SIS Epidemic Spreading Under Multilayer Population Dispersal in Patchy Environments

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Abstract—In this article, we study susceptible–infected–susceptible (SIS) epidemic spreading models under population dispersal on multilayer networks. We consider a patchy environment in which each patch comprises individuals belonging to different classes. Individuals disperse to other patches on a multilayer network, in which each layer corresponds to a class. The dispersal on each layer is modeled by a continuous-time Markov chain (CTMC). At each time, individuals disperse according to their CTMC and subsequently interact with the local individuals in the patch according to an SIS model. We establish the existence of various equilibria under different parameter regimes and establish their (almost) global asymptotic stability using Lyapunov techniques. We also derive simple conditions that highlight the influence of the multilayer network on the stability of these equilibria. For this model, we study optimal intervention strategies using a convex optimization framework. Finally, we numerically illustrate the influence of the multilayer network structure and the effectiveness of the optimal intervention strategies.

Index Terms—Epidemic models, multilayer networks, optimal intervention, population dispersal.

I. INTRODUCTION

Understanding processes underlying the spread of social activities, beliefs, and influence is of foundational interest for the efficient design of sociotechnical systems. Deterministic epidemic propagation models have been extensively used to study such spreading processes in the context of epidemics [2], [3]; the spread of computer viruses [4], [5]; routing in mobile communication networks [6]; and the spread of rumors [7]. While classical deterministic propagation models [8] rely on the assumption that the overall population is well mixed, several generalizations have been explored that incorporate the sparse interaction network among individuals or subpopulations into the model [9], [10], [11], [12], [13].

In this article, we focus on a class of such models in which subpopulations are distributed across spatial patches, and individuals interact within the patch using a classical epidemic propagation model and interact across patches by physically moving to other patches [14], [15], [16], [17]. Individuals may belong to different categories based on their features, such as age groups, socioeconomic status, and social preferences, which determine their dispersal pattern. Using Lyapunov techniques, we characterize the steady-state behavior of the model under different parameter regimes and characterize the influence of individuals’ dispersal patterns on the epidemic dynamics.

Epidemic models have been extensively studied in the literature. The two most widely studied models are the 1) susceptible–infected–susceptible (SIS) and 2) susceptible–infected–recovered (SIR) models, wherein individuals are classified into one of the three compartments, i.e., susceptible, infected, or recovered, and the dynamics of the fraction of the population in each compartment is studied [8]. Some common generalizations of the SIR/SIS models include the SEIR model [11], [18], where an additional compartment “exposed” is introduced, SIRS [3], where individuals get temporary immunity after recovery and then become susceptible again, and SIRI [19], [20], where, after recovery, agents become susceptible with a different rate of infection.

Networked epidemic models attempt to capture the heterogeneity and structured interactions among subpopulations. Several approaches have been developed to this end. A popular approach to networked epidemic models considers subpopulations as nodes in the interaction graph and models epidemic propagation at each node based on the local subpopulation as well as subpopulations at neighboring nodes [9], [10], [11], [12], [21], [22], [23], [24]. These models implicitly assume that the number of individuals at each node remains constant (if there is no birth or death) and that interactions with neighboring nodes do not involve the dispersal of individuals. Variants of these models with time-varying interaction graphs have also been studied [25], [26], [27].

Another approach to networked epidemic models uses heterogeneous mean-field theory and considers random interaction graphs among individuals. The individuals are classified based on their degree in the interaction graph, and the coupled dynamics of individuals in different classes is studied [28], [29].
The third approach to networked epidemic models considers patchy environments with population dispersal. Each patch contains a subpopulation, and the connectivity of the patches is modeled using a dispersal graph. Individuals within each patch interact according to classical epidemic models and disperse to neighboring patches in the dispersal graph [14], [15], [16]. Continuum approximations of these models have been studied using reaction–diffusion processes [30], [31]. A closely related class of models is called multicity models [32], [33], in which the individuals are identified by their patches and the model keeps track of the distribution of individuals from each patch. Alternative epidemic models with population flows have also been studied [34], [35], [36], [37].

Multilayer epidemic models have also been studied. Classical epidemic models have been extended to include heterogeneity due to age groups in epidemic propagation [8]. Multilayer networked epidemic models have also been used to study epidemic spread under competitive viruses [38], [39], [40].

The epidemic spread with dispersal on a multilayer network of patches has been modeled and studied in [41], wherein, at each time, individuals randomly move to another patch, participate in epidemic propagation, and then return to their home patch. A multispecies SEIR epidemic model with population dispersal has been studied in [17], wherein each species may have a different dispersal pattern corresponding to each layer in the multilayer graph. SIR epidemic dynamics with multilayer population dispersal have been studied in [42].

The problem of optimal intervention in terms of designing networks and allocating resources for efficiently mitigating epidemics has also received significant attention. A prominent approach leverages a static convex optimization framework to determine optimal intervention parameters such that the convergence rate for the disease-free equilibrium (DFE) is maximized [43], [44], [45], [46], [47]. Some works have also explored dynamic optimization [48], [49] as well as feedback control [50] for designing interventions.

In this article, we focus on the class of networked epidemic models that consider patchy environments with population dispersal. Individuals may belong to different categories based on their features, such as age groups, socioeconomic status, and social preferences, which determine their dispersal pattern. We consider a multilayer model in which each layer corresponds to a category of individuals and captures the associated dispersal pattern. Individuals within each patch can travel across patches according to a continuous-time Markov Chain (CTMC) characterizing their dispersal pattern and upon reaching a new patch participate in the local SIS epidemic process. We extend the results for the deterministic network SIS model [11], [12], [21], [22] to the networked SIS model with population dispersal and characterize its steady-state and stability properties. We also study optimal intervention strategies for epidemic containment using our model. Finally, we numerically illustrate that the derived model approximates well the stochastic model with a finite population. We illustrate the influence of the network topology on the transient properties of the model. We also illustrate the effectiveness of optimal intervention strategies.

The rest of this article is organized as follows. In Section II, we derive the epidemic model under multilayer dispersal as a continuum limit to two interacting stochastic processes. In Section III, we characterize the existence and stability of disease-free and endemic equilibrium for the derived model with strongly connected multilayer interaction. In Section IV, we relax the strong connectivity assumption. We study optimal intervention strategies in Section V and draw additional insights on the ideas in this article through numerical examples in Section VI. Finally, Section VII concludes this article.

### A. Mathematical Notation

For any two real vectors \( x, y \in \mathbb{R}^n \), we denote \( x \geq y \) if \( x_i \geq y_i \) for all \( i \in \{1, \ldots, n\} \), \( x \gg y \) if \( x_i > y_i \) for all \( i \in \{1, \ldots, n\} \), \( x > y \) if \( x_i > y_i \) for all \( i \in \{1, \ldots, n\} \), and \( x \neq y \).

