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Competitive networked bi-virus spread: Existence of coexistence equilibria ☆

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ABSTRACT

The paper studies multi-competitive continuous-time epidemic processes. We consider the setting where two viruses are simultaneously prevalent, and the spread occurs due to individual-to-individual interaction. In such a setting, an individual is either not affected by any of the viruses, or infected by one and exactly one of the two viruses. One of the equilibrium points is the *coexistence equilibrium*, i.e., multiple viruses simultaneously infect separate fractions of the population. We provide a sufficient condition for the existence of a coexistence equilibrium. We identify a condition such that for certain pairs of spread matrices either every coexistence equilibrium lies on a line that is locally exponentially attractive, or there is no coexistence equilibrium. We then provide a condition that, for certain pairs of spread matrices, rules out the possibility of the existence of a coexistence equilibrium, and, as a consequence, establishes global asymptotic convergence to the endemic equilibrium of the dominant virus. Finally, we provide a mitigation strategy that employs one virus to ensure that the other virus is eradicated. The theoretical results are illustrated using simulations.

1. Introduction

In February 1918 a deadly influenza pandemic (popularly known as the Spanish flu) swept across the globe. It lasted until 1920, and caused approximately 50 million deaths [1]. Influenza viruses have continued to spread across the globe in recurring epidemics [2]. Given that the spread of infectious diseases has an enormous impact on society, the study of spread has been an active area of research since Bernoulli's seminal paper [3]. The overarching goal of these research directions is to find conditions that would cause an epidemic to become eradicated, and leverage the knowledge of these conditions to design spread control strategies. To this end, various infection models have been proposed and studied in the literature; susceptible–infected (SI), susceptible–infected–susceptible (SIS), susceptible–infected–removed (SIR), etc. In this paper, we focus on the susceptible–infected–susceptible (SIS) model.

More specifically, we consider networked SIS models, where each node in the network represents a large population and interconnections between nodes capture the possibility of the virus spreading between populations. (Networked) SIS models have been studied extensively using discrete-time [4–8] and continuous-time dynamics [9–11]. In the present paper, we will focus on continuous-time dynamics.

All of the aforementioned works consider the single-virus setting. A more general setup is one in which more than one virus could be simultaneously active in a population. More specifically, in a bi-virus (two virus) setting with each virus spreading across its own contact network, one possibility is for the viruses to be competitive [12]. Examples include the simultaneous spread of multiple strains of a virus [13–15], and the spread of two different viruses that cannot simultaneously infect a host (such as influenza and the common cold) [16].

This paper deals with the competitive case. That is, say the two viruses circulating are virus 1 and virus 2, an individual is either healthy or infected by virus 1 or infected by virus 2; it *cannot* be infected by both viruses 1 and 2 at the same time. Recovery from a virus does not confer long-term immunity; the individual becomes susceptible to both the viruses. Several families of models have been proposed in the literature to better understand the (possibly complex) phenomena that is exhibited when multiple viruses simultaneously circulate in a population, and compete with each other so as to infect

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the susceptible population. The major ones being (i) the SIR model, first devised for two competing strains in [17], subsequently extended to account for various real-world scenarios (by means of introduction of additional compartments), for instance, record of infection with each of the two strains [18], transmission not just by person-to-person contact but also via environment [19], possibility of some fraction of the population being in quarantine [20], etc., and generalized to admit arbitrary number of strains in [21,22]; and (ii) the SIS model, first devised for two competing viral strains in a single population in [23]. Note that several other models have been devised to understand the behavior of multi-strain epidemics; see, for instance, De Leenheer and Pilyugin [24] and Gao et al. [25], with De Leenheer and Pilyugin [24] remarkably even factoring in the possibility of mutation between the strains. The present paper focuses on the continuous-time competitive networked bivirus SIS model.

Competitive SIS epidemics have been studied extensively in the literature. Specifically, the papers [23,26–31] consider a single (sub)population i.e., no network. While clearly not applicable for settings with multiple (sub)population nodes, these papers nonetheless have the advantage of being able to account for various real-world constraints such as effects of immunization, quarantine, etc.

Overcoming the drawbacks in the aforesaid papers, several other works have considered the presence of *an arbitrary but finite* number of (sub)population nodes, with very mild restrictions (namely, strong connectedness) imposed on the structure of the graph that captures how the various nodes are connected with each other. In particular, see [32–42]. For a recent overview of this subtopic, see [43]. The limiting behavior of competitive bi-virus SIS models have been recently studied in [34]. It is well-known that competitive multi-virus propagation exhibits richer behavior in comparison to single-virus propagation [17]. One possible outcome of competitive multi-virus propagation is *co-existence* (i.e., multiple strains coexist in a population by infecting separate fractions of each population node), while another is *competitive exclusion* (i.e., the spread parameters of one strain dominate those of the other strains, thereby causing those strains to become eradicated). The papers [32,35,36,38,44] provided conditions for coexistence in networked SIS models. In particular, analysis of the various equilibria of a competing continuous-time time-invariant bi-virus model has been provided in [36], whereas a necessary and sufficient condition for a coexistence equilibrium has been established [35, Theorem 6]. However, the results obtained in [34–36,38] are restrictive in the following sense: (i) [36, Theorems 6 and 7] rely on the assumption that the spread parameters with respect to each virus is the *same* for every population; (ii) [35, Theorem 6] is reliant on the assumption that the set of spread parameters for each virus is a scaled version of that of other viruses; (iii) the setting in [38] assumes that the healing and infection rate for each agent is the same, and (iv) coexistence equilibrium is not explored in depth in [34].

Our contributions for the networked competitive bi-virus SIS model are as follows:

(i) A sufficient condition for the existence of a coexistence equilibrium that neither insists on the spread parameters being the same for all agents nor on them being scaled versions of each other; see Theorem 1. Later on, we will see that the set of choices of system parameters for which the conditions in Theorem 1 are fulfilled does not lie on a set of measure zero in the space of free parameters,[1] which, as we will see later in the paper, is in sharp contrast to the results in [36, Theorems 6 and 7], [35, Theorem 6], and [34, Proposition 3.9].

(ii) A condition which guarantees that, for certain pairs of spread matrices, every coexistence equilibrium lies on a line, which is locally exponentially attractive. If said condition is violated, then there is no coexistence equilibrium. See Theorem 2.

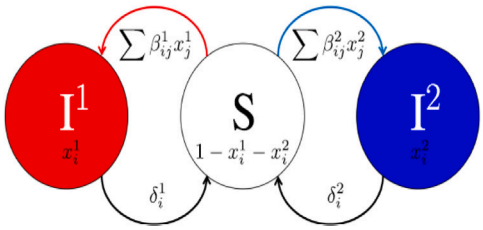

Fig. 1. Visualization of the model for the case when $m = 2$. An individual is either susceptible (S), infected with virus 1 (I^1), or infected with virus 2 (I^2).

(iii) A condition which, for certain pairs of spread matrices, precludes the existence of a coexistence equilibrium, and as a consequence leads to the single-virus endemic equilibrium of the dominant virus being globally asymptotically stable; see Theorem 3.

(iv) Design of an open-loop control strategy such that the spread dynamics converge to the single-virus endemic equilibrium of a desired virus; see Theorem 4.

A summary of the contribution that the present paper makes and what gaps in the literature it addresses has been provided in Table 1.

Notations

We denote the set of real numbers by $\mathbb{R}$, and the set of non-negative real numbers by $\mathbb{R}_+$. For a positive integer n, we use $[n]$ to denote the set $\{1, \dots, n\}$. The ith entry of a vector x is denoted by x_i. The element in the ith row and jth column of a matrix M is denoted by M_{ij}. We use $\mathbf{0}$ and $\mathbf{1}$ to denote vectors whose entries all equal 0 and 1, respectively, and use I to denote the identity matrix, while the sizes of the vectors and matrices are to be understood from the context. For a vector x, we denote the square matrix with x along the diagonal by $\Delta(x)$. 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 $i \in [n]$, $j \in [2]$, 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., $s(M) = \max\{\mathrm{Re}(\lambda) : \lambda \in \sigma(M)\}$. We denote a subset by $P \subseteq Q$, a proper subset by $P \subset Q$, and set difference by $P \setminus Q$. Given two sets A and B, $A \cap B$ denotes the intersection of the two sets. For a set $\mathcal{M}$ with a boundary, we denote the boundary as $\partial\mathcal{M}$, and the interior as $\mathrm{Int}(\mathcal{M}) := \mathcal{M} \setminus \partial\mathcal{M}$.

2. Problem formulation

In this section, we detail a model of multi-viral spread across a population network. We then formally state the problems being investigated. Finally, pertinent assumptions and definitions are introduced for later use.

Consider a set of n nodes, where $n \geq 2$. Each node represents a population of individuals. Further, the number of individuals in a population is fixed.[2] We suppose that two viruses (hereafter referred to as virus 1 and virus 2) are spreading in some (possibly all) of the n nodes. The spread could occur both between individuals in the same population node, and also between individuals across different population nodes. The viruses are assumed to be *competitive*, i.e., an individual in node i (where $i \in [n]$) is infected either by virus 1 or by virus 2 but not by *both* viruses 1 and 2 at the same time. Let, at time t, $N_i^1(t)$ and $N_i^2(t)$ represent the set of individuals in node i that

[1] A precise definition of the term free parameters appears in Section III after Theorem 2.

[2] SIS models with variable population sizes have also been considered in the literature; see, for instance, Brauer and van den Driessche [48].

Table 1
Comparison of the results in this paper with some of the other results in the literature.

Comparison of the results in this paper with other results		
Paper	Setting	Contribution
Castillo-Chavez et al. [45]	$n = 3$ case	Castillo-Chavez et al. [45, Theorem 3.2] provides a necessary and sufficient condition for the local stability of the boundary equilibria.
Li et al. [44]	$n = 2$ case	Li et al. [44, Theorem 5.2] guarantees the existence of coexistence equilibrium.
Martcheva and Pilyugin [26], Gjini et al. [46] and Dénes et al. [30]	$n = 1$ case, but with the possibility of simultaneous infection by two viruses	A sufficient condition for the coexistence of two viruses has been provided; see, for instance, Martcheva and Pilyugin [26, Theorem 3.2].
Martcheva [27]	$n = 1$ case, but time-varying healing and infection rates	A sufficient condition for the coexistence of two viral strains has been provided in [27, Corollary 5.3].
Liu et al. [36] and Paré et al. [35]	Arbitrary but finite n, and arbitrary network topologies	The results [36, Theorems 6 and 7] and [35, Theorem 6] establish the existence of a line of coexistence equilibria, for certain choices of parameters that lie on a set of measure zero.
Santos et al. [47]	Arbitrary but finite n, but special classes of graphs, and the assumption that $\delta_i^k = 1$ for all $i \in [n]$ and $k \in [2]$	A condition which establishes one virus as being dominant has been provided in [47, Theorem 21]. Santos et al. [47, Theorem 21] identifies a condition which establishes one virus as being dominant.
Doshi et al. [40]	Arbitrary but finite n, and arbitrary network topologies	Doshi et al. [40, Theorem 5.4] secures the existence of, and global asymptotic convergence to, a finite set of coexistence equilibria.
Ye et al. [34]	Arbitrary but finite n, and arbitrary network topologies	A specific choice of parameters that gives rise to a set of locally exponentially attractive coexistence equilibria has been identified in [34, Proposition 3.9], while necessary conditions for the existence of co-existence equilibria are identified in [34, Corollary 3.11].
This paper	Arbitrary but finite n, and arbitrary network topologies	A sufficient condition for existence of a co-existence equilibrium (with a novel proof technique); a necessary and sufficient condition for every co-existence equilibrium to lie on a line; design of a control scheme that guarantees convergence to a desired single-virus endemic equilibrium

are infected with virus 1 and with virus 2, respectively. Then, $N_i^1(t) \cap N_i^2(t) = \emptyset$. To be more specific, assuming node i gets infected with both the viruses at time t, then it is indeed *separate fractions* of node i that are getting infected with both the viruses. Assuming an individual in node i is infected with virus 1 (resp. virus 2), said individual recovers from virus 1 (resp. virus 2) based on its healing rate with respect to virus 1 (resp. virus 2). Thereafter, the same individual becomes susceptible to being infected by either virus 1 or by virus 2. Consequently, there could exist t_1 and t_2, with $t_1 \neq t_2$, such that $N_i^1(t_1) \cap N_i^2(t_2) \neq \emptyset$. The spread of both the viruses in a population of n nodes could be represented by a two-layer graph $\mathcal{G} = \{\mathcal{V}, E_1, E_2\}$, where $\mathcal{V} = \{1, 2, \dots, n\}$ [32]. The edge sets E_1 and E_2 determine the contact spreading network for virus 1 and virus 2, respectively.

