied in epidemiology [1]. Various epidemic models have been proposed in order to model such a spreading process. For example, Bernoulli developed one of the first known models inspired by the smallpox virus [2]. Other notable examples include the Susceptible-Infected-Susceptible (SIS), Susceptible-Infected-Recovered (SIR), and Susceptible-Exposed-Infected-Recovered (SEIR) models [3]–[5]. In this paper, we focus on continuous-time SIS models [6].

Traditional SIS models usually deal with one group of “fully connected” individuals (i.e., each pair of individuals comes in contact with each other) [6]. Recently, distributed SIS models have been proposed to study multi-group of individuals, implicitly assuming that each group is fully connected [7]–[9]. Another thread of research in the study of distributed SIS epidemic models considers a system consisting of $n > 1$ interactive individuals, instead of groups, and studies the evolution of each individual’s probability of being infected. Such a model is described by either a discrete-time system [10]–[14] or a continuous-time system [15]–[18]. The first probability-based continuous-time model was proposed by Van Mieghem et al. [15] in which the underlying neighbor graph is assumed to be undirected. The same model on a directed neighbor graph has been recently studied by Khanafer et al. [18] for both strongly and weakly connected neighbor graphs. The system defined in [18] admits the same mathematical expression as that in [7], as the result of a mean field approximation on a 2nd state Markov chain model. For a survey covering of this area, see [19].

Lately, the idea of competing SIS virus models has been studied in [20]–[24]. The models can be used to understand how competing opinions spread on different social networks. The idea of competing viruses has also been explored for an SIR model in [25]. In [20], a homogeneous model (i.e., all individuals have the same infection and healing rates), with both viruses spreading over the same undirected connected graph, is analyzed. Specifically, the paper provides the set of equilibria and sufficient conditions for local stability for all equilibria except the coexisting equilibrium (i.e., both viruses infect the whole network). In [21], a heterogeneous model (i.e., different individuals have differing infection and healing rates) is studied by assuming undirected connected graphs for both viruses and analyzing the equilibria and their stability. Particularly, co-existence of the epidemic states from both viruses is shown but with no stability analysis. In [23], a sufficient condition for the survival of a single virus is established, assuming that the virus, homogeneous in healing rate, propagates over undirected regular graphs. In our recent paper [26], a distributed, continuous-time, multi-group, bi-virus model has been analyzed in which two competing viruses spread over possibly different directed strongly connected graphs. Limiting behaviors of the network are characterized by analyzing the equilibria of the system, including coexisting equilibria, and their stability. Recently, the idea of competing viruses has been generalized to multiple competing viruses [27], [28].

Another recent thread of research in epidemic networks is to model and analyze the effects of human awareness. In [29], the single virus SIS model is modified to reflect the scenario that individuals may become alert, if not yet infected, when their neighbors are infected. Based on this modified model, the effects of information dissemination were considered in [30], [31] and an optimal dissemination strategy was studied to promote preventive behaviors in the network. Other recent work on human awareness include [32]–[35], all for single virus models.

In this paper, we study a continuous-time bi-virus model with human awareness. The model is derived from a network of $n > 1$ group of fully connected individuals. In this model, two competing viruses diffuse over two (possibly different) networks with the same node set. An individual
may be infected by individuals in its own group as well as by individuals from its nearest-neighbor groups. Neighbor relationships among the \( n \) groups are described by a directed graph \( \mathbb{G} \) on \( n \) vertices with an arc from vertex \( j \) to vertex \( i \) whenever the individuals in group \( i \) can be infected by those in group \( j \). Thus, the neighbor graph \( \mathbb{G} \) has self-arcs at all \( n \) vertices and the directions of arcs in \( \mathbb{G} \) represent the directions of epidemic contagion. We assume that \( \mathbb{G} \) is strongly connected and is the union of the two spreading graphs of the two viruses. Thus, each spreading graph is a spanning subgraph of \( \mathbb{G} \). When contacting infected individuals in their own and neighboring groups, individuals may either be infected by one of the two viruses with a virus-dependent infection rate or become alert. Alert individuals may be infected by either virus but with a smaller virus-dependent infection rate, and also stimulates awareness in the network. Limiting behaviors of the model are studied by analyzing the equilibria and their stability and running simulations; these results are also compared with those of the model without human awareness.

