

EPIDEMIC MODELS UNDER MOBILITY ON MULTI-LAYER NETWORKS

By

Vishal Abhishek

A THESIS

Submitted to
Michigan State University
in partial fulfillment of the requirements
for the degree of

Mechanical Engineering – Master of Science

2021

ABSTRACT

EPIDEMIC MODELS UNDER MOBILITY ON MULTI-LAYER NETWORKS

By

Vishal Abhishek

We study epidemic spreading models namely, SIS and SIR models, under mobility on multi-layer networks. 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 in the multi-layer network of spatially-distributed patches move according to their CTMC and subsequently interact with the local individuals in the patch according to SIS or SIR models. 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 multi-layer network on the stability of these equilibria. 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.

Next, we extend some of the results to the case of weakly connected networks. Here, we use the notion of strongly connected components and input to state stability to study the stability of equilibria.

Finally, we consider a resource allocation problem to maximize the rate of convergence to an equilibrium. We show that under certain assumptions the problem can be formulated as a geometric program. We provide numerical illustrations to corroborate the results.

ACKNOWLEDGEMENTS

I would like to express my sincere thanks to my advisor Prof. Vaibhav Srivastava, without whom this work would not have been possible. I express my deepest gratitude for his continuous guidance and motivation. I would like to thank my committee members Prof. Ranjan Mukherjee and Prof. Xiaobo Tan for giving their valuable time and inputs.

I would also like to thank all the members of D-CYPHER Lab for making my work at the lab fruitful as well as cheerful.

Lastly, I would like to thank my parents for their sacrifices and continuous support.

Vishal Abhishek

TABLE OF CONTENTS

LIST OF FIGURES	v
CHAPTER 1 INTRODUCTION	1
1.1 Epidemic Models	1
1.2 Epidemic Models under Mobility	2
1.3 Resource Allocation	3
1.4 Thesis Organization	4
1.5 Mathematical Notations	4
CHAPTER 2 EPIDEMIC MODELS UNDER MOBILITY ON SINGLE-LAYER NETWORKS	5
2.1 SIS Model under Markovian Mobility	5
2.2 Analysis of SIS Model under Markovian Mobility	7
2.3 Numerical Illustrations	15
CHAPTER 3 EPIDEMIC MODELS UNDER MOBILITY ON MULTI-LAYER NETWORKS	18
3.1 SIS Model under Multi-layer Markovian Mobility	18
3.2 Analysis of SIS Model under Multi-layer Markovian Mobility	20
3.3 Numerical Illustrations	30
3.4 SIR Model under Multi-layer Markovian Mobility	32
3.5 Numerical Illustrations	37
CHAPTER 4 SIS EPIDEMIC MODEL UNDER MOBILITY ON MULTI-LAYER NETWORKS: WEAKLY CONNECTED CASE	39
4.1 SIS Model under Mobility with Non-strongly Connected Layers	39
4.2 Stability Analysis	41
CHAPTER 5 RESOURCE ALLOCATION	44
5.1 Resource allocation	44
5.1.1 Single layer mobility	44
5.1.2 Multilayer mobility	46
5.2 Numerical Illustration	46
CHAPTER 6 CONCLUSIONS	49
APPENDIX	50
BIBLIOGRAPHY	61

LIST OF FIGURES

Figure 2.1:	Stochastic simulation of epidemic spread under mobility. Line graph, $n = 20$, $\nu(i) = 0.2$, $q_{ij} = \frac{\nu(i)}{D_{out}}$, $p_i(0) = 0.01$. Each iteration in stochastic model corresponds to time-step 0.01 sec.	15
Figure 2.2:	Simulation of deterministic model of epidemic spread under mobility, with same equilibrium distribution of population over 4 different graph structure with stable endemic equilibrium. $n = 20$, $p_i(0) = 0.01$	16
Figure 2.3:	Stable disease-free equilibrium with curing rates computed as per the λ_2 sufficient condition (statement (iv), Corollary 1) for stability of disease-free equilibrium. Graph: Complete, $n = 20$, $p_i(0) = 0.01$	17
Figure 3.1:	Stochastic simulation of epidemic spread under mobility. Complete-Line graphs, $n = 20$, $\nu(i) = 0.2$, $q_{ij} = \frac{\nu(i)}{D_{out}}$, $p_i(0) = 0.01$. Each iteration in stochastic model corresponds to time-step 0.01 sec.	30
Figure 3.2:	Simulation of deterministic model of epidemic spread under 2 layer mobility, over different graph structure with stable endemic equilibrium. $n = 10$, $p_i(0) = 0.01$	31
Figure 3.3:	Simulation of deterministic model of SIR epidemic spread under 2 layer mobility, over Line-Ring graph structure. $n = 10$, $p_i(0) = 0.01$	38
Figure 4.1:	Non-strongly connected multilayer network with shaded sink components	39
Figure 5.1:	Decay rate λ against maximum allowable cost C . Graph1: Line, Graph 2: Ring, $n = 10$, $\nu_i = 0.2$	48

CHAPTER 1

INTRODUCTION

In this thesis, we study epidemic models: namely, SIS (Susceptible-Infected-Susceptible) and SIR (Susceptible-Infected-Recovered) models, under mobility on multi-layer networks. The following sections introduce the work done.

1.1 Epidemic Models

Contagion dynamics are used to model a variety of phenomenon such as spread of influence, disease and rumors. Epidemic propagation models are as a class of contagion models that have been used in the context of disease spread [1, 2], spread of computer viruses [3, 4], routing in mobile communication networks [5], and spread of rumors [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 thesis, we consider a generalized epidemic propagation model in 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 classical SIS/SIR models where the dynamics of the fraction of the population in each category [2] is studied, the Network 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 [7, 8, 8, 9, 10]. Authors in [11, 12] study network epidemic dynamics in discrete time setting.

Some common generalizations of the SIR/SIS models include: SEIR model [7, 13], where an additional classification “exposed” is introduced, SIRS [2, 12], where individuals get temporary immunity after recovery and then become susceptible again, and SIRI [14, 15], where after recovery, agents become susceptible with a different rate of infection. The network epidemic dynamics have also been studied for time-varying networks [16, 17, 18].

1.2 Epidemic Models under Mobility

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 [19, 20]. Epidemic spread in a patchy environment with population dispersal has been modeled and studied in [21, 22, 23]. 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 thesis.

Epidemic spread with mobility on a multiplex network of patches has been modeled and studied in [24]. Authors of this work consider a discrete 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 [25] 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 this work is identical to the multi-layer mobility model studied in this thesis and it reduces to the single layer mobility model for a single

species. In contrast to this work, we focus on SIS epidemic model and study endemic equilibria for the general multiplex network.

In this work, we study a coupled epidemic-mobility model comprised of a set of patches located in a multi-layer network of spatially distributed regions. Individuals within each patch (region) can travel across regions according to a Continuous Time Markov Chain (CTMC) characterising their mobility pattern and upon reaching a new region participate in the local SIS epidemic process. We extend the results for the deterministic network SIS and SIR model [8, 9, 10, 11] to the proposed model and characterize its steady state and stability properties.

We extend the results for the SIS model to the case of weakly connected networks. Here, we use the notion of strongly connected components to divide the nodes of the multi-layer networks into several batches and analyze the stability of epidemic model over these nodes only. We use the notion of input to state stability to incorporate the effects of the remaining nodes.

1.3 Resource Allocation

We formulate a resource allocation problem for the SIS model under markovian mobility where we allocate resources so as to have the disease free equilibrium (DFE) as the stable equilibrium. We consider two types of resources:

- i. Preventive resource: This can be used to change the infection rate such that $\beta_i \in [\underline{\beta}_i, \bar{\beta}_i]$. This resource is applied to a node with cost function $f_i(\beta_i)$.
- ii. Corrective resource: This can be used to change the recovery rate such that $\delta_i \in [\underline{\delta}_i, \bar{\delta}_i]$.

The corresponding cost function is $g_i(\delta_i)$.

We show that under certain assumptions the problem can be formulated as a geometric program.

1.4 Thesis Organization

Chapter 2 discusses SIS epidemic model under mobility over single layer networks. Chapter 3 discusses epidemic models: SIS and SIR under mobility on multi-layer networks. Chapter 4 extends the results for weakly connected networks. Chapter 5 discusses resource allocation formulation and its solution as a geometric program. Finally, Chapter 6 concludes the thesis. First, we give below mathematical notations used in this thesis:

1.5 Mathematical Notations

For any two real vectors $\mathbf{x}, \mathbf{y} \in \mathbb{R}^n$, we denote:

$\mathbf{x} \gg \mathbf{y}$, if $x_i > y_i$ for all $i \in \{1, \dots, n\}$,

$\mathbf{x} \geq \mathbf{y}$, if $x_i \geq y_i$ for all $i \in \{1, \dots, n\}$,

$\mathbf{x} > \mathbf{y}$, if $x_i \geq y_i$ for all $i \in \{1, \dots, n\}$ and $\mathbf{x} \neq \mathbf{y}$.

For a square matrix G , radial abscissa $\mu : \mathbb{R}^{n \times n} \rightarrow \mathbb{R}$ is defined by

$$\mu(G) = \max\{\operatorname{Re}(\lambda) \mid \lambda \text{ is an eigenvalue of } G\},$$

where $\operatorname{Re}(\cdot)$ denotes the real part of the argument. Spectral radius ρ 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 $\mathbf{x} = [x_1, \dots, x_n]^\top$, $X = \operatorname{diag}(\mathbf{x})$ is a diagonal matrix with $X_{ii} = x_i$ for all $i \in \{1, \dots, n\}$.

CHAPTER 2

EPIDEMIC MODELS UNDER MOBILITY ON SINGLE-LAYER NETWORKS

In this chapter, we study the SIS model under mobility on a single-layer network. The single layer corresponds to the presence of one mobility pattern with its characteristic Markov Chain and digraph. We assume that the digraph is strongly connected. We give complete characterization of the equilibria of the system, including its existence, uniqueness and stability. We also give numerical illustrations to support our results.

2.1 SIS Model under Markovian Mobility

We consider n sub-populations of individuals that are located in distinct spatial regions. We assume the individuals within each sub-population can be classified into two categories: (i) susceptible, and (ii) infected. Let $p_i \in [0, 1]$ (respectively, $1 - p_i$) be the fraction of infected (respectively, susceptible) individuals within sub-population $i \in \{1, \dots, n\}$. We assume that the individuals within each sub-population can travel to regions associated with other sub-populations. Let the connectivity of these regions be modeled by a digraph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$, where $\mathcal{V} = \{1, \dots, n\}$ is the node set and $\mathcal{E} \subset \mathcal{V} \times \mathcal{V}$ is the edge set. We model the mobility of individuals on graph $\mathcal{G}$ using a Continuous Time Markov Chain (CTMC) with a stationary generator matrix Q , whose (i, j) -th entry is q_{ij} . The entry $q_{ij} \geq 0$, $i \neq j$, is the instantaneous transition rate from node i to node j , and $-q_{ii} = \nu_i$ is the total rate of transition out of node i , i.e., $\nu_i = \sum_{j \neq i} q_{ij}$. Here, $q_{ij} > 0$, if $(i, j) \in \mathcal{E}$; and $q_{ij} = 0$, otherwise. Let $x_i(t) \in (0, 1)$ be the fraction of the total population that constitutes the sub-population at node i at time t . It follows that $\sum_{i=1}^n x_i = 1$. Define $\mathbf{p} := [p_1, \dots, p_n]^\top$ and $\mathbf{x} := [x_1, \dots, x_n]^\top$.