Let $p_i^1(t) \in [0, 1]$ and $p_i^2(t) \in [0, 1]$ denote the infection ratios in node $i \in \mathcal{V}$ at time $t \in \mathbb{R}_{\geq 0}$ with respect to virus 1 and virus 2. Then the infection ratio $p_i^k(t)$ of virus $k = 1, 2$, in node $i \in \mathcal{V}$ will evolve as follows.

$$\dot{p}_i^k(t) = -\delta_i^k p_i^k(t) + \Big(1 - \sum_{l=1}^{2} p_i^l(t)\Big)\Big(\sum_{j=1}^{n} \beta_{ij}^k p_j^k(t)\Big). \tag{1}$$

Here, δ_i^k represents the recovery rate of an individual with virus k in node i, while β_{ij}^k represents the spread rate of virus k from node i to node j. Note that all individuals within a population have the same healing (resp. infection) rates, while individuals belonging to different populations may have different healing (resp. infection) rates [49]. See Fig. 1 for a pictorial depiction of the model.

Then, by defining the vectors $p^1(t) = [p_1^1(t), \dots, p_n^1(t)]^\top$ and $p^2(t) = [p_1^2(t), \dots, p_n^2(t)]^\top$, (1) can be written as

$$\dot{p}^k(t) = \Big(-D^k + \Big(I - \sum_{l=1}^{2} \Delta(p^l(t))\Big) B^k\Big) p^k(t), \tag{2}$$

where D^k is the diagonal matrix with δ_i^k on the diagonal, while B^k is the matrix of β_{ij}^k. The system in (2) has state variable $(p^1(t), p^2(t))$, and is a mean-field approximation of a coupled Markov process that captures the SIS bi-virus spread; see [32,33,36]. We have the following remarks.

Remark 1. For the case when $n = 1$, model (2) is subsumed by the multi-strain model proposed in [27], due to the fact that the model in [27] allows for the healing and infection rates to be non-negative periodic functions. When $n = 1$, (2) is a special case also of the model in [31], given that the latter allows for: (i) the infection rate to be not deterministic (it is in fact governed by a Levy process), and (ii) the presence of an arbitrary but finite number of strains.

Remark 2. For the case when $n = 2$, model (2) coincides with the model studied in [44].

Furthermore, we can let $p(t) := [p^1(t), p^2(t)]^\top$. Then, with $A^k(p(t)) := \big(-D^k + (I - \sum_{l=1}^{2} \Delta(p^l(t)))B^k\big)$ for $k = 1, 2$, the dynamics of $p(t)$ are given by

$$\dot{p}(t) = \begin{bmatrix} A^1\big(p(t)\big) & 0 \\ 0 & A^2\big(p(t)\big) \end{bmatrix} p(t). \tag{3}$$

2.1. Problem statements

For the model (3), we formally state the problems being investigated in this paper.

(i) Identify a sufficient condition for the existence of a coexistence equilibrium, i.e., $(\hat{p}^1, \hat{p}^2)$ such that $\hat{p}^1 > \mathbf{0}$ and $\hat{p}^2 > \mathbf{0}$.
(ii) Identify a condition such that for certain pairs of spread matrices B^1 and B^2 either (i) every coexistence equilibrium $(\hat{p}^1, \hat{p}^2)$ such that $\hat{p}^1 > \mathbf{0}$ and $\hat{p}^2 > \mathbf{0}$ lies on a line, or (ii) there is no coexistence equilibrium.
(iii) Identify a condition that precludes the existence of a coexistence equilibrium, i.e., any $(\hat{p}^1, \hat{p}^2)$ such that $\hat{p}^1 > \mathbf{0}$ and $\hat{p}^2 > \mathbf{0}$.
(iv) How can the healing rates of virus 2, i.e., δ_i^2, be chosen to ensure that the system converges to the single-virus endemic equilibrium of virus 1?

2.2. Positivity assumptions

In order for (3) to be well-defined and realistic, we make the following assumption.

Assumption 1. The model parameters satisfy $\delta_i^k > 0$ and $\beta_{ij}^k \geq 0$ for all $i, j \in [n]$ and $k \in [2]$.

Note that if Assumption 1 holds, then for all $k \in [2]$, B^k is a non-negative matrix and D^k is a positive diagonal matrix. Moreover, recall that a square matrix M is said to be irreducible if, replacing the non-zero elements of M with ones and interpreting it as an adjacency matrix, the corresponding graph is strongly connected. Then, noting that non-zero elements in B^k represent directed edges in the set E_k, we see that B^k is irreducible whenever the kth layer of the multi-layer network $\mathcal{G}$ is strongly connected.

Thanks to Assumption 1, we can restrict our analysis to the sets $\mathcal{F} := \{p^k(t) \in [0,1]^n, \forall k \in [2]\}$ and $\mathcal{F}^k := \{p^k(t) \in [0,1]^n\}$. Since $p_i^k(t)$ is to be interpreted as a fraction of a population, these sets represent the sensible domain of the system. That is, if $p^k(t)$ takes values outside of $\mathcal{F}^k$, then those values would lack physical meaning. The following lemma shows that $p(t)$ never leaves $\mathcal{F}$.

Lemma 1. *Let Assumption 1 hold. Then the set $\mathcal{F}$ is positively invariant with respect to (3)*

Proof. Consider $p(t) \in \mathcal{F}$. If $p_i^k(t) = 1$, then $\dot{p}_i^k(t) < 0$, so if $p_i^k(0) \leq 1$ then $p_i^k(t) \leq 1$, for all $t \geq 0$, $k \in [2], i \in [n]$. Further, if $p_i^k(t) = 0$ then $\dot{p}_i^k(t) \geq 0$, for all $t \geq 0$. □

It can be easily verified that $(\mathbf{0}, \mathbf{0})$ is an equilibrium of (2), and is referred to as the healthy state. A sufficient condition for convergence to the healthy state has been provided by Liu et al. [36]. Any non-zero equilibrium in $\mathcal{F}$ is known as an *endemic* equilibrium, which can be further categorized as follows: Equilibria of the form $(\mathbf{0}, \bar{p}^k)$ are referred to as the *single-virus endemic equilibria* or boundary equilibria. Note that in the single-virus setting, an endemic equilibrium, when it exists, is *unique* [50, Theorem 2.1]. It turns out that indeed $\tilde{p}^1$ (resp. $\tilde{p}^2$) is the endemic equilibrium of virus 1 (resp. virus 2) [34, Section 2.2]. The equilibria of the form $(\bar{p}^1, \bar{p}^2)$, where $\bar{p}^k$ for $k = 1, 2$ are non-negative vectors with at least one positive entry in $\bar{p}^k$ for $k = 1, 2$ are referred to as *coexistence equilibria*. It turns out that any non-zero equilibrium of (2) must necessarily satisfy the following: $\mathbf{0} \ll p^k \ll \mathbf{1}$, and, furthermore, $\sum_{k=1}^2 p^k \ll \mathbf{1}$; see Lemma 6 in Appendix.

3. Coexistence of viruses

In this section, we present the main results of the paper; all of which pertain to the existence (or lack thereof) of a coexistence equilibrium. The proofs are deferred to Appendix. The following theorem provides a sufficient condition for the existence of a coexistence equilibrium.

Theorem 1. *Consider the SIS model (3) under Assumption 1. Suppose that B^1 and B^2 are irreducible matrices, and that $s(B^1 - D^1) > 0$ and $s(B^2 - D^2) > 0$. If*

$$s(-D^1 + (I - \Delta(\tilde{p}^2))B^1) > 0 \tag{4}$$

$$s(-D^2 + (I - \Delta(\tilde{p}^1))B^2) > 0. \tag{5}$$

with $\tilde{p}^1$ and $\tilde{p}^2$ being the single-virus endemic equilibria of viruses 1 and 2, respectively, then there exists at least one coexistence equilibrium $(\hat{p}^1, \hat{p}^2) \gg \mathbf{0}$ in $\mathcal{F}$ such that $\hat{p}^1 + \hat{p}^2 \leq \mathbf{1}$.

Proof. See Appendix. □

With each virus satisfying the condition for the existence of its single-virus endemic equilibrium, Theorem 1 states that if, for each virus, the largest real part of any eigenvalue of the matrix of the dynamics linearized around the single-virus endemic equilibrium of the other virus is positive, then both the viruses can *simultaneously* infect separate fractions of each population node.

Remark 3. Due to Liu et al. [36, Proposition 1], conditions (4) and (5) in Theorem 1 are equivalent to $\rho((I - \Delta(\tilde{p}^2))(D^1)^{-1}B^1) > 1$ and $\rho((I - \Delta(\tilde{p}^1))(D^2)^{-1}B^2) > 1$, respectively. This is consistent with an interpretation of $\rho((I - \Delta(\tilde{p}^2))(D^1)^{-1}B^1)$ and $\rho((I - \Delta(\tilde{p}^1))(D^2)^{-1}B^2)$ as the invasion reproduction numbers[3] of virus 1 invading virus 2 and virus 2 invading virus 1, respectively. The invasion reproduction number is defined for an invading pathogen, introduced into a setting with another, endemic pathogen at equilibrium. It is defined as the average number of secondary infections caused by an individual infected by the invading pathogen, at the time of introduction [52]. In line with this interpretation, Theorem 1 shows that coexistence is possible whenever both invasion reproduction numbers are greater than one.

Theorem 1 guarantees existence of a coexistence equilibrium in the bi-virus setup.[4] It turns out that the condition in Theorem 1 implies the existence of a finite set of coexistence equilibria. Furthermore, the aforementioned set is globally attractive; for any non-zero initial infection levels with respect to both virus 1 and virus 2, the system converges to some point in the set of coexistence equilibria, see [40, Theorem 5.4]. Note that [40, Theorem 5.4] builds upon [38, Theorem 4.3]. Moreover, the result in [40, Theorem 5.4] relies on the notion of monotone dynamical systems (MDS).[5] While competitive bi-virus systems are monotone [34], competitive tri-virus systems are not [55, Theorem 1]. As a consequence, the proof technique in [40, Theorem 5.4] cannot be adapted to scenarios where there are more than two viruses. Our proof relies on fixed point mapping, and can possibly be extended for scenarios involving more than two viruses. Another result that has improved upon Theorem 1, by using the Poincaré–Hopf theorem [56] and Morse–Smale inequalities [57], is [41, Corollary 3.9], which gives a lower bound on the number of coexistence equilibria.

Observe that the works [35,36] also study multi-competitive virus spread, and identify special scenarios where coexistence equilibria can exist. In particular, Liu et al. [36, Theorems 6 and 7] and, particularized for the bi-virus setting, Paré et al. [35, Theorem 6] establish the existence of infinitely many coexistence equilibria, thus implying that a coexistence equilibrium in the bi-virus setup is not necessarily unique. In order to compare our result with Paré et al. [35, Theorem 6], we recall the same in the next proposition. Prior to so doing, we need to introduce the following: For the case when there is only one virus in the network (i.e., no competition), the dynamics can, by dropping the notation for virus index, be immediately obtained from (1), as given below:

$$\dot{p}_i(t) = -\delta_i p_i(t) + \big(1 - p_i(t)\big)\Big(\sum_{j=1}^{n} \beta_{ij} p_j(t)\Big). \tag{6}$$

In vector form, (6) can be written as follows:

$$\dot{p}(t) = [-D + (I - \Delta(p(t)))B]p(t). \tag{7}$$

where p is the vector of all p_i.

Proposition 1 (*[35, Theorem 6]*). *Suppose that $\delta_i^1 = \upsilon\delta_i^2 > 0$, $\forall i \in [n]$, $\beta_{ij}^1 = \nu\beta_{ij}^2$ $\forall \beta_{ij}^k \neq 0$ $k \in [2]$, $\nu > 0$, the matrix B^1 is non-negative and irreducible, and $s(-D^1 + B^1) > 0$. We have that $(\hat{p}^1, \hat{p}^2)$ with $\hat{p}^k > \mathbf{0}$ $\forall k \in [2]$ is an equilibrium of (1) if and only if $\hat{p}^k \gg \mathbf{0}$ for $k \in [2]$, $\hat{p}^i = \alpha^{ik}\hat{p}^k$, $\forall i, k \in [2]$, for some constants $\alpha^{ik} > 0$ such that $\tilde{p} = \hat{p}^1 + \hat{p}^2$, where $\tilde{p}$ is the non-zero endemic state of (7).*

We now explore the relationship between Theorem 1 and Paré et al. [35, Theorem 6].