The model considered here is also related to patch forwarding in computer virus epidemic networks in which virus patches have similar functions in computer networks as human awareness in epidemic networks [36], [37].

A. Preliminaries

For any positive integer \( n \), we use \([n]\) to denote the set \( \{1, 2, \ldots, n\} \). A vector \( \mathbf{x} \) is a column vector and \( \mathbf{x}^t \) denotes its transpose. Similarly, we use \( A^t \) for the transpose of a matrix \( A \). The \( i \)th entry of a vector \( \mathbf{x} \) will be denoted by \( x_i \). The \( ij \)th entry of a matrix \( A \) will be denoted by \( a_{ij} \) and, also, by \([A]_{ij}\) when convenient. We use \( 0 \) and \( I \) to denote the vectors whose entries all equal 0 and 1, respectively, and \( I \) to denote the identity matrix, while the dimension of the vectors and matrices is to be understood from the context. For any vector \( \mathbf{x} \in \mathbb{R}^n \), we use \( \text{diag}(\mathbf{x}) \) or \( X \) to denote the \( n \times n \) diagonal matrix whose \( i \)th diagonal entry equals \( x_i \). Similarly, we use \( X^* \) and \( \bar{X} \) to denote diagonal matrices \( \text{diag}(\mathbf{x})^* \) and \( \text{diag}(\bar{x}) \), respectively. For any two sets \( A \) and \( B \), we use \( A \cup B \) to denote the set of elements in \( A \) but not in \( B \), and \( A \subset B \) to denote that \( A \) is a subset of \( B \).

For any two real vectors \( \mathbf{a}, \mathbf{b} \in \mathbb{R}^n \), we write \( \mathbf{a} \geq \mathbf{b} \) if \( a_i \geq b_i \) for all \( i \in [n] \), \( \mathbf{a} > \mathbf{b} \) if \( a_i > b_i \) for all \( i \in [n] \), and \( \mathbf{a} \neq \mathbf{b} \) if \( a_i \neq b_i \) for all \( i \in [n] \). Similarly, for any two real matrices \( A, B \in \mathbb{R}^{m \times n} \), we write \( A \geq B \) if \( a_{ij} \geq b_{ij} \) for all \( i \in [m] \) and \( j \in [n] \), \( A > B \) if \( a_{ij} > b_{ij} \) for all \( i \in [m] \) and \( A \neq B \), and \( A \neq B \) if \( a_{ij} 
eq b_{ij} \) for all \( i \in [m] \) and \( j \in [n] \).

For a real square matrix \( M \), we use \( \rho(M) \) to denote the spectral radius of \( M \) and \( s(M) \) to denote the largest real part among the eigenvalues of \( M \), i.e.,

\[
\rho(M) = \max \{ |\lambda| : \lambda \in \sigma(M) \},
\]

\[
s(M) = \max \{ \Re(\lambda) : \lambda \in \sigma(M) \},
\]

where \( \sigma(M) \) denotes the spectrum of \( M \).

For any two nonnegative vectors \( \mathbf{a} \) and \( \mathbf{b} \in \mathbb{R}^n \), we say that \( \mathbf{a} \) and \( \mathbf{b} \) have the same sign pattern if they have zero entries and positive entries in the same places, i.e., for all \( i \in [n] \), \( a_i = 0 \) if and only if \( b_i = 0 \) and \( a_i > 0 \) if and only if \( b_i > 0 \). A square matrix is called irreducible if it cannot be permuted to a block upper triangle matrix. A real square matrix is called Metzler if its off-diagonal entries are all nonnegative.

Definition 1: Consider an autonomous system

\[
\dot{x}(t) = f(x(t)),
\]

where \( f : \mathcal{D} \rightarrow \mathbb{R}^n \) is a locally Lipschitz map from a domain \( \mathcal{D} \subset \mathbb{R}^n \) into \( \mathbb{R}^n \). Let \( z \) be an equilibrium of (1) and \( \mathcal{E} \subset \mathcal{D} \) be a domain containing \( z \). When the equilibrium \( z \) is asymptotically stable such that for any \( x(0) \in \mathcal{E} \) we have \( \lim_{t \to \infty} x(t) = z \), then \( \mathcal{E} \) is a domain of attraction for \( z \).