For a square matrix \( G \), spectral abscissa \( \mu : \mathbb{R}^{n \times n} \to \mathbb{R} \) is defined by

\[
\mu(G) = \max\{\Re(\lambda) \mid \lambda \text{ is an eigenvalue of } G\}
\]

where \( \Re(\cdot) \) denotes the real part of the argument. Spectral radius \( \rho \) is defined by

\[
\rho(G) = \max\{|\lambda| \mid \lambda \text{ is an eigenvalue of } G\}
\]

where \( |\cdot| \) denotes the absolute value of the argument. For any vector \( x = [x_1, \ldots, x_n]^T \), \( X = \text{diag}(x) \) is a diagonal matrix with \( X_{ii} = x_i \) for all \( i \in \{1, \ldots, n\} \). Let \( \otimes \) denote the Kronecker product and \( \oplus \) denote the matrix direct sum.
II. SIS MODEL WITH MULTILAYER POPULATION DISPERAL

We consider $n$ subpopulations of individuals that are located in distinct spatial regions (patches). We assume that the individuals within each patch can be classified into two categories: 1) susceptible and 2) infected. We assume that the individuals within each patch are further grouped into $m$ classes, deciding how they travel to other patches. Let the connectivity of these patches corresponding to the dispersal pattern of each class $\alpha \in \{1, \ldots, m\}$ be modeled by a digraph $G^\alpha = (\mathcal{V}, \mathcal{E}^\alpha)$, where $\mathcal{V}$ and $\mathcal{E}^\alpha$ are the node (patch) set and the edge set. We model the dispersal of individuals on each graph $G^\alpha$ using a CTMC with generator matrix $Q^\alpha$, whose $(i, j)$th entry is $q^\alpha_{ij}$. The entry $q^\alpha_{ij} > 0$, if $i \neq j$, is the instantaneous transition rate from node $i$ to node $j$, and $q^\alpha_{ii}$ is the total rate of transition out of node $i$, i.e., $\nu^\alpha_i = \sum_{j \neq i} q^\alpha_{ij}$. Here, $q^\alpha_{ij} > 0$, if $(i, j) \in \mathcal{E}^\alpha$, and $q^\alpha_{ij} = 0$, otherwise.

We model the interaction of population dispersal with the epidemic process as follows. At each time $t$, individuals of each class $\alpha$ within each node move on graph $G^\alpha$ according to the CTMC with generator matrix $Q^\alpha$ and then interact with individuals within their current node according to an SIS epidemic process. For the epidemic process at node $i$ and for individuals in class $\alpha$, let $\beta^\alpha > 0$ and $\delta^\alpha > 0$ be the infection and recovery rates, respectively. We let $B^\alpha > 0$ and $D^\alpha > 0$ be the positive and nonnegative diagonal matrices with entries $\beta^\alpha_i$ and $\delta^\alpha_i$, $i \in \{1, \ldots, n\}$, respectively. Let $B = \oplus_{\alpha=1}^m B^\alpha$ and $D = \oplus_{\alpha=1}^m D^\alpha$.

Let $x^\alpha_i(t)$ be the number of individuals of class $\alpha$ at node $i$ at time $t$. Let $p^\alpha_i(t) \in [0, 1]$ (respectively, $1 - p^\alpha_i(t)$) be the fraction of infected (respectively, susceptible) subpopulation of class $\alpha$ at patch $i$. Let

$$
p^\alpha := \begin{bmatrix} p^1_i \\ \vdots \\ p^m_i \end{bmatrix}, \quad \alpha^\alpha := \begin{bmatrix} x^1_i \\ \vdots \\ x^n_i \end{bmatrix}, \quad p := \begin{bmatrix} p^1 \\ \vdots \\ p^m \end{bmatrix}, \quad \text{and } x := \begin{bmatrix} x^1 \\ \vdots \\ x^n \end{bmatrix}.
$$

Define $P^\alpha := \text{diag}(p^\alpha)$ and $P := \text{diag}(p)$. For clarity of exposition, we make the following assumption on the connectivity of the dispersal graphs at each layer. We will relax this condition later in Section IV.

**Assumption 1 (Strong connectivity):** Digraph $G^\alpha$ is strongly connected, for all $\alpha \in \{1, \ldots, m\}$, which is equivalent to matrices $Q^\alpha$ being irreducible [51]. A digraph is said to be strongly connected if each node can be reached from every other node by traversing directed edges.

Assumption 1 ensures that the population of every class of individuals in every patch is always nonzero, and it is initially nonzero. We now derive the continuous-time dynamics that capture the interaction of population dispersal and the epidemic dynamics under Assumption 1.

Let $L = \oplus_{\alpha=1}^m L^\alpha \in \mathbb{R}^{nm \times nm}$, where $L^\alpha(x) \in \mathbb{R}^{n \times n}$ is a matrix with entries

$$
l^\alpha_{ij}(x) = \begin{cases} s^\alpha_{ij} + x^\alpha_i \frac{q^\alpha_{ij} x^\alpha_j}{x^\alpha_i}, & \text{if } i = j \\
q^\alpha_{ij} x^\alpha_j, & \text{otherwise}. \end{cases}
$$

Let $F(x) = 1_m \otimes F_{\text{blk}}(x) \in \mathbb{R}^{nm \times nm}$, where $F_{\text{blk}}(x) = [F^1(x), \ldots, F^m(x)] \in \mathbb{R}^{n \times n}$, and $F^\alpha \in \mathbb{R}^{n \times n}$ is a diagonal matrix with entries $f^\alpha_i(x) := \frac{x^\alpha_i}{\sum_{j} x^\alpha_j}$ for $i \in \{1, \ldots, n\}$, i.e., the fraction of total population at node $i$ contributed by class $\alpha$.

**Proposition 1 (SIS model with population dispersal):** Under Assumption 1, the dynamics of the fractions of the infected subpopulation $p$ and the number of individuals $x^\alpha$ under multilayer population dispersal model with generator matrices $Q^\alpha$, and infection and recovery matrices $B$ and $D$, respectively, are

$$\dot{p} = (BF(x) - D - L(x))p - PB^\alpha F(x)p \quad (1a)$$

$$\dot{x}^\alpha = (Q^\alpha)^T x^\alpha. \quad (1b)$$

**Proof:** Consider a small time increment $h > 0$ at time $t$. Then, the number of individuals of class $\alpha$ present at node $i$ after the evolution of CTMC in time interval $[t, t+h)$ is

$$x^\alpha_i(t+h) = x^\alpha_i(t)(1 - q^\alpha_i h) + \sum_{j \neq i} q^\alpha_{ij} x^\alpha_j(t)h + o(h). \quad (2)$$

After the dispersal, individuals within each node interact according to SIS dynamics. Thus, the number of infected individuals of class $\alpha$ present at node $i$ is

$$x^\alpha_i(t+h)p^\alpha_i(t+h) = -x^\alpha_i(t)d^\alpha_i p^\alpha_i(t)h + x^\alpha_i(t)\delta^\alpha_i p^\alpha_i(t)(1 - p^\alpha_i(t))h + x^\alpha_i(t)p^\alpha_i(t)(1 - \nu^\alpha_i h) + \sum_{j \neq i} q^\alpha_{ij} p^\alpha_j(t)h + o(h), \quad (3)$$

where $p^\text{avg}_i$ is the fraction of infected population at node $i$ and is given by

$$p^\text{avg}_i = \sum_{\alpha} f^\alpha_i p^\alpha_i.$$

The first two terms on the right-hand side of (3) correspond to the epidemic process within each node, whereas the last two terms correspond to infected individuals coming from other nodes due to dispersal. Using the expression of $x^\alpha_i$ from (2) in (3) and taking the limit $h \to 0^+$ gives

$$\dot{p}^\alpha = -d^\alpha p^\alpha + \delta^\alpha p^\alpha \cdot p^\text{avg}(1 - p^\alpha) - \sum_{j \neq i} l^\alpha_{ij} p^\alpha_j - \sum_{j \neq i} l^\alpha_{ij} p^\alpha_j. \quad (4)$$

Writing above in vector form gives

$$\dot{p}^\alpha = -(D^\alpha - L^\alpha(x^\alpha))p^\alpha + B^\alpha F_{\text{blk}}(x)p^\alpha - P^\alpha B^\alpha F_{\text{blk}}(x)p. \quad (5)$$

Similarly taking limits in (2) yields

$$\dot{x}^\alpha_i = -\nu^\alpha_i x^\alpha_i + \sum_{j \neq i} q^\alpha_{ij} x^\alpha_j. \quad (6)$$

Rewriting (4) and (6) in vector form establishes the proposition.