[3] The term reproduction number is also referred to as reproductive number in the literature; see, for instance, Hyman and Li [51].

[4] Theorem 1 is the same as [39, Corollary 1]. It is an improvement of a similar result in [44, Theorem 5.2], wherein the same is established for $n = 2$; and of Doshi et al. [38, Theorem 4.3] where all nodes have the same healing and infection rates.

[5] The notion of MDS was pioneered by Morris Hirsch in [53]. For a detailed overview of MDS, the reader is referred to Smith [54].

Proposition 2. *Suppose that*

(i) $\delta_i^1 = \upsilon\delta_i^2 > 0$ *for* $i \in [n]$;
(ii) $\beta_{ij}^1 = \upsilon\beta_{ij}^2$ *for all* $\beta_{ij}^k \neq 0$ $k \in \{1,2\}$ $\upsilon > 0$;

with $D^1 = \Delta(\delta^1)$, $B^1 = [\beta_{ij}^1]_{n\times n}$ *non-negative and irreducible, and* $s(-D^1 + B^1) > 0$. *Then, with* $\tilde{p}^1, \tilde{p}^2$ *being the single-virus endemic equilibrium of viruses 1 and 2, respectively, it follows that*

$$s(-D^1 + (I - \Delta(\tilde{p}^2))B^1) = 0$$
$$s(-D^2 + (I - \Delta(\tilde{p}^1))B^2) = 0.$$

Proof. See Appendix. □

As a consequence of Proposition 2, Theorem 1 and Paré et al. [35, Theorem 6] *cannot* be applied at the same time, i.e., the conditions in Theorem 1 and Proposition 1 are mutually exclusive.

While Theorem 1 provides conditions for the existence of coexistence equilibrium, a related problem is finding conditions under which no coexistence equilibrium can exist. As a first step in this direction, we devise a test that *disqualifies* an arbitrary point (p^1, p^2) in the state space from being a coexistence equilibrium of system (3).

Proposition 3. *Consider a bi-virus state* $\mathbf{0} \ll (p^1, p^2) \ll \mathbf{1}$ *with* B^1, B^2 *irreducible and* $D^1 = D^2 = I$, *where* $\rho(B^1) > 1$ *and* $\rho(B^2) > 1$. *If* $(B^2 - B^1)p^1 < \mathbf{0}$, *or if* $(B^2 - B^1)p^1 > \mathbf{0}$, *then* (p^1, p^2) *is not an equilibrium of the system* (3).

Proof. See Appendix. □

Note that Proposition 3 does *not* preclude the existence of a coexistence equilibrium; if *every* point (p^1, p^2) in the state space fulfills the conditions of Proposition 3, then a coexistence equilibrium, (p^1, p^2) where $p^1 > \mathbf{0}$ and $p^2 > \mathbf{0}$, does not exist.

It turns out that given one of the spread matrices, say B^1, there could be several B^2 obeying a specific functional form (but different from the one identified in [34, Proposition 3.9]), that yield a connected set, such that every element in this set is a non-zero equilibrium point. Furthermore, this set comprises an interval of a straight line. The following theorem establishes the same.

Theorem 2. *Consider system* (3) *under Assumption* 1. *Suppose that* $D^1 = D^2 = I$, *and that* B^1 *is an irreducible, non-negative matrix with* $\rho(B^1) > 1$. *Let* $\tilde{p}$ *be the unique solution to*

$$(I - \Delta(p))B^1 p = p \tag{8}$$

such that $\mathbf{0} \ll \tilde{p} \ll \mathbf{1}$. *Suppose* $b > \mathbf{0}$.

(i) Consider some $z \in \mathbb{R}^n$ *such that* $z^\top \tilde{p} = 0$. *If* $B^2 = B^1 + bz^\top$ *is an irreducible non-negative matrix, then every coexistence equilibrium of system* (3) *is of the form* $(p^1, p^2) = (c\tilde{p}, (1-c)\tilde{p})$ *for some* $c \in (0,1)$. *Further, the line of coexistence equilibria* $(c\tilde{p}, (1-c)\tilde{p})$ *is locally exponentially attractive.*
(ii) Consider some $z \in \mathbb{R}^n$ *such that* $z^\top \tilde{p} \neq 0$. *If* $B^2 = B^1 + bz^\top$ *is an irreducible non-negative matrix, then system* (3) *has no coexistence equilibrium.*

Proof. See Appendix. □

In words, Theorem 2 states that, assuming a bi-virus network is constructed in a particular way, either every point in the interval of a straight line, with each end of the interval corresponding to the single-virus endemic equilibrium associated with each of the viruses, is a coexistence equilibrium (thus obtaining a connected set of equilibria); or no coexistence equilibrium exists. This further implies that said line is the unique set of coexistence equilibria.

Observe that the results in Proposition 3 and Theorem 2 rely on the assumption that $D^1 = D^2 = I$, which begets the following question: is there a loss of generality in using the aforesaid assumption? In order to answer this, we recall the following result.

Lemma 2 ([34, Lemma 3.7])**.** *Consider two bivirus network systems* $\mathcal{S}$ *and* $\hat{\mathcal{S}}$, *defined by quadruples* B^1, D^1, B^2, D^2 *and* $\hat{B}^k = (D^k)^{-1}B^k$, $\hat{D}^k = I$ *for* $k = 1,2$, *respectively. Then, the two systems have the same equilibrium sets and the (local) stability properties of each equilibrium are the same.*

Specifically, Lemma 2 states that there is no loss of generality in assuming $D^1 = D^2 = I$. Consequently, the findings of Proposition 3 and Theorem 2 are applicable even if D^k for $k = 1,2$ are arbitrary positive diagonal matrices that are not necessarily equal to each other.

Note that if the condition in Theorem 2 is fulfilled, then the bivirus system has an infinite number of coexistence equilibria. A question that one is faced with at this point is as follows: do *almost all* bivirus networks possess an infinite number of equilibria? In order to answer this question, we recall the following result:

Proposition 4 ([34, Theorem 3.6])**.** *For generic parameter matrices* D^i, B^i, $i = 1,2$, *the bivirus equation set* (3) *has a finite number of equilibria. If* $D^i = I$, $i = 1,2$, *then for generic parameter matrices* B^i, $i = 1,2$ *the same conclusion holds.*

In order to understand the ramifications of Proposition 4, and how that relates with statement (i) in Theorem 2, we introduce the following. Free parameters in D^i, B^i, $i = 1,2$ are those positions in D^i, B^i, $i = 1,2$, that are free to take any value in $\mathbb{R}_+$; these free parameters can be collected in a vector, with the dimension of the vector equaling the sum total of the free parameters in matrices D^1, D^2, B^1 and B^2. Each numerical choice of said vector of free parameters yields a system, whose dynamics are as given in (3). A property (in this case, that of having a finite number of equilibria) being true for *almost all* choices of free parameters means that it is true for all choices of free parameters except those lying on a set of measure zero. In the context of Theorem 2, observe that, since by assumption, $D^1 = D^2 = I$, and since all off-diagonal terms in matrices D^1, D^2 are fixed to zero, it is clear that the matrices D^1, D^2 have no free parameters. Since no restrictions are imposed on any of the entries in matrices B^1 and B^2, all entries in these matrices are free parameters. Given that Proposition 4 says that for almost all choices of B^i, $i = 1,2$, system (3) has a finite number of equilibria, it follows that for almost all choices of B^1, the set of numerical choices of free parameters of B^2 for which the condition in statement *(i)* of Theorem 2 is fulfilled has measure zero.

In a similar vein, with respect to Proposition 2, note that since D^1 and B^1 are scaled versions of D^2 and B^2, respectively, the elements along the diagonal of D^2 and (in general) all elements in B^2 are free parameters, while none of the elements in D^1 and B^1 are free parameters. The choices of free parameters of D^2 and B^2 for which the conditions in Proposition 2 are fulfilled lies on a set of measure zero in the corresponding space of free parameters; see [34, Section 3.2.1]. The set of choices of free parameters that fulfill Proposition 2 is contained within the set of choices of free parameters that fulfill the conditions in Theorem 2, as illustrated by the following. By setting $z = 0$ in statement *(i)* of Theorem 2, we recover conditions (i) and (ii) from Proposition 2 with $\upsilon = 1$ (assuming $\delta_i^1 = 1$, for each $i \in [n]$), that is, Liu et al. [36, Theorem 6] and Paré et al. [35, Theorem 6] for two viruses, (with $\upsilon = 1$) which guarantees the existence of a line of coexistence equilibria (and is a necessary condition according to Paré et al. [35, Theorem 6]). Furthermore, in so doing, statement *(i)* of Theorem 2 strengthens [36, Theorem 6] (and adds to Paré et al. [35, Theorem 6] in the bi-virus case when $\upsilon = 1$) due to the guarantee of local exponential attractivity to the line of coexistence equilibria.

Remark 4. One key insight that Theorem 2 provides is as follows: Suppose that we are interested in constructing bivirus networks for which we would like to obtain infinitely many coexistence equilibria. Then, statement (i) in Theorem 2 says that purely from knowledge of parameters corresponding to virus 1, we can obtain said construction. To see this, consider the following: Suppose that we are given B^1 such that B^1 is irreducible non-negative and $\rho(B^1) > 1$. Since $\rho(B^1) > 1$,

there exists an endemic equilibrium corresponding to virus 1, call it $\tilde{p}^1$, where $\mathbf{0} \ll \tilde{p}^1 \ll \mathbf{1}$, see [50, Theorem 2.1]. An exact characterization of $\tilde{p}^1$ can be obtained from [58, Theorem 5]. Consequently, with a suitable choice of z such that $z^\top \tilde{p}^1 = 0$ and with some choice of $b \gg \mathbf{0}$, it might be perhaps possible to *design* B^2 such that $B^2 = B^1 + bz^\top$. Due to Theorem 2 statement i), it follows that the corresponding bi-virus system will possess infinitely many coexistence equilibria. Provision of a systematic procedure for the construction of a bivirus network in the aforementioned manner is beyond the scope of the present paper.

The following result makes use of a nontrivial condition to eliminate the possibility of coexistence equilibrium in a bi-virus setting, and establishes one virus as being dominant.

Theorem 3. *Consider system (3) under Assumption 1. Suppose that $D^1 = D^2 = I$, and that B^1 is an irreducible, non-negative matrix with $\rho(B^1) > 1$. Let $\tilde{p}^1$ be the unique solution to*

$$(I - \Delta(p^1))B^1 p^1 = p^1 \tag{9}$$

such that $\mathbf{0} \ll \tilde{p}^1 \ll \mathbf{1}$. Consider some $z \in \mathbb{R}^n$ such that $z^\top \tilde{p}^1 > 0$, and some $b \gg \mathbf{0}$. If $B^2 = B^1 + bz^\top$ is an irreducible non-negative matrix with $\rho(B^2) > 1$, and $\tilde{p}^2$ is the unique solution to

$$(I - \Delta(p^2))B^2 p^2 = p^2, \tag{10}$$

such that $\mathbf{0} \ll \tilde{p}^2 \ll \mathbf{1}$, then the only equilibria of (3) are $(\mathbf{0}, \mathbf{0})$ and $(\tilde{p}^1, \mathbf{0})$, which are unstable, and $(\mathbf{0}, \tilde{p}^2)$, which is locally exponentially stable. Moreover, the equilibrium $(\mathbf{0}, \tilde{p}^2)$ is asymptotically stable with a domain of attraction that includes Int($\mathcal{F}$).

Proof. See Appendix. □

Theorem 3 establishes one virus as being dominant. Note that [47, Theorem 21] also provides a condition for establishing one virus as dominant. However, since the condition in Theorem 3 involves matrix inequalities, the condition in [47, Theorem 21] does not imply the condition in Theorem 3; see [47, Definition 11].

4. Leveraging one virus to eradicate another

It turns out that in a bi-virus setting, where one virus is malignant and the other virus is benign, we can leverage the benign virus in order to help eradicate the malignant virus, as stated in the following theorem.

Theorem 4. *Consider the bi-virus SIS model (3) under Assumption 1. Suppose that B^1 and B^2 are irreducible matrices; $s(B^1 - D^1) > 0$; $s(B^2 - D^2) > 0$; and $E^2 \subseteq E^1$, where E^1 and E^2 are as defined in Section 2. If the healing rates for virus 2 fulfill*

$$\delta_i^2 > \max_{j \in [n]} \left\{ \frac{(B^2)_{ij}}{((D^1)^{-1}B^1)_{ij}} \right\}_{(B^1)_{ij} > 0}, \tag{11}$$

for all $i \in [n]$, then the only locally asymptotically stable equilibrium in $\mathcal{F}$ is $(\tilde{p}^1, \mathbf{0})$ with $\mathbf{0} \ll \tilde{p}^1 \ll \mathbf{1}$.