II. THE MODEL

Consider a network consisting of \( n > 1 \) groups of individuals, labeled \( 1 \) to \( n \). There are two competing viruses diffused over the network. Individuals cannot be infected with the two viruses simultaneously. An individual may be infected with one of the two viruses only by those in its own and neighboring groups. Neighbor relationships among the \( n \) groups are described by a directed graph \( \mathbb{G} \) on \( n \) vertices with an arc from vertex \( j \) to vertex \( i \) whenever the individuals in group \( i \) can be infected by those in group \( j \). Thus, the neighbor graph \( \mathbb{G} \) has self-arcs at all \( n \) vertices and the directions of arcs in \( \mathbb{G} \) represent the directions of contagion. Each virus spreads over a spanning subgraph of \( \mathbb{G} \). The two subgraphs can be different. Their union is the neighbor graph \( \mathbb{G} \). It will be assumed that both of the two subgraphs are strongly connected and, thus, so is \( \mathbb{G} \).

Each individual has four possible states including susceptible, infected with virus 1, infected with virus 2, and alert state. An alert individual is still susceptible but is cautious, and therefore less susceptible than when not alert. Let \( S_i(t) \) and \( A_i(t) \) respectively denote the number of susceptible and alert individuals in group \( i \) at time \( t \geq 0 \), and let \( I_1^i(t) \) and \( I_2^i(t) \) respectively denote the number of individuals infected with virus 1 and virus 2 in group \( i \) at time \( t \geq 0 \). Assume that the total number of individuals in each group \( i \), denoted by \( N_i \), does not change over time. In other words, \( S_i(t) + I_1^i(t) + I_2^i(t) + A_i(t) = N_i \), for all \( i \in [n] \) and \( t \geq 0 \), which implies that birth rate equals death rate. Let \( \mu_i \) and \( \bar{\mu}_i \) be the birth rate and death rate of group \( i \), respectively. Since \( N_i \) is constant, \( \mu_i = \bar{\mu}_i \). Individuals are born as susceptible.

We use \( x_1^i(t) \) and \( x_2^i(t) \) to denote the portion of infected individuals in group \( i \) with virus 1 and virus 2, respectively, and use \( y_i(t) \) to denote the portion of alert individuals in group \( i \), i.e.,

\[
x_1^i(t) = \frac{I_1^i(t)}{N_i}, \quad x_2^i(t) = \frac{I_2^i(t)}{N_i}, \quad \text{and} \quad y_i(t) = \frac{A_i(t)}{N_i}.
\]

The dynamics of \( x_1^i(t), x_2^i(t) \), and \( y_i(t) \) are as follows:

\[
\dot{x}_1^i(t) = -\delta_1^i x_1^i(t) + (1 - x_1^i(t) - x_2^i(t) - y_i(t)) \sum_{j=1}^n \beta_{ij} x_j^i(t)
\]

\[
+ y_i(t) \sum_{j=1}^n \bar{\beta}_{ij} x_j^i(t).
\]
\( x_i^2(t) = -\delta_i^2 x_i^2(t) + (1 - x_1^2(t) - x_2^2(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^2 x_j^2(t) + y_i(t) \sum_{j=1}^{n} \tilde{\beta}_{ij}^2 x_j^2(t), \) (3)

\( y_i(t) = -\mu_i y_i(t) \)

\( -y_i(t) \sum_{j=1}^{n} \beta_{ij} x_j^2(t) - y_i(t) \sum_{j=1}^{n} \beta_{ij}^2 x_j^2(t) + (1 - x_1^2(t) - x_2^2(t) - y_i(t)) \sum_{j=1}^{n} \kappa_{ij} (x_j^2(t) + x_j^2(t)) + (1 - x_1^2(t) - x_2^2(t) - y_i(t)) \sum_{j=1}^{n} \tilde{\kappa}_{ij} y_j(t). \) (4)

We call \( \delta_i^2 \) and \( \delta_{ij}^2 \) healing rates, \( \beta_{ij}, \beta_{ij}^2 \), \( \tilde{\beta}_{ij}, \) and \( \tilde{\beta}_{ij}^2 \) infection rates, and \( \kappa_{ij}, \tilde{\kappa}_{ij} \) alerting rates of the system. It is worth noting that \( \beta_{ij} < \beta_{ij}^2 \) and \( \tilde{\beta}_{ij} < \tilde{\beta}_{ij}^2 \) for all \( i, j \in [n] \). The derivation of the model is omitted due to space limitations and will be included in an expanded version of the paper.

