SIS Epidemic Model under Mobility on Multi-layer Networks

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Abstract—We study the influence of heterogeneous mobility patterns in a population on the SIS epidemic model. In particular, we consider a patchy environment in which each patch comprises individuals belonging to the different classes, e.g., individuals in different socio-economic strata. We model the mobility of individuals of each class across different patches through an associated Continuous Time Markov Chain (CTMC). The topology of these multiple CTMCs constitute the multi-layer network of mobility. At each time, individuals move in the multi-layer network of spatially-distributed patches according to their CTMC and subsequently interact with the local individuals in the patch according to an SIS epidemic model. We derive a deterministic continuum limit model describing these mobility-epidemic interactions. We establish the existence of a Disease-Free Equilibrium (DFE) and an Endemic Equilibrium (EE) under different parameter regimes and establish their (almost) global asymptotic stability using Lyapunov techniques. We derive simple sufficient conditions that highlight the influence of the multi-layer network on the stability of DFE. Finally, we numerically illustrate that the derived model provides a good approximation to the stochastic model with a finite population and also demonstrate the influence of the multi-layer network structure on the transient performance.

I. INTRODUCTION

Contagion dynamics are used to model a variety of phenomena such as spread of influence, disease and rumors. Epidemic propagation models are a class of contagion models that have been used in the context of disease spread\textsuperscript{1} \textsuperscript{2}, spread of computer viruses\textsuperscript{3} \textsuperscript{4}, routing in mobile communication networks\textsuperscript{5}, and spread of rumors\textsuperscript{6}. Epidemic propagation in patchy environments refers to the epidemic spread process in an environment comprised of disjoint spatially distributed regions (patches). In these models, individuals interact within each patch and also move across different patches according to a CTMC.

In this paper, we consider a generalized epidemic propagation model in a patchy environment in which individuals within each patch belong to multiple classes, and individuals within each class move according to an associated CTMC. This leads to a multi-layer mobility model and we study its interaction with epidemic propagation. Using Lyapunov techniques, we characterize the steady state behavior of the model under different parameter regimes and characterize the influence of mobility on epidemic dynamics.

Epidemic models have been extensively studied in the literature. The two most widely studied models are SIS (Susceptible-Infected-Susceptible) and SIR (Susceptible-Infected-Recovered) models, wherein individuals are classified into one of the three categories: susceptible, infected or recovered. In contrast to the classical SIS/SIR models where the dynamics of the fraction of the population in each category\textsuperscript{3} \textsuperscript{4} is studied, the networked models consider patches clustered into different nodes, and the patch-level dynamics is determined by the local SIS/SIR interactions as well as the interactions with neighboring patches in the network graph\textsuperscript{7} \textsuperscript{10}. While most of studies on SIR/SIS epidemic models focus on continuous-time dynamics, the authors in\textsuperscript{11} \textsuperscript{12} study network epidemic dynamics in discrete time setting.

Some common generalizations of the SIR/SIS models include: SEIR model\textsuperscript{7} \textsuperscript{13}, where an additional classification “exposed” is introduced, SIRS\textsuperscript{2} \textsuperscript{12}, where individuals get temporary immunity after recovery and then become susceptible again, and SIRI\textsuperscript{4} \textsuperscript{14} \textsuperscript{16}, where after recovery, agents become susceptible with a different rate of infection. The network epidemic dynamics have also been studied for time-varying networks\textsuperscript{17} \textsuperscript{19}.

The terms population dispersal and network mobility have been used interchangeably in the literature. Epidemic spread under mobility has been modeled and analyzed as reaction-diffusion process in\textsuperscript{20} \textsuperscript{21}. Epidemic spread in a patchy environment with population dispersal has been modeled and studied in\textsuperscript{22} \textsuperscript{24}. In these works, the mobility or dispersal patterns depend on the state (susceptible or infected) of the individuals, and conditions for global stability of the disease-free equilibrium and an endemic equilibrium are derived. When the mobility patterns are identical for all individuals, then these models reduce to a model similar to the single-layer version of the multi-layer model studied in this paper.

Epidemic spread with mobility on a multiplex network of patches has been modeled and studied in\textsuperscript{25}. Authors of this work consider a discrete-time model in which, at each time, individuals randomly move to another node, participate in epidemic propagation and then return to their home node. A multi-species SEIR epidemic model with population dispersal has been analyzed in\textsuperscript{26} and conditions for the global stability of a disease-free equilibrium are derived. Stability results for endemic equilibrium for the single species case are also derived. The population dispersal model in\textsuperscript{26} is identical to the multi-layer mobility model studied in this paper. In contrast to\textsuperscript{26}, we focus on SIS epidemic model and completely characterize the properties of the model, including existence, uniqueness, and stability of both disease-free and endemic equilibria.