**Remark 1 (Comparison with the classical networked SIS model):** We now compare our model (1) with the classical...
networked SIS dynamics defined on a single-layer network \[ \dot{p} = (B - D)p - PBp \] \hspace{1cm} (7)
where \( B > 0 \) is the infection rate matrix, whose entries \( b_{ij} \)s determine the rate at which the infection may be transmitted from node \( i \) to node \( j \), and \( D > 0 \) is a diagonal recovery rate matrix. The model (7) implicitly assumes that the subpopulation size at each node is a constant, while in model (1), subpopulations disperse across nodes. For a fair comparison, we specialize model (1) to a single layer and assume that the population dispersal dynamics (1b) operates at its steady state \( x^* \). This reduces dynamics (1a) to
\[ \dot{p} = (B - D - L(x^*))p - PBp. \]
\hspace{1cm} (8)
Since \( B \) is a diagonal matrix, it has a smaller number of parameters than matrix \( B \). Thus, model (8) leverages the population dispersal dynamics to reduce the number of parameters in the infection rate matrix in a principled way. In several contexts, the data associated with population dispersal may be easier to obtain than the internode infection rate data. It is also noteworthy that the nonnegative diagonal entries of \( L(x^*) \) contribute to increasing the effective recovery rate, while its nonpositive off-diagonal entries contribute to the effective internode infection rates.

III. ANALYSIS OF SIS MODEL WITH MULTILAYER POPULATION DISPERSAL

In this section, we analyze the SIS model with multilayer population dispersal (1) under the following standard assumptions.

**Assumption 2:** For each layer \( \alpha \), there exists a node \( k_\alpha \) such that \( \delta^\alpha_{k_\alpha} > 0 \). \( \square \)

Let \( \pi^\alpha \) be the right eigenvector of \((Q^\alpha)^\top\) associated with eigenvalue at 0. We assume that \( \pi^\alpha \) is scaled such that its inner product with the associated left eigenvector \( 1_\alpha \) is unity, i.e., \( 1_\alpha^\top \pi^\alpha = 1 \). Define \( Q = \oplus_{\alpha=1}^\alpha Q^\alpha \) and \( \pi = [\pi^1, \ldots, \pi^m]^\top \), where \( N^\alpha \) is the total number of individuals belonging to class \( \alpha \), for \( \alpha \in \{1, \ldots, m\} \). We call an equilibrium point \((p^*, x^*)\), an endemic equilibrium point if at equilibrium the disease does not die out, i.e., \( p^* \neq 0 \); otherwise, we call it a DFE point. Let \( F(x^*) = F(\pi) \) and \( L^* := L(x^*) = L(\pi) \).

**Theorem 2 (Existence and stability of equilibria):** For the SIS model with multilayer population dispersal (1) under Assumption 1, the following statements hold.

i) If \( p(0) \in [0,1]^{nm} \), then \( p(t) \in [0,1]^{nm} \) for all \( t > 0 \). Also, if \( p(0) > 0_{nm} \), then \( p(t) > 0_{nm} \) for all \( t > 0 \).

ii) The model admits a DFE at \((p^*, x^*) = (0_{nm}, \pi)\).

iii) The model admits an endemic equilibrium at \((p^*, x^*) = (p_{end}, \pi), p_{end} > 0 \), if and only if \( \mu(BF^* - D - L^*) > 0 \).

iv) The DFE is globally asymptotically stable if and only if \( \mu(BF^* - D - L^*) < 0 \) and is unstable otherwise.

v) The endemic equilibrium is almost globally asymptotically stable if \( \mu(BF^* - D - L^*) > 0 \) with region of attraction \( p(0) \in [0,1]^{nm} \setminus \{0_{nm}\} \).

**Proof:** The first part of statement (i) follows from the fact that \( \dot{p} \) is either directed tangent or inside of the region \( [0,1]^{nm} \) at its boundary, which comprises surfaces with \( p^\alpha_i = 0 \) or 1. This can be seen from (4). For the second part of (i), rewrite (1a) as
\[ \dot{p} = ((I - P)BF(x) + A(x))p - E(t)p \]
\hspace{1cm} (9)
where \( L(x) = C(x) - A(x) \) with \( C(x) \) composed of the diagonal terms of \( L(x) \), \( A(x) \) is the nonnegative matrix corresponding to the off-diagonal terms, and \( E(t) = C(x(t)) + D \) is a diagonal matrix. Now, consider a variable change \( z(t) := e^L\int_0^t e^{-L\tau}E(\tau)d\tau p(t) \). Differentiating \( z(t) \) and using (9) yields
\[ \dot{z} = e^L\int_0^t e^{(\tau - t)E(\tau)}((I - P)BF(x) + A(x))e^{-E(t)} dz(t) \]
\hspace{1cm} (10)
Now, the coefficient matrix of \( z(t) \) is always nonnegative and strongly connected. The rest of the proof is the same as in [12, Th. 4.2(i)].

The second statement follows by inspection.

For the proof of the third statement, we refer the reader to the Appendix of the technical report [52].

**Stability of disease-free equilibria:** To prove the fourth statement, we begin by establishing sufficient conditions for instability. The linearization of (1) at \((p, x) = (0, \pi)\) is
\[ \frac{\dot{p}}{\dot{x}} = \begin{bmatrix} BF^* - D - L^* & 0 & p \\ 0 & Q^\top & x \end{bmatrix} \]
\hspace{1cm} (11)
Since the system matrix in (11) is block diagonal, its eigenvalues are the eigenvalues of the block-diagonal submatrices. Furthermore, since spectral abscissa \( \mu(Q^\top) \) is zero, a sufficient condition for instability of the DFE is that \( \mu(BF^* - D - L^*) > 0 \).

For the case of \( \mu(BF^* - D - L^*) \leq 0 \), we now show that the DFE is a globally asymptotically stable equilibrium. It can be seen from the definitions of matrices \( F^* \) and \( L^* \) that under Assumption 1, \((BF^* - D - L^*) \) is an irreducible Metzler matrix. Together with \( \mu(BF^* - D - L^*) \leq 0 \), it implies that there exists a positive diagonal matrix \( R \) such that
\[ R(BF^* - D - L^*) + (BF^* - D - L^*)^\top R = -K \]
where \( K \) is a positive-semidefinite matrix [22, Proposition 1(iv), Lemma A.1]. Define \( \bar{L} := L(x) - L^*, \bar{F} := F(x) - F^* \) and \( r := ||R|| \), where \( ||R|| \) denotes the induced two norms of the matrix. Recall \((Q^\top)^\top\) has exactly one eigenvalue at zero and all other eigenvalues have negative real parts. The right and left eigenvectors associated with the eigenvalue at zero are \( \pi^\alpha \) and \( 1_\alpha \), respectively. Let \( y^\alpha \in \mathbb{R}^{n \alpha - 1} \) be the projection of \( x^\alpha \) to the orthogonal space of \( \pi^\alpha \). Let the dynamics (1b) projected onto the orthogonal space of \( \pi^\alpha \) be \( \tilde{y}^\alpha = \Gamma^\top y^\alpha \). It follows that \( \Gamma^\top \) is Hurwitz and \( y^\alpha = 0_{n\alpha-1} \) is a globally asymptotically stable equilibrium point. Let \( y = [y^1, \ldots, y^m]^\top \) and \( \Gamma = \oplus_{\alpha=1}^m \Gamma^\top \). Also, with a given population of each class \( N^\alpha \), we can write \( F(x) \) and \( L(x) \) as functions of \( y \) alone, and it can be seen that \(||\bar{F}(y)||\) and \(||\bar{L}(y)||\) are positive-definite functions of \( y \). Rewriting dynamics (1) using transformed variables \( p \) and \( y \), we get
\[ \dot{p} = (BF^* - D - L^*)p - PB(y)p + (BF^* - D - L^*)p \]
\hspace{1cm} (12a)
\[ \dot{y} = \Gamma y. \]
\hspace{1cm} (12b)
Consider the Lyapunov function \( V(p) = p^\top R p \). Then
\[
\dot{V} = 2p^\top R \dot{p} = p^\top (R(BF^* - D - L^*) + (BF^* - D - L^*)^\top R) p
+ 2p^\top R(B\tilde{F} - \tilde{L}) p - 2p^\top RPB(F + F^*) p
= -p^\top Kp + 2p^\top R(B(I - P)\tilde{F} - \tilde{L}) p - 2p^\top RPB^* p
\leq -2p^\top RPB^* p + 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|)
\]
where \( k_1, b > 0 \) are appropriate positive constants. Pick \( \epsilon \in (0, 1) \), and it follows that:
\[
\dot{V} \leq -2(1 - \epsilon)p^\top RPB^* p - 2\epsilon p^\top RPB^* p
+ 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|)
\leq -2(1 - \epsilon)p^\top RPB^* p - k_2\|p\|_3^3 + 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|)
\leq -2(1 - \epsilon)p^\top RPB^* p - k_2\|p\|_3^3 + \rho_1(\|y\|_\infty)
\leq -2(1 - \epsilon)p^\top RPB^* p
\]
for \( \|p\|_\infty \geq \rho_2(\|y\|_\infty) =: \sqrt{\frac{2\epsilon\|y\|_\infty}{k_2}}. \)