The model described by (2)-(4) can be written in matrix form as follows:

\[ x^1(t) = (-D^1 + B^1 - X^1(t)B^1 - X^2(t)B^1)x^1(t) - Y(t)B^1 x^1(t) + Y(t)B^1 x^1(t), \]

\[ x^2(t) = (-D^2 + B^2 - X^2(t)B^2 - X^1(t)B^2)x^2(t) - Y(t)B^2 x^2(t) + Y(t)B^2 x^2(t), \]

\[ y(t) = -My(t) - Y(t)B^1 x^1(t) - Y(t)B^2 x^2(t) + (I - X^1(t) - X^2(t) - Y(t))(K x^1(t) + K x^2(t) + Ky(t)), \] (5)

where \( x^1(t), x^2(t), y(t) \) are the column vectors obtained by stacking up \( x_1^1(t), \) \( x_2^1(t), \) and \( y_1(t) \), respectively. \( B^1, B^2, B^1, B^2, K, \tilde{K} \) are the matrices of \( \beta_{ij}, \beta_{ij}^2, \tilde{\beta}_{ij}, \tilde{\beta}_{ij}^2, \kappa_{ij}, \tilde{\kappa}_{ij} \), respectively. \( X^1(t) = \text{diag}(x^1(t)), X^2(t) = \text{diag}(x^2(t)), Y(t) = \text{diag}(y(t)), D^1 = \text{diag}(\delta^1), D^2 = \text{diag}(\delta^2), \) and \( M = \text{diag}(\mu) \).

Remark 1: The model in (5) subsumes some existing epidemic models. If \( y_i(t) = 0 \) for all \( i \in [n] \) and \( t \geq 0 \) (i.e., without alert individuals), then the model simplifies to the bi-virus model [26], in which case (5) reduces to

\[ \dot{x}^1(t) = (-D^1 + B^1 - X^1(t)B^1 - X^2(t)B^1)x^1(t), \]

\[ \dot{x}^2(t) = (-D^2 + B^2 - X^2(t)B^2 - X^1(t)B^2)x^2(t), \] (6)

If \( x_i^2(t) = 0 \) for all \( i \in [n] \) and \( t \geq 0 \), the model further simplifies to the single virus SIS model [18]

\[ \dot{z}(t) = (-D + B - Z(t)B)z(t), \] (7)

where \( z_i(t) \) is the proportion of infected individuals in group \( i \). If \( x_i^2(t), \mu_i, \) and \( \tilde{\kappa}_{ij} \) all equal zero for all \( i, j \in [n] \) and \( t \geq 0 \), then the model becomes a heterogeneous version of the single virus SIS model with human awareness [29]. Thus, the model considered here can be regarded as a generalized version of those in [18], [26], [29]. It is worth noting that after taking human awareness into account, birth rates \( \mu_i \) directly play a role in the model (note the first term in (4)), which is not the case for the single virus [18], bi-virus [26], or human awareness models [29].

We impose the following set of assumptions on the parameters throughout the paper.

Assumption 1: For all \( i \in [n] \), we have \( \delta_i^2, \delta_{ij}^2, \mu_i \geq 0 \). The matrices \( B^1, B^2, B^1, B^2, K, \tilde{K} \) are nonnegative and irreducible. The matrices \( K \) and \( \tilde{K} \) are nonnegative.

The non-negativity assumption on the matrices \( B^1, B^2, B^1, B^2, K, \tilde{K} \) and \( \tilde{K} \) is equivalent to \( \beta_{ij}, \beta_{ij}^2, \beta_{ij}^2, \kappa_{ij}, \tilde{\kappa}_{ij} \geq 0 \) for all \( i, j \in [n] \). The assumption of \( B^1 \) and \( B^2 \) being irreducible matrices is equivalent to requiring that the graphs of the single virus 1 and 2 are both strongly connected (though they can be different). It is worth emphasizing that the graphs of \( B^1 \) and \( B^2 \) are the same as the graphs of \( B^1 \) and \( B^2 \), respectively. We will specify the graphs of \( K \) and \( \tilde{K} \) later.