We model the interaction of mobility with the epidemic process as follows. At each time t , individuals at each node move on graph $\mathcal{G}$ according to the CTMC with generator matrix Q and 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 $\delta_i \geq 0$ be the infection and recovery rate, respectively. We let $B > 0$ and $D \geq 0$ be the positive and non-negative diagonal matrices with entries β_i and δ_i , $i \in \{1, \dots, n\}$, respectively. Similarly we define P as a diagonal matrix with entries p_i . We now derive the continuous time dynamics that captures the interaction of mobility and the SIS epidemic dynamics.

Proposition 1 (SIS model under mobility) *The dynamics of the fractions of the infected sub-population $\mathbf{p}$ and the fractions of the total population $\mathbf{x}$ that constitute the sub-population at each node under Markovian mobility model with generator matrix Q , and infection and recovery matrices B and D , respectively, are*

$$\dot{\mathbf{p}} = (B - D - L(\mathbf{x}))\mathbf{p} - P\mathbf{B}\mathbf{p} \quad (2.1a)$$

$$\dot{\mathbf{x}} = Q^\top \mathbf{x}, \quad (2.1b)$$

where $L(\mathbf{x})$ is a matrix with entries

$$l_{ij}(\mathbf{x}) = \begin{cases} \sum_{j \neq i} q_{ji} \frac{x_j}{x_i}, & \text{if } i = j, \\ -q_{ji} \frac{x_j}{x_i}, & \text{otherwise.} \end{cases}$$

Proof: Consider a small time increment $h > 0$ at time t . Then the fraction of the total population present at node i after the evolution of CTMC in time-interval $[t, t + h)$ is

$$x_i(t + h) = x_i(t)(1 - \nu_i h) + \sum_{j \neq i} q_{ji} x_j(t) h + o(h). \quad (2.2)$$

Individuals within each node interact according to SIS dynamics. Thus, the fraction of infected population present at node i is:

$$\begin{aligned} x_i(t + h)p_i(t + h) = & -x_i(t)\delta_i p_i(t)h + x_i(t)\beta_i p_i(t)(1 - p_i(t))h \\ & + x_i(t)p_i(t)(1 - \nu_i h) + \sum_{j \neq i} q_{ji} p_j(t)x_j(t)h + o(h). \end{aligned} \quad (2.3)$$

The first two terms on the right side of (2.3) 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 from (2.2) in (2.3) and taking the limit $h \rightarrow 0^+$ gives

$$\dot{p}_i = -\delta_i p_i + \beta_i p_i (1 - p_i) + \sum_{j \neq i} q_{ji} (p_j - p_i) \frac{x_j}{x_i}. \quad (2.4)$$

Similarly taking limits in (2.2) yields

$$\dot{x}_i = -\nu_i x_i + \sum_{j \neq i} q_{ji} x_j. \quad (2.5)$$

Rewriting (2.4) and (2.5) in vector form establishes the proposition. $\square$

Remark 1 (*Comparison with other models*) *The epidemic propagation models in theoretical ecology incorporate spatial aspects by using a partial differential equation that is obtained by adding a spatial diffusion operator to the infected population dynamics [26]. Since, Laplacian matrix is a diffusion operator on a graph, dynamics (2.1) can be interpreted as a network equivalent of the population models with spatial aspects. The dependence of the Laplacian matrix on $\mathbf{x}$ in (2.1) is more general than the constant diffusion coefficient discussed in [26].* $\square$

2.2 Analysis of SIS Model under Markovian Mobility

In this section, we analyze the SIS model under mobility (2.1) under the following standard assumption:

Assumption 1 *Digraph $\mathcal{G}$ is strongly connected which is equivalent to matrix Q being irreducible [27].* $\square$

Let $\mathbf{v}$ be the right eigenvector of $Q^\top$ associated with eigenvalue at 0. We assume that $\mathbf{v}$ is scaled such that its inner product with the associated left eigenvector $\mathbf{1}_n$ is unity, i.e., $\mathbf{1}_n^\top \mathbf{v} = 1$. We call an equilibrium point $(\mathbf{p}^*, \mathbf{x}^*)$, an endemic equilibrium point, if at equilibrium the disease does not die out, i.e., $\mathbf{p}^* \neq 0$, otherwise, we call it a disease-free equilibrium point. Let $L^* := L(\mathbf{x}^*) = L(\mathbf{v})$.

Theorem 1 (*Existence and Stability of Equilibria*) *For the SIS model under Markovian mobility (2.1) with Assumption 1, the following statements hold*

- i. if $\mathbf{p}(0) \in [0, 1]^n$, then $\mathbf{p}(t) \in [0, 1]^n$ for all $t > 0$. Also, if $\mathbf{p}(0) > \mathbf{0}_n$, then $\mathbf{p}(t) \gg \mathbf{0}_n$ for all $t > 0$;*
- ii. the model admits a disease-free equilibrium at $(\mathbf{p}^*, \mathbf{x}^*) = (\mathbf{0}_n, \mathbf{v})$;*
- iii. the model admits an endemic equilibrium at $(\mathbf{p}^*, \mathbf{x}^*) = (\bar{\mathbf{p}}, \mathbf{v})$, $\bar{\mathbf{p}} \gg 0$, if and only if $\mu(B - D - L^*) > 0$;*
- iv. the disease-free equilibrium is globally asymptotically stable if and only if $\mu(B - D - L^*) \leq 0$ and is unstable otherwise;*
- v. the endemic equilibrium is almost globally asymptotically stable if $\mu(B - D - L^*) > 0$ with region of attraction $\mathbf{p}(0) \in [0, 1]^n$ such that $\mathbf{p}(0) \neq \mathbf{0}_n$.*

Proof: The first part of statement (i) follows from the fact that $\dot{\mathbf{p}}$ is either directed tangent or inside of the region $[0, 1]^n$ at its boundary which are surfaces with $p_i = 0$ or 1 . For the second part of (i), we rewrite (3.1a) as:

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

where $L(\mathbf{x}) = C(\mathbf{x}) - A(\mathbf{x})$ with $C(\mathbf{x})$ composed of the diagonal terms of $L(\mathbf{x})$, $A(\mathbf{x})$ is the non-negative matrix corresponding to the off-diagonal terms, and $E(t) = C(\mathbf{x}(t)) + D$ is a diagonal matrix. Now, consider a variable change $\mathbf{y}(t) := e^{\int_0^t E(t)dt} \mathbf{p}(t)$. The rest of the proof is same as in [8, Theorem 4.2 (i)].

The second statement follows by inspection.

The proof of the third statement is presented in Appendix A.1.

Stability of disease-free equilibria: To prove the fourth statement, we begin by establishing sufficient conditions for instability. The linearization of (2.1) at $(\mathbf{p}, \mathbf{x}) = (\mathbf{0}, \mathbf{v})$ is

$$\begin{bmatrix} \dot{\mathbf{p}} \\ \dot{\mathbf{x}} \end{bmatrix} = \begin{bmatrix} B - D - L^* & 0_{n \times n} \\ 0_{n \times n} & Q^\top \end{bmatrix} \begin{bmatrix} \mathbf{p} \\ \mathbf{x} \end{bmatrix}. \quad (2.6)$$

Since the system matrix in (2.6) is block-diagonal, its eigenvalues are the eigenvalues of the block-diagonal sub-matrices. Further, since radial abscissa $\mu(Q^\top)$ is zero, a sufficient condition for instability of the disease-free equilibrium is that $\mu(B - D - L^*) > 0$.

For the case of $\mu(B - D - L^*) \leq 0$, we now show that the disease-free equilibrium is a globally asymptotically stable equilibrium. Since $(B - D - L^*)$ is an irreducible Metzler matrix with $\mu(B - D - L^*) \leq 0$, there exists a positive diagonal matrix R such that

$$R(B - D - L^*) + (B - D - L^*)^\top R = -K,$$

where K is a positive semi-definite matrix [10, Proposition 1 (iv), Lemma A.1]. Define $\tilde{L} := L(\mathbf{x}) - L^*$ and $r := \|R\|$, where $\|\cdot\|$ denotes the induced two norm of the matrix.

Since $\mathbf{x}(0) \gg 0$, under Assumption 1, $x_i(t)$ is lower bounded by some positive constant and hence, $\tilde{L}$ is bounded and continuously differentiable. Since $\mathbf{x}$ is bounded and exponentially converges to $\mathbf{x}^*$, it follows that $\|\tilde{L}(x)\|$ locally exponentially converges to $\|\tilde{L}(\mathbf{x}^*)\| = 0$ and $\int_0^t \|\tilde{L}\| dt$ is bounded for all $t > 0$.

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

$$\begin{aligned} \dot{V} &= \mathbf{p}^\top R \dot{\mathbf{p}} + \dot{\mathbf{p}}^\top R \mathbf{p} - 2nr \|\tilde{L}\| \\ &= \mathbf{p}^\top (R(B - D - L^*) + (B - D - L^*)^\top R) \mathbf{p} \\ &\quad - 2\mathbf{p}^\top R(L(\mathbf{x}) - L^*) \mathbf{p} - 2\mathbf{p}^\top RPB \mathbf{p} - 2nr \|\tilde{L}\| \\ &= -\mathbf{p}^\top K \mathbf{p} - 2\mathbf{p}^\top R \tilde{L}(\mathbf{x}) \mathbf{p} - 2\mathbf{p}^\top RPB \mathbf{p} \\ &\quad - 2nr \|\tilde{L}\| \\ &\leq -\mathbf{p}^\top K \mathbf{p} + 2nr \|\tilde{L}\| - 2nr \|\tilde{L}\| - 2\mathbf{p}^\top RPB \mathbf{p} \\ &\leq -2\mathbf{p}^\top RPB \mathbf{p} \leq 0. \end{aligned} \quad (2.7)$$

Since all the signals and their derivatives are bounded, it follows that $\ddot{V}(t)$ is bounded and hence $\dot{V}$ is uniformly continuous in t . Therefore from Barbalat's lemma and its application to Lyapunov-like functions [28, Lemma 4.3, Chapter 4] it follows that $\dot{V} \rightarrow 0$ as $t \rightarrow \infty$. Consequently, from (3.8), $\mathbf{p}^\top RPB\mathbf{p} \rightarrow 0$. Since $R > 0$, $B > 0$ and $p_i \geq 0$, $\mathbf{p}(t) \rightarrow \mathbf{0}$ as $t \rightarrow \infty$. This establishes global attractivity of the disease-free equilibrium point. We now establish its stability.