In this paper, we study a coupled epidemic-mobility model...
The individuals within each patch are further grouped into sub-populations defined by $x > X$. The matrix with entries $x$ is the instantaneous transition rate from node $i$ to node $j$, and $-q_{ij} = \mu_i$ is the total rate of transition out of node $i$, i.e., $\mu_i = \sum_{j \neq i} q_{ij}$. Here, $q_{ij} > 0$, if $(i, j) \in E^\alpha$, and $q_{ij} = 0$, otherwise. Let $x_i^\alpha(t)$ be the number of individuals of class $\alpha$ in patch $i$ at time $t$. Let $p_i^\alpha \in [0, 1]$ (respectively, $1 - p_i^\alpha$) be the fraction of infected (respectively, susceptible) sub-population of class $\alpha$ at patch $i$. Define $p^\alpha := [p_1^\alpha, \ldots, p_n^\alpha]^\top$, $x^\alpha := [x_1^\alpha, \ldots, x_n^\alpha]^\top$, $p := [(p_1^\alpha)^\top, \ldots, (p_n^\alpha)^\top]^\top$ and $x := [(x_1^\alpha)^\top, \ldots, (x_n^\alpha)^\top]^\top$.

We model the interaction of mobility 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 $i$, let $\beta_i > 0$ and $\delta_i > 0$ be the infection and recovery rate, respectively. We let $B^\alpha > 0$ and $D^\alpha > 0$ be the positive and non-negative diagonal matrices with entries $\beta_i$ and $\delta_i$, $i \in \{1, \ldots, n\}$, respectively. Let $B$ and $D$ be the positive and non-negative diagonal matrices with block-diagonal entries $B^\alpha$ and $D^\alpha$, $\alpha \in \{1, \ldots, m\}$, respectively. Let $P^\alpha := \text{diag}(p^\alpha)$ and $P := \text{diag}(p)$. We now derive the continuous time dynamics that captures the interaction of mobility and the epidemic dynamics.

**Proposition 1 (SIS model under mobility):** The dynamics of the fractions of the infected sub-population $p$ and the number of individuals $x^\alpha$ under multi-layer Markovian mobility model with generator matrices $Q^\alpha$, and infection and recovery matrices $B$ and $D$, respectively, are

\begin{equation}
\dot{p} = (BF(x) - D - L(x))p - PB F(x)p
\end{equation}

\begin{equation}
\dot{x}^\alpha = (Q^\alpha)^\top x^\alpha,
\end{equation}

where $L$ is an $nm \times nm$ block-diagonal matrix with block-diagonal terms $L^\alpha$, $\alpha \in \{1, \ldots, m\}$, $L^\alpha(x)$ is a matrix with entries

\[
l_{ij}^\alpha(x) = \begin{cases} \sum_{j \neq i} q_{ij} \frac{x_j^\alpha}{z_j}, & \text{if } i = j, \\ -q_{ij} \frac{x_i^\alpha}{z_i}, & \text{otherwise}, \end{cases}
\]

$F(x) := [F^\top(x), \ldots, F^\top(x)]^\top$ be a row-concatenated $nm \times nm$ matrix with each $n \times nm$ block-row as $F^\top(x) := [F^1(x), \ldots, F^m(x)]$, and $F^\alpha$ as a diagonal matrix with entries $f_{ii}^\alpha(x) := \sum_{j \neq i} q_{ij} \frac{x_j^\alpha}{z_j}$, i.e., the fraction of total population at node $i$ contributed by class $\alpha$.

**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

\[
x_i^\alpha(t + h) = x_i^\alpha(t)(1 - \nu_i^\alpha h) + \sum_{j \neq i} q_{ij}^\alpha x_j^\alpha(t) h + o(h).
\]
After the mobility, individuals within each node interact according to SIS dynamics. Thus, the fraction of infected population present at node $i$ is:

$$x_i^0(t + h)p_i^0(t + h) = -x_i^0(t)\delta p_i^0(t)h + x_i^0(t)\beta_i p_i(t)(1 - p_i^0(t))h + x_i^0(t)p_i^0(t)(1 - \nu_i^0 h) + \sum_{j \neq i} q_{ij}^0 p_j^0 x_j^0(t)h + o(h). \quad (3)$$

where $\bar{p}_i$ is the fraction of infected population at node $i$ and is given as:

$$\bar{p}_i := \sum_{\alpha} f_i^\alpha p_i^\alpha.$$ 

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

$$\dot{\bar{p}}_i = -\delta_i p_i^0 + \beta_i \bar{p}_i(1 - p_i^0) - l_i^0 p_i^0 - \sum_{j \neq i} l_{ij}^0 p_j^0. \quad (4)$$

Writing above in vector form gives:

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

Similarly taking limits in (2) yields

$$\dot{x}_i^0 = -\nu_i^0 x_i^0 + \sum_{j \neq i} q_{ij}^0 x_j^0. \quad (6)$$

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

III. ANALYSIS OF SIS MODEL UNDER MULTI-LAYER MARKOVIAN MOBILITY

In this section, we analyze the SIS model under multi-layer mobility (11) under the following standard assumption:

**Assumption 1**: Digraph $G^\alpha$ is strongly connected, for all $\alpha \in \{1, \ldots, m\}$, which is equivalent to matrices $Q^\alpha$ being irreducible [27].