Lemma 1: Suppose that Assumption 1 holds. Then, \( x_1^1(t), x_2^1(t), x_1^2(t) + x_2^2(t), y_i(t), x_1^1(t) + x_2^2(t) + y_i(t) \in [0,1] \) for all \( i \in [n] \) and \( t \geq 0 \).

Lemma 1 implies that the set

\[ D = \{(x^1, x^2, y) | x^1 \geq 0, x^2 \geq 0, y \geq 0, x^1 + x^2 + y \leq 1 \} \] (8)

is invariant with respect to the system defined by (5). Since \( x_1^1, x_2^1, \) and \( y_i \) denote the proportion of individuals in group \( i \) being infected by virus 1, infected by virus 2, and alert, respectively, and \( 1 - x_1^1 - x_2^2 - y \) denotes the proportion of susceptible individuals in group \( i \), it is natural to assume their initial values are in \([0,1]\), or the values will lack physical meaning. Therefore, in this paper, we focus on the analysis of (5) only on the domain \( D \), as defined in (8).

III. EQUILIBRIA AND THEIR STABILITY

We call an equilibrium \((x^1, x^2, y)\) of system (5) the healthy state if \( x^1 = x^2 = 0 \), no matter what value \( y \) is, since at such an equilibrium, all individuals in the network are healthy. It can be seen that \( x^1 = x^2 = y = 0 \) is a trivial healthy state. If a healthy state is with \( y > 0 \), we also call it an alert state, which implies that all individuals are healthy, but some of them are alert. We will show that system (5) also admits epidemic states which are equilibria with nonzero \( x^1 \) and/or \( x^2 \). In this section, we study the stability of the healthy states and the epidemic states of (5).

The following theorem provides a sufficient condition for global stability of healthy states.

Theorem 1: Suppose that Assumption 1 holds, \( s(-D^1 + B^1) \leq 0 \), and \( s(-D^2 + B^2) \leq 0 \). Then, system (5) asymptotically enters the set of healthy states. Suppose, in addition, that \( \tilde{K} \) is irreducible. If \( s(-M + \tilde{K}) \leq 0 \), then system (5) has a unique equilibrium \((0,0,0)\), which is asymptotically stable with domain of attraction \( D \) defined in (8). If \( s(-M + \tilde{K}) > 0 \), then system (5) has two equilibria, the trivial healthy state \((0,0,0)\), which is asymptotically stable with domain of attraction \( \{(x^1, x^2, 0) | x^1 \geq 0, x^2 \geq 0, x^1 + x^2 \leq 1\} \), and a unique alert state \((0,0,\tilde{y})\) with...
\( \vec{y} \gg 0 \), which is asymptotically stable with domain of attraction \( D \setminus \{ (x^1, x^2, 0) | x^1 \geq 0, x^2 \geq 0, x^1 + x^2 \leq 1 \} \).

In the bi-virus model (6) without human awareness, the condition \( s(-D^1 + B^1) \leq 0 \) and \( s(-D^2 + B^2) \leq 0 \) guarantees that all individuals will finally become susceptible (see Theorem 2 in [26]). This is not necessarily the case in system (5), in which human awareness is taken into account.

Theorem 1 implies that it is possible for individuals to remain in the alert state even if both viruses have died out, depending on the birth rates, the admonition rates, and the communication graph.

To prove the theorem, we need the following result for the single-virus model (7).

**Proposition 1:** Suppose that \( \delta_i \geq 0 \) for all \( i \in [n] \) and that matrix \( B \) is nonnegative and irreducible. If \( s(-D + B) \leq 0 \), then \( 0 \) is the unique equilibrium of system (7) which is asymptotically stable with domain of attraction \([0, 1]^n \). If \( s(-D + B) > 0 \), then system (7) has two equilibria, \( 0 \) and \( x^* \gg 0 \) which is asymptotically stable with domain of attraction \([0, 1]^n \ \setminus \ \{ 0 \} \).