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

$$\begin{aligned} V(\mathbf{p}(0), 0) &= \mathbf{p}(0)^\top R\mathbf{p}(0) \\ &\geq V(\mathbf{p}(t), t) \\ &\geq \mathbf{p}(t)^\top R\mathbf{p}(t) - 2 \frac{nrk\|\mathbf{x}(0) - \mathbf{x}^*\|}{\alpha} \\ &\geq R_{\min} \|\mathbf{p}(t)\|^2 - 2 \frac{nrk\|\mathbf{x}(0) - \mathbf{x}^*\|}{\alpha}, \end{aligned}$$

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

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

It follows using stability of $\mathbf{x}$ dynamics, that for any $\epsilon > 0$, there exists $\delta > 0$, such that $\|\mathbf{x}(0) - \mathbf{x}^*\|^2 + \|\mathbf{p}(0)\|^2 \leq \delta^2 \Rightarrow \|\mathbf{p}(t)\|^2 + \|\mathbf{x}(t) - \mathbf{x}^*\|^2 \leq \epsilon^2$. 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 (3.1a), if $p_i(t) \rightarrow 0$ as $t \rightarrow \infty$, for some $i \in \{1, \dots, n\}$, then $\mathbf{p}(t) \rightarrow \mathbf{0}$ as $t \rightarrow \infty$.*

Proof: The dynamics of p_i are

$$\dot{p}_i = (\beta_i - \delta_i - l_{ii}(\mathbf{x}))p_i - \sum_{j \neq i} l_{ij}(\mathbf{x})p_j - \beta_i p_i^2. \quad (2.8)$$

It can be easily seen that $\ddot{p}_i$ is bounded and hence $\dot{p}_i$ is uniformly continuous in t . Now if $p_i(t) \rightarrow 0$ as $t \rightarrow \infty$, it follows from Barbalat's lemma [28, Lemma 4.2] that $\dot{p}_i \rightarrow 0$. Therefore, from (2.8) and the fact that $-l_{ij}(\mathbf{x}) \geq 0$ and $p_i \geq 0$, it follows that $p_j(t) \rightarrow 0$ for all j such that $-l_{ij}(\mathbf{x}) \neq 0$. Using Assumption 1 and applying the above argument at each node implies $\mathbf{p}(t) \rightarrow \mathbf{0}$. $\square$

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

$$\begin{aligned} \dot{\tilde{\mathbf{p}}} &= (B - D - L(\mathbf{x}) - PB)\mathbf{p} \\ &= (B - D - L^* - P^*B)\mathbf{p}^* + (B - D - L^* - P^*B)\tilde{\mathbf{p}} \\ &\quad - \tilde{L}(\mathbf{x})\mathbf{p} - \tilde{P}B\mathbf{p} \\ &= (B - D - L^* - P^*B)\tilde{\mathbf{p}} - \tilde{L}(\mathbf{x})\mathbf{p} - \tilde{P}B\mathbf{p}. \end{aligned}$$

where $(B - D - L^* - P^*B)\mathbf{p}^* = \mathbf{0}$, as $(\mathbf{p}^*, \mathbf{x}^*)$ is an equilibrium point.

Note that $(B - D - L^* - P^*B)$ is an irreducible Metzler matrix. The Perron-Frobenius theorem for irreducible Metzler matrices [27] implies $\mu(B - D - L^* - P^*B) = 0$ and the associated eigenvector $\mathbf{p}^* \gg \mathbf{0}_n$. Also, this means there exists a positive-diagonal matrix R_2 and a positive semi-definite matrix K_2 such that

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

Similar to the proof of the fourth statement, take $V_2(\tilde{\mathbf{p}}, t) = \tilde{\mathbf{p}}^\top R_2 \tilde{\mathbf{p}} - 2nr_2 \int_0^t \|\tilde{L}\| dt$,

where $r_2 := \|R_2\|$. Then,

$$\begin{aligned}
\dot{V}_2 &= \tilde{\mathbf{p}}^\top R_2 \dot{\tilde{\mathbf{p}}} + \dot{\tilde{\mathbf{p}}}^\top R_2 \tilde{\mathbf{p}} - 2nr_2 \|\tilde{L}\| \\
&= \tilde{\mathbf{p}}^\top (R_2(B - D - L^* - P^*B) \\
&\quad + (B - D - L^* - P^*B)^\top R_2) \tilde{\mathbf{p}} \\
&\quad - 2\tilde{\mathbf{p}}^\top R_2 \tilde{L}(\mathbf{x}) \mathbf{p} - 2\tilde{\mathbf{p}}^\top R_2 \tilde{P} B \mathbf{p} - 2nr_2 \|\tilde{L}\| \\
&= -\tilde{\mathbf{p}}^\top K_2 \tilde{\mathbf{p}} - 2\tilde{\mathbf{p}}^\top R_2 \tilde{L}(\mathbf{x}) \mathbf{p} - 2\tilde{\mathbf{p}}^\top R_2 \tilde{P} B \mathbf{p} - 2nr_2 \|\tilde{L}\| \\
&\leq -\tilde{\mathbf{p}}^\top K_2 \tilde{\mathbf{p}} + 2nr_2 \|\tilde{L}\| - 2nr_2 \|\tilde{L}\| - 2\tilde{\mathbf{p}}^\top R_2 \tilde{P} B \mathbf{p} \\
&\leq -2\tilde{\mathbf{p}}^\top R_2 \tilde{P} B \mathbf{p} = -2 \sum_{i=1}^n (R_2)_i \beta_i \tilde{p}_i^2 p_i \leq 0.
\end{aligned}$$

It can be easily shown that $\ddot{V}_2$ is bounded implying $\dot{V}_2$ is uniformly continuous. Applying Barbalat's lemma [28, Lemma 4.2] gives $\dot{V}_2 \rightarrow 0$ as $t \rightarrow \infty$. Now, since R_2 and B are positive diagonal matrices this implies that $\tilde{p}_i p_i \rightarrow 0$, for each i . Using Lemma 1, and the fact that $\mathbf{p} = \mathbf{0}$ is an unstable equilibrium for $\mu(B - D - L^*) > 0$, we have $\tilde{\mathbf{p}} \rightarrow \mathbf{0}$ as long as $\mathbf{p}(0) \neq \mathbf{0}$. Stability can be established similarly to the disease-free equilibrium case. This concludes the proof of the theorem. $\square$

Corollary 1 (*Stability of disease-free equilibria*) *For the SIS epidemic model under Markovian mobility (2.1) with Assumption 1 and the disease-free equilibrium $(\mathbf{p}^*, \mathbf{x}^*) = (\mathbf{0}_n, \mathbf{v})$ the following statements hold*

- i. *a necessary condition for stability is $\delta_i > \beta_i - \nu_i$, for each $i \in \{1, \dots, n\}$;*
- ii. *a necessary condition for stability is that there exists some $i \in \{1, \dots, n\}$ such that $\delta_i \geq \beta_i$;*
- iii. *a sufficient condition for stability is $\delta_i \geq \beta_i$, for each $i \in \{1, \dots, n\}$;*
- iv. *a sufficient condition for stability is*

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

where $\mathbf{w}$ is a positive left eigenvector of L^* such that $\mathbf{w}^\top L^* = 0$ with $\max_i w_i = 1$, $m = \min_i (\delta_i - \beta_i)$, $W = \text{diag}(\mathbf{w})$, and λ_2 is the the second smallest eigenvalue of $\frac{1}{2}(WL^* + L^{*\top}W)$.

Proof: We begin by proving the first two statements. First, we note that $L_{ii}^* = \nu_i$. This can be verified by evaluating $L^* = L(\mathbf{v})$ and utilising the fact that $Q^\top \mathbf{v} = \mathbf{0}$. The necessary and sufficient condition for the stability of disease-free equilibrium is $\mu(B - D - L^*) \leq 0$. Since, $B - D - L^*$ is an irreducible Metzler matrix, a necessary condition for $\mu \leq 0$ is that its diagonal terms are strictly negative, i.e., $\beta_i - \delta_i - \nu_i < 0$, for each $i \in \{1, \dots, n\}$. This gives the statement (i).

Perron-Frobenius theorem for irreducible Metzler matrices implies that there exists a real eigenvalue equal to μ with positive eigenvector, i.e., $(B - D - L^*)\mathbf{y} = \mu\mathbf{y}$, where $\mathbf{y} \gg \mathbf{0}_n$. Since, $\mu \leq 0$, written component-wise for i^* , where $y_{i^*} = \min(y_i)$:

$$\begin{aligned} & (\beta_{i^*} - \delta_{i^*} - \nu_{i^*})y_{i^*} - \sum_{j \neq i^*} l_{ij}y_j \leq 0 \\ \Rightarrow & (\beta_{i^*} - \delta_{i^*})y_{i^*} \leq (\nu_{i^*} + \sum_{j \neq i^*} l_{ij})y_{i^*} + \sum_{j \neq i^*} l_{ij}(y_j - y_{i^*}) \\ \Rightarrow & (\beta_{i^*} - \delta_{i^*})y_{i^*} \leq \sum_{j \neq i^*} l_{ij}(y_j - y_{i^*}) \\ \Rightarrow & \beta_{i^*} - \delta_{i^*} \leq 0. \end{aligned}$$

This proves the statement (ii).

Since, L^* is a Laplacian matrix, if $\delta_i \geq \beta_i$, for each $i \in \{1, \dots, n\}$, from Gershgorin disks theorem [27], $\mu \leq 0$, which proves the third statement.

For the last statement, we use an eigenvalue bound for perturbed irreducible Laplacian matrix of a digraph [29, Theorem 6], stated below:

Let $H = L + \Delta$, where L is an $n \times n$ irreducible Laplacian matrix and $\Delta \neq 0$ is a

non-negative diagonal matrix, then

$$\operatorname{Re}(\lambda(H)) \geq \frac{\lambda_2}{\left(1 + \sqrt{1 + \frac{\lambda_2}{\sum_i w_i \Delta_i}}\right)^2 n + 1} > 0,$$

where, $\mathbf{w}$ is a positive left eigenvector of L such that $\mathbf{w}^\top L = 0$ with $\max_i w_i = 1$, $W = \operatorname{diag}(\mathbf{w})$, and λ_2 is the second smallest eigenvalue of $\frac{1}{2}(WL + L^\top W)$.

Now, in our case necessary and sufficient condition for stability of disease-free equilibrium is:

$$\begin{aligned} \operatorname{Re}(\lambda(L^* + D - B)) &= \operatorname{Re}(\lambda(L^* + \Delta + mI)) \\ &= \operatorname{Re}(\lambda(L^* + \Delta)) + m \geq 0 \end{aligned}$$

where, $m = \min_i(\delta_i - \beta_i)$ and $\Delta = D - B - mI$. Applying the eigenvalue bound with $H = L^* + \Delta$ gives the sufficient condition (iv). $\square$

Remark 2 *It can be shown that $\mathbf{v}$ is the left eigenvector associated with eigenvalue zero for both Q and L^* , i.e., $\mathbf{v}^\top Q = \mathbf{v}^\top L^* = 0$ and thus can be re-scaled to compute $\mathbf{w} = \frac{1}{\max_i(v_i)} \mathbf{v}$.* $\square$

Remark 3 *For a given graph and the associated mobility transition rates in dynamics (2.1), let $m = \min_i(\delta_i - \beta_i)$ and $i^* = \operatorname{argmin}_i(\delta_i - \beta_i)$. Then, there exist δ_i 's, $i \neq i^*$, that satisfy statement (iv) of Corollary 1 if $m > m_{\text{lower}}$, where*

$$m_{\text{lower}} = -\frac{\lambda_2}{4n + 1}.$$

$\square$

Remark 4 *(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, λ_2 is a measure of "intensity" of mobility and m 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.* $\square$

2.3 Numerical Illustrations

We start with numerical simulation of epidemic model with mobility in which we treat epidemic spread as well as mobility as stochastic processes. We take 20 simulations with same initial conditions and parameters and take the average of the results. The fraction of infected populations for different cases are shown in Fig. 2.1. We take a line graph and the mobility transition rates being equal among out going neighbors of a node. The two cases relate to the stable disease-free equilibrium and stable endemic equilibrium respectively. We have chosen heterogeneous curing or infection rates to elucidate the influence of mobility. If the curing rates, infection rates and the initial fraction of infected population is same for all the nodes, mobility does not play any role. The corresponding simulations of the deterministic model as per Proposition 1 are also shown for comparison. Figure 2.1 (a) corresponds to the case $\delta_i \geq \beta_i$ for each i , whereas Fig. 2.1 (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.