Proof. See Appendix. □

Theorem 4 represents a strategy to eradicate one of the viruses in a bi-virus system, made possible by leveraging the fact that one virus has a stronger set of spread parameters than the other. Theorem 4 addresses question (iv) in Section 2.1. We discuss an interesting interpretation of the strategy in Theorem 4, and of the merits of the same in the following remarks.

Remark 5 (*Virus as Vaccine*)**.** Since the strategy given in Theorem 4 ensures local asymptotic convergence to the single-virus endemic equilibrium of the benign virus, it could also be interpreted in the following sense: the benign virus effectively acts as a *vaccine* against the malignant virus. In the context of battling epidemic outbreaks, where the goal is to minimize the mortality rate, this strategy could potentially provide health administration officials with an effective tool. ■

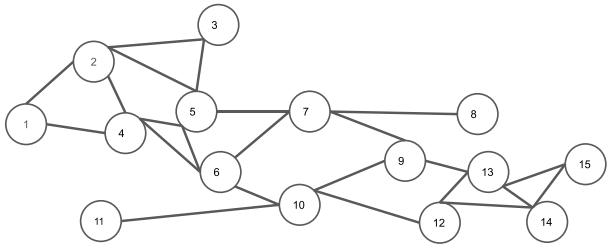

Fig. 2. Spread network for virus 1.

The mitigation strategies detailed in this section can be compared as follows. On the one hand, assuming that the objective of public health officials is solely to eradicate one virus in a bi-virus system while considering resource constraints (e.g., availability of vaccines, drugs, ventilators, etc.), it may be more feasible to implement the strategy given in Theorem 4. On the other hand, this strategy requires the persistence of one virus, which may be undesirable. Observe that since the condition in Theorem 4 involves adjusting healing rates, it can be viewed as an allocation of healing resources but under the assumption that there are enough resources to meet the demand.

Given that both Theorems 3 and 4 establish one virus as dominating the other virus, it is natural to ask whether Theorem 3 implies and is implied by Theorem 4. We address the same in the following. Theorem 3 says that if $B^2 = B^1 + bz^\top$, for some $b \gg \mathbf{0}$ and z such that $z^\top \tilde{p}^1 > 0$, where $\tilde{p}^1$ is the unique solution to Eq. (9), then virus 2 dominates virus 1. Setting $D^k = I$ for $k = 1, 2$ in Theorem 4 (and there is no loss of generality in doing so; see [34, Lemma 3.7]), it can be immediately observed that $B^1 > B^2$, which, due to Ye et al. [34, Corollary 3.10] further implies that virus 1 dominates virus 2. Indeed, post a suitable adjustment of notation in Theorem 4 (i.e., essentially replace index 1 with index 2 and vice-versa), it can be readily seen that $B^2 > B^1$, which implies that virus 2 dominates virus 1. Note that for the condition in Theorem 3 to be satisfied, we require $B^2 = B^1 + bz^\top$ where the vector z satisfies $z^\top \tilde{p}^1 > 0$. However, the vector z does not necessarily need to have all its elements to be strictly positive. Hence, $B^2 = B^1 + bz^\top$ does not necessarily imply that $B^2 > B^1$ or $B^1 > B^2$. Thus, the condition in Theorem 3 does not imply the condition in Theorem 4. It also turns out that the condition in Theorem 4 does not imply the condition in Theorem 3; to see this, consider the following: Suppose that $B^2 > B^1$, then, for some $b' \gg \mathbf{0}$ and $\bar{z}$, we have $B^2 = B^1 + b'\bar{z}^\top$. Note that such a $\bar{z}$ need not necessarily satisfy $\bar{z}^\top \tilde{p}^1 > 0$. In conclusion, Theorem 3 (resp. Theorem 4) does not subsume Theorem 4 (resp. Theorem 3).

5. Simulations

In this section, we present a number of simulations to illustrate our theoretical findings. In particular, we consider a network having 15 population nodes, thus, $n = 15$. In all simulated scenarios we consider two competing viruses, namely virus 1 and virus 2. We denote the average infection ratio of virus k, i.e., $\frac{1}{n}\sum_i^n p_i^k(t)$, by $\bar{p}^k(t)$. The spread parameter β_{ij}^k is set to one if node j is a neighbor of node i; otherwise β_{ij}^k is set to zero. The spread network for virus 1 is as shown in Fig. 2.

In the simulation depicted in Fig. 3, the contact network of each virus is the same, i.e., $E^1 = E^2$. We chose $\delta_i^1 = 1.5$ for $i \in [8]$, and $\delta_i^1 = 2$ for $i \in [15] \setminus [8]$. Mirroring this pattern, we chose $\delta_i^2 = 2$ for $i \in [8]$, and $\delta_i^2 = 1.5$ for $i \in [15] \setminus [8]$. As initial conditions, we set $p_i^1(0) = 0.5$ and $p_i^2(0) = 0.3$ for all $i \in [15]$. With these choices of parameters, it turns out that $s(B^1 - D^1) = 2.5032$, and $s(B^2 - D^2) = 2.5188$. Hence, both viruses fulfill the conditions in [36, Theorem 3], thus providing the existence

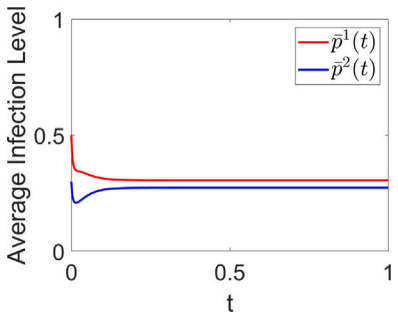

Fig. 3. Simulation with two viruses (red and blue), converging to a coexistence equilibrium. The average infection ratio of virus k is denoted by $\bar{p}^k(t)$.

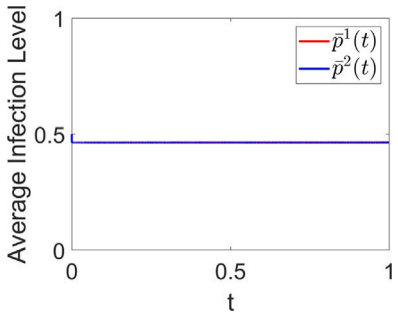

Fig. 4. Simulation with two viruses (red and blue). With $z^\top = [\text{ones}(1,14), -14.0608]$ (z being a column vector), $b = 0.1 * \text{ones}(15,1)$, and letting $B^2 = B^1 + bz^\top$, neither virus is able to push out the other; thereby leading to the existence of a coexistence equilibrium point.

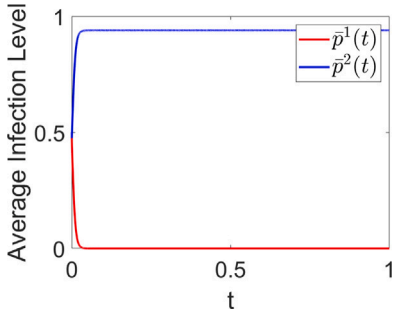

Fig. 5. Simulation with two viruses (red and blue). With $z = [\text{ones}(14,1); 14.0608]$, $b = 0.1 * \text{ones}(15,1)$, and letting $B^2 = B^1 + bz^\top$, the infection level with respect to virus 1 dies out, thereby precluding the possibility of the existence of a coexistence equilibrium.

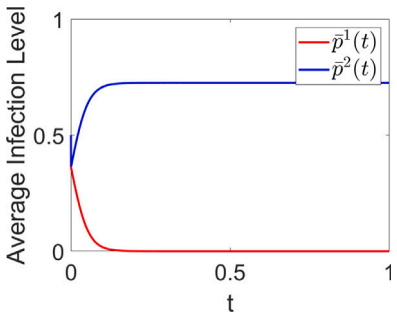

Fig. 6. Simulation with two viruses (red and blue). The average infection ratio of virus k is denoted by $\bar{p}^k(t)$. The single-virus endemic equilibrium of virus 1 is unstable, whereas that of virus 2 is asymptotically stable.

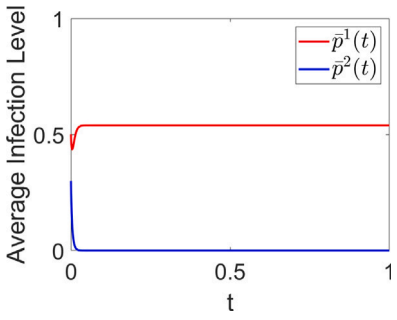

Fig. 7. Simulation with two viruses (red and blue). The healing rates of virus 2 are changed to fulfill Theorem 4. Virus 1 persists and reaches its single-virus endemic equilibrium, whereas virus 2 dies out.

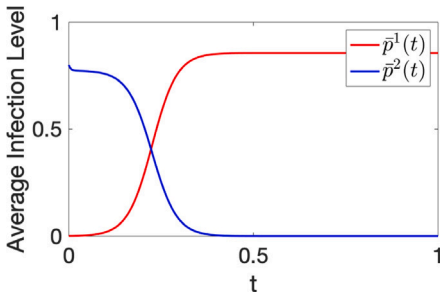

Fig. 8. Simulation with reproduction numbers analogous to Covid variants, with Omicron ($\bar{p}^1(t)$) depicted in red and Delta ($\bar{p}^2(t)$) depicted in blue. While the Delta variant starts out close to its single-virus endemic equilibrium, it is eventually overtaken by Omicron, despite the latter barely being present in the population initially.

of exactly two single-virus endemic equilibria, namely $(\tilde{p}^1, \mathbf{0})$ and $(\mathbf{0}, \tilde{p}^2)$. Note, $\tilde{p}^1$ can be approximated by setting $p^1(0) > \mathbf{0}$ and $p^2(0) = \mathbf{0}$, and running the simulation for a sufficiently long period of time T. Then, assuming that $\tilde{p}^1 \approx p^1(T)$, and, with an analogous approximation for virus 2, $\tilde{p}^2 \approx p^2(T)$, we obtain $s((I - \Delta(\tilde{p}^2))B^1 - D^1) = 2.126$, and $s((I - \Delta(\tilde{p}^1))B^2 - D^2) = 2.147$. Consequently, this pair of viruses fulfills the conditions for Theorem 1. In line with the result in Theorem 1, there exists a coexistence equilibrium; see Fig. 3. Moreover, our simulations show that the viral infection levels appear to converge to a coexistence equilibrium . Additionally, irrespective of how the initial condition is varied within $\mathcal{F}$, excluding $p^1(0) = \mathbf{0}$ or $p^2(0) = \mathbf{0}$, we observe that all simulations converge to the same coexistence equilibrium, which suggests that the coexistence equilibrium might be unique, as well as asymptotically stable.

For the simulation depicted in Fig. 5, we set the initial conditions to be $p_i^1(0) = 0.5$ and $p_i^2(0) = 0.5$ for all $i \in [15]$. The matrix B^1 is the same as that for the simulation depicted in Fig. 3, except that all entries in the last column are increased by 10. The healing rates are $\delta_i^k = 1$ for $i \in [15]$ and $k \in [2]$. We choose z to be a vector with all entries except the last one being equal to 1; the last entry equals -14.0608. Observe that $z^\top \tilde{p}^1 = 0$, where $\tilde{p}^1$ is obtained as described in the simulation for Fig. 3. We choose b to be a column vector with all entries being equal to 0.1. We set $B^2 = B^1 + bz^\top$, and observe that B^2 is an irreducible non-negative matrix. Consistent with the result in Theorem 2 (statement i)), a coexistence equilibrium point exists; see Fig. 4. Next, we choose z to be a column vector with all entries except the last one being equal to 1; the last entry equals 14.0608. Note that with this choice of z, $z^\top \tilde{p}^1 \neq 0$. We choose vector b as described for Fig. 3, and accordingly construct B^2. Consistent with the result in Theorem 2 (statement (ii)), it can be seen that the infection level with respect to virus 1 decays to zero (see red line in Fig. 5); thus implying that a coexistence equilibrium does not exist.