Here, \( k_2 > 0 \) is an appropriate constant and \( \rho_1 \) is a suitable class \( K \) function. Since \( 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|) \) is a positive-definite function of \( y \), existence of \( \rho_1 \) follows from [53, Lemma 4.3]. \( \rho_2 \) is also a class \( K \) function. Since (13) is a continuous negative-definite function of \( p \in [0, 1]^{nm} \), it follows from [53, Th. 4.19] that dynamics (12a) is input to state stable with respect to input \( y \).
Note that the origin is globally asymptotically stable for (12b). Now, using [53, Lemma 4.7] for the cascaded system (12a), (12b) implies that the origin is globally asymptotically stable equilibrium for the cascaded system.

**Stability of endemic equilibria:** Finally, we prove the fifth statement. To this end, we first establish an intermediate result.

**Lemma 3:** For the dynamics (1a), if \( p_0(t) \to 0 \) as \( t \to \infty \), for some \( i \in \{1, \ldots, n\} \) and \( \alpha \in \{1, \ldots, m\} \), then \( p(t) \to 0 \) as \( t \to \infty \).

**Proof:** It can be easily seen from (4) that \( \tilde{p}_i^\alpha \) is bounded, and hence, \( \tilde{p}_i^\alpha \) is uniformly continuous in \( t \). Now if \( p_j^\alpha(t) \to 0 \) as \( t \to \infty \), it follows from Barbalat’s lemma [54, Lemma 4.2] that \( \tilde{p}_i^\alpha \to 0 \). Therefore, from (4) and the fact that \( -l_j^\alpha(x) \geq 0 \) and \( p_j^\alpha \geq 0 \), it follows that \( p_j^\alpha(t) \to 0 \) for all \( j \) such that \( -l_j^\alpha(x) \neq 0 \). Using Assumption 1 and applying the above argument for each class at each node implies \( p(t) \to 0 \).

Define \( \tilde{p} := p - p^* \), \( P^* := \text{diag}(p^*) \), and \( \tilde{P} := \text{diag}(\tilde{p}) \). Then
\[
\dot{\tilde{p}} = (BF - D - L - PBF)p
= (BF^* - D - L^* - P^*BF^*) \tilde{p}
+ (BF^* - D - L^* - P^*BF^*) \tilde{p}
+ (BF^* - D - L^* - P^*BF^*) \tilde{p}
= ((I - P^*)BF^* - D - L^*) \tilde{p} + ((I - P)BF^* - D - L^*) \tilde{p}
- PBF^* \tilde{p}
\]
where \( (BF^* - D - L^* - P^*BF^*)p^* = 0 \), as \( (p^*, x^*) \) is an equilibrium point.

Note that \( (BF^* - D - L^* - P^*BF^*) = ((I - P^*)BF^* - D - L^*) \) is an irreducible Metzler matrix and \( p^* \gg 0 \) is an eigenvector associated with eigenvalue at zero. Therefore, the Perron–Frobenius theorem for irreducible Metzler matrices [51] implies \( \mu((I - P^*)BF^* - D - L^*) = 0 \). Also, this means there exists a positive-diagonal matrix \( R_2 \) and a positive-semidefinite matrix \( K_2 \) such that
\[
R_2((I - P^*)BF^* - D - L^*)
+ ((I - P^*)BF^* - D - L^*) \tilde{p} = -K_2.
\]

Consider the cascaded system
\[
\dot{\tilde{p}} = ((I - P^*)BF^* - D - L^*) \tilde{p} + ((I - P)BF^*(y - \tilde{L}(y)))p - \tilde{P}BF^* p
\]
(\ref{eq:14a})
\[
y = \tilde{y} \gamma y.
\]
(\ref{eq:14b})

Similar to the proof of the fourth statement, take \( V_2(\tilde{p}) = \tilde{p}^\top R_2 \tilde{p} \). Then
\[
\dot{V}_2 = 2\tilde{p}^\top R_2 \tilde{p}
= \tilde{p}^\top (R_2((I - P^*)BF^* - D - L^*)
+ ((I - P^*)BF^* - D - L^*) \tilde{p}
+ 2\tilde{p}^\top R_2((I - P)BF - \tilde{L}) p - 2\tilde{p}^\top R_2 \tilde{P}BF^* p
- \tilde{p}^\top K_2 \tilde{p} + 2\tilde{p}^\top R_2((I - P)BF - \tilde{L}) p
- 2\tilde{p}^\top R_2 \tilde{P}BF^* p
\leq -2\epsilon \tilde{p}^\top R_2 \tilde{P}BF^* p + k_2b(\|\tilde{F}\| + \|\tilde{L}\|), k_2, b > 0
\]
where \( k_2, b > 0 \) are appropriate positive constants. Pick \( \epsilon \in (0, 1) \), and it follows that
\[
\dot{V}_2 \leq -2(1 - \epsilon)p^\top R_2 \tilde{P}BF^* p + 2\epsilon p^\top R_2 \tilde{P}BF^* p + \rho_4(\|y\|)
\leq -2(1 - \epsilon)p^\top R_2 \tilde{P}BF^* p - \rho_3(\|\tilde{p}\|) + \rho_4(\|y\|)
\leq -2(1 - \epsilon)p^\top R_2 \tilde{P}BF^* p
\]
for \( \|\tilde{p}\| \geq \rho_5(\|y\|) =: \frac{\epsilon^2}{\rho_4(\|y\|)} \). Here, \( \rho_4 \) and \( \rho_5 \) are suitable class \( K \) functions and \( \rho_3 \) a class \( K_\infty \) function. The existence of these functions follows from [53, Lemma 4.3]. The remainder of the proof follows analogously to the proof of the fourth statement.