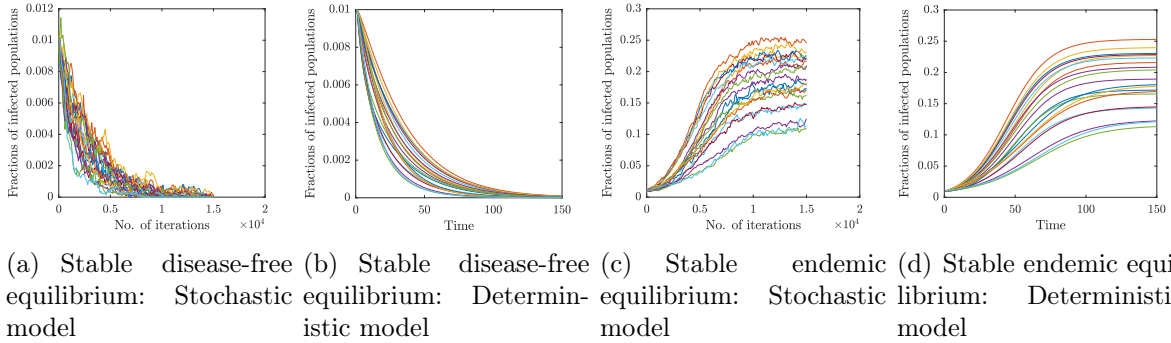


Figure 2.1: Stochastic simulation of epidemic spread under mobility. Line graph, $n = 20$, $\nu(i) = 0.2$, $q_{ij} = \frac{\nu(i)}{D_{out}}$, $p_i(0) = 0.01$. Each iteration in stochastic model corresponds to time-step 0.01 sec.

Once we have established the correctness of deterministic model predictions with the stochastic simulations, we study the simulations of deterministic model only. We study the effect of mobility over 4 different mobility graph structure - line graph, ring graph, star graph and a complete graph. First we keep the equilibrium distribution of population same for all

the four graphs 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. 2.2 shows the fractions of infected population trajectories for 20 nodes connected with 4 different graph structures. The nodes have heterogeneous curing rates and these rates are the same across different graph structures. The values of equilibrium fractions are affected by the presence of mobility and are different for different graph structures. As seen in Fig. 2.2, star graph has the widest distribution of equilibrium infected fraction values whereas complete graph has the narrowest of the four.

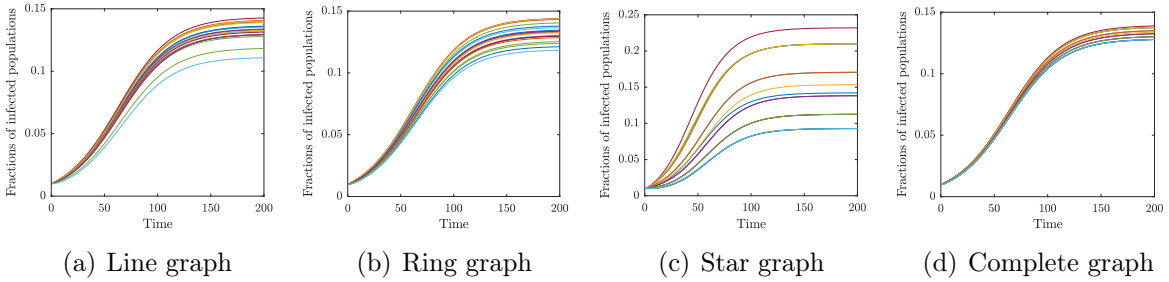


Figure 2.2: Simulation of deterministic model of epidemic spread under mobility, with same equilibrium distribution of population over 4 different graph structure with stable endemic equilibrium. $n = 20$, $p_i(0) = 0.01$.

Next, we verify the statement (iv) of Corollary 1, where one can have some curing rates δ_i less than the infection rates β_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 λ_2 . We take a given set of values of β_i . Next, we compute $m_{\text{lower}} = -\frac{\lambda_2}{4n+1}$ and take 0.8 times of this value as m in order to compute δ_i 's that satisfy statement (iv) of Corollary 1. For our case the values are: $\beta_i = 0.3$, $\lambda_2 = 0.2105$, $m_{\text{lower}} = -0.0026$, $m = 0.8 m_{\text{lower}} = -0.0021$, $\delta_1 = \delta_n = \beta_i + m$ and the rest δ_i computed to satisfy the condition which gives $\delta_1 = \delta_n = 0.2979$ and $\delta_i = 0.3198$ for $i \in \{2, \dots, n-1\}$. Fig. 2.3 shows the trajectories of infected fraction populations. As can be seen the trajectories converge to the disease-free equilibrium.

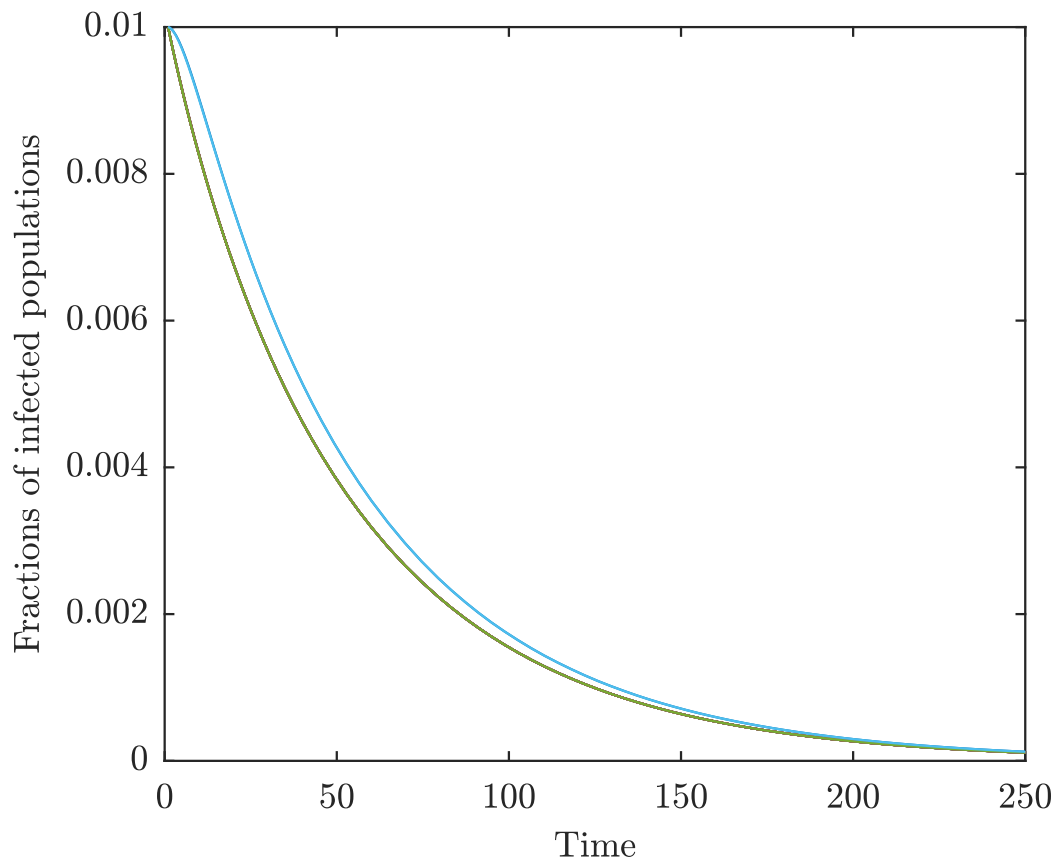


Figure 2.3: Stable disease-free equilibrium with curing rates computed as per the λ_2 sufficient condition (statement (iv), Corollary 1) for stability of disease-free equilibrium.
Graph: Complete, $n = 20$, $p_i(0) = 0.01$.

CHAPTER 3

EPIDEMIC MODELS UNDER MOBILITY ON MULTI-LAYER NETWORKS

In this chapter, we study SIS and SIR models under mobility on multi-layer networks. The presence of multi-layer arises from the presence of different mobility patterns with their own Markov chains and digraphs. We give complete characterization for existence, uniqueness and stability of equilibria. We give numerical illustrations to support our results.

3.1 SIS Model under Multi-layer Markovian Mobility

We consider n sub-population of individuals that are located in distinct spatial regions (patches). We assume the individuals within each patch can be classified into two categories: (i) susceptible, and (ii) infected. We assume that the individuals within each patch are further grouped into m classes which decide how they travel to other patches. Let the connectivity of these patches corresponding to the mobility pattern of each class $\alpha \in \{1, \dots, m\}$ be modeled by a digraph $\mathcal{G}^\alpha = (\mathcal{V}, \mathcal{E}^\alpha)$, where $\mathcal{V} = \{1, \dots, n\}$ is the node (patch) set and $\mathcal{E}^\alpha \subset \mathcal{V} \times \mathcal{V}$ is the edge set. We model the mobility of individuals on each graph $\mathcal{G}^\alpha$ using a Continuous Time Markov Chain (CTMC) with generator matrix Q^α , whose (i, j) -th entry is q_{ij}^α . The entry $q_{ij}^\alpha \geq 0$, $i \neq j$, is the instantaneous transition rate from node i to node j , and $-q_{ii}^\alpha = \nu_i^\alpha$ is the total rate of transition out of node i , i.e., $\nu_i^\alpha = \sum_{j \neq i} q_{ij}^\alpha$. Here, $q_{ij}^\alpha > 0$, if $(i, j) \in \mathcal{E}^\alpha$; and $q_{ij}^\alpha = 0$, otherwise. Let $x_i^\alpha(t)$ be the number of individuals of class α 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 α at patch i . Define $\mathbf{p}^\alpha := [p_1^\alpha, \dots, p_n^\alpha]^\top$, $\mathbf{x}^\alpha := [x_1^\alpha, \dots, x_n^\alpha]^\top$, $\mathbf{p} := [(\mathbf{p}^1)^\top, \dots, (\mathbf{p}^m)^\top]^\top$ and $\mathbf{x} := [(\mathbf{x}^1)^\top, \dots, (\mathbf{x}^m)^\top]^\top$.

We model the interaction of mobility with the epidemic process as follows. At each time t , individuals of each class α within each node move on graph $\mathcal{G}^\alpha$ according to the CTMC with generator matrix Q^α 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 $\delta_i \geq 0$ be

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

Proposition 2 (SIS model under mobility) *The dynamics of the fractions of the infected sub-population $\mathbf{p}$ and the number of individuals $\mathbf{x}^\alpha$ under multi-layer Markovian mobility model with generator matrices Q^α , and infection and recovery matrices B and D , respectively, are*

$$\dot{\mathbf{p}} = (BF(\mathbf{x}) - D - L(\mathbf{x}))\mathbf{p} - PBF(\mathbf{x})\mathbf{p} \quad (3.1a)$$

$$\dot{\mathbf{x}}^\alpha = (Q^\alpha)^\top \mathbf{x}^\alpha, \quad (3.1b)$$

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

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

$F(\mathbf{x}) := [\bar{F}^\top(\mathbf{x}), \dots, \bar{F}^\top(\mathbf{x})]^\top$ be a row-concatenated $nm \times nm$ matrix with each $n \times nm$ block-row as $\bar{F}(\mathbf{x}) := [F^1(\mathbf{x}), \dots, F^m(\mathbf{x})]$, and F^α as a diagonal matrix with entries $f_i^\alpha(\mathbf{x}) := \frac{x_i^\alpha}{\sum_\alpha x_i^\alpha}$, i.e., the fraction of total population at node i contributed by class α .