For the following simulation, we set $p_i^1(0) = 0.5$ and $p_i^2(0) = 0.3$, for all $i \in [15]$. For the simulation depicted in Fig. 6, B^1 is same as that for the simulation depicted in Fig. 3. The healing rates are $\delta_i^k = 1$,

for $i \in [15]$ and $k \in [2]$. We choose z to be a column vector with all entries being equal to 0.01, and note that $z^\top \tilde{p}^1 > 0$, where $\tilde{p}^1$ is obtained as described in the simulation for Fig. 3. We choose b to be a column vector with all entries being equal to 0.1. We set $B^2 = B^1 + bz^\top$, and note that B^2 is irreducible. Further, $s(-D^1 + B^1) = 3.1599$, and therefore $s(-D^1 + B^1) > 0$, which implies $\rho(B^1) > 1$. Likewise, $s(-D^2 + B^2) = 3.1729$, and therefore $s(-D^2 + B^2) > 0$, which implies $\rho(B^2) > 1$. Thus, the aforementioned choice of parameters fulfills the criteria in Theorem 3. In line with the result in Theorem 3, the single-virus endemic equilibrium corresponding to virus 1 is unstable (see red line in Fig. 6), while the single-virus endemic equilibrium corresponding to virus 2 is asymptotically stable (see blue line in Fig. 6).

The simulations depicted in Fig. 7 was initialized at the coexistence equilibrium from Fig. 3, with all parameters the same as in that simulation, except for the healing rate with respect to virus 2. The healing rates of virus 2, i.e., δ_i^2, are chosen as in (11). More specifically, $\delta_i^2 = 4$ for $i \in [15]$. With these choices of parameters, it turns out that $s(B^1 - D^1) = 2.5032$, and $s(B^2 - D^2) = 0.1599$. Given that the choice of δ_i^2 fulfills the inequality in (11), it follows that, consistent with the result in Theorem 4, virus 1 persists and reaches its single-virus endemic equilibrium (see red line in Fig. 7), whereas virus 2 is eradicated (see blue line in Fig. 7).

To relate the consequences of Theorem 4 to a real-world epidemic, the simulations depicted in Fig. 8 feature two viruses with similar basic reproduction numbers to the Covid-19 variants Omicron (red) and Delta (blue). Specifically, the healing parameters for virus 1 were chosen as $\delta_i^1 = 0.51$ for $i \in [15]$ to obtain $\rho((D^1)^{-1}B^1) = 8.2$, emulating the estimated basic reproduction number of the Omicron variant [59]. For virus 2, setting $\delta_i^2 = 0.81$ for $i \in [15]$ ensures that $\rho((D^2)^{-1}B^2) = 5.1$, emulating the estimated basic reproduction number of the Delta variant [60]. Furthermore, the initial conditions were set to $p_i^1(0) = 0.001$ and $p_i^2(0) = 0.7$ for all $i \in [15]$, representing a situation where the Delta variant is endemic in the population whereas the Omicron variant has just appeared. From Theorem 4 it follows that the only locally stable equilibrium is the single-virus endemic equilibrium of the Omicron variant. As seen in Fig. 8, despite the disadvantageous initial condition, the Omicron variant will eventually beat out the Delta variant, similar to what was witnessed in real-world data by Paton et al. [61]. In this sense, the Omicron variant may be thought of as a type of *vaccine* against the Delta variant, as discussed in Remark 5. However, it should be noted that these simulation parameters and the underlying assumptions may not be adequate models of Covid-19 spread.

6. Conclusions

The paper dealt with the existence of a coexistence equilibrium in a competitive bi-virus networked SIS model. We provided a sufficient condition, and a necessary condition, for the existence of a coexistence equilibrium. Further, we identified a condition, the fulfillment of which guarantees that, for certain special pairs of spread matrices, every coexistence equilibrium lies on a line; the violation of the said condition guarantees that there does not exist any coexistence equilibrium. Lastly, we devised a mitigation strategy, which employs one virus for eradicating the other.

There are several promising directions that could be pursued. A natural question is to ascertain whether the sufficient condition for existence of a coexistence equilibrium can be further strengthened to guarantee uniqueness and global (or at least local) asymptotic stability of the said equilibrium. Another line of work could involve devising closed-loop control strategies for steering the dynamics to the disease-free equilibrium, and to the boundary equilibrium of the benign virus, respectively. Yet another line of future investigation may revolve around characterizing observability in a bi-virus setting. Finally, it is of interest to consider the problem of leveraging one virus to eradicate another virus but under the caveat that there are constraints on the availability of healing resources.

Preliminaries

In this section, we recall some preliminary results, pertinent to the analysis of system (3). A real square matrix is said to be Metzler if all elements outside the diagonal are non-negative. We require the following result for Metzler matrices.

Lemma 3 ([36, Proposition 1]). *Suppose that Λ is a negative diagonal matrix and N is an irreducible non-negative matrix. Let M be the irreducible Metzler matrix $M = \Lambda + N$. Then, $s(M) < 0$ if and only if $\rho(-\Lambda^{-1}N) < 1$, $s(M) = 0$ if and only if $\rho(-\Lambda^{-1}N) = 1$, and $s(M) > 0$ if and only if, $\rho(-\Lambda^{-1}N) > 1$.* ■

We will also be making use of the following variants of the Perron–Frobenius theorem for irreducible matrices.

Lemma 4 ([62, Chapter 8.3] [63, Theorem 2.7]). *Suppose that N is an irreducible non-negative matrix. Then,*

(i) $r = \rho(N)$ is a simple eigenvalue of N.
(ii) There is an eigenvector $\zeta \gg \mathbf{0}$ corresponding to the eigenvalue r.
(iii) $x > \mathbf{0}$ is an eigenvector only if $Nx = rx$ and $x \gg \mathbf{0}$.
(iv) If A is a non-negative matrix such that $A < N$, then $\rho(A) < \rho(N)$. ■

Lemma 5 ([63, Lemma 2.3]). *Suppose that M is an irreducible Metzler matrix. Then $r = s(M)$ is a simple eigenvalue of M, with an eigenvector $\zeta \gg \mathbf{0}$.* ■

The following lemma pertains to system (3), providing a constraint on any endemic equilibrium.

Lemma 6. *Consider system (3) under Assumption 1. Suppose, for all $k \in [2]$, that B^k is irreducible. If $p = (p^1, p^2) \in \mathcal{F}$ is an equilibrium of (3), then, for each $k \in [2]$, either $p^k = \mathbf{0}$, or $\mathbf{0} \ll p^k \ll \mathbf{1}$. Moreover, $\sum_{k=1}^2 p^k \ll \mathbf{1}$.* ■

Proof. Consider an equilibrium $p \in \mathcal{F}$ of system (3). Assume, by way of contradiction, that $\sum_{k=1}^2 p_i^k \geq 1$ for some $i \in [n]$. Plugged into (1) under Assumption 1, we obtain

$$\sum_{k=1}^{2} \dot{p}_i^k(t) \leq -\sum_{k=1}^{2} \delta_i^k p_i^k < 0, \tag{12}$$

where (12) follows from (i) Assumption 1, (ii) $\sum_{k=1}^2 p_i^k \geq 1$ and (iii) that $p \in \mathcal{F}$. Note that (12) is a contradiction of the fact that p is an equilibrium, following from the assumption $\sum_{k=1}^2 p_i^k \geq 1$ for some $i \in [n]$. Therefore, $\sum_{k=1}^2 p^k \ll \mathbf{1}$.

Now, for all $k \in [2]$, p^k is a equilibrium of (2), so we have

$$\begin{aligned} &(-D^k + (I - \sum_{l=1}^{2} \Delta(p^l))B^k)p^k = 0, \\ \implies &(I - \sum_{l=1}^{2} \Delta(p^l))(D^k)^{-1}B^k p^k = p^k. \end{aligned} \tag{13}$$

Then, since $\mathbf{0} \ll p^k \ll \mathbf{1}$, $(I - \sum_{l=1}^2 \Delta(p^l))(D^k)^{-1}B^k$ is an irreducible non-negative matrix for all $k \in [2]$. Now, for some $k \in [2]$, assume by way of contradiction that $p^k > \mathbf{0}$, with $p_i^k = 0$ for all $i \in W$, where $W \subset [n]$ is nonempty. By the properties of irreducible non-negative matrices, $((I - \sum_{l=1}^2 \Delta(p^l))(D^k)^{-1}B^k p^k)_j > 0$ for some $j \in W$. Since $p_j^k = 0$, this contradicts (13), and therefore we must either have $p^k \gg \mathbf{0}$, or $p^k = \mathbf{0}$, for each $k \in [2]$. □

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Declaration of competing interest

There are no conflicts of interest.

Appendix

Proof of Theorem 1. Recall that for $k \in [2]$, Assumption 1 implies that D^k is a positive diagonal matrix, and therefore invertible. Furthermore, note that $(I + \Delta((D^1)^{-1}B^1p^1))$ and $(I + \Delta((D^2)^{-1}B^2p^2))$ are positive diagonal matrices whenever $p^1 \geq 0$ and $p^2 \geq 0$, and are then also invertible. Define the maps $T^1(p^1,p^2) : [0,1]^n \times [0,1]^n \to [0,1]^n$, and $T^2(p^1,p^2) : [0,1]^n \times [0,1]^n \to [0,1]^n$, such that

$$T^1(p^1,p^2) = (I + \Delta((D^1)^{-1}B^1p^1))^{-1} \times (I - \Delta(p^2))(D^1)^{-1}B^1p^1$$
$$T^2(p^1,p^2) = (I + \Delta((D^2)^{-1}B^2p^2))^{-1} \times (I - \Delta(p^1))(D^2)^{-1}B^2p^2.$$

For $i \in [n]$, the ith components of the maps are

$$T_i^1(p^1,p^2) = \frac{(1-p_i^2)((D^1)^{-1}B^1p^1)_i}{1+((D^1)^{-1}B^1p^1)_i},$$
$$T_i^2(p^1,p^2) = \frac{(1-p_i^1)((D^2)^{-1}B^2p^2)_i}{1+((D^2)^{-1}B^2p^2)_i}.$$

Note that the scalar function $s/(1+s)$ is increasing in s, and for $k \in [2]$, the matrix $(D^k)^{-1}B^k$ is non-negative. Therefore, T_i^k is an increasing function in p_j^k for all $i,j \in [n]$. Moreover, T_i^1 is a decreasing function in p_i^2 and T_i^2 is a decreasing function in p_i^1, for all $i \in [n]$. Hence, for any $p^1,p^2 \in [0,1]^n$, if $v \geq z$ it follows that

$$\begin{aligned} &T^1(v,p^2) \geq T^1(z,p^2),\ T^1(p^1,v) \leq T^1(p^1,z),\\ &T^2(v,p^2) \leq T^2(z,p^2),\ T^2(p^1,v) \geq T^2(p^1,z). \end{aligned} \tag{14}$$

The inequalities in (14) state that $T^k(p^1,p^2)$ is increasing in its kth argument and decreasing in its other argument. Let $p = (p^1,p^2)$, and let $T(p) : [0,1]^{2n} \to [0,1]^{2n}$ be the map $T(p) = (T^1(p),T^2(p))$. A fixed point of $T(p)$ fulfills

$$\begin{aligned} p^1 &= (I + \Delta((D^1)^{-1}B^1p^1))^{-1} \times (I - \Delta(p^2))(D^1)^{-1}B^1p^1\\ p^2 &= (I + \Delta((D^2)^{-1}B^2p^2))^{-1} \times (I - \Delta(p^1))(D^2)^{-1}B^2p^2. \end{aligned} \tag{15}$$

Pre-multiplying the first line (resp. second line) of (15) by $(I + \Delta((D^1)^{-1}B^1p^1))$ (resp. $(I + \Delta((D^2)^{-1}B^2p^2))$) gives us

$$\begin{aligned} (I + \Delta((D^1)^{-1}B^1p^1))p^1 &= (I - \Delta(p^2))(D^1)^{-1}B^1p^1\\ (I + \Delta((D^2)^{-1}B^2p^2))p^2 &= (I - \Delta(p^1))(D^2)^{-1}B^2p^2. \end{aligned} \tag{16}$$

Rearranging (16), and making use of the identity $\Delta(u)v = \Delta(v)u$ yields

$$\begin{aligned} (I - \Delta(p^1) - \Delta(p^2))(D^1)^{-1}B^1p^1 &= p^1,\\ (I - \Delta(p^1) - \Delta(p^2))(D^2)^{-1}B^2p^2 &= p^2. \end{aligned} \tag{17}$$

Making use of the fact that diagonal matrices commute, pre-multiplying the first line (resp. second line) of (17) by D^1 (resp. D^2), and rearranging terms gives us

$$\begin{aligned} (-D^1 + (I - \Delta(p^1) - \Delta(p^2))B^1)p^1 &= \mathbf{0},\\ (-D^2 + (I - \Delta(p^1) - \Delta(p^2))B^2)p^2 &= \mathbf{0}. \end{aligned} \tag{18}$$

Comparing (18) with (2), it follows that a fixed point of $T(p)$ constitutes an equilibrium of system (3) and vice versa. It suffices to show that $T(p)$ has a fixed point $\hat{p} = (\hat{p}^1,\hat{p}^2) \gg \mathbf{0}$, such that $\hat{p}^1 + \hat{p}^2 \leq \mathbf{1}$.