Let $v^\alpha$ be the right eigenvector of $(Q^\alpha)^T$ associated with eigenvalue at 0. We assume that $v^\alpha$ is scaled such that its inner product with the associated left eigenvector $1_\alpha$ is unity, i.e., $1_\alpha^T v^\alpha = 1$. Define $v := [N^1(v^1)^T, \ldots, N^m(v^m)^T]^T$, where $N^\alpha$ is the total number of individuals belonging to class $\alpha$, for $\alpha \in \{1, \ldots, m\}$. We call an equilibrium point $(\bar{p}^*, x^*)$, an endemic equilibrium point, if at equilibrium the terms correspond to infected individuals coming from other nodes due to mobility. After the mobility, individuals within each node interact to epidemic process within each node, whereas the last two terms correspond to infected individuals coming from other nodes due to mobility. Using the expression of $x_i^0$ from (2) in (3) and taking the limit $h \to 0^+$ gives

$$\dot{\bar{p}}_i = -\delta_i p_i^0 + \beta_i \bar{p}_i(1 - p_i^0) - l_i^0 p_i^0 - \sum_{j \neq i} l_{ij}^0 p_j^0. \quad (4)$$

Writing above in vector form gives:

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

Similarly taking limits in (2) yields

$$\dot{x}_i^0 = -\nu_i^0 x_i^0 + \sum_{j \neq i} q_{ij}^0 x_j^0. \quad (6)$$

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

(iii) the model admits an endemic equilibrium at $(\bar{p}^*, x^*) = (\bar{p}, v)$, $\bar{p} \gg 0$, if and only if $\mu(BF^* - D - L^*) > 0$;

(iv) the disease-free equilibrium is globally asymptotically stable if and only if $\mu(BF^* - D - L^*) \leq 0$ and is unstable otherwise;

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

Proof: The first part of statement (i) follows from the fact that $\bar{p}$ is either tangent or directed inside of the region $[0, 1]^{nm}$ at its boundary which are surfaces with $p_i^0 = 0$ or 1. This can be seen from (4). For the second part of (i), we rewrite (1.3) as:

$$\dot{p} = ((I - P)BF(x) + A(x))p - E(t)p.$$

where $L(x) = C(x) - A(x)$ with $C(x)$ composed of the diagonal terms of $L(x)$, $A(x)$ is the non-negative matrix corresponding to the off-diagonal terms, and $E(t) = C(x(t)) + D$ is a diagonal matrix. Now, consider a variable change $y(t) := e^{\int_0^t E(\tau) d\tau} p(t)$. Differentiating $y(t)$ and using above gives:

$$\dot{y} = e^{\int_0^t E(\tau) d\tau}((I - P)BF(x) + A(x))e^{\int_0^t E(\tau) d\tau} e^{\int_0^t E(\tau) d\tau} p = e^{\int_0^t E(\tau) d\tau}((I - P)BF(x) + A(x))e^{\int_0^t E(\tau) d\tau} e^{\int_0^t E(\tau) d\tau} y.$$

Now, the coefficient matrix of $y$ above is always non-negative and strongly connected. The rest of the proof is the same as in [3] Theorem 4.2 (i).

The second statement follows by inspection. The proof of the third statement is presented in Appendix A.

Stability of disease-free equilibria: To prove the fourth statement, we begin by establishing sufficient conditions for instability. The linearization of (1) at $(p, x) = (0, v)$ is

$$\begin{bmatrix} \dot{p} \\ \dot{x} \end{bmatrix} = \begin{bmatrix} BF^* - D - L^* & 0 \\ 0 & Q^* \end{bmatrix} \begin{bmatrix} p \\ x \end{bmatrix}. \quad (7)$$

Since the system matrix in (7) is block-diagonal, its eigenvalues are the eigenvalues of the block-diagonal sub-matrices. Further, since radial abscissa $\mu(Q^*)$ is zero, a sufficient condition for instability of the disease-free equilibrium is that $\mu(BF^* - D - L^*) > 0$.

For the case of $\mu(BF^* - D - L^*) \leq 0$, we now show that the disease-free equilibrium is a globally asymptotically stable equilibrium. It can be seen from the definitions of matrices $F^*$ and $L^*$, that under Assumption (11) $(BF^* - D - L^*)$ is an irreducible Metzler matrix. Together with $\mu(BF^* - D - L^*) \leq 0$, implies there exists a positive diagonal matrix $R$ such that

$$R(BF^* - D - L^*) + (BF^* - D - L^*)^T R = -K,$$

where $K$ is a positive semi-definite matrix. Let $L := L(x) - L^*$, $F := F(x) - F^*$ and $r := \|R\|$, where $\|\cdot\|$ denotes the the induced two norm of the matrix.

Since $x(0) \gg 0$, under Assumption (11) $x_i^0(t)$ is lower bounded by some positive constant and hence, $L$ and $F$
are bounded and continuously differentiable. Since $x$ is bounded and exponentially converges to $x^*$, it follows that $\|L(x)\|$ and $\|F(x)\|$ locally exponentially converge to 0 and $\int_0^t \|L\| dt$ and $\int_0^t \|F\| dt$ are bounded for all $t > 0$.