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

$$x_i^\alpha(t + h) = x_i^\alpha(t)(1 - \nu_i^\alpha h) + \sum_{j \neq i} q_{ji}^\alpha x_j^\alpha(t)h + o(h). \quad (3.2)$$

After the mobility, individuals within each node interact according to SIS dynamics. Thus, the fraction of infected population present at node i is:

$$\begin{aligned}
& x_i^\alpha(t+h)p_i^\alpha(t+h) \\
&= -x_i^\alpha(t)\delta_i p_i^\alpha(t)h + x_i^\alpha(t)\beta_i \bar{p}_i(t)(1-p_i^\alpha(t))h \\
&+ x_i^\alpha(t)p_i^\alpha(t)(1-\nu_i^\alpha h) + \sum_{j \neq i} q_{ji}^\alpha p_j^\alpha x_j^\alpha(t)h + o(h).
\end{aligned} \tag{3.3}$$

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 (3.3) 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^α from (3.2) in (3.3) and taking the limit $h \rightarrow 0^+$ gives

$$\dot{p}_i^\alpha = -\delta_i p_i^\alpha + \beta_i \bar{p}_i (1 - p_i^\alpha) - l_{ii}^\alpha p_i^\alpha - \sum_{j \neq i} l_{ij}^\alpha p_j^\alpha. \tag{3.4}$$

Writing above in vector form gives:

$$\dot{\mathbf{p}}^\alpha = (-D^\alpha - L^\alpha(\mathbf{x}^\alpha))\mathbf{p}^\alpha + B^\alpha \bar{\mathbf{F}}(\mathbf{x})\mathbf{p} - P^\alpha B^\alpha \bar{\mathbf{F}}(\mathbf{x})\mathbf{p}. \tag{3.5}$$

Similarly taking limits in (3.2) yields

$$\dot{x}_i^\alpha = -\nu_i^\alpha x_i^\alpha + \sum_{j \neq i} q_{ji}^\alpha x_j^\alpha. \tag{3.6}$$

Rewriting (3.4) and (3.6) in vector form establishes the proposition. $\square$

3.2 Analysis of SIS Model under Multi-layer Markovian Mobility

In this section, we analyze the SIS model under multi-layer mobility (3.1) under the following standard assumption:

Assumption 2 *Digraph $\mathcal{G}^\alpha$ is strongly connected, for all $\alpha \in \{1, \dots, m\}$, which is equivalent to matrices Q^α being irreducible [27].* $\square$

Let $\mathbf{v}^\alpha$ be the right eigenvector of $(Q^\alpha)^\top$ associated with eigenvalue at 0. We assume that $\mathbf{v}^\alpha$ is scaled such that its inner product with the associated left eigenvector $\mathbf{1}_n$ is unity, i.e., $\mathbf{1}_n^\top \mathbf{v}^\alpha = 1$. Define $\mathbf{v} := [N^1(\mathbf{v}^1)^\top, \dots, N^m(\mathbf{v}^m)^\top]^\top$, where N^α is the total number of individuals belonging to class α , for $\alpha \in \{1, \dots, m\}$. We call an equilibrium point $(\mathbf{p}^*, \mathbf{x}^*)$, an endemic equilibrium point, if at equilibrium the disease does not die out, i.e., $\mathbf{p}^* \neq \mathbf{0}$, otherwise, we call it a disease-free equilibrium point. Let $F^* := F(\mathbf{x}^*) = F(\mathbf{v})$ and $L^* := L(\mathbf{x}^*) = L(\mathbf{v})$. It can be verified that F^* admits the splitting, $F^* = I - M$, where I is the identity matrix of appropriate dimensions and M is a Laplacian matrix.

Theorem 2 (*Existence and Stability of Equilibria*) *For the SIS model under multi-layer Markovian mobility (3.1) with Assumption 2, the following statements hold*

- i. if $\mathbf{p}(0) \in [0, 1]^{nm}$, then $\mathbf{p}(t) \in [0, 1]^{nm}$ for all $t > 0$. Also, if $\mathbf{p}(0) > \mathbf{0}_{nm}$, then $\mathbf{p}(t) \gg \mathbf{0}_{nm}$ for all $t > 0$;
- ii. the model admits a disease-free equilibrium at $(\mathbf{p}^*, \mathbf{x}^*) = (\mathbf{0}_{nm}, \mathbf{v})$;
- iii. the model admits an endemic equilibrium at $(\mathbf{p}^*, \mathbf{x}^*) = (\bar{\mathbf{p}}, \mathbf{v})$, $\bar{\mathbf{p}} \gg \mathbf{0}$, 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 $\mathbf{p}(0) \in [0, 1]^{nm}$ such that $\mathbf{p}(0) \neq \mathbf{0}_{nm}$.

Proof: The first part of statement (i) follows from the fact that $\dot{\mathbf{p}}$ is either tangent or directed inside of the region $[0, 1]^{nm}$ at its boundary which are surfaces with $p_i^\alpha = 0$ or 1. This can be seen from (3.4). For the second part of (i), we rewrite (3.1a) as:

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

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

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

Now, the coefficient matrix of $\mathbf{y}$ above is always non-negative and strongly connected. The rest of the proof is same as in [8, Theorem 4.2 (i)].

The second statement follows by inspection.

The proof of the third statement is presented in Appendix A.2.

Stability of disease-free equilibria: To prove the fourth statement, we begin by establishing sufficient conditions for instability. The linearization of (3.1) at $(\mathbf{p}, \mathbf{x}) = (\mathbf{0}, \mathbf{v})$ is

$$\begin{bmatrix} \dot{\mathbf{p}} \\ \dot{\mathbf{x}} \end{bmatrix} = \begin{bmatrix} BF^* - D - L^* & 0 \\ 0 & Q^\top \end{bmatrix} \begin{bmatrix} \mathbf{p} \\ \mathbf{x} \end{bmatrix}. \quad (3.7)$$

Since the system matrix in (3.7) is block-diagonal, its eigenvalues are the eigenvalues of the block-diagonal sub-matrices. Further, since radial abscissa $\mu(Q^\top)$ 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 2, $(BF^* - D - L^*)$ is an irreducible Metzler matrix. Together with $\mu(BF^* - D - L^*) \leq 0$, implies there exists a positive diagonal matrix R such that

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

where K is a positive semi-definite matrix [10, Proposition 1 (iv), Lemma A.1]. Define $\tilde{L} := L(\mathbf{x}) - L^*$, $\tilde{F} := F(\mathbf{x}) - F^*$ and $r := \|R\|$, where $\|\cdot\|$ denotes the induced two norm of the matrix.

Since $\mathbf{x}(0) \gg 0$, under Assumption 2, $x_i^\alpha(t)$ is lower bounded by some positive constant and hence, $\tilde{L}$ and $\tilde{F}$ are bounded and continuously differentiable. Since $\mathbf{x}$ is bounded and exponentially converges to $\mathbf{x}^*$, it follows that $\|\tilde{L}(\mathbf{x})\|$ and $\|\tilde{F}(\mathbf{x})\|$ locally exponentially converge to 0 and $\int_0^t \|\tilde{L}\|dt$ and $\int_0^t \|\tilde{F}\|dt$ are bounded for all $t > 0$.

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

$$\begin{aligned}
\dot{V} &= 2\mathbf{p}^\top R \dot{\mathbf{p}} - 2nmr(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&= \mathbf{p}^\top (R(BF^* - D - L^*) + (BF^* - D - L^*)^\top R) \mathbf{p} \\
&\quad + 2\mathbf{p}^\top R(B\tilde{F} - \tilde{L})\mathbf{p} - 2\mathbf{p}^\top RPBF\mathbf{p} \\
&\quad - 2nmr(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&= -\mathbf{p}^\top K\mathbf{p} + 2\mathbf{p}^\top R(B\tilde{F} - \tilde{L})\mathbf{p} - 2\mathbf{p}^\top RPBF\mathbf{p} \\
&\quad - 2nmr(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&\leq -\mathbf{p}^\top K\mathbf{p} + 2nmr(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&\quad - 2nmr(B\|\tilde{F}\| + \|\tilde{L}\|) - 2\mathbf{p}^\top RPBF\mathbf{p} \\
&\leq -2\mathbf{p}^\top RPBF\mathbf{p} \leq 0.
\end{aligned} \tag{3.8}$$

Since all the signals and their derivatives are bounded, it follows that $\ddot{V}(t)$ is bounded and hence $\dot{V}$ is uniformly continuous in t . Therefore from Barbalat's lemma and its application to Lyapunov-like functions [28, Lemma 4.3, Chapter 4] it follows that $\dot{V} \rightarrow 0$ as $t \rightarrow \infty$. Consequently, from (3.8), $\mathbf{p}^\top RPBF\mathbf{p} \rightarrow 0$. Since $R > 0$, $B > 0$, $F \geq 0$ with $F_{kk} > 0$ and $p_k \geq 0$, $\mathbf{p}(t) \rightarrow \mathbf{0}$ as $t \rightarrow \infty$. This establishes global attractivity of the disease-free equilibrium point. We now establish its stability.

We note that since, for $\mathbf{x} \gg 0$, $(B\|\tilde{F}\| + \|\tilde{L}\|)$ is a real analytic function of $\mathbf{x}$, $\exists$ a region $\|\mathbf{x} - \mathbf{x}^*\| < \delta_1$ in which $(B\|\tilde{F}\| + \|\tilde{L}\|) \leq k_1\|\mathbf{x} - \mathbf{x}^*\|$ for some $k_1 > 0$. Also, since $\mathbf{x} - \mathbf{x}^*$ is globally exponentially stable, $\|\mathbf{x}(t) - \mathbf{x}^*\| \leq k_2 e^{-\alpha t} \|\mathbf{x}(0) - \mathbf{x}^*\|$ for $k_2, \alpha > 0$. Thus, if $\|\mathbf{x}(0) - \mathbf{x}^*\| < \frac{\delta_1}{k_2}$, then $(B\|\tilde{F}\| + \|\tilde{L}\|) \leq k_1 k_2 e^{-\alpha t} \|\mathbf{x}(0) - \mathbf{x}^*\|$. This implies

$\int_0^t (B\|\tilde{F}\| + \|\tilde{L}\|)dt \leq \frac{k}{\alpha}\|\mathbf{x}(0) - \mathbf{x}^*\|$, where $k := k_1 k_2$. Now, since $\dot{V}(\mathbf{p}, t) \leq 0$,

$$\begin{aligned} V(\mathbf{p}(0), 0) &= \mathbf{p}(0)^\top R \mathbf{p}(0) \\ &\geq V(\mathbf{p}(t), t) \\ &\geq \mathbf{p}(t)^\top R \mathbf{p}(t) - 2 \frac{nmrk\|\mathbf{x}(0) - \mathbf{x}^*\|}{\alpha} \\ &\geq R_{\min}\|\mathbf{p}(t)\|^2 - 2 \frac{nmrk\|\mathbf{x}(0) - \mathbf{x}^*\|}{\alpha}, \end{aligned}$$