Next we consider the scenario in which at least one of \( s(-D^1 + B^1) \) and \( s(-D^2 + B^2) \) is greater than zero. Toward this end, we will consider two cases of system (5) separately, which will be specified shortly.

Before doing so, we calculate the Jacobian matrix of any equilibrium of system (5), which will be used later.

Suppose that \((\vec{x}^1, \vec{x}^2, \vec{y})\) is an equilibrium of system (5). Then, the Jacobian matrix of the equilibrium, denoted by \( J(\vec{x}^1, \vec{x}^2, \vec{y}) \) is given in (9) in which

\[
\begin{align*}
\vec{B}^1 &= \text{diag}(B^1 \vec{x}^1), \\
\vec{B}^2 &= \text{diag}(B^2 \vec{x}^2), \\
K_x &= \text{diag}(K(\vec{x}^1 + \vec{x}^2)), \\
\bar{K}_y &= \text{diag}(\bar{K} \vec{y}).
\end{align*}
\]

**A. Case with \( \bar{k}_{ij} = 0 \)**

In the case when \( \bar{k}_{ij} = 0 \) for all \( i,j \in [n] \), susceptible individuals may become alert only when they contact or observe infected individuals, which means that they are not affected by the behaviors of alert individuals. Such a situation is possible when alert individuals protect themselves by changing their personal habits which are private and cannot be observed by others.

With \( \bar{k}_{ij} = 0 \) for all \( i,j \in [n] \), system (5) becomes

\[
\begin{align*}
\dot{x}^1(t) &= (-D^1 + B^1 - X^1(t)B^1 - X^2(t)B^1)x^1(t) - Y(t)B^1 x^1(t) + Y(t)\bar{B}^1 x^1(t), \\
\dot{x}^2(t) &= (-D^2 + B^2 - X^2(t)B^2 - X^1(t)B^2)x^2(t) - Y(t)B^2 x^2(t) + Y(t)\bar{B}^2 x^2(t), \\
\dot{y}(t) &= -M_y(t)(I - X^1(t) - X^2(t) - Y(t))K(x^1(t) + x^2(t)).
\end{align*}
\]

We first consider the case when one of \( s(-D^1 + B^1) \) and \( s(-D^2 + B^2) \) is greater than zero. Without loss of generality, suppose that \( s(-D^1 + B^1) > 0 \) and \( s(-D^2 + B^2) \leq 0 \).

Suppose that \( (\vec{x}^1, \vec{x}^2, \vec{y}) \) is an equilibrium of system (10). We characterize the expressions of \( \vec{x}^1, \vec{x}^2, \) and \( \vec{y} \) in the following.

Since \( x^1_1(t), x^2_1(t) \) and \( y_1(t) \) are always nonnegative by Lemma 1, from (3), we have

\[
\begin{align*}
\dot{x}^1_1(t) &\leq -\delta^1_1 x^1_1(t) + (1 - x^1_1(t)) \sum_{j=1}^n \beta^1_{ij} y_j(t), \\
\dot{x}^2_1(t) &\leq -\delta^2_1 x^2_1(t) + (1 - x^2_1(t)) \sum_{j=1}^n \beta^2_{ij} y_j(t),
\end{align*}
\]

which implies that the trajectory of \( x^2_1(t) \) is bounded above by a single-virus model. From Assumption 1 and Proposition 1, it follows that \( x^2_1(t) \) will asymptotically converge to 0 as \( t \to \infty \), and thus for any equilibrium of (10), there holds \( \vec{x}^2 = 0 \).

From the third equation in (10), we have

\[
M \vec{y} + \tilde{Y} \vec{B}^1 \vec{x}^1 + \tilde{Y} \vec{B}^2 \vec{x}^2 = (I - \tilde{X}^1 - \tilde{X}^2 - \tilde{Y})K(\vec{x}^1 + \vec{x}^2).
\]

Since \( \vec{x}^2 = 0 \), it follows that

\[
M \vec{y} + \tilde{Y} \vec{B}^1 \vec{x}^1 = (I - \tilde{X}^1 - \tilde{Y})K\vec{x}^1,
\]

from which, we have

\[
(M + \text{diag}(B^1 \vec{x}^1) + \text{diag}(K\vec{x}^1)) \vec{y} = (I - \tilde{X}^1)K\vec{x}^1.
\]