Consider the Lyapunov-like function $V(p, t) = p^\top R p - 2n \text{mr} \int_0^t (B\|F\| + \|\tilde{L}\|) dt$. It follows from the above arguments that $V$ is bounded. Therefore,

$$V = 2p^\top R p - 2n \text{mr} (B\|F\| + \|\tilde{L}\|)$$

$$= p^\top (R(BF^* - D - L^*) + (BF^* - D - L^*)^\top R)p$$

$$+ 2p^\top (BF^* - L)p - 2p^\top R PB F p$$

$$- 2n \text{mr}(B\|F\| + \|\tilde{L}\|)$$

$$= -p^\top K p + 2p^\top R(BF^* - \tilde{L})p - 2p^\top R PB F p$$

$$- 2n \text{mr}(B\|F\| + \|\tilde{L}\|)$$

$$\leq -p^\top K p + 2n \text{mr}(B\|F\| + \|\tilde{L}\|)$$

$$- 2n \text{mr}(B\|F\| + \|\tilde{L}\|) - 2p^\top R PB F p$$

$$\leq -2p^\top R PB F p \leq 0. \quad (8)$$

Since all the signals and their derivatives are bounded, it follows that $V(t)$ is bounded and hence $V$ is uniformly continuous in $t$. Therefore from Barbalat’s lemma and its application to Lyapunov-like functions [28, Lemma 4.3], it follows that $V \to 0$ as $t \to \infty$. Consequently, from (3), $p^\top R PB F p \to 0$. Since $B > 0$, $D > 0$ with $F_{kk} > 0$ and $p_k \geq 0$, $p(t) \to 0$ as $t \to \infty$. This establishes global attractivity of the disease-free equilibrium point. We now establish its stability.

We note that since, for $x \geq 0$, $(B\|F\| + \|\tilde{L}\|)$ is a real analytic function of $x$, 3 is a region $\|x - x^*\| < \delta_1$ in which $(B\|F\| + \|\tilde{L}\|) \leq k_1 \|x - x^*\|$ for some $k_1 > 0$. Also, since $x - x^*$ is globally exponentially stable, $\|x(t) - x^*\| \leq k_2 e^{-\alpha t} \|x(0) - x^*\|$ for $k_2, \alpha > 0$. Thus, if $\|x(0) - x^*\| < \frac{\delta_1}{k_2}$, then $(B\|F\| + \|\tilde{L}\|) \leq k_1 k_2 e^{-\alpha t} \|x(0) - x^*\|$. This implies $\int_0^t (B\|F\| + \|\tilde{L}\|) dt \leq k_2 \|x(0) - x^*\|$, where $k := k_1 k_2$. Now, since $V(p, t) \leq 0$,

$$V(p, 0) = p(0)^\top R p(0)$$

$$\geq V(p(t), t)$$

$$\geq p(t)^\top R p(t) - 2 \text{mr} k \|x(0) - x^*\|$$

$$\geq R_{\text{min}} \|p(t)\|^2 - 2 \text{mr} k \|x(0) - x^*\|,$$

where $R_{\text{min}} = \min_i \{R_i\}$. Equivalently,

$$\|p(t)\|^2 \leq \frac{r}{R_{\text{min}}} \|p(0)\|^2 + 2 \text{mr} k \|x(0) - x^*\| \alpha R_{\text{min}}.$$ 

It follows using stability of $x$ dynamics, that for any $\varepsilon > 0$, there exists $\delta > 0$, such that $\|x(0) - x^*\|^2 + \|p(0)\|^2 \leq \delta^2 \Rightarrow \|p(t)\|^2 + \|x(t) - x^*\|^2 \leq \varepsilon^2$. This establishes stability. Together, global attractivity and stability prove the fourth statement.

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

**Lemma 1:** For the dynamics (3.3), if $p_i(t) \to 0$ as $t \to \infty$, for some $i \in \{1, \ldots, n\}$ and $\alpha \in \{1, \ldots, m\}$, then $p_i(t) \to 0$ as $t \to \infty$.

**Proof:** It can be easily seen from (4) that $p_i^n$ is bounded and hence $\tilde{p}_i^n$ is uniformly continuous in $t$. Now if $p_i^n(t) \to 0$ as $t \to \infty$, it follows from Barbalat’s lemma [28, Lemma 4.2] that $\tilde{p}_i^n \to 0$. Therefore, from (4) and the fact that $-l_{ij}^0(x) \geq 0$ and $p_i^n \geq 0$, it follows that $p_{ij}^n(t) \to 0$ for all $j$ such that $-l_{ij}^0(x) \neq 0$. Using Assumption 01 and applying the above argument for each class at each node implies $p_i(t) \to 0$.

Define $\tilde{p} := p - p^*$, $P := \text{diag}(p^*)$ and $\tilde{P} := \text{diag}(\tilde{p})$. Then

$$\dot{p} = (BF - D - L - PB F) p$$

$$= (BF^* - D - L^* - P^* BF^*) \tilde{p}$$

$$+ (BF^* - D - L^* - P^* BF^*) \tilde{p}$$

$$+ (BF^* - D - L^* - P^* BF^*) \tilde{p}$$

$$+ (I - P^*) BF^* - D - L^* \tilde{p} + (I - P) BF^* - D - L^* \tilde{p}$$

$$- P^* BF^*.$$ 

where we have used $(BF^* - D - L^* - P^* BF^*) p^* = 0$, 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 its positive eigenvector associated with eigenvalue at zero. Therefore, the Perron-Frobenius theorem for irreducible Metzler matrices [27] implies $\mu((I - P^*) BF^* - D - L^*) = 0$. Also, this means there exists a positive-diagonal matrix $R_2$ and a positive semi-definite matrix $K_2$ such that