**Remark 2:** It should be noted that dynamics (1) has an equilibrium point on the boundary of its domain, and the standard Lyapunov analysis assumes that the equilibrium point lies in the interior of the domain. However, since we have shown that \( [0, 1]^{nm} \) is the invariant set for the \( p \) dynamics, similar conclusions can be drawn using LaSalle’s invariance principle [53]. Similarly, the input-to-state stability [53, Lemma 4.7] cannot be directly used. However, its proof relies on [53, Ths. 4.18 and 4.19], which can be extended to our positive system by constructing invariant sets that are the intersection of \( [0, 1]^{nm} \) and the invariant sets in the proof of [53, Ths. 4.18 and 4.19].
For the last statement, we use an eigenvalue bound for perturbed irreducible Laplacian matrix of a digraph [55, Th. 6], stated as follows.

Let $H = A + \Delta$, where $A$ is an $n \times n$ irreducible Laplacian matrix and $\Delta \neq 0$ is a nonnegative diagonal matrix. Then

$$\text{Re}(\lambda(H)) \geq \frac{\lambda_2}{\left(1 + \sqrt{1 + \frac{\lambda_2}{\sum_{i \neq j} l_{ij}^{\alpha}}}ight)^2} > 0,$$

where $w$ is a positive left eigenvector of $A$ such that $w^TA = 0$ with $\max_i w_i = 1$, $W = \text{diag}(w)$, and $\lambda_2$ is the second smallest eigenvalue of $1/(2(WA + A^TW))$.

Now, in our case, the necessary and sufficient condition for the stability of DFE is

$$\text{Re}(\lambda(BM + L^* + D - sI)) = \text{Re}(\lambda(BM + L^* + \Delta)) + s \geq 0,$$

where $s = \min_{i,\alpha}(\delta_{\alpha}^i - \beta_{\alpha}^i)$ and $\Delta = D - B - sI$. Applying the eigenvalue bound with $H = BM + L^* + \Delta$ gives sufficient condition (iv).

\textbf{Proof:} We begin by proving the first two statements. First, we note that \( (L^*)^a_{\alpha} = \nu_{\alpha}^a \). This can be verified by evaluating $L^* = L(\pi)$ and utilizing the fact that $Q = \pi$. The necessary and sufficient condition for the stability of DFE is $\mu(BF^* - D - L^*) \leq 0$. Note that $BF^* - D - L^*$ is an irreducible Metzler matrix. The Perron–Frobenius theorem for irreducible Metzler matrices implies that there exists a real eigenvalue equal to $\mu$ with a positive eigenvector, i.e., $(BF^* - D - L^*)z = \mu z$, where $z \gg 0$. Rename components of $z$ as $z_{(n(1-1)+i)} = z_{i}^{\alpha} = \nu_{\alpha}^{i}$, $i \in \{1, \ldots, m\}$, $\alpha \in \{1, \ldots, n\}$. Let for each $i \in \{1, \ldots, n\}$, $\nu_{\alpha}^{i} = \min\{z_{i}^{1}, \ldots, z_{i}^{m}\}$. Since $\mu \leq 0$, written componentwise for the $(n(1-1)+i)$th component of $(BF^* - D - L^*)z$, we have

$$\sum_{\alpha} \beta_{\alpha}^{i} f_{i}^{\alpha} z_{i}^{\alpha} - (\delta_{\alpha}^{i} + \nu_{\alpha}^{i}) z_{i}^{\alpha} - \sum_{j \neq i} l_{ij}^{\alpha} z_{j}^{\alpha} \leq 0$$

$$\Rightarrow (\beta_{\alpha}^{i} - \delta_{\alpha}^{i} - \nu_{\alpha}^{i}) z_{i}^{\alpha} \leq \sum_{\alpha} \beta_{\alpha}^{i} f_{i}^{\alpha} (z_{i}^{\alpha} - z_{i}^{\alpha})$$

$$+ \sum_{j \neq i} l_{ij}^{\alpha} z_{j}^{\alpha}$$

$$\Rightarrow \beta_{\alpha}^{i} - \delta_{\alpha}^{i} - \nu_{\alpha}^{i} < 0.$$

Here, we have used facts: $\sum_{\alpha} f_{i}^{\alpha} = 1, f_{i}^{\alpha} > 0, l_{ij}^{\alpha} \leq 0$, and that there exists $j \in \{1, \ldots, n\}$ such that $l_{ij}^{\alpha} < 0$. This proves the first statement.

The second statement follows similarly to the first statement by selecting $z_{i}^{\alpha} = \min\{z_{1}^{\alpha}, \ldots, z_{n}^{\alpha}\}$ and using the additional fact $\nu_{\alpha}^{i} + \sum_{j \neq i} l_{ij}^{\alpha} = 0$.

Let $F^* = I - M$, where $M$ is the Laplacian matrix that can be seen from the definition of $F$. Now, $BF^* - D - L^* = B - D - (BM + L^*)$. Since $(BM + L^*)$ is a Laplacian matrix, if $\delta_{\alpha}^{i} \geq \beta_{\alpha}^{i}$, for each $i \in \{1, \ldots, n\}$ and $\alpha \in \{1, \ldots, m\}$, from Gersgorin disks theorem [51], $\mu \leq 0$, which proves the third statement.

\textbf{Remark 3:} For a given multilayer graph and the associated dispersal transition rates in dynamics (1), let $s = \min_{i,\alpha}(\delta_{\alpha}^{i} - \beta_{\alpha}^{i})$ and $(i^*, \alpha^*) = \argmin_{i,\alpha}(\delta_{\alpha}^{i} - \beta_{\alpha}^{i})$. Then, there exist $\delta_{\alpha}^{i}$, $(i, \alpha) \neq (i^*, \alpha^*)$, which satisfy statement (iv) of Corollary 4 if $s > s_{\text{lower}}$, where

$$s_{\text{lower}} = -\frac{\lambda_2}{4mn + 1}.$$

\textbf{Remark 4 (Influence of population dispersal on the stability of DFE):} Statement (iv) of Corollary 4 characterizes the influence of population dispersal on the stability of disease-free equilibria. In particular, $\lambda_2$ is a measure of the “intensity” of population dispersal and $s$ is a measure of the largest deficit in the recovery rate compared with the infection rate among nodes. The sufficient condition in statement (iv) states explicitly how population dispersal can allow for stability of DFE even under a deficit in recovery rate at some nodes.

IV. SIS MODEL UNDER MULTILAYER POPULATION DISPERSAL: NONSTRONGLY CONNECTED LAYERS

In this section, we relax Assumption 1, so that the digraph representing population dispersal on a layer need not be strongly connected. We first derive a reduced model and then present a stability analysis.

A. Reduced Model for Nonstrongly Connected Layers

As discussed in [51, Ch. 10], a CTMC is a closed dynamical flow system, and accordingly, every individual of each class $\alpha$ eventually resides within the sinks of $G^{\alpha}$ [51, Th. 10.13]. Let $\mathcal{V}^{\alpha} = \{V_1^{\alpha}, \ldots, \hat{V}_{\alpha}^{n_{\alpha}}\} \subset \{1, \ldots, n\}$ be the nodes in the sinks of $G^{\alpha}$, and let $\hat{G}^{\alpha}$ be the subgraph of $G^{\alpha}$ induced by these nodes. Let $\mathcal{V} \setminus \mathcal{V}^{\alpha} = \{\hat{V}_1^{\alpha}, \ldots, \hat{V}_{(n-n_{\alpha})}\}$.
Let \( \tilde{p}^\alpha_i(t) = p^\alpha_{ij}(t) \), \( \tilde{x}^\alpha_i(t) = x^\alpha_{ij}(t) \), \( \hat{p}^\alpha_i(t) = p^\alpha_{ij} \), and \( \hat{x}^\alpha_i(t) = x^\alpha_{ij} \). Define

\[
\hat{p}^\alpha = \begin{bmatrix}
\hat{p}^1_1 \\
\vdots \\
\hat{p}^m_n \\
\hat{p}^n_m \\
\end{bmatrix}, \quad \hat{x}^\alpha = \begin{bmatrix}
\hat{x}^1_1 \\
\vdots \\
\hat{x}^m_n \\
\hat{x}^n_m \\
\end{bmatrix}, \quad \tilde{p} = \begin{bmatrix}
\tilde{p}^1 \\
\vdots \\
\tilde{p}^m \\
\tilde{p}^n \\
\end{bmatrix}, \quad \tilde{x} = \begin{bmatrix}
\tilde{x}^1 \\
\vdots \\
\tilde{x}^m \\
\tilde{x}^n \\
\end{bmatrix}.
\]