Note that \( (M + \text{diag}(B^1 \vec{x}^1) + \text{diag}(K\vec{x}^1)) \) is a diagonal matrix. If all birth rates \( \mu_i > 0 \), then this matrix is necessarily nonsingular. Therefore,

\[
\vec{y} = (M + \text{diag}(B^1 \vec{x}^1) + \text{diag}(K\vec{x}^1))^{-1} (I - \tilde{X}^1)K\vec{x}^1. \quad (11)
\]

Employing this expression, \( \vec{x}^2 = 0 \), and the first equation in (10), it follows that

\[
\begin{align*}
\epsilon K\vec{x}^1 &= \text{diag}((B^1 - \tilde{B}^1)\vec{x}^1) (M + \text{diag}(B^1 \vec{x}^1) + \text{diag}(K\vec{x}^1))^{-1} (I - \tilde{X}^1)K\vec{x}^1. \quad (12)
\end{align*}
\]

The discussion above leads to the following lemma.

**Lemma 2:** Suppose that \( s(-D^1 + B^1) > 0 \) and \( s(-D^2 + B^2) \leq 0 \). Suppose that \( \mu_i > 0 \) for all \( i \in [n] \). Then, the equilibria of system (10) are those states \((\vec{x}^1, 0, \vec{y})\) satisfying (11) and (12).

For the bi-virus model without human awareness (6), it has been shown in [26] that if \( s(-D^1 + B^1) > 0 \) and \( s(-D^2 + B^2) \leq 0 \), the system has two equilibria, the healthy state \((0, 0)\) and a unique epidemic state (see Theorem 3 in [26]). But this is not always the case for system (10) when human awareness is taken into account. To see this, we consider a homogeneous case under the following assumption.

**Assumption 2:** The graphs of \( \tilde{K} \) and \( B^1 \) are the same. For all \( i,j \in [n] \) such that \((i,j)\) is a directed edge in the graph of \( B^1 \), there holds \( \kappa_{ij} = \kappa > 0 \), \( \beta^1_{ij} = \beta^1 > 0 \), and \( \tilde{\beta}^1_{ij} = \tilde{\beta}^1 > 0 \).

It is worth emphasizing that the graph of \( \tilde{B}^1 \) is also the same as the graph of \( B^1 \), and that \( \beta^1 > \tilde{\beta}^1 \), which is consistent with the assumption that alert individuals have lower infection rates compared with susceptible individuals.
Suppose that Assumption 2 holds. Then, $K = \kappa A$, $B^1 = \beta^1 A$, and $B^2 = \beta^2 A$, where $A$ is the adjacency matrix of the graph of $B^1$, i.e., the spreading graph of virus 1. Suppose, in addition, that $\mu_i = 0$ for all $i \in [n]$. Then, from the third equation in (10) and $\dot{x}_2^2 = 0$, it can be verified that

$$\dot{y}(t) = -My(t) - Y(t) \bar{B}_1 x_1(t) - Y(t) \bar{B}_2 x_2(t) + (I - X_1(t) - X_2(t) - Y(t)) \bar{K} y(t).$$

From this and the first equation in (10), we have

$$\dot{x}_1(t) = (-D^1 + \beta^1 A - \beta^1 X_1(t) A)x_1(t) - (\beta^1 - \beta^2) Y(t) A x_2(t)$$

$$= (-D^1 + (\beta^1 - \alpha^1) A - (\beta^1 - \alpha^1) X_1(t) A)x_1(t),$$

where

$$\alpha^1 = \frac{\kappa(\beta^1 - \beta^2)}{\kappa + \beta^1}.$$

It can be verified that $\alpha^1 < \beta^1$. Thus, the above dynamics of $x_1$ is a single virus model.