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

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

It follows using stability of $\mathbf{x}$ dynamics, that for any $\epsilon > 0$, there exists $\delta > 0$, such that $\|\mathbf{x}(0) - \mathbf{x}^*\|^2 + \|\mathbf{p}(0)\|^2 \leq \delta^2 \Rightarrow \|\mathbf{p}(t)\|^2 + \|\mathbf{x}(t) - \mathbf{x}^*\|^2 \leq \epsilon^2$. 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 2 *For the dynamics (3.1a), if $p_i^\alpha(t) \rightarrow 0$ as $t \rightarrow \infty$, for some $i \in \{1, \dots, n\}$ and $\alpha \in \{1, \dots, m\}$, then $\mathbf{p}(t) \rightarrow \mathbf{0}$ as $t \rightarrow \infty$.*

Proof: It can be easily seen from (3.4) that $\dot{p}_i^\alpha$ is bounded and hence $\dot{p}_i^\alpha$ is uniformly continuous in t . Now if $p_i^\alpha(t) \rightarrow 0$ as $t \rightarrow \infty$, it follows from Barbalat's lemma [28, Lemma 4.2] that $\dot{p}_i^\alpha \rightarrow 0$. Therefore, from (3.4) and the fact that $-l_{ij}^\alpha(\mathbf{x}) \geq 0$ and $p_i^\alpha \geq 0$, it follows that $p_j^\alpha(t) \rightarrow 0$ for all j such that $-l_{ij}^\alpha(\mathbf{x}) \neq 0$. Using Assumption 2 and applying the above argument for each class at each node implies $\mathbf{p}(t) \rightarrow \mathbf{0}$. $\square$

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

$$\begin{aligned}
\dot{\tilde{\mathbf{p}}} &= (BF - D - L - PBF)\mathbf{p} \\
&= (BF^* - D - L^* - P^*BF^*)\mathbf{p}^* \\
&\quad + (BF^* - D - L^* - P^*BF^*)\tilde{\mathbf{p}} \\
&\quad + (B\tilde{F} - \tilde{L})\mathbf{p} - PB\tilde{F}\mathbf{p} - \tilde{P}BF^*\mathbf{p} \\
&= ((I - P^*)BF^* - D - L^*)\tilde{\mathbf{p}} + ((I - P)B\tilde{F} - \tilde{L})\mathbf{p} \\
&\quad - \tilde{P}BF^*\mathbf{p}.
\end{aligned}$$

where we have used $(BF^* - D - L^* - P^*BF^*)\mathbf{p}^* = \mathbf{0}$, as $(\mathbf{p}^*, \mathbf{x}^*)$ is an equilibrium point.

Note that $(BF^* - D - L^* - P^*BF^*) = ((I - P^*)BF^* - D - L^*)$ is an irreducible Metzler matrix and $\mathbf{p}^* \gg 0$ 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

$$\begin{aligned}
&R_2((I - P^*)BF^* - D - L^*) \\
&\quad + ((I - P^*)BF^* - D - L^*)^\top R_2 = -K_2.
\end{aligned}$$

Similar to the proof of the fourth statement, take $V_2(\tilde{\mathbf{p}}, t) = \tilde{\mathbf{p}}^\top R_2 \tilde{\mathbf{p}} - 2nmr_2 \int_0^t (B\|\tilde{F}\| +$

$\|\tilde{L}\|)dt$, where $r_2 := \|R_2\|$. Then,

$$\begin{aligned}
\dot{V}_2 &= 2\tilde{\mathbf{p}}^\top R_2 \dot{\tilde{\mathbf{p}}} - 2nmr_2(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&= \tilde{\mathbf{p}}^\top (R_2((I - P^*)BF^* - D - L^*) \\
&\quad + ((I - P^*)BF^* - D - L^*)^\top R_2)\tilde{\mathbf{p}} \\
&\quad + 2\tilde{\mathbf{p}}^\top R_2((I - P)B\tilde{F} - \tilde{L})\mathbf{p} - 2\tilde{\mathbf{p}}^\top R_2\tilde{P}BF^*\mathbf{p} \\
&\quad - 2nmr_2(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&= -\tilde{\mathbf{p}}^\top K_2\tilde{\mathbf{p}} + 2\tilde{\mathbf{p}}^\top R_2((I - P)B\tilde{F} - \tilde{L})\mathbf{p} \\
&\quad - 2\tilde{\mathbf{p}}^\top R_2\tilde{P}BF^*\mathbf{p} - 2nmr_2(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&\leq -\tilde{\mathbf{p}}^\top K_2\tilde{\mathbf{p}} + 2nmr_2(B\|\tilde{F}\| + \|\tilde{L}\|) \\
&\quad - 2nmr_2(B\|\tilde{F}\| + \|\tilde{L}\|) - 2\tilde{\mathbf{p}}^\top R_2\tilde{P}BF^*\mathbf{p} \\
&\leq -2\tilde{\mathbf{p}}^\top R_2\tilde{P}BF^*\mathbf{p} \\
&\leq -2 \sum_{k=1}^{nm} (R_2)_k \beta_k F_{kk}^* \tilde{p}_k^2 p_k \leq 0.
\end{aligned}$$

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 $\ddot{V}_2$ is bounded implying $\dot{V}_2$ is uniformly continuous. Applying Barbalat's lemma [28, Lemma 4.2] gives $\dot{V}_2 \rightarrow 0$ as $t \rightarrow \infty$. This implies that $\tilde{p}_k p_k \rightarrow 0$. Using Lemma 2, and the fact that $\mathbf{p} = \mathbf{0}$ is an unstable equilibrium for $\mu(BF^* - D - L^*) > 0$, we have $\tilde{\mathbf{p}} \rightarrow \mathbf{0}$ as long as $\mathbf{p}(0) \neq \mathbf{0}$. Stability can be established similarly to the disease-free equilibrium case. This concludes the proof of the theorem. $\square$

Corollary 2 (*Stability of disease-free equilibria*) *For the SIS epidemic model under Multi-layer Markovian mobility (3.1) with Assumption 2 and the disease-free equilibrium $(\mathbf{p}^*, \mathbf{x}^*) = (\mathbf{0}, \mathbf{v})$ the following statements hold*

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

ii. a necessary condition for stability is that there exists some $i \in \{1, \dots, n\}$ such that

$$\delta_i \geq \beta_i;$$

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

iv. a sufficient condition for stability is

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

where $\mathbf{w}$ is a positive left eigenvector of $(BM + L^*)$ such that $\mathbf{w}^\top (BM + L^*) = 0$ with $\max_i w_i = 1$, $s = \min_i (\delta_i - \beta_i)$, $W = \text{diag}(\mathbf{w})$, and λ_2 is the second smallest eigenvalue of $\frac{1}{2}(W(BM + L^*) + (BM + L^*)^\top W)$.

Proof: We begin by proving the first two statements. First, we note that $(L^\alpha)_{ii}^* = \nu_i^\alpha$. This can be verified by evaluating $L^* = L(\mathbf{v})$ and utilising the fact that $Q^\top \mathbf{v} = \mathbf{0}$. 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 μ with positive eigenvector, i.e., $(BF^* - D - L^*)\mathbf{y} = \mu\mathbf{y}$, where $\mathbf{y} \gg \mathbf{0}$. Rename components of $\mathbf{y}$ as $y_{(n\alpha+i)} = y_i^\alpha$ to write $\mathbf{y} = [(\mathbf{y}^1)^\top, \dots, (\mathbf{y}^m)^\top]^\top$.

Let for each $i \in \{1, \dots, n\}$, $y_i^{k_i} = \min\{y_i^1, \dots, y_i^m\}$. Since $\mu \leq 0$, written component-wise

for $(nk_i + i)$ -th component

$$\begin{aligned}
& \sum_{\alpha} \beta_i f_i^{*\alpha} y_i^{\alpha} - (\delta_i + \nu_i^{k_i}) y_i^{k_i} - \sum_{j \neq i} l_{ij}^{*k_i} y_j^{k_i} \leq 0 \\
& \Rightarrow \sum_{\alpha} \beta_i f_i^{*\alpha} y_i^{k_i} + \sum_{\alpha} \beta_i f_i^{*\alpha} (y_i^{\alpha} - y_i^{k_i}) - (\delta_i + \nu_i^{k_i}) y_i^{k_i} \\
& \quad - \sum_{j \neq i} l_{ij}^{*k_i} y_j^{k_i} \leq 0 \\
& \Rightarrow (\beta_i - \delta_i - \nu_i^{k_i}) y_i^{k_i} \leq - \sum_{\alpha} \beta_i f_i^{*\alpha} (y_i^{\alpha} - y_i^{k_i}) + \sum_{j \neq i} l_{ij}^{*k_i} y_j^{k_i} \\
& \Rightarrow (\beta_i - \delta_i - \nu_i^{k_i}) y_i^{k_i} < 0 \\
& \Rightarrow \beta_i - \delta_i - \nu_i^{k_i} < 0.
\end{aligned}$$

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 $j \in \{1, \dots, n\}$ such that $l_{ij}^{*k_i} < 0$. This proves the statement (i).

Let $y_i^{k_i}$ be $\min\{y_1^1, \dots, y_n^m\}$. Similar to the proof of the first statement

$$\begin{aligned}
& \sum_{\alpha} \beta_i f_i^{*\alpha} y_i^{\alpha} - (\delta_i + \nu_i^{k_i}) y_i^{k_i} - \sum_{j \neq i} l_{ij}^{*k_i} y_j^{k_i} \leq 0 \\
& \Rightarrow \sum_{\alpha} \beta_i f_i^{*\alpha} y_i^{k_i} + \sum_{\alpha} \beta_i f_i^{*\alpha} (y_i^{\alpha} - y_i^{k_i}) - (\delta_i + \nu_i^{k_i}) y_i^{k_i} \\
& \quad - \sum_{j \neq i} l_{ij}^{*k_i} y_i^{k_i} - \sum_{j \neq i} l_{ij}^{*k_i} (y_j^{k_i} - y_i^{k_i}) \leq 0 \\
& \Rightarrow (\beta_i - \delta_i) y_i^{k_i} \leq - \sum_{\alpha} \beta_i f_i^{*\alpha} (y_i^{\alpha} - y_i^{k_i}) + \sum_{j \neq i} l_{ij}^{*k_i} (y_j^{k_i} - y_i^{k_i}) \\
& \Rightarrow (\beta_i - \delta_i) y_i^{k_i} \leq 0 \\
& \Rightarrow \beta_i - \delta_i \leq 0.
\end{aligned}$$

Here we have used an additional fact: $\nu_i^{k_i} + \sum_{j \neq i} l_{ij}^{*k_i} = 0$. This proves statement (ii).

Let $F^* = I - M$ where M is a Laplacian matrix which can be seen from the definition of F . Now $BF^* - D - L^* = B - D - (BM + L^*)$. Since $(BM + L^*)$ is an irreducible Laplacian

matrix, if $\delta_i \geq \beta_i$, for each $i \in \{1, \dots, n\}$, from Gershgorin disks theorem [27], $\mu \leq 0$, which proves the third statement.