Let \( \tilde{L}^\alpha(x) \in \mathbb{R}^{n^\alpha \times n^\alpha} \) be the matrix with entries

\[
(\tilde{L}^\alpha)_{ij}(x) = \begin{cases}
\sum_{v \in V} q_{iv}^\alpha \frac{x^k_i}{x^k_j}, & \text{if } \tilde{v}^\alpha_i = \tilde{v}^\alpha_j \\
-q_{iv}^\alpha \frac{x^k_i}{x^k_j}, & \text{otherwise}
\end{cases}
\]

for each \( \tilde{v}^\alpha_i, \tilde{v}^\alpha_j \in V^\alpha \). Likewise, let \( \tilde{L}(x) \in \mathbb{R}^{n \times n} \) be the matrix with entries

\[
(\tilde{L})_{ij}(x) = -q_{ij} \frac{x^k_i}{x^k_j},
\]

for \( \tilde{v}^\alpha_i, \tilde{v}^\alpha_j \in V^\alpha \) and \( \tilde{v}^\alpha_i \in V \). Consider the multi-layer population dispersal on nonstrongly connected multiple layers (16), under Assumption 3, the following statements hold.

1) The DFE \( (\bar{p}, x) = (0, \pi) \) is globally asymptotically stable if and only if \( \mu(BF^* - \bar{D} - \bar{L}^*) \leq 0 \) and is unstable otherwise.

2) The endemic equilibrium is almost globally asymptotically stable if \( \mu(BF^* - \bar{D} - \bar{L}^*) > 0 \) with region of attraction \( p(0) \in (0, 1)^n \) such that \( p(0) \neq 0_n \).

Proof: We start with establishing the first statement. Let \( c_1 = F(x)p \) and \( c_2 = L(x)p \). Note that entries of \( F \) and \( L \) are either zero or exponentially converge to zero, and \( p \in [0, 1] \). Therefore, \( c_1 \) and \( c_2 \) exponentially converge to the origin.

Under Assumption 3, \( (BF^* - \bar{D} - \bar{L}^*) \) is an irreducible Metzler matrix. Together with \( \mu(BF^* - \bar{D} - \bar{L}^*) \leq 0 \), it implies that there exists a positive diagonal matrix \( \bar{R} \) such that

\[
\bar{R}(BF^* - \bar{D} - \bar{L}^*) + (BF^* - \bar{D} - \bar{L}^*)^T \bar{R} = -\bar{K}
\]

where \( \bar{K} \) is a positive-semidefinite matrix. Consider the Lyapunov function \( V(p) = p^T \bar{R}p \).

\[
\dot{V} = 2p^T \bar{R} \dot{p} = p^T \left( \bar{R}(BF^* - \bar{D} - \bar{L}^*) + (BF^* - \bar{D} - \bar{L}^*)^T \bar{R} \right) p + 2p^T \bar{R}(\tilde{F} - \tilde{L})p - 2p^T \bar{R} \bar{B}(\tilde{F} - \tilde{L})p + 2p^T \bar{R}(I - \bar{P}) \bar{B}c_1 + 2p^T c_2
\]

An illustration of the reduction in Corollary 5 for a small bilayer graph is presented in the Appendix.

B. Stability Analysis

Note that at equilibrium, every \( x^\alpha_k \) for \( k \in V \setminus V^\alpha \) is zero, and hence, the block diagonal matrix \( \bar{L}(x) \), at equilibrium, comprises strongly connected Laplacian matrices as the diagonal blocks. Let \( \bar{L}^* \) and \( \bar{F}^* \) denote the equilibrium values of \( \bar{L}(x) \) and \( \bar{F}(x) \). Then, similar to Theorem 2, the matrix \( (BF^* - \bar{D} - \bar{L}^*) \) determines the existence and stability of equilibrium point. The matrix \( (BF^* - \bar{D} - \bar{L}^*) \) may comprise multiple diagonal blocks that are irreducible. Consider a scenario with a two-layered graph in which layer 1 has two strongly connected sinks with node sets \( V^1_1 \) and \( V^1_2 \), and layer 2 also has two strongly connected sinks with node sets \( V^2_1 \) and \( V^2_2 \). Suppose that \( V^1_1 \cap V^2_2 = \emptyset \) is an empty set, while \( V^1_1 \cap V^2_2 \) is nonempty. Then, \( (BF^* - \bar{D} - \bar{L}^*) \) will have three irreducible blocks associated with \( V^1 \cup V^2_1, V^2_2, \) and \( V^2_2 \). Since each of these blocks can be individually analyzed, for simplicity, we assume that \( (BF^* - \bar{D} - \bar{L}^*) \) is irreducible.

Assumption 3: The matrix \( (BF^* - \bar{D} - \bar{L}^*) \) is irreducible.

In addition, for every strongly connected sink component in each layer \( \alpha \), there exists a node \( k \) such that \( \delta^\alpha_k > 0 \).
Thus, minimizing $\mu(BF^* - D - L^*)$ is same as minimizing $\mu(BF^* + \hat{D} + L)$. Note that $(BF^* + \hat{D} + L)$ is also an irreducible nonnegative matrix. We now recall the following result for irreducible nonnegative matrices.

**Lemma 7 (see [51, Th. 10.2]):** Let $M$ be an irreducible nonnegative matrix with its spectral abscissa $\mu(M)$. Then

$$\mu(M) = \inf \{ \lambda \in \mathbb{R} : Mu \leq \lambda u, \text{ for } u \gg 0 \}.$$  

Using Lemma 7, it follows that minimizing $\mu(M)$ is equivalent to minimizing $\lambda$ such that

$$\frac{(Mu)_i}{\lambda u_i} \leq 1, \quad u_i > 0. \quad (18)$$

**Assumption 4:** We assume that the cost functions $f_i^\alpha(\beta_i^\alpha)$ and $g_i^\alpha(\delta_i^\alpha) = g_i^\alpha(\Delta + 1 - \delta_i^\alpha)$ are polynomials [56, Sec. 4.5] in $\beta_i^\alpha$ and $\delta_i^\alpha$, respectively.

We now pose the optimization problem to maximize the convergence rate for the DFE

$$\text{minimize} \quad \lambda$$

subject to

$$\frac{1}{\lambda u_i} \left( (BF^* + \hat{D} + L)u \right)_i \leq 1, \quad i \in \{1, \ldots, nm\}$$

$$\sum_{i=1}^{n} \sum_{\alpha=1}^{m} f_i^\alpha(\beta_i^\alpha) + g_i^\alpha(\delta_i^\alpha) \leq C$$

$$\delta_i^\alpha \leq \delta_i^\alpha \leq \beta_i^\alpha, \quad i \in \{1, \ldots, n\}, \alpha \in \{1, \ldots, m\}$$

$$\Delta + 1 - \delta_i^\alpha \leq \delta_i^\alpha \leq \Delta + 1 - \delta_i^\alpha, \quad i \in \{1, \ldots, n\}, \alpha \in \{1, \ldots, m\} \quad (19)$$

where $C > 0$ is the allocation budget. Under Assumption 4, optimization problem (19) is a geometric program [56] and can be solved efficiently.