Recall that $(\tilde{p}^1,\mathbf{0})$ and $(\mathbf{0},\tilde{p}^2)$ are single-virus endemic equilibria of system (3). Consider $T^1(\tilde{p}^1,y^2)$. By assumption, $(\tilde{p}^1,\mathbf{0})$ is an equilibrium of (3), therefore $T^1(\tilde{p}^1,\mathbf{0}) = \tilde{p}^1$. By the inequalities in (14) we have $T^1(\tilde{p}^1,p^2) \leq \tilde{p}^1$, and thus $T^1(p^1,p^2) \leq \tilde{p}^1$, for all $p^1 \leq \tilde{p}^1$. Analogously, it can be shown that we have $T^2(p^1,p^2) \leq \tilde{p}^2$, for all $p^2 \leq \tilde{p}^2$. Thus,

$$T(p^1,p^2) \leq (\tilde{p}^1,\tilde{p}^2), \tag{19}$$

whenever $(p^1,p^2) \leq (\tilde{p}^1,\tilde{p}^2)$.

Now, by assumption, $s(-D^1+(I-\Delta(\tilde{p}^2))B^1) > 0$, and since D^1 and $(I-\Delta(\tilde{p}^2))$ are positive diagonal matrices and B^1 is an irreducible and non-negative matrix, $(-D^1 + (I - \Delta(\tilde{p}^2))B^1)$ is an irreducible Metzler matrix. Therefore, by Lemma 3 and the fact that diagonal matrices commute, we have $\rho((I - \Delta(\tilde{p}^2))(D^1)^{-1}B^1) > 1$. Further, since $((I - \Delta(\tilde{p}^2))(D^1)^{-1}B^1)$ is an irreducible non-negative matrix, by item *(i)* in Lemma 4 we know that $\lambda^1 = \rho((I - \Delta(\tilde{p}^2))(D^1)^{-1}B^1)$ is a simple eigenvalue of this matrix. Furthermore, by item *(ii)* in Lemma 4, we know that the eigenspace of λ^1 is spanned by a vector $\bar{p}^1 \gg \mathbf{0}$. Analogously, we get $\lambda^2 = \rho((I - \Delta(\tilde{p}^1))(D^2)^{-1}B^2) > 1$, and the corresponding eigenvector $\bar{p}^2 \gg \mathbf{0}$.

With the eigenvectors $\bar{p}^1,\bar{p}^2$ in place, we see that since $(D^1)^{-1}B^1$ and $(D^2)^{-1}B^2$ are irreducible non-negative matrices, we have $((D^1)^{-1}B^1\bar{p}^1)_i > 0$, $((D^2)^{-1}B^2\bar{p}^2)_i > 0$, for all $i \in [n]$. Further, given that $\bar{p}^1 \gg \mathbf{0}, \bar{p}^2 \gg \mathbf{0}, \tilde{p}^1 \gg \mathbf{0}$, and $\tilde{p}^2 \gg \mathbf{0}$, we have $\tilde{p}_i^1/\bar{p}_i^1 > 0$, and $\tilde{p}_i^2/\bar{p}_i^2 > 0$, for all $i \in [n]$. Moreover, note that $\lambda^1 - 1 > 0$ and $\lambda^2 - 1 > 0$. Hence, there exist $\epsilon^1 > 0$ and $\epsilon^2 > 0$ such that

$$\begin{aligned} \epsilon^1 &< \min\left\{\frac{\lambda^1-1}{\max_{i\in[n]}((D^1)^{-1}B^1\bar{p}^1)_i}, \min_{i\in[n]}\frac{\tilde{p}_i^1}{\bar{p}_i^1}\right\},\\ \epsilon^2 &< \min\left\{\frac{\lambda^2-1}{\max_{i\in[n]}((D^2)^{-1}B^2\bar{p}^2)_i}, \min_{i\in[n]}\frac{\tilde{p}_i^2}{\bar{p}_i^2}\right\}. \end{aligned} \tag{20}$$

From (20) it follows that

$$\begin{aligned} 1 + \max_{i\in[n]}((D^1)^{-1}B^1\epsilon^1\bar{p}^1)_i &< \lambda^1,\\ 1 + \max_{i\in[n]}((D^2)^{-1}B^2\epsilon^2\bar{p}^2)_i &< \lambda^2. \end{aligned} \tag{21}$$

Employing (21) it follows that, for all $i \in [n]$, we have

$$\begin{aligned} T_i^1(\epsilon^1\bar{p}^1,\tilde{p}^2) &= \frac{((I - \Delta(\tilde{p}^2))(D^1)^{-1}B^1\epsilon^1\bar{p}^1)_i}{1+((D^1)^{-1}B^1\epsilon^1\bar{p}^1)_i}\\ &= \frac{\lambda^1\epsilon^1\bar{p}_i^1}{1+((D^1)^{-1}B^1\epsilon^1\bar{p}^1)_i} > \epsilon^1\bar{p}_i^1,\\ T_i^2(\tilde{p}^1,\epsilon^2\bar{p}^2) &= \frac{((I - \Delta(\tilde{p}^1))(D^2)^{-1}B^2\epsilon^2\bar{p}^2)_i}{1+((D^2)^{-1}B^2\epsilon^2\bar{p}^2)_i}\\ &= \frac{\lambda^2\epsilon^2\bar{p}_i^2}{1+((D^2)^{-1}B^2\epsilon^2\bar{p}^2)_i} > \epsilon^2\bar{p}_i^2. \end{aligned}$$

Given that (20) implies $\epsilon^1\bar{p}^1 < \tilde{p}^1$ and $\epsilon^2\bar{p}^2 < \tilde{p}^2$, by the inequalities in (14) we have $T^1(\epsilon^1\bar{p}^1,p^2) > \epsilon^1\bar{p}^1$ whenever $\epsilon^2\bar{p}^2 \leq p^2 \leq \tilde{p}^2$, and $T^2(p^1,\epsilon^2\bar{p}^2) > \epsilon^2\bar{p}^2$ whenever $\epsilon^1\bar{p}^1 \leq p^1 \leq \tilde{p}^1$. Further application of the inequalities in (14) yields

$$T^1(p^1,p^2) > \epsilon^1\bar{p}^1,\ \ T^2(p^1,p^2) > \epsilon^2\bar{p}^2, \tag{22}$$

whenever $(\epsilon^1\bar{p}^1,\epsilon^2\bar{p}^2) \leq (p^1,p^2) \leq (\tilde{p}^1,\tilde{p}^2)$. Then, (19) and (22) show that $(\epsilon^1\bar{p}^1,\epsilon^2\bar{p}^2) \leq T(p^1,p^2) \leq (\tilde{p}^1,\tilde{p}^2)$ whenever $(\epsilon^1\bar{p}^1,\epsilon^2\bar{p}^2) \leq (p^1,p^2) \leq (\tilde{p}^1,\tilde{p}^2)$. By Brouwer's fixed point theorem [64, Theorem 9.3], there exists at least one fixed point of $T(p)$ in the domain $\{p = (p^1,p^2) : (\epsilon^1\bar{p}^1,\epsilon^2\bar{p}^2) \leq (p^1,p^2) \leq (\tilde{p}^1,\tilde{p}^2)\}$. Recall that a fixed point of $T(p)$ is equivalent to an equilibrium of (3), hence, by Lemma 6, any fixed point of $T(p)$ must fulfill $p^1 + p^2 \leq \mathbf{1}$. In conclusion, system (3) has at least one coexistence equilibrium $(\hat{p}^1,\hat{p}^2) \gg \mathbf{0}$ in $\mathcal{F}$, such that $\hat{p}^1 + \hat{p}^2 \leq \mathbf{1}$. ■

Proof of Proposition 2. Suppose that there are matrices D^1 and B^1 obeying conditions *(i)–(ii)* in the statement of Proposition 2, with the matrix B^1 being non-negative and irreducible. Further, note that with the given assumptions, $s(-D^1 + B^1) > 0$ implies that $s(-D^2 + B^2)$. Let $\tilde{p}^1$ and $\tilde{p}^2$ be the unique single-virus endemic equilibria for virus 1 and 2,

respectively. It follows from (2), and the fact that D^1, D^2 are invertible, that $\tilde{p}^1, \tilde{p}^2$ fulfill

$$\begin{aligned}(I-\Delta(\tilde{p}^1))(D^1)^{-1}B^1\tilde{p}^1 &= \tilde{p}^1,\\ (I-\Delta(\tilde{p}^2))(D^2)^{-1}B^2\tilde{p}^2 &= \tilde{p}^2.\end{aligned} \tag{23}$$

Since $B^1 = \nu B^2$, $D^1 = \nu D^2$ gives $(D^1)^{-1}B^1 = (D^2)^{-1}B^2$, from (23), it is immediate that $\tilde{p}^1 = \tilde{p}^2 = \tilde{p}$, and therefore

$$\begin{aligned}(I-\Delta(\tilde{p}))(D^1)^{-1}B^1\tilde{p} &= \tilde{p},\\ (I-\Delta(\tilde{p}))(D^2)^{-1}B^2\tilde{p} &= \tilde{p}.\end{aligned} \tag{24}$$

By Lemma 6 we have $\tilde{p} \ll \mathbf{1}$, implying that $(I-\Delta(\tilde{p}))$ is a positive diagonal matrix. Then, for $k \in [2]$, it follows that $(I-\Delta(\tilde{p}))(D^k)^{-1}B^k$ is irreducible and non-negative. Therefore, item *(iii)* in Lemma 4 can be applied to (24), from which it follows that $\rho((I-\Delta(\tilde{p}))(D^1)^{-1}B^1) = 1$ and $\rho((I-\Delta(\tilde{p}))(D^2)^{-1}B^2) = 1$. Applying Lemma 3 we obtain

$$\begin{aligned}s(-D^1 + (I-\Delta(\tilde{p}^2))B^1) &= 0,\\ s(-D^2 + (I-\Delta(\tilde{p}^1))B^2) &= 0.\end{aligned} \tag{25}$$

This concludes the proof. ■

Proof of Proposition 3. Suppose that (p^1, p^2) is an equilibrium of (2). Let the left Perron eigenvector of $(I-\Delta(p^1)-\Delta(p^2))B^2$ be $u \gg \mathbf{0}$, with corresponding eigenvalue $\rho((I-\Delta(p^1)-\Delta(p^2))B^2)$, so that $u^\top p^1 = 1$. Suppose that $(B^2-B^1)p^1 < \mathbf{0}$. Then

$$\begin{aligned}&(B^2-B^1)p^1 < \mathbf{0}\\ \Leftrightarrow\ &(I-\Delta(p^1)-\Delta(p^2))(B^2-B^1)p^1 < \mathbf{0}\\ \Leftrightarrow\ &[-I+(I-\Delta(p^1)-\Delta(p^2))B^2]p^1 < \mathbf{0}\\ \Rightarrow\ &u^\top[-I+(I-\Delta(p^1)-\Delta(p^2))B^2]p^1 < 0\\ \Rightarrow\ &\rho((I-\Delta(p^1)-\Delta(p^2))B^2) \neq 1.\end{aligned} \tag{26}$$

Since $\rho((I-\Delta(p^1)-\Delta(p^2))B^2) = 1$ at a coexistence equilibrium, we have a contradiction. Now, suppose that $(B^2-B^1)p^1 > \mathbf{0}$. Then

$$\begin{aligned}&(B^2-B^1)p^1 > \mathbf{0}\\ \Leftrightarrow\ &(I-\Delta(p^1)-\Delta(p^2))(B^2-B^1)p^1 > \mathbf{0}\\ \Leftrightarrow\ &[-I+(I-\Delta(p^1)-\Delta(p^2))B^2]p^1 > \mathbf{0}\\ \Rightarrow\ &u^\top[-I+(I-\Delta(p^1)-\Delta(p^2))B^2]p^1 > 0\\ \Rightarrow\ &\rho((I-\Delta(p^1)-\Delta(p^2))B^2) \neq 1.\end{aligned} \tag{27}$$

Since $\rho[(I-\Delta(p^1)-\Delta(p^2))B^2] = 1$ at a coexistence equilibrium, this contradicts (p^1, p^2) being a coexistence equilibrium of system (3). ■