$$R_2 ((I - P^*) BF^* - D - L^*)$$

$$+ ((I - P^*) BF^* - D - L^*)^\top R_2 = -K_2.$$ 

Similar to the proof of the fourth statement, take $V_2 (\tilde{p}, t) = \tilde{p}^\top R_2 \tilde{p} - 2 nm \text{mr} \int_0^t (B\|F\| + \|\tilde{L}\|) dt$, where $r_2 := \|R_2\|$. Then,

$$V_2 = 2 \tilde{p}^\top R_2 \tilde{p} - 2 nm \text{mr} (B\|F\| + \|\tilde{L}\|)$$

$$= \tilde{p}^\top (R_2 ((I - P^*) BF^* - D - L^*)$$

$$+ ((I - P^*) BF^* - D - L^*)^\top R_2) \tilde{p}$$

$$+ 2 \tilde{p}^\top R_2 ((I - P) BF^* - D - L^*) \tilde{p} - 2 \tilde{p}^\top R_2 \tilde{p} BF^* p$$

$$- 2 nm \text{mr} (B\|F\| + \|\tilde{L}\|)$$

$$= -\tilde{p}^\top K_2 \tilde{p} + 2 \tilde{p}^\top R_2 ((I - P) BF^* - D - L^*) \tilde{p}$$

$$- 2 \tilde{p}^\top R_2 \tilde{p} BF^* p$$

$$\leq -2 \tilde{p}^\top R_2 \tilde{p} BF^* p$$

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The last inequality above follows from the fact that $R_2 > 0$, $B > 0$ and $F \geq 0$ with diagonal terms $F_{kk} > 0$. It can be
easily shown that $\bar{V}_2$ is bounded implying $\bar{V}_2$ is uniformly continuous. Applying Barbalat’s lemma \cite[Lemma 4.2]{ref6} gives $\bar{V}_2 \to 0$ as $t \to \infty$. This implies that $p_k \to 0$. Using Lemma \ref{lemma4} and the fact that $p = 0$ is an unstable equilibrium for $\mu(BF^* - D - L^*) > 0$, we have $p \to 0$ as long as $p(0) \neq 0$. Stability can be established similarly to the disease-free equilibrium case. This concludes the proof of the theorem. \hfill $\blacksquare$

**Corollary 1** (Stability of disease-free equilibrium): For the SIS epidemic model under Multi-layer Markovian mobility \ref{assumption1} with Assumption \ref{assumption2} and the disease-free equilibrium $(\nu^*, x^*) = (0, v)$ the following statements hold:

(i) a necessary condition for stability is that for each $i \in \{1, \ldots, n\}$, $\exists \alpha \in \{1, \ldots, m\}$ such that $\delta_i > \beta_i - \nu_i^*$;

(ii) a necessary condition for stability is that there exists some $i \in \{1, \ldots, n\}$ such that $\delta_i \geq \beta_i$;

(iii) a sufficient condition for stability is $\delta_i \geq \beta_i$, for each $i \in \{1, \ldots, n\}$;

(iv) a sufficient condition for stability is

$$\lambda_2 \left(1 + \sqrt{1 + \frac{\lambda_2}{\sum_i w_i (\delta_i - \beta_i - s)}}\right)^2 nm + 1 + s \geq 0,$$

where $w$ is a positive left eigenvector of $(BM + L^*)$ such that $w^T(BM + L^*) = 0$ with $\max_i w_i = 1$, $s = \min_i (\delta_i - \beta_i)$, $W = \text{diag}(w)$, and $\lambda_2$ is the second smallest eigenvalue of $\frac{1}{2}(W(BM + L^*) + (BM + L^*)^T W)$.

**Proof**: We begin by proving the first two statements. First, we note that $(L^*)_{ik} = \nu_i^*$. This can be verified by evaluating $L^* = L(v)$ and utilising the fact that $Q^Tv = 0$. The necessary and sufficient condition for the stability of disease-free equilibrium is $\mu(BF^* - D - L^*) \leq 0$. Note that $BF^* - D - L^*$ is an irreducible Metzler matrix. Perron-Frobenius theorem for irreducible Metzler matrices implies that there exists a real eigenvalue equal to $\mu$ with positive eigenvector, i.e., $(BF^* - D - L^*)y = \mu y$, where $y \succ 0$. Rename components of $y$ as $y_{(n+1)i} = y_i^*$ to write $y = \left( (y_1^*, \ldots, y_m^*)^T \right)^T$.

Let for each $i \in \{1, \ldots, n\}$, $y_i^{k_i} = \min\{y_i^1, \ldots, y_i^m\}$. Since $\mu \leq 0$, write component-wise for $(nk_i + i)^{th}$ component

$$\sum_\alpha \beta_i f_{i,\alpha}^* y_i^{*\alpha} - (\delta_i + \nu_i^{k_i}) y_i^{k_i} - \sum_j l_{ij}^{k_i} y_j \leq 0$$

$$\Rightarrow \sum_\alpha \beta_i f_{i,\alpha}^* y_i^{*\alpha} y_i^{*\alpha} + \sum_\alpha \beta_i f_{i,\alpha}^* (y_i^{*\alpha} - y_i^{k_i}) - (\delta_i + \nu_i^{k_i}) y_i^{k_i}$$