For the last statement, we use an eigenvalue bound for perturbed irreducible Laplacian matrix of a digraph [29, Theorem 6], stated below:

Let $H = A + \Delta$, where A is an $n \times n$ irreducible Laplacian matrix and $\Delta \neq 0$ is a non-negative diagonal matrix, then

$$\operatorname{Re}(\lambda(H)) \geq \frac{\lambda_2}{\left(1 + \sqrt{1 + \frac{\lambda_2}{\sum_i w_i \Delta_i}}\right)^2 n + 1} > 0,$$

where, $\mathbf{w}$ is a positive left eigenvector of A such that $\mathbf{w}^\top A = 0$ with $\max_i w_i = 1$, $W = \operatorname{diag}(\mathbf{w})$, and λ_2 is the second smallest eigenvalue of $\frac{1}{2}(WA + A^\top W)$.

Now, in our case necessary and sufficient condition for stability of disease-free equilibrium is:

$$\begin{aligned} \operatorname{Re}(\lambda(BM + L^* + D - B)) &= \operatorname{Re}(\lambda(BM + L^* + \Delta + sI)) \\ &= \operatorname{Re}(\lambda(BM + L^* + \Delta)) + s \\ &\geq 0, \end{aligned}$$

where, $s = \min_i(\delta_i - \beta_i)$ and $\Delta = D - B - sI$. Applying the eigenvalue bound with $H = BM + L^* + \Delta$ gives the sufficient condition (iv). $\square$

Remark 5 For given graphs and the associated mobility transition rates in dynamics (3.1), let $s = \min_i(\delta_i - \beta_i)$ and $i^* = \operatorname{argmin}_i(\delta_i - \beta_i)$. Then, there exist δ_i 's, $i \neq i^*$, that satisfy statement (iv) of Corollary 3 if $s > s_{\text{lower}}$, where

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

$\square$

Remark 6 (*Influence of mobility on stability of disease-free equilibrium.*) The statement (iv) of Corollary 3 characterizes the influence of mobility on the stability of disease-free equilibria. In particular, λ_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. $\square$

3.3 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. 3.1. The corresponding simulations of the deterministic model as per Proposition 2 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 3.1 (a) corresponds to the case $\delta_i \geq \beta_i$ for each i , whereas Fig. 3.1 (c) corresponds to the case $\delta_i < \beta_i$ for each i . The results support statements (iii) and (ii) of Corollary 3 and lead to, respectively, the stable disease-free equilibrium and the stable endemic equilibrium.

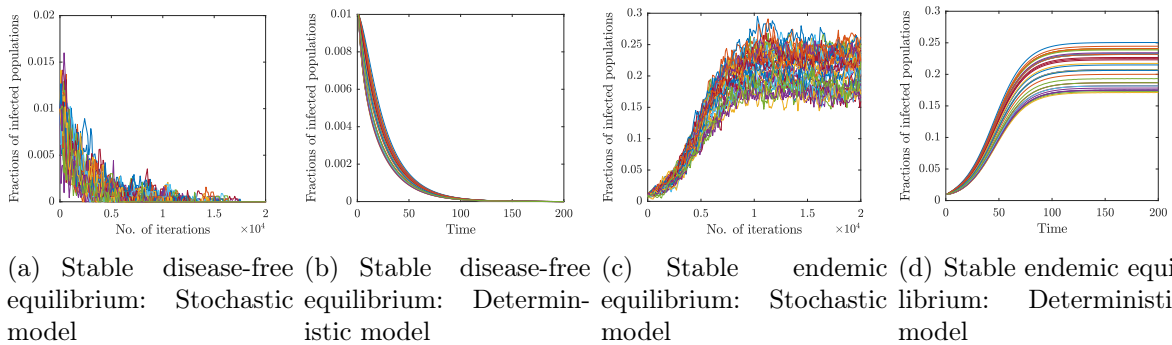


Figure 3.1: Stochastic simulation of epidemic spread under mobility. Complete-Line graphs, $n = 20$, $\nu(i) = 0.2$, $q_{ij} = \frac{\nu(i)}{D_{out}}$, $p_i(0) = 0.01$. Each iteration in stochastic model corresponds to time-step 0.01 sec.

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. 3.2 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.

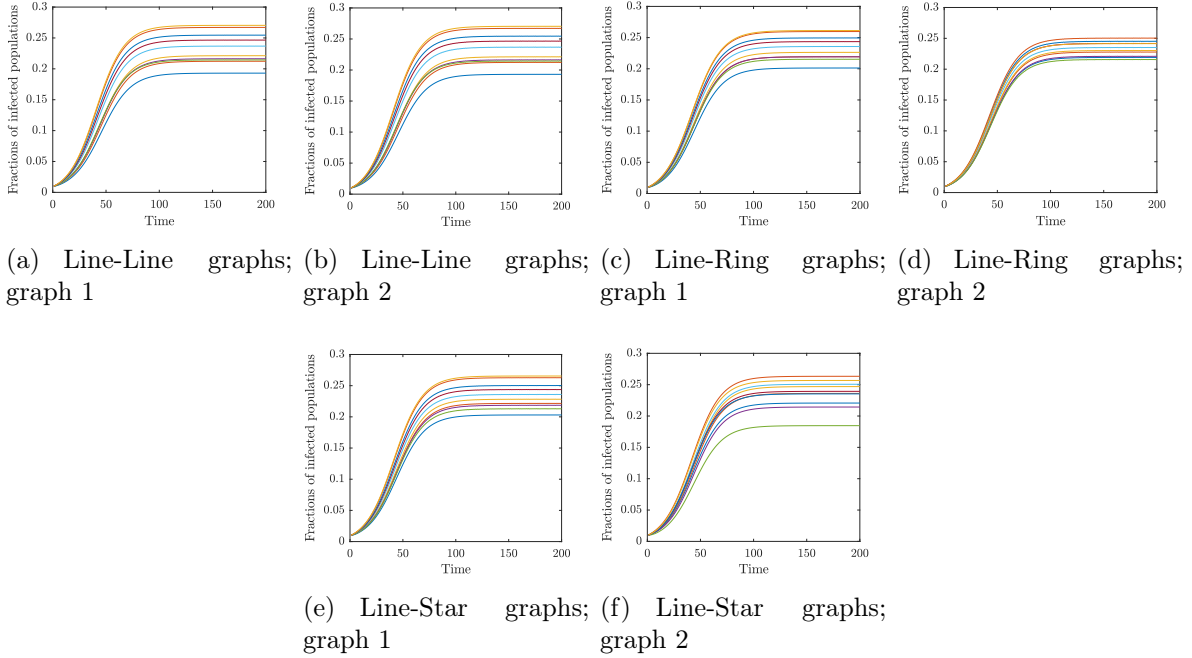


Figure 3.2: Simulation of deterministic model of epidemic spread under 2 layer mobility, over different graph structure with stable endemic equilibrium. $n = 10$, $p_i(0) = 0.01$.

3.4 SIR Model under Multi-layer Markovian Mobility

We consider n sub-populations of individuals that are located in distinct spatial regions (patches). We assume that the individuals within each patch can be classified into three categories: (i) susceptible, (ii) infected and (iii) recovered. Additionally, we assume that these individuals are further grouped into m classes depending on how they travel to other patches. Let the connectivity of these patches corresponding to the mobility pattern of each class $\alpha \in \{1, \dots, m\}$ be modeled by a digraph $\mathcal{G}^\alpha = (\mathcal{V}, \mathcal{E}^\alpha)$, where $\mathcal{V} = \{1, \dots, n\}$ is the node (patch) set and $\mathcal{E}^\alpha \subset \mathcal{V} \times \mathcal{V}$ is the edge set. We model the mobility of individuals on each graph $\mathcal{G}^\alpha$ using a Continuous Time Markov Chain (CTMC) with generator matrix Q^α , whose (i, j) -th entry is q_{ij}^α . The entry $q_{ij}^\alpha \geq 0$, $i \neq j$, is the instantaneous transition rate from node i to node j , and $-q_{ii}^\alpha = \nu_i^\alpha$ is the total rate of transition out of node i , i.e., $\nu_i^\alpha = \sum_{j \neq i} q_{ij}^\alpha$. Here, $q_{ij}^\alpha > 0$, if $(i, j) \in \mathcal{E}^\alpha$; and $q_{ij}^\alpha = 0$, otherwise. Let $x_i^\alpha(t)$ be the number of individuals of class α in patch i at time t . Let $p_i^\alpha \in [0, 1]$ (respectively, $s_i^\alpha \in [0, 1]$) be the fraction of infected (respectively, susceptible) individuals within individuals of class α at patch i . Define $\mathbf{p}^\alpha := [p_1^\alpha, \dots, p_n^\alpha]^\top$, $\mathbf{s}^\alpha := [s_1^\alpha, \dots, s_n^\alpha]^\top$, $\mathbf{x}^\alpha := [x_1^\alpha, \dots, x_n^\alpha]^\top$, $\mathbf{p} := [(\mathbf{p}^1)^\top, \dots, (\mathbf{p}^m)^\top]^\top$, $\mathbf{s} := [(\mathbf{s}^1)^\top, \dots, (\mathbf{s}^m)^\top]^\top$ and $\mathbf{x} := [(\mathbf{x}^1)^\top, \dots, (\mathbf{x}^m)^\top]^\top$.

For the epidemic process at node i , let $\beta_i > 0$ and $\delta_i \geq 0$ be the infection and recovery rate, respectively. We let $B^\alpha > 0$ and $D^\alpha \geq 0$ be the positive and non-negative diagonal matrices with entries β_i and δ_i , $i \in \{1, \dots, n\}$, respectively. Let B and D be the positive and non-negative diagonal matrices with block-diagonal entries B^α and D^α , $\alpha \in \{1, \dots, m\}$, respectively. Let $P^\alpha := \text{diag}(\mathbf{p}^\alpha)$, $P := \text{diag}(\mathbf{p})$ and $S := \text{diag}(\mathbf{s})$. We now derive the continuous time dynamics that captures the interaction of mobility and the SIR epidemic dynamics.

Proposition 3 (*SIR model under mobility*) *The*

dynamic model for SIR epidemic process with multi-layer Markovian mobility is

$$\dot{\mathbf{s}} = -SBF(\mathbf{x})\mathbf{p} - L(\mathbf{x})\mathbf{s} \quad (3.9a)$$

$$\dot{\mathbf{p}} = (SBF(\mathbf{x}) - D - L(\mathbf{x}))\mathbf{p} \quad (3.9b)$$

$$\dot{\mathbf{x}}^\alpha = (Q^\alpha)^\top \mathbf{x}^\alpha, \quad (3.9c)$$

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

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

$F(\mathbf{x}) := [\bar{F}^\top(\mathbf{x}), \dots, \bar{F}^\top(\mathbf{x})]^\top$ be a row-concatenated $nm \times nm$ matrix with each $n \times nm$ block-row as $\bar{F}(\mathbf{x}) := [F^1(\mathbf{x}), \dots, F^m(\mathbf{x})]$, and F^α as a diagonal matrix with entries $f_i^\alpha(\mathbf{x}) := \frac{x_i^\alpha}{\sum_\alpha x_i^\alpha}$, i.e., the fraction of total population at node i contributed by class α .