Proof of Theorem 2. Note that for any $p^2 \in \mathbb{R}^n$ we must have one of the following.

$$bz^\top p^2 > \mathbf{0}, \text{ or } bz^\top p^2 < \mathbf{0}, \text{ or } bz^\top p^2 = \mathbf{0}. \tag{28}$$

Assume that (p^1, p^2) is a coexistence equilibrium. Hence, from Lemma 6 it follows that $\mathbf{0} \ll (p^1, p^2) \ll \mathbf{1}$. Then, by Proposition 3 we cannot have $bz^\top p^2 > \mathbf{0}$ or $bz^\top p^2 < \mathbf{0}$. Therefore $bz^\top p^2 = \mathbf{0}$, and thus

$$p^1 + p^2 = (I-\Delta(p^1)-\Delta(p^2))(B^1p^1 + B^2p^2) \tag{29}$$

$$= (I-\Delta(p^1)-\Delta(p^2))(B^1p^1 + [B^1 + bz^\top]p^2) \tag{30}$$

$$= (I-\Delta(p^1)-\Delta(p^2))B^1(p^1+p^2). \tag{31}$$

With $y := p^1 + p^2$, (31) becomes

$$y = (I-\Delta(y))B^1 y \tag{32}$$

Note that (32) is the same equation as (8). Therefore, (32) has the same unique positive solution $y = \tilde{p}$, and thus $p^1 + p^2 = \tilde{p}$ for every coexistence equilibrium (p^1, p^2). Further, the coexistence equilibrium equations are

$$p^1 = (I-\Delta(\tilde{p}))B^1p^1 \tag{33}$$

$$p^2 = (I-\Delta(\tilde{p}))B^2p^2 \tag{34}$$

Since B^1 is an irreducible non-negative matrix where $\mathbf{0} \ll \tilde{p} \ll \mathbf{1}$ solves (8), we know that $(I-\Delta(\tilde{x}))B^1$ has a simple unity eigenvalue with the corresponding eigenvector $\tilde{p}$. Moreover, we see that

$$(I-\Delta(\tilde{p}))B^2\tilde{p} = (I-\Delta(\tilde{p}))(B^1 + bz^\top)\tilde{p} \tag{35}$$

$$= (I-\Delta(\tilde{p}))B^1\tilde{p} \tag{36}$$

$$= \tilde{p}, \tag{37}$$

and since B^2 is an irreducible non-negative matrix, this tells us that $(I-\Delta(\tilde{p}))B^2$ has a simple unity eigenvalue with the corresponding eigenvector $\tilde{p}$. Thus, (33) and (34), combined with $(p^1, p^2) \gg \mathbf{0}$, imply that p^1 and p^2 are both parallel to $\tilde{p}$. Therefore, every coexistence equilibrium is of the form $(p^1, p^2) = (c\tilde{p}, (1-c)\tilde{p})$ for some $c \in (0,1)$. Local exponential attractivity of the line of coexistence equilibria $(c\tilde{p}, (1-c)\tilde{p})$, then, follows from [34, Proposition 3.9].

Now, note that by the same arguments as for (32), it follows that

$$y = (I-\Delta(y))B^2 y \tag{38}$$

Eqs. (32) and (38) must have a common solution if there exists a coexistence equilibrium. However, note that

$$(I-\tilde{p})B^2\tilde{p} = (I-\tilde{p})(B^1 + bz^\top)\tilde{p} \tag{39}$$

$$= \tilde{p} + (I-\tilde{p})bz^\top\tilde{p}. \tag{40}$$

From (40) it can be seen that if $z^\top\tilde{p} = 0$, Eqs. (32) and (38) have a common solution $\tilde{p}$. However, if $z^\top\tilde{p} \neq 0$, it follows that Eqs. (32) and (38) cannot have a common solution, and therefore there can be no coexistence equilibrium in the system. ■

In order to prove the claim in Theorem 3, we need the following lemma.

Lemma 7 (*[34, Corollary 3.16]*). *For the bivirus system in (3) with generic parameter matrices, suppose there are no coexistence equilibria. Then precisely one of the boundary equilibria is an attractive equilibrium, and Int($\mathcal{F}$) is in its domain of attraction.*

In words, Lemma 7 says that if there exists no coexistence equilibrium then one of the boundary equilibria is globally stable.

Proof of Theorem 3. Since $z^\top\tilde{p}^1 > 0$, by Theorem 2 there is no coexistence equilibrium, so the only equilibria are $(\mathbf{0}, \mathbf{0})$, $(\tilde{p}^1, \mathbf{0})$ and $(\mathbf{0}, \tilde{p}^2)$. Since, by assumption, $\rho(B^1) > 1$ and $\rho(B^2) > 1$, from [36, Theorem 3] it follows that $(\mathbf{0}, \mathbf{0})$ is unstable. Consider the Jacobian of (3) at $(\tilde{p}^1, \mathbf{0})$, which takes the following form:

$$J(\tilde{p}^1, \mathbf{0}) = \begin{bmatrix} -I + (I-\Delta(\tilde{p}^1))B^1 - \Delta(B^1\tilde{p}^1) & -\Delta(B^1\tilde{p}^1) \\ 0 & -I + (I-\Delta(\tilde{p}^1))B^2 \end{bmatrix}. \tag{41}$$

The matrix $J(\tilde{p}^1, \mathbf{0})$ is unstable if $L^1 = -I + (I-\Delta(\tilde{p}^1))B^2$ is unstable. Note that L^1 is an irreducible Metzler matrix, so if $L^1\tilde{p}^1 > \mathbf{0}$ then $s(L^1) > 0$. Since

$$L^1\tilde{p}^1 = (-I + (I-\Delta(\tilde{p}^1))(B^1 + bz^\top))\tilde{p}^1 \tag{42}$$

$$= (I-\Delta(\tilde{p}^1))z^\top\tilde{p}^1 b \tag{43}$$

$$> \mathbf{0}, \tag{44}$$

where inequality (44) is due to the fact that, by assumption, $z^\top\tilde{p}^1$ and $b \gg \mathbf{0}$, while $(I-\Delta(\tilde{p}^1))$ is positive diagonal, which implies that $bz^\top\tilde{p}^1 \gg \mathbf{0}$. Consequently, it follows that $s(L^1) > 0$, and therefore $(\tilde{p}^1, \mathbf{0})$ is an unstable equilibrium. Now, consider the Jacobian of (3) at $(\mathbf{0}, \tilde{p}^2)$, which takes the following form:

$$J(\mathbf{0}, \tilde{p}^2) = \begin{bmatrix} -I + (I-\Delta(\tilde{p}^2))B^1 & 0 \\ -\Delta(B^2\tilde{p}^2) & -I + (I-\Delta(\tilde{p}^2))B^2 - \Delta(B^2\tilde{p}^2) \end{bmatrix}. \tag{45}$$

The matrix $J(\mathbf{0}, \tilde{p}^2)$ is stable if, and only if, the matrices $-I + (I-\Delta(\tilde{p}^2))B^1$ and $-I + (I-\Delta(\tilde{p}^2))B^2 - \Delta(B^2\tilde{p}^2)$ are stable. Observe that since $\tilde{p}^2$ is the unique solution to (10) it follows that

$$(I-\Delta(\tilde{p}^2))B^2\tilde{p}^2 = \tilde{p}^2$$

$$\implies (-I + (I - \Delta(\tilde{p}^2))B^2)\tilde{p}^2 = \mathbf{0}. \tag{46}$$

Note that $\tilde{p}^2 \gg \mathbf{0}$. Hence, since $(-I+(I-\Delta(\tilde{p}^2))B^2)$ is irreducible Metzler, applying Lemma 5 to (46) we have that $s(-I+(I-\Delta(\tilde{p}^2))B^2) = 0$. Since $\Delta(B^2\tilde{p}^2)$ is a non-negative matrix, it follows that $-I + (I - \Delta(\tilde{p}^2))B^2 > -I + (I - \Delta(\tilde{p}^2))B^2 - \Delta(B^2\tilde{p}^2)$. Hence, from [65, Theorem 2.1], we have that $s(-I+(I-\Delta(\tilde{p}^2))B^2) > s(-I+(I-\Delta(\tilde{p}^2))B^2-\Delta(B^2\tilde{p}^2))$, which further implies that $s(-I + (I - \Delta(\tilde{p}^2))B^2-\Delta(B^2\tilde{p}^2)) < 0$.

It remains to show that $L^2 = -I + (I - \Delta(\tilde{p}^2))B^1$ is stable. Since L^2 is an irreducible Metzler matrix and $\tilde{p}^2 \gg \mathbf{0}$, it suffices to show that $L^2\tilde{p}^2 < \mathbf{0}$, thereby implying $s(L^2) < 0$. Note that

$$\begin{aligned} L^2\tilde{p}^2 &= (-I + (I - \Delta(\tilde{p}^2))(B^2 - bz^\top))\tilde{p}^2 \\ &= -(I - \Delta(\tilde{p}^2))z^\top\tilde{p}^2 b, \end{aligned} \tag{47}$$

and since $b > \mathbf{0}$ by assumption and $(I - \Delta(\tilde{p}^2))$ is a positive diagonal matrix, it must be shown that $z^\top\tilde{p}^2 > 0$. By way of contradiction, assume that $z^\top\tilde{p}^2 \leq 0$. If $z^\top\tilde{p}^2 < 0$ then (47) is greater than $\mathbf{0}$, implying that $s(L^2) > 0$. Since $s(L^1) > 0$, the conditions for Theorem 1 are fulfilled, implying that a coexistence equilibrium exists, which is a contradiction. If $z^\top\tilde{p}^2 = 0$, then $(I - \Delta(\tilde{p}^2))B^1\tilde{p}^2 = \tilde{p}^2$, which by the uniqueness of single-virus endemic equilibria implies that $\tilde{p}^1 = \tilde{p}^2$, contradicting the prior assumption $z^\top\tilde{p}^1 > 0$. Hence, $z^\top\tilde{p}^2 < 0$, ensuring that L^2 is stable. Therefore, $s(J(\mathbf{0}, \tilde{p}^2)) < 0$, which, from [66, Theorem 4.15 and Corollary 4.3], implies that the equilibrium point $(\mathbf{0}, \tilde{p}^2)$ is locally exponentially stable.

Since the existence of a coexistence equilibrium has been ruled out, Lemma 7 implies that the equilibrium $(\mathbf{0}, \tilde{p}^2)$ has a domain of attraction that includes $\mathrm{Int}(\mathcal{F})$. ■

Proof of Theorem 4. In order to prove this result, we need the following lemma.

Lemma 8 (*[34, Corollary 3.10]*). *Consider the SIS model (3) under Assumption 1. Suppose that B^1 and B^2 are irreducible matrices, and that $s(B^1 - D^1) > 0$ and $s(B^2 - D^2) > 0$. If $(D^1)^{-1}B^1 > (D^2)^{-1}B^2$ then there are exactly three equilibria in $[0, 1]^{2n}$, namely the healthy state, which is unstable, $(\mathbf{0}, \tilde{p}^2)$ with $\mathbf{0} \ll \tilde{p}^2 \ll \mathbf{1}$, which is unstable, and $(\tilde{p}^1, \mathbf{0})$ with $\mathbf{0} \ll \tilde{p}^1 \ll \mathbf{1}$, which is locally exponentially stable.*

Proof of Theorem 4. Note that with δ_i^2 given by (11) for all $i \in [n]$, since B^1 and B^2 are irreducible non-negative matrices we have $\delta_i^2 > 0$ for all $i \in [n]$. Therefore (11) is consistent with Assumption 1. Then, it follows from (i) the healing rate in (11), and (ii) $E^2 \subseteq E^1$, that $(D^1)^{-1}B^1 > (D^2)^{-1}B^2$. Hence, since, by assumption, $s(B^1 - D^1) > 0$ and $s(B^2 - D^2) > 0$, the conditions for Lemma 8 are met. Therefore, the only locally asymptotically stable equilibrium in $\mathcal{F}$ is $(\tilde{p}^1, \mathbf{0})$ with $\mathbf{0} \ll \tilde{p}^1 \ll \mathbf{1}$. ■

References

[1] N.P. Johnson, J. Mueller, Updating the accounts: Global mortality of the 1918–1920 “Spanish" influenza pandemic, Bull. Hist. Med. (2002) 105–115.

[2] C.W. Potter, A history of influenza, J. Appl. Microbiol. 91 (4) (2001) 572–579.