$$- \sum_\alpha l_{ij}^{k_i} y_j \leq 0$$

$$\Rightarrow \beta_i - \delta_i - \nu_i^{k_i} y_i^{k_i} \leq - \sum_\alpha \beta_i f_{i,\alpha}^* (y_i^{*\alpha} - y_i^{k_i}) + \sum_\alpha l_{ij}^{k_i} y_j$$

$$\Rightarrow \beta_i - \delta_i - \nu_i^{k_i} y_i^{k_i} < 0$$

$$\Rightarrow \beta_i - \delta_i < \nu_i^{k_i}$$

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

Let $y_i^{k_i} = \min\{y_i^1, \ldots, y_i^m\}$. Similar to the proof of the first statement

$$\sum_\alpha \beta_i f_{i,\alpha}^* y_i^{*\alpha} - (\delta_i + \nu_i^{k_i}) y_i^{k_i} - \sum_\alpha l_{ij}^{k_i} y_j \leq 0$$

$$\Rightarrow \sum_\alpha \beta_i f_{i,\alpha}^* y_i^{k_i} + \sum_\alpha \beta_i f_{i,\alpha}^* (y_i^{*\alpha} - y_i^{k_i}) - (\delta_i + \nu_i^{k_i}) y_i^{k_i}$$

$$- \sum_\alpha l_{ij}^{k_i} y_j \leq 0$$

$$\Rightarrow (\beta_i - \delta_i) y_i^{k_i} \leq - \sum_\alpha \beta_i f_{i,\alpha}^* (y_i^{*\alpha} - y_i^{k_i}) + \sum_\alpha l_{ij}^{k_i} (y_j^{*\alpha} - y_j^{k_i})$$

$$\Rightarrow (\beta_i - \delta_i) y_i^{k_i} \leq 0$$

$$\Rightarrow \beta_i - \delta_i \leq 0.$$
Remark 2: (Influence of mobility on stability of disease-free equilibrium.) The statement (iv) of Corollary 1 characterizes the influence of mobility on the stability of disease-free equilibria. In particular, \( \lambda_2 \) is a measure of “intensity” of mobility and \( s \) is a measure of largest deficit in the recovery rate compared with infection rate among nodes. The sufficient condition in statement (iv) states explicitly how mobility can allow for stability of disease-free equilibrium even under deficit in recovery rate at some nodes.

IV. Numerical Illustrations

We start with numerical simulation of epidemic model with multi-layer mobility in which we treat epidemic spread as well as mobility as stochastic processes. The fraction 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 take two mobility network layers: a complete graph and a line graph with the mobility transition rates being equal among out going neighbors of a node for both the graphs. The two cases relate to the stable disease-free equilibrium and stable endemic equilibrium respectively. If the curing rates, infection rates and the initial fraction of infected population are the same for all the nodes, mobility does not play any role. Therefore, we have chosen heterogeneous curing or infection rates to elucidate the influence of mobility. Figure 1 (a) corresponds to the case \( \delta_i \geq \beta_i \) for each \( i \), whereas Fig. 1 (c) corresponds to the case \( \delta_i < \beta_i \) for each \( i \). The results support statements (iii) and (ii) of Corollary 1 and lead to, respectively, the stable disease-free equilibrium and the stable endemic equilibrium.

Once we have established the correctness of deterministic model predictions with the stochastic simulations, we study the simulations using only the deterministic model. We study the effect of multi-layer mobility over different pairs of mobility graph structures - line-line graph, line-ring graph and line-star graph. We choose different population size for the two mobility layers and take the mobility transition rates such as to keep the equilibrium distribution of population the same for both the layers across all pairs (taken as uniform equilibrium distribution) by using instantaneous transition rates from Metropolis-Hastings algorithm [30]. This shows the effect of different mobility graph structure on epidemic spread while the equilibrium population distribution remains the same. Fig. 2 shows the fractions of infected population trajectories for 10 nodes connected with different pairs of graph structures. The values of equilibrium fractions are affected by the presence of mobility and are different for different graph structures.

![Fig. 1. Stochastic simulation of epidemic spread under mobility. Complete-Line graphs, \( n = 20 \), \( \nu(i) = 0.2 \), \( q_{ij} = \frac{1}{|D_{out}|} \), \( p_i(0) = 0.01 \). Each iteration in stochastic model corresponds to time-step 0.01 sec.](image)

![Fig. 2. Simulation of deterministic model of epidemic spread under 2 layer mobility, over different graph structure with stable endemic equilibrium. \( n = 10 \), \( p_i(0) = 0.01 \).](image)

Next, we verify the statement (iv) of Corollary 1 for a single layer mobility model, where one can have some curing rates \( \delta_i \) less than the infection rates \( \beta_i \) but still have stable disease-free equilibrium. We take a complete graph of \( n = 20 \) nodes with given mobility transition rates which give us
\(\mathbf{w}, L^*\) and \(\lambda_2\). We take a given set of values of \(\beta_i\). Next, we compute \(s_{\text{lower}} = -\frac{\lambda_2}{4nm+1}\) and take 0.8 times of this value as \(s\) in order to compute \(\delta_i\)’s that satisfy statement (iv) of Corollary 1. For our case the values are: \(\beta_i = 0.3, \lambda_2 = 0.2105, s_{\text{lower}} = -0.0026, s = 0.8 s_{\text{lower}} = -0.0021,\delta_1 = \delta_n = \beta_i + s\) and the rest \(\delta_i\) computed to satisfy the condition which gives \(\delta_1 = \delta_n = 0.2979\) and \(\delta_i = 0.3198\) for \(i \in \{2, \ldots, n-1\}\). Fig. 3 shows the trajectories of infected fraction populations. As can be seen the trajectories converge to the disease-free equilibrium.