**VI. NUMERICAL ILLUSTRATIONS**

In this section, we illustrate our results through numerical simulations. For simplicity, in all our simulations, we choose the same recovery and infection rates at any given node $i$ across each layer $\alpha$, i.e., $\beta_i^\alpha = \beta_i$ and $\delta_i^\alpha = \delta_i$, for each $\alpha$. In addition, we choose functions $f_i^\alpha$ and $g_i^\alpha$ independent of $i$ and $\alpha$ and omit these indices.

**A. Comparison of Deterministic and Stochastic Models**

We start with a numerical simulation of the epidemic model with multilayer population dispersal in which we treat epidemic spread as well as population dispersal as stochastic processes. We take two population dispersal network layers: a complete graph and a line graph with 20 nodes each. The population dispersal transition rates are selected equally among outgoing neighbors of a node for both graphs with total transition rate $\nu^i = 0.1$, for each $i$ and $\alpha$. For the stochastic simulations, the initial sizes of subpopulations at each node are selected as

$$500 \times \{7, 5, 3, 1, 5, 7, 8, 9, 6, 7, 7, 7, 5, 9, 8, 6, 10, 9, 10, 5\},$$

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Comparison of the stochastic and deterministic epidemic model. (d) Stable endemic equilibrium: Deterministic model. (b) Stable DFE: Deterministic model. (c) Stable endemic equilibrium: Stochastic model. (a) Stable DFE: Stochastic model.

Fig. 1. Comparison of the stochastic and deterministic epidemic spread with population dispersal on a two-layer graph with $n = 20$ nodes. The layers correspond to complete and line graphs, respectively. In each layer, individuals move to their neighbors with equal probability with total transition rate $\nu_i^\alpha = 0.1$. The initial fraction of the infected population at each node is $\rho_i^\alpha(0) = 0.01$. Each iteration in the stochastic model corresponds to time step $0.01$ s. Different trajectories correspond to the fraction of the infected population at each node in both layers. Some trajectories are overlapping. (a) Stable DFE: Stochastic model. (b) Stable DFE: Deterministic model. (c) Stable endemic equilibrium: Stochastic model. (d) Stable endemic equilibrium: Deterministic model.

500 $\times$ \{3, 3, 2, 1, 2, 3, 4, 4, 5, 3, 3, 4, 4, 3, 4, 2, 6, 3, 3, 4\} in layers 1 and 2, respectively.

If the recovery rates, infection rates, and the initial fraction of the infected population are the same for all the nodes, population dispersal does not play any role. Therefore, we have chosen heterogeneous recovery rates across nodes to elucidate the influence of population dispersal. The curing rates $\{\delta_1, \ldots, \delta_{20}\}$ are arbitrarily selected as

\{0.3, 0.22, 0.21, 0.25, 0.3, 0.21, 0.23, 0.24, 0.21, 0.22, 0.25, 0.21, 0.3, 0.28, 0.22, 0.26, 0.21, 0.3, 0.28, 0.25\}.

The fractions of infected populations for different cases are shown in Fig. 1. The corresponding simulations of the deterministic model as per Proposition 1 are also shown for comparison. We consider two cases corresponding to the stable DFE and stable endemic equilibrium, respectively. Fig. 1(a) corresponds to $\beta_i = 0.2$, for each node, i.e., the case $\delta_i \geq \beta_i$ for each $i$, whereas Fig. 1(c) corresponds to $\beta_i = 0.31$, for each node, i.e., the case $\delta_i < \beta_i$ for each $i$. The results support statements (ii) and (iii) of Corollary 4 and lead to the stable endemic equilibrium and the stable DFE, respectively.

B. Influence of Network Structure on Epidemic Propagation

Once we have established the correctness of deterministic model predictions with the stochastic simulations, we perform the simulations using only the deterministic model. We study the effect of multilayer population dispersal over different pairs of population dispersal graph structures: complete-line graph, complete-ring graph, and complete-star graph. The number of nodes in each layer is selected as 10. We choose different population sizes for the two population dispersal layers and take the population dispersal transition rates to keep the equilibrium distribution of population the same for both layers across all pairs (taken as uniform equilibrium distribution) by using instantaneous transition rates from the Metropolis–Hastings algorithm [57]. The total transition rate is selected as $\nu_i^\alpha = 0.1$, for each $i$ and $\alpha$. This shows the effect of different population dispersal graph structures on epidemic spread, while the equilibrium population distribution remains the same. We select the infection rate $\beta_i = 0.31$, for each $i$, and the recovery rates $\{\delta_1, \ldots, \delta_{10}\}$ as

\{0.3, 0.22, 0.21, 0.25, 0.3, 0.21, 0.23, 0.24, 0.21, 0.22, 0.21\}.

Fig. 2 shows the fractions of infected population trajectories for ten nodes connected with different pairs of graph structures. The values of equilibrium fractions are affected by the presence of population dispersal and are different for different graph structures.

Next, we verify statement (iv) of Corollary 4, for a single-layer population dispersal model, where some recovery rates $\delta_i$ may be lesser than the infection rates $\beta_i$ but the DFE may still be stable. We take a complete graph of $n = 20$ nodes and select the population dispersal transition rates equally among outgoing neighbors of a node and the total transition rate $\nu_i = 0.1$, for each node $i$. These choices fix the values of $\nu$, $L^*$, and $\lambda_2$. Next, we compute $s_{\text{lower}} = -\frac{\lambda_2}{4n^2+1} = -0.0013$ and take $s = 0.8s_{\text{lower}} = -0.0010$. We select $\beta_i = 0.3$, $\delta_i = \delta_n = \beta_i + s$ and the rest $\delta_i$ are assumed to be the same and are computed to satisfy the condition in statement (iv) of Corollary 4. This yields $\delta_1 = \delta_n = 0.2990$ and $\delta_i = 0.3099$ for $i \in \{2, \ldots, n-1\}$. Fig. 3(a) shows the trajectories of infected fraction populations. As can be seen, the trajectories converge to the DFE.

To further compare model (1) with the classical networked SIS model (7), we consider a single-layer line graph with 20 nodes, infection rates $\beta_i = 0.31$, and curing rates the same as in Section VI-A. The networked infection matrix $B$ for the networked SIS model is obtained by equally distributing $\beta_i$ among the node and its neighbors. Such choice corresponds to each susceptible individual at each time selecting uniformly among neighboring nodes and interacting with the individuals in that node. The trajectories for node 1 for the two models are shown in Fig. 3(b). It can be seen that the two trajectories have significantly different steady-state values.
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Fig. 2. Simulation of the deterministic model of epidemic spread for two-layer graphs with different structures. Each graph has ten nodes, and the fraction of infected population at each node in both layers is $p_i(0) = 0.01$. (a) Complete-line graphs; graph 1. (b) Complete-line graphs; graph 2. (c) Complete-ring graphs; graph 1. (d) Complete-ring graphs; graph 2. (e) Complete-star graphs; graph 1. (f) Complete-star graphs; graph 2.

Fig. 3. (a) Illustration of statement (iv) of Corollary 4. A single-layer complete graph with 20 nodes is considered with an initial fraction of the infected population $p_i(0) = 0.01$ at each node. The nodes belong to two categories corresponding to the deficit and excess recovery rate, and the two trajectories correspond to each category. The recovery rates are selected to satisfy the sufficient condition in statement (iv) of Corollary 4 for the stability of DFE. (b) Comparison of node 1 trajectories for the SIS model with population dispersal (1) and the classical networked SIS model (7) with a single-layer 20-node line graph, $p_i(0) = 0.01$ and $\nu_i = 0.01$.