From Proposition 1, if $s(-D^1 + (\beta^1 - \alpha^1) A) \leq 0$, then $x_1$ has a unique zero equilibrium, in which case, from the (10), an equilibrium must have the form $(0, 0, \tilde{y})$ with $\tilde{y}$ being any vector in $[0, 1]^n$. The stability of each equilibrium can be determined by checking the corresponding Jacobian matrix given in (9). Specifically, in this case, from (9), the Jacobian matrix equals

$$\begin{bmatrix}
\beta^1 (I - \bar{Y}) A - D^1 + \beta^1 Y A & 0 & 0 \\
0 & (I - \bar{Y}) B^2 - D^2 + \bar{Y} \bar{B}^2 & 0 \\
* & * & 0
\end{bmatrix},$$

where $*$ means that the corresponding submatrix is nonzero but does not affect the stability. Note that $(0, 0, \tilde{y})$ is stable if and only if $s(\beta^1 (I - \bar{Y}) A - D^1 + \beta^1 Y A) < 0$ and $s((I - \bar{Y}) B^2 - D^2 + \bar{Y} \bar{B}^2) < 0$. Since $(I - \bar{Y}) B^2 - D^2 + \bar{Y} \bar{B}^2 = (-D^2 + B^2) - \bar{Y} (B^2 - \bar{B}^2)$, $-D^2 + B^2$ is an irreducible Metzler matrix, and $Y(B^2 - \bar{B}^2)$ is a nonnegative matrix, it follows that $s((I - \bar{Y}) B^2 - D^2 + \bar{Y} \bar{B}^2) < 0$ if $s(-D^2 + B^2) \leq 0$. Thus, $(0, 0, \tilde{y})$ is stable if and only if $s(\beta^1 (I - \bar{Y}) A - D^1 + \beta^1 Y A) < 0$. Note that $(0, 0, 0)$ is unstable since $s(\beta^1 A - D^1) = s(-D^1 + B^1) > 0$.

From Proposition 1, if $s(-D^1 + (\beta^1 - \alpha^1) A) > 0$, system (10) has a unique epidemic equilibrium $(\tilde{x}_1, 0, \tilde{y})$ where $\tilde{x}_1^2 \gg 0$ is the unique nonzero solution of

$$(-D^1 + (\beta^1 - \alpha^1) A - (\beta^1 - \alpha^1) X_1(t) A)x_1 = 0,$$

and, from (13) and the fact that $Ax_1 \gg 0$,

$$\tilde{y} = \frac{\kappa}{\kappa + \beta^1} (1 - \tilde{x}_1).$$

We have thus proved the following theorem.

**Theorem 2:** Suppose that $s(-D^1 + B^1) > 0$ and $s(-D^2 + B^2) \leq 0$. Suppose that $\mu_i = 0$ for all $i \in [n]$ and $\alpha^1 > 0$, then system (10) has another epidemic state $(\tilde{x}_1, 0, \tilde{y})$, where $\tilde{x}_1^2 > 0$ and $\tilde{y}$ are determined by (14) and (15), respectively.
Theorem 4: Suppose that Assumption 1 holds, \( s(-D_1 + B_1) > 0 \), and \( s(-D_2 + B_2) \leq 0 \). Suppose that \( \bar{K} \) is irreducible. If \( s(-M + \bar{K}) \leq 0 \), then system (5) has two equilibria, the trivial healthy state \((0, 0, 0)\), which is asymptotically stable with domain of attraction \( \{(0, x^1, y)|x^1 \geq 0, y \geq 0, x^1 + y \leq 1\} \), and a unique epidemic state \((\bar{x}^1, 0, 0)\) with \( \bar{x}^1 \gg 0 \), which is asymptotically stable with domain of attraction \( D \setminus \{(0, x^1, y)|x^1 \geq 0, y \geq 0, x^1 + y \leq 1\} \).

IV. CONCLUSION

In this paper, we have presented the derivation of a continuous-time bi-virus model with human awareness in a network of \( n > 1 \) groups of fully connected individuals. We have introduced and studied the healthy and epidemic states of the proposed model, and established several sufficient conditions for convergence to the different equilibria. Proofs of the results that have been left out because of space limitations, and some simulations illustrating the main results can be found in an expanded version of the paper available from the authors.

For future work, we would like to further explore the co-existing epidemic equilibria, and provide conditions for convergence to these equilibria. We would also like to incorporate a control input to the system to drive susceptible individuals to the alert state, under some reasonable constraints.

REFERENCES


[34] M. Ogura and V. M. Preciado. Epidemic processes over adaptive networks of the authors.