**Fig. 3.** Stable disease-free equilibrium with curing rates computed as per the \(\lambda_2\) sufficient condition (statement (iv), Corollary 1) for stability of disease-free equilibrium. Graph: Complete, \(n = 20, p_i(0) = 0.01\).

**V. CONCLUSIONS**

We derived a continuous-time model for epidemic propagation under Markovian mobility across multi-layer network of patches. The epidemic spread within each node has been modeled as SIS population model with individuals traveling across the nodes with different mobility patterns modeled as layers of a multi-layer network. The derived model has been analyzed to establish the existence and stability of disease-free equilibrium and an endemic equilibrium under different conditions. Some necessary and some sufficient conditions for stability of disease-free equilibrium have been established. We also provided numerical studies to support our results and elucidated the effect of mobility on epidemic propagation.

**APPENDIX**

**A. Proof of Theorem 1 (iii): Existence of an endemic equilibrium**

Here we assume that there exists at least one node with positive recovery rate, i.e., \(\delta_i > 0\) for at least one \(i\). The case with no recovery at all nodes is trivial and leads to \(p^* = 1\).

We first state some properties of M-matrices, which we will use in the proof.

**Theorem 2 (Properties of M-matrix, [31]):** For a real Z-matrix (i.e., a matrix with all off-diagonal terms non-positive) \(A \in \mathbb{R}^{n \times n}\), the following statements are equivalent to \(A\) being a non-singular M-matrix

(i) **Stability:** real part of each eigenvalue of \(A\) is positive;

(ii) **Inverse positivity:** \(A^{-1} \geq 0\) (for irreducible \(A, A^{-1} > 0\));

(iii) **Regular splitting:** \(A\) has a convergent regular splitting, i.e., \(A\) has a representation \(A = M - N\), where \(M^{-1} \geq 0, N \geq 0\) (called regular splitting), with \(M^{-1}N\) convergent, i.e., \(\rho(M^{-1}N) < 1\);

(iv) **Convergent regular splitting:** every regular splitting of \(A\) is convergent. Further, for a singular M-matrix (i.e. singular Z-matrix with real part of eigenvalues non-negative) regular splitting of \(A\) gives \(\rho(M^{-1}N) = 1\);

(v) **Semi-positivity:** there exists \(x \geq 0\) such that \(Ax \geq 0\);

(vi) **Modified semi-positivity:** there exists \(x > 0\) such that \(y = Ax > 0\) and matrix \(A\) defined by

\[
\hat{A}_{ij} = \begin{cases} 1 & \text{if } A_{ij} \neq 0 \text{ or } y_i \neq 0, \\ 0 & \text{otherwise} \end{cases}
\]

is irreducible.

A consequence of Theorem 2 (vi) is that an irreducible Laplacian matrix perturbed with a non-negative diagonal matrix with at least one positive element is a non-singular M-matrix (take \(x = 1 \gg 0\)). This implies that block diagonal submatrices of the matrix \(L^* + D\) are all non-singular M-matrices (since \(\delta_i \geq 0\) with strict inequality for at least one \(i\)) and hence \(L^* + D\) is a non-singular M-matrix. Similar arguments imply \(B^{-1}(L^* + D)\) is a non-singular M-matrix.

We show below that in the case of \(\mu(BF^* - D - L^*) > 0\) there exists an endemic equilibrium \(P^* \gg 0\), i.e.,

\[
\dot{p}|_{p=p^*} = (BF^* - D - L^* - P^*BF^*)p^* = 0. \tag{9}
\]

We use Brouwer’s fixed point theorem, similar to the derivation in [31]. We split the non-negative matrix \(F^*\) as \(F^* = I - M\), where \(M\) is a Laplacian matrix. Rearranging the terms and writing the above as an equation in \(p\) to be satisfied at \(p^*\) leads to

\[
(L^* + D)((L^* + D)^{-1}B - I)p = (PB + (I - P)BM)p = B(P + (I - P)M)p. \tag{10}
\]

Define \(A := (L^* + D)^{-1}B\). Since \(A^{-1} = B^{-1}(L^* + D)\) is a non-singular M-matrix, its inverse \(A\) is non-negative [31]. Rearranging (10) leads to

\[
p = H(p) = (I + A(P + (I - P)M))^{-1}Ap. \tag{11}
\]

Now we show that \(H(p)\) as defined above is a monotonic function in the sense that \(p_2 \geq p_1\) implies \(H(p_2) \geq H(p_1)\). Define \(\tilde{p} := p_2 - p_1\) and \(\tilde{P} := \text{diag}(\tilde{p})\). Then,
H(p₂) − H(p₁)
= (A⁻¹ + P₂ + (I − P₂)M)⁻¹ p₂
− (A⁻¹ + P₁ + (I − P₁)M)⁻¹ p₁
= (A⁻¹ + P₂ + (I − P₂)M)⁻¹ (p₂ − (A⁻¹ + P₂ + (I − P₂)M) (A⁻¹ + P₁ + (I − P₁)M)⁻¹ p₁)
= (A⁻¹ + P₂ + (I − P₂)M)⁻¹ (p₂ − (A⁻¹ + P₂ + (I − P₂)M) (A⁻¹ + P₁ + (I − P₁)M)⁻¹ (I − diag ((I − M)(A⁻¹ + P₁ + (I − P₁)M)⁻¹ p₁)) p)
(12)