[3] D. Bernoulli, Essai d’une nouvelle analyse de la mortalité causée par la petite vérole, et des avantages de l’inoculation pour la prévenir, Hist. l’Acad. R. Sci.(Paris) Avec Mem. (1760) 1–45.

[4] L.J. Allen, Some discrete-time SI, SIR, and SIS epidemic models, Math. Biosci. 124 (1) (1994) 83–105.

[5] H.J. Ahn, B. Hassibi, Global dynamics of epidemic spread over complex networks, in: Proceedings of the 52nd IEEE Conference on Decision and Control, 2013, pp. 4579–4585.

[6] Y. Wang, D. Chakrabarti, C. Wang, C. Faloutsos, Epidemic spreading in real networks: An eigenvalue viewpoint, in: Proceedings of the 22nd International Symposium on Reliable Distributed Systems, 2003, IEEE, 2003, pp. 25–34.

[7] D. Chakrabarti, Y. Wang, C. Wang, J. Leskovec, C. Faloutsos, Epidemic thresholds in real networks, ACM Trans. Inf. Syst. Secur. 10 (4) (2008) 1–26.

[8] S. Gracy, P.E. Paré, H. Sandberg, K.H. Johansson, Analysis and distributed control of periodic epidemic processes, IEEE Trans. Control Netw. Syst. 8 (1) (2021) 123–134.

[9] P. Van Mieghem, J. Omic, R. Kooij, Virus spread in networks, IEEE/ACM Trans. Netw. 17 (1) (2009) 1–14.

[10] A. Khanafer, T. Başar, B. Gharesifard, Stability of epidemic models over directed graphs: A positive systems approach, Automatica 74 (2016) 126–134.

[11] A. Khanafer, T. Başar, Information spread in networks: Control, games, and equilibria, in: Proceedings of the 2014 Information Theory and Applications Workshop, ITA, IEEE, 2014, pp. 1–10.

[12] A.S. Ackleh, K. Deng, X. Wang, Competitive exclusion and coexistence for a quasilinear size-structured population model, Math. Biosci. 192 (2) (2004) 177–192.

[13] P. Minayev, N. Ferguson, Improving the realism of deterministic multi-strain models: implications for modelling influenza A, J. R. Soc. Interface 6 (35) (2009) 509–518.

[14] K.L. Laurie, W. Horman, L.A. Carolan, K.F. Chan, D. Layton, A. Bean, D. Vijaykrishna, P.C. Reading, J.M. McCaw, I.G. Barr, Evidence for viral interference and cross-reactive protective immunity between influenza B virus lineages, J. Infect. Dis. 217 (4) (2018) 548–559.

[15] A. Wu, V.T. Mihaylova, M.L. Landry, E.F. Foxman, Interference between rhinovirus and influenza A virus: A clinical data analysis and experimental infection study, Lancet Microbe 1 (6) (2020) e254–e262.

[16] K.F. Chan, L.A. Carolan, D. Korenkov, J. Druce, J. McCaw, P.C. Reading, I.G. Barr, K.L. Laurie, Investigating viral interference between influenza a virus and human respiratory syncytial virus in a ferret model of infection, J. Infect. Dis. 218 (3) (2018) 406–417.

[17] M.E. Newman, Threshold effects for two pathogens spreading on a network, Phys. Rev. Lett. 95 (10) (2005) 108701.

[18] A.J. Kucharski, V. Andreasen, J.R. Gog, Capturing the dynamics of pathogens with many strains, J. Math. Biol. 72 (2016) 1–24.

[19] M. Martcheva, X.-Z. Li, Competitive exclusion in an infection-age structured model with environmental transmission, J. Math. Anal. Appl. 408 (1) (2013) 225–246.

[20] M. Nuño, Z. Feng, M. Martcheva, C. Castillo-Chavez, Dynamics of two-strain influenza with isolation and partial cross-immunity, SIAM J. Appl. Math. 65 (3) (2005) 964–982.

[21] M. Fudolig, R. Howard, The local stability of a modified multi-strain SIR model for emerging viral strains, PLoS One 15 (12) (2020) e0243408.

[22] C. Zhang, S. Gracy, T. Başar, P.E. Paré, A networked competitive multi-virus SIR model: Analysis and observability, IFAC-PapersOnLine 55 (13) (2022) 13–18.

[23] C. Castillo-Chavez, H.W. Hethcote, V. Andreasen, S.A. Levin, W.M. Liu, Epidemiological models with age structure, proportionate mixing, and cross-immunity, J. Math. Biol. 27 (3) (1989) 233–258.

[24] P. De Leenheer, S.S. Pilyugin, Multistrain virus dynamics with mutations: a global analysis, Math. Med. Biol.: J. IMA 25 (4) (2008) 285–322.

[25] S. Gao, M. Shen, X. Wang, J. Wang, M. Martcheva, L. Rong, A multi-strain model with asymptomatic transmission: Application to COVID-19 in the US, J. Theoret. Biol. 565 (2023) 111468.

[26] M. Martcheva, S.S. Pilyugin, The role of coinfection in multidisease dynamics, SIAM J. Appl. Math. 66 (3) (2006) 843–872.

[27] M. Martcheva, A non-autonomous multi-strain SIS epidemic model, J. Biol. Dyn. 3 (2–3) (2009) 235–251.

[28] S. Madec, E. Gjini, Predicting n-strain coexistence from co-colonization interactions: epidemiology meets ecology and the replicator equation, Bull. Math. Biol. 82 (11) (2020) 142.

[29] M. Sun, X. Fu, Competitive dual-strain SIS epidemiological models with awareness programs in heterogeneous networks: two modeling approaches, J. Math. Biol. 87 (1) (2023) 14.

[30] A. Dénes, Y. Muroya, G. Röst, Global stability of a multistrain SIS model with superinfection, Math. Biosci. Eng. 14 (2) (2016) 421–435.

[31] C. Chen, Y. Kang, Dynamics of a stochastic multi-strain SIS epidemic model driven by Lévy noise, Commun. Nonlinear Sci. Numer. Simul. 42 (2017) 379–395.

[32] F.D. Sahneh, C. Scoglio, Competitive epidemic spreading over arbitrary multilayer networks, Phys. Rev. E 89 (6) (2014) 062817.

[33] A. Santos, Bi-virus Epidemics over Large-scale Networks: Emergent Dynamics and Qualitative Analysis (Ph.D. thesis), Carnegie Mellon University, 2014.

[34] M. Ye, B.D. Anderson, J. Liu, Convergence and equilibria analysis of a networked bivirus epidemic model, SIAM J. Control Optim. 60 (2) (2022) S323–S346.

[35] P.E. Paré, J. Liu, C.L. Beck, A. Nedić, T. Başar, Multi-competitive viruses over time-varying networks with mutations and human awareness, Automatica 123 (2021) 109330.

[36] J. Liu, P.E. Paré, A. Nedić, C.Y. Tang, C.L. Beck, T. Başar, Analysis and control of a continuous-time bi-virus model, IEEE Trans. Autom. Control 64 (12) (2019) 4891–4906.

[37] C. Granell, S. Gómez, A. Arenas, Dynamical Interplay between Awareness and Epidemic Spreading in Multiplex Networks, Phys. Rev. Lett. 111 (12) (2013) 128701.

[38] V. Doshi, S. Mallick, D.Y. Eun, Competing epidemics on graphs-global convergence and coexistence, in: IEEE INFOCOM 2021-IEEE Conference on Computer Communications, IEEE, 2021, pp. 1–10.

[39] A. Janson, S. Gracy, P.E. Paré, H. Sandberg, K.H. Johansson, Networked multi-virus spread with a shared resource: Analysis and mitigation strategies, 2020, https://arxiv.org/pdf/2011.07569.pdf.
[40] V. Doshi, S. Mallick, D.Y. Eun, Convergence of Bi-Virus Epidemic Models With Non-Linear Rates on Networks – A Monotone Dynamical Systems Approach, IEEE/ACM Trans. Netw. (2022).
[41] B.D. Anderson, M. Ye, Equilibria Analysis of a networked bivirus epidemic model using Poincar\'e–Hopf and Manifold Theory, SIAM J. Appl. Dyn. Syst. 22 (4) (2023) 2856–2889.
[42] S. Gracy, B.D. Anderson, M. Ye, C.A. Uribe, Competitive Networked Bivirus SIS spread over Hypergraphs, in: 2024 American Control Conference, ACC, IEEE, 2024, URL https://arxiv.org/pdf/2309.14230.pdf, Note: in press.
[43] M. Ye, B.D. Anderson, Competitive epidemic spreading over networks, IEEE Control Syst. Lett. 7 (2022) 545–552.
[44] J. Li, Z. Ma, S.P. Blythe, C. Castillo-Chavez, Coexistence of pathogens in sexually-transmitted disease models, J. Math. Biol. 47 (2003) 547–568.
[45] C. Castillo-Chavez, W. Huang, J. Li, Competitive exclusion and coexistence of multiple strains in an SIS STD model, SIAM J. Appl. Math. 59 (5) (1999) 1790–1811.
[46] E. Gjini, C. Valente, R. Sa-Leao, M.G.M. Gomes, How direct competition shapes coexistence and vaccine effects in multi-strain pathogen systems, J. Theoret. Biol. 388 (2016) 50–60.
[47] A. Santos, J. Moura, J. Xavier, Bi-virus SIS epidemics over networks: Qualitative analysis, IEEE Trans. Netw. Sci. Eng. 2 (1) (2015) 17–29.
[48] F. Brauer, P. van den Driessche, Models for transmission of disease with immigration of infectives, Math. Biosci. 171 (2) (2001) 143–154.
[49] A. Lajmanovich, J.A. Yorke, A deterministic model for gonorrhea in a nonhomogeneous population, Math. Biosci. 28 (3–4) (1976) 221–236.
[50] A. Fall, A. Iggidr, G. Sallet, J.-J. Tewa, Epidemiological models and Lyapunov functions, Math. Model. Nat. Phenom. 2 (1) (2007) 62–83.
[51] J.M. Hyman, J. Li, An intuitive formulation for the reproductive number for the spread of diseases in heterogeneous populations, Math. Biosci. 167 (1) (2000) 65–86.
[52] T.C. Porco, S.M. Blower, Designing HIV vaccination policies: subtypes and cross-immunity, Interfaces 28 (3) (1998) 167–190.
[53] M.W. Hirsch, Stability and convergence in strongly monotone dynamical systems, J. Reine Angew. Math. (1988).
[54] H.L. Smith, Monotone Dynamical Systems: An Introduction to the Theory of Competitive and Cooperative Systems: An Introduction to the Theory of Competitive and Cooperative Systems, vol. 41, American Mathematical Soc., 2008.
[55] S. Gracy, M. Ye, B.D. Anderson, C.A. Uribe, Towards understanding the endemic behavior of a competitive tri-virus SIS networked model, SIAM J. Appl. Dyn. Syst. 23 (2) (2024) 1372–1410.
[56] J. Milnor, D.W. Weaver, Topology from the Differentiable Viewpoint, vol. 21, Princeton University Press, 1997.
[57] S. Smale, Differentiable dynamical systems, Bull. Am. Math. Soc. 73 (6) (1967) 747–817.
[58] P.V. Mieghem, J. Omic, R. Kooij, Virus spread in networks, IEEE/ACM Trans. Netw. 17 (1) (2009) 1–14.
[59] Y. Liu, J. Rocklöv, The effective reproductive number of the Omicron variant of SARS-CoV-2 is several times relative to Delta, J. Travel Med. 29 (3) (2022) taac037.
[60] Y. Liu, J. Rocklöv, The reproductive number of the Delta variant of SARS-CoV-2 is far higher compared to the ancestral SARS-CoV-2 virus, J. Travel Med. 28 (7) (2021) taab124.
[61] R.S. Paton, C.E. Overton, T. Ward, The rapid replacement of the SARS-CoV-2 Delta variant by Omicron (B. 1.1. 529) in England, Sci. Transl. Med. 14 (652) (2022) eabo5395.
[62] C. Meyer, Matrix Analysis and Applied Linear Algebra, in: Other Titles in Applied Mathematics, SIAM, 2000.
[63] R. Varga, Matrix Iterative Analysis, Springer Series in Computational Mathematics, Springer Berlin Heidelberg, 1999.
[64] R.M. Starr, The brouwer fixed-point theorem, in: General Equilibrium Theory: An Introduction, second ed., Cambridge University Press, 2011, pp. 99–108.
[65] R.S. Varga, Matrix properties and concepts, in: Matrix Iterative Analysis, Springer, 2009, pp. 1–30.
[66] H. Khalil, Nonlinear Systems, in: Pearson Education, Prentice Hall, 2002.