C. Optimal Intervention for Epidemic Containment

We now illustrate budget-constrained optimal intervention strategies in a multilayer network. We consider two layers: layer 1 as a line graph and layer 2 as a ring graph. We use population dispersal transition rates such that the outgoing rates to neighboring nodes are equal and the total outgoing transition rate at each node is fixed and equal to 0.2. The total number of individuals in layers 1 and 2 are 300 and 500, respectively. We adopt the following cost functions:

$$f(\beta_i) = \frac{1}{\beta_i} - 1$$
$$g(\delta_i) = \frac{1}{\Delta + 1 - \delta_i} - \frac{1}{\Delta + 1 - \bar{\delta}_i} = \frac{1}{\delta_i} - \frac{1}{\Delta + 1 - \bar{\delta}_i}.$$ 

The bounds on the infection and recovery rates are $\underline{\beta}_i = 0.1$, $\bar{\beta}_i = 0.4$, $\underline{\delta}_i = 0.1$, and $\bar{\delta}_i = 0.4$. We compute the optimal infection and recovery rate by solving the optimization problem (19). We also solve the resource allocation problem using a naïve strategy, in which the budget is allocated equally to each node to modify recovery and infection rates within their bounds. Fig. 4(a) shows $\mu(BF^* - D - L^*)$ achieved using the optimal intervention as well as the naïve strategy versus the allocation budget $C$. It can be seen that $\mu$ is positive for very low values of budget implying unstable DFE. As the allocation budget $C$ increases, $\mu$ saturates around a value of $-0.3$. Fig. 4(b) shows the resource used by each strategy versus the allocation budget. Note that the naïve strategy uses lesser resources compared with the optimal strategy. This is due to the fact that equal allocation of budget leads to unused resources. In particular, the recovery rates reach their upper limit before the infection rates reach their lower limit, and subsequently, any additional resource available for recovery remains unused.

VII. CONCLUSION

In this article, we derived a continuous-time model for epidemic propagation with population dispersal across a multilayer...
network of patches. The epidemic spread within each patch was modeled as an SIS model with individuals traveling across the patches with different dispersal patterns modeled as layers of a multilayer network. The derived model was analyzed to establish the existence and stability of a DFE and an endemic equilibrium under different conditions. Some necessary and sufficient conditions for the stability of DFE were established. We studied the optimal intervention for epidemic containment using a geometric program that maximizes the decay rate of DFE under a budget constraint. We also presented numerical studies to support our results and elucidate the effect of population dispersal on epidemic propagation.

While this article focused on studying the interaction of population dispersal dynamics with the epidemic spread dynamics, several recent works focused on the interaction of epidemic dynamics with human behavioral and societal dynamics [58], [59], [60], [61], [62], [63], [64], [65], [66]. It would be interesting to explore the joint interactions of the epidemic, population dispersal, behavioral, and societal dynamics.

APPENDIX

ILLUSTRATIVE EXAMPLE OF THE REDUCTION IN SECTION IV

We further illustrate the system of equations in Proposition 1 and Corollary 5 using a simple two-layer graph shown in Fig. 5. The reader may also refer to the technical report [67] for a single-layer description of these dynamics.

For the two-layer graph in Fig. 5, the generator matrices associated with the population dispersal Markov chain are

\[
Q^1 = \begin{bmatrix}
-q_{12} & q_{12} & 0 \\
0 & -q_{23} & q_{23} \\
0 & q_{32} & -q_{32}
\end{bmatrix}
\quad \text{and} \quad
Q^2 = \begin{bmatrix}
-q_{12} & q_{12} & 0 \\
0 & -q_{21} & q_{21} \\
0 & q_{32} & -q_{32}
\end{bmatrix}.
\]

The Laplacian matrices associated with each layer are

\[
L^1(x) = \begin{bmatrix}
0 & 0 & 0 \\
-q_{12} x_1 & -q_{21} x_2 & 0 \\
0 & -q_{31} x_2 & -q_{32} x_3
\end{bmatrix}
\quad \text{and} \quad
L^2(x) = \begin{bmatrix}
0 & 0 & 0 \\
q_{12} x_1^2 & q_{21} x_2^2 & 0 \\
-q_{31} x_2^2 & -q_{32} x_3^2 & 0
\end{bmatrix}.
\]

In addition

\[
F_j(x) = \begin{bmatrix}
x_1^j \\
\frac{x_2^j}{x_1^j + x_2^j} \\
\frac{x_3^j}{x_1^j + x_3^j}
\end{bmatrix}, \quad j \in \{1, 2\}.
\]

For brevity, we focus on dynamics in layer 1. The dynamics (5) can be specialized to this example to get

\[
\dot{p}^1 = (-D^1 - L^1(x^1))p^1 + (I - P^1)B^1 \left( F_1(x)p^1 + F_2(x)p^2 \right).
\]

Note that nodes 2 and 3 form a strongly connected sink component in layer 1, while nodes 1 and 2 form a strongly connected sink component in layer 2. Thus, \( \bar{v}_1^1 = 2, \bar{v}_2^1 = 3, \bar{v}_3^1 = 1 \), and \( \bar{v}_2^2 = 2 \). In addition, \( \bar{v}_1^2 = 1 \) and \( \bar{v}_3^2 = 3 \). For the reduced model, we define

\[
\dot{p}^1 = \left[ p_{1j}^1 \right] = \dot{p}^2 = \left[ p_{2j}^2 \right], \quad \bar{x}^1 = \begin{bmatrix} x_2^1 \\ x_3^1 \end{bmatrix}, \quad \bar{x}^2 = \begin{bmatrix} x_2^2 \\ x_3^2 \end{bmatrix}
\]

\[
\dot{p}^1 = p_1^1, \dot{p}^2 = p_{32}^2, \bar{x}^1 = x_1^1, \text{ and } \bar{x}^2 = x_3^2.
\]

We now write dynamics (20) restricted to nodes 2 and 3

\[
\dot{p}^1 = -\bar{D}^1 \bar{p}^1 - \left[ \begin{bmatrix}
q_{12} x_1^1 + q_{12} x_1^2 \\
q_{21} x_1^2 \\
q_{31} x_1^2
\end{bmatrix} \right] \bar{p}^1 - \left[ \begin{bmatrix}
-q_{12} x_2^1 \\
-q_{21} x_2^2 \\
-q_{31} x_3^2
\end{bmatrix} \right] \bar{p}^2 \quad \text{as } \bar{L}^1(\bar{x}^1)
\]

\[
+ (I - \bar{P}^1)\bar{B}^1 \left( \begin{bmatrix}
\frac{x_2^1}{x_1^1 + x_2^1} \\
\frac{x_3^1}{x_1^1 + x_3^1} \\
0
\end{bmatrix} \bar{p}^1 + \begin{bmatrix}
0 \\
0 \\
0
\end{bmatrix} \bar{p}^2 \right) \quad \text{as } \bar{F}^{11}(\bar{x}^1)
\]

\[
+ \left[ \begin{bmatrix}
\frac{x_2^1}{x_1^1 + x_2^1} \\
\frac{x_3^1}{x_1^1 + x_3^1} \\
0
\end{bmatrix} \bar{p}^1 + \begin{bmatrix}
0 \\
0 \\
0
\end{bmatrix} \bar{p}^2 \right] \quad \text{as } \bar{F}^{12}(\bar{x}^1)
\]

(21)

It can be verified that dynamics (21) is consistent with Corollary 5, and the matrices defined in (21) are consistent with the definitions in Section IV.

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