Since (A⁻¹ + P₂ + (I − P₂)M) = B⁻¹(L⁺ + D) + P₂ + (I − P₂)M is a non-singular M-matrix (consider theorem [2] (vi) with \( x = 1 \gg 0 \)), its inverse and hence the first term above is non-negative. The second term is shown to be non-negative as below

\[
(\text{I} - \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I} - \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I})
\]
\[
= \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I}
\]
\[
= \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I}
\]
\[
= \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I}
\]
\[
= \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I}
\]
\[
= \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I}
\]
\[
= \text{diag} \left( (\text{I} - \text{M})(A^{-1} + P \text{I} + (I - P \text{I})M)^{-1} P \text{I} \right) \text{I}
\]
\[
\geq 0,
\]
where we have used the identity
\[
(I + X)^{-1} = I - (I + X)^{-1}X,
\]
and \(M1 = 0\), as \(M\) is a Laplacian matrix. The last inequality in (13) holds as \(A^{-1}1 = B^{-1}(L^* + D)1 = B^{-1}D1 \geq 0\) and \((A^{-1} + P + (I - P)M)^{-1}1 \geq 0\), since it is the inverse of an M-matrix. The last term in the last line of (12) is \(\hat{p} \geq 0\). This implies that \(H(p)\) is a monotonic function. Also, argument similar to above can be used to show that \(H(p) \leq 1\) for all \(0 \leq p \leq 1\). Therefore, \(H(1) \leq 1\).

Applying the converse of Theorem [2] (iv), with Z-matrix as \((L^* + D) - BF^*\), where \((L^* + D)^{-1} \geq 0\), \(BF^* \geq 0\) implies \(\mu(BF^* - (D + L^*)) > 0\) if and only if \(R_0 = \rho(AF^*) = \rho(A(I - M)) > 1\). Now, \(A\) is a block-diagonal matrix with block-diagonal terms as \(A^\alpha = (L^{\alpha} + D^{\alpha})^{-1}B^\alpha\), which are inverse of irreducible non-singular M-matrices and hence are positive. Using the expression for \(F\) gives \(AF^* = [(A^1)^T F^T (x^*)] \ldots, (A^{\alpha})^T F^T (x^*)]^T\). Since \(A^\alpha > 0\) and \(F^* > 0\) with no zero column, \(AF^* > 0\) and hence irreducible. Since \(AF^*\) is an irreducible non-negative matrix, Perron-Frobenius theorem implies \(\rho(AF^*)\) is a simple eigenvalue satisfying \(AF^* u = \rho(AF^*) u = R_0 u\) with \(u \gg 0\).

Using \(F^* = I - M\) implies:

\[
Au = R_0 u + AM u = (R_0 - 1) u + (I + AM) u.
\]
(15)

Define \(U := \text{diag}(u)\) and \(\gamma := \frac{R_0 - 1}{R_0}\). Putting \(p = \epsilon u\), we show that \(\exists \epsilon_0\) such that \(\epsilon \in (0, \epsilon_0)\) implies \(H(\epsilon u) \geq \epsilon u\) as below:

\[
H(\epsilon u) - \epsilon u
= (I + \epsilon AM)^{-1}(R_0 - 1)u + (I + AM)u - \epsilon u
\]
\[
= (I + AM)^{-1}(R_0 - 1)u + (I + AM)u - \epsilon u
\]
\[
= (I + AM)^{-1}(R_0 - 1)u + (I + AM)u - \epsilon u
\]
\[
= (R_0 - 1)(A^{-1} + M)^{-1}A^{-1}u
\]
\[
= (R_0 - 1)(A^{-1} + M)^{-1}A^{-1}u
\]
\[
\geq 0.
\]
(17)

The last inequality follows as \(\gamma\) and \(u\) are both positive, and \((A^{-1} + M)^{-1}F^* = (B^{-1}(L^* + D))^{-1}F^* > 0\) as \(B^{-1}(L^* + D) + M\) is an irreducible M-matrix and hence its inverse is positive and \(F^* \geq 0\) with no zero column. Since \(K(\epsilon)\) is a continuous function of \(\epsilon\), \(\exists \epsilon_0\) such that \(\epsilon_0 > \epsilon > 0\) implies \(K(\epsilon) \gg 0\) and therefore, \(H(\epsilon u) \geq \epsilon u\). Therefore there exists an \(\epsilon > 0\) such that \(H(\epsilon u) - \epsilon u \gg 0\) or equivalently, \(H(\epsilon u) \geq \epsilon u\). Taking the closed compact set \(J = [\epsilon u, 1]\), \(H(p) : J \rightarrow J\) is a continuous function of \(p\). Brouwer’s fixed point theorem implies there exists a fixed point of \(H\) in \(J\). This proves the existence of an endemic equilibrium \(p^* \gg 0\) when \(\mu(BF^* - D - L^*) > 0\) or equivalently \(R_0 > 1\).

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