Proof: The proof follows similarly to that in Proposition 2. $\square$

We analyze the SIR model under multi-layer mobility (3.9) under the strongly connected assumption: Assumption 2 as well as following standard assumption:

Assumption 3 *There exists a node k such that $\delta_k > 0$.* $\square$

Let $\mathbf{v}^\alpha$ be the right eigenvector of $(Q^\alpha)^\top$ associated with eigenvalue at 0. We assume that $\mathbf{v}^\alpha$ is scaled such that its inner product with the associated left eigenvector $\mathbf{1}_n$ is unity, i.e., $\mathbf{1}_n^\top \mathbf{v}^\alpha = 1$. Define $\mathbf{v} := [N^1(\mathbf{v}^1)^\top, \dots, N^m(\mathbf{v}^m)^\top]^\top$, where N^α is the total number of individuals belonging to class α , for $\alpha \in \{1, \dots, m\}$.

Theorem 3 (*Existence and properties of equilibria*) *For the SIR model with multi-layer Markovian mobility (3.9) under Assumptions 2 and 3, the following statements hold*

i. if $\mathbf{p}(0)$ and $\mathbf{s}(0) \in [0, 1]^{nm}$, then $\mathbf{p}(t)$ and $\mathbf{s}(t) \in [0, 1]^{nm}$ for all $t > 0$;

ii. if $\mathbf{p}(0) > 0$ and $\mathbf{s}^\alpha(0) > 0$ for each α , then $\mathbf{p}(t) \gg 0$ and $\mathbf{s}(t) \gg 0$ for all $t > 0$;

iii. the equilibrium points $(\mathbf{p}^*, \mathbf{s}^*, \mathbf{x}^*)$ belong to the set

$$\{(\mathbf{0}, [k_1 \mathbf{1}_n^\top, k_2 \mathbf{1}_n^\top, \dots, k_m \mathbf{1}_n^\top]^\top, \mathbf{v}) \mid k_1, k_2, \dots, k_m \in \mathbb{R}_{\geq 0}\};$$

iv. the set of equilibria

$\{(\mathbf{0}, [k_1 \mathbf{1}_n^\top, k_2 \mathbf{1}_n^\top, \dots, k_m \mathbf{1}_n^\top]^\top, \mathbf{v}) \mid k_1, k_2, \dots, k_m \in \mathbb{R}_{\geq 0}\}$ is globally asymptotically attractive.

Proof: (i) and (ii) follow similarly to the proof in Theorem 2. Define $L^* := L(\mathbf{x}^*)$, $S^* := \text{diag}(\mathbf{s}^*)$ and $F^* := F(\mathbf{x}^*)$. To establish statement (iii), premultiply (3.9a) and (3.9b) with $\mathbf{x}^{*\top}$ at equilibrium

$$-\mathbf{x}^{*\top} S^* B F^* \mathbf{p}^* = 0 \quad (3.10a)$$

$$\mathbf{x}^{*\top} S^* B F^* \mathbf{p}^* - \mathbf{x}^{*\top} D \mathbf{p}^* = 0. \quad (3.10b)$$

Here, we have used the fact that $\mathbf{x}^{*\top} L^* = 0$, which can be seen from the fact that $\mathbf{x}^\top L(\mathbf{x}) = \mathbf{x}^\top Q$. Also, since $\mathbf{x}^* \gg \mathbf{0}$ and $S^* B F^* \mathbf{p}^* \geq \mathbf{0}, D \mathbf{p}^* \geq \mathbf{0}$, (3.10) yields

$$S^* B F^* \mathbf{p}^* = 0 \quad (3.11a)$$

$$D \mathbf{p}^* = 0. \quad (3.11b)$$

Using Assumption 3 in (3.11b) implies $p_k^{*\alpha} = 0$ for each α at node k with $\delta_k > 0$. Using (3.11) in (3.9b) at equilibrium gives $L^* \mathbf{p}^* = \mathbf{0}$ or equivalently $L^{*\alpha} \mathbf{p}^{*\alpha} = \mathbf{0}$ for each α . Therefore under strong connectivity assumption of each layer (Assumption 2) $\mathbf{p}^* = \mathbf{0}$. Further using (3.11a) in (3.9a) at equilibrium yields $L^* \mathbf{s}^* = \mathbf{0}$, or equivalently $L^{*\alpha} \mathbf{s}^{*\alpha} = \mathbf{0}$ which gives: $\mathbf{s}^{*\alpha} = k_\alpha \mathbf{1}_n$ for each α . This proves statement (iii).

For statement (iv), consider a Lyapunov candidate function $V_3 = \mathbf{x}^\top (2\mathbf{s} + \mathbf{p})$. It follows

that

$$\begin{aligned}
\dot{V}_3 &= \mathbf{x}^\top (-2SBF\mathbf{p} - 2L\mathbf{s} + SBF\mathbf{p} - D\mathbf{p} - L\mathbf{p}) \\
&\quad + \mathbf{x}^\top Q(2\mathbf{s} + \mathbf{p}) \\
&= \mathbf{x}^\top (-SBF\mathbf{p} - D\mathbf{p}) \\
&\leq 0.
\end{aligned}$$

Now, using LaSalle's invariance theorem [31, Theorem 4.4], all trajectory asymptotically goes to the largest invariant set with $\dot{V}_3 = 0$. This further implies all trajectory asymptotically goes to an invariant set with $D\mathbf{p} = 0$ and $SBF\mathbf{p} = 0$. Using this fact in (3.9b) at equilibrium expanded for each mobility layer under Assumptions 2 and 3 implies $\mathbf{p}^* = \mathbf{0}$ is globally attractive.

Next consider a Lyapunov candidate function $V_4 = \mathbf{s}^\top X^* \mathbf{s} - 2nmr \int_0^t (\|\tilde{L}\|) dt$ with $X^* := \text{diag}(\mathbf{x}^*)$ and $r := \|X^*\|$. Then,

$$\begin{aligned}
\dot{V}_4 &= 2\mathbf{s}^\top X^* \dot{\mathbf{s}} - 2nmr(\|\tilde{L}\|) \\
&= -2\mathbf{s}^\top X^* BFS\mathbf{p} + \mathbf{s}^\top (X^*(-L) + (-L)^\top X^*)\mathbf{s} \\
&\quad - 2nmr(\|\tilde{L}\|) \\
&= -2\mathbf{s}^\top X^* BFS\mathbf{p} - \mathbf{s}^\top (X^*(L^*) + (L^*)^\top X^*)\mathbf{s} \\
&\quad - \mathbf{s}^\top (X^*(\tilde{L}) + (\tilde{L})^\top X^*)\mathbf{s} - 2nmr(\|\tilde{L}\|) \\
&\leq -2\mathbf{s}^\top X^* BFS\mathbf{p} - \mathbf{s}^\top (X^*(L^*) + (L^*)^\top X^*)\mathbf{s} \\
&\quad + 2nmr(\|\tilde{L}\|) - 2nmr(\|\tilde{L}\|) \\
&\leq -2\mathbf{s}^\top X^* BFS\mathbf{p} - \mathbf{s}^\top (X^*(L^*) + (L^*)^\top X^*)\mathbf{s} \\
&\leq -\mathbf{s}^\top (X^*(L^*) + (L^*)^\top X^*)\mathbf{s} \leq 0.
\end{aligned}$$

The last inequality follows as the matrix $X^*(L^*) + (L^*)^\top X^*$ is a symmetric Laplacian and hence a symmetric positive semi-definite matrix. To see this, note that $(X^*(L^*) + (L^*)^\top X^*)\mathbf{1} = X^*(L^*)\mathbf{1} + (L^*)^\top X^*\mathbf{1} = \mathbf{0} + (L^*)^\top \mathbf{x}^* = \mathbf{0}$. Additionally, this matrix is a block

diagonal matrix with block elements as strongly connected symmetric Laplacian matrices. Using Barbalat's lemma, we get $\dot{V}_4 \rightarrow 0$. This in turn leads to $\mathbf{s} \rightarrow [k_1 \mathbf{1}_n^\top, k_2 \mathbf{1}_n^\top, \dots, k_m \mathbf{1}_n^\top]^\top$. This proves statement (iv). $\square$

An epidemic outbreak is an event in which the total number of infected individuals in the system (summed over all the layers and nodes) increase before eventually reaching a disease-free state. As evident from Theorem 3, the total number of infected individuals ultimately goes to zero. The epidemic outbreak is characterized by the increase in the size of the infected population in the early phase of the transient response.

Define $s_{\max}(t)$ as the greatest element in $\mathbf{s}(t)$ taken over all layers and nodes.

Corollary 3 (*Epidemic outbreak*) *For the SIR epidemic model under multi-layer Markovian mobility (3.9) under Assumption 2, the following statements hold*

- i. For a single layer network, if $s_{\max}(0)B - D \leq 0$ then there is no epidemic outbreak and total infected population monotonically decreases to zero;*
- ii. If $S(0)BF(0) - D > 0$, then there is an epidemic outbreak at $t = 0$.*

Proof: Using (3.9b), we first write the expression for the rate of change of total infected population for the system, $N_I = \mathbf{x}^\top \mathbf{p}$:

$$\begin{aligned}
\dot{N}_I &= \mathbf{x}^\top \dot{\mathbf{p}} + \dot{\mathbf{x}}^\top \mathbf{p} \\
&= \mathbf{x}^\top (SBF(\mathbf{x}) - D - L(\mathbf{x}))\mathbf{p} + \mathbf{x}^\top Q\mathbf{p} \\
&= \mathbf{x}^\top (SBF(\mathbf{x}) - D)\mathbf{p}
\end{aligned} \tag{3.12}$$

where (3.12) follows using $\mathbf{x}^\top L(\mathbf{x}) = \mathbf{x}^\top Q$, a consequence of definitions of matrices $L(\mathbf{x})$ and Q . It can be shown from (3.9a) that $s_{\max}(t)$ monotonically decreases with time. This is a consequence of negative first term and negative Laplacian second term in the right hand side of (3.9a). Now, for the special case of a single layer network $F(\mathbf{x}) = I$, therefore in the right hand side of (3.12), we can see that $SB - D \leq s_{\max}(t)B - D \leq s_{\max}(0)B - D$. Further,

since $\mathbf{x}$ and $\mathbf{p}$ are non-negative, if $s_{\max}(0)B - D \leq 0$, then for a single layer network the right hand side of (3.12) is non-positive and hence N_I monotonically decreases. This proves statement (i).

Statement (ii) follows by evaluating $SBF - D$ at $t = 0$ and making it positive to make right side of (3.12) positive at $t = 0$ and hence N_I increases at $t = 0$ giving rise to an initial outbreak. $\square$

3.5 Numerical Illustrations

In this section, we numerically illustrate our results on multi-layer SIR epidemic model.

We choose different population size for the two mobility layers and select the mobility transition rates using the Metropolis-Hastings algorithm [30] such that the equilibrium distribution of population is the same for both the layers (taken as uniform equilibrium distribution).

Figures 3.3 (a) and (b) show the fractions of infected population whereas Figures 3.3 (c) and (d) show the fraction of susceptible population trajectories for 10 nodes connected with 2-layers of graph structures. Layer 1 is line graph and layer 2 is ring graph. The initial population distribution at the 10 nodes for layer 1 and layer 2 are

$$5 \times [700, 500, 300, 100, 500, 700, 800, 900, 600, 500], \quad \text{and}$$

$$5 \times [300, 300, 200, 100, 200, 300, 400, 400, 500, 200],$$

respectively. The infection and curing rates for the 10 nodes are

$$[0.31, 0.32, 0.35, 0.36, 0.5, 0.3, 0.3, 0.1, 0.1, 0.1], \quad \text{and}$$

$$[0.3, 0.22, 0.21, 0.25, 0.3, 0.21, 0.23, 0.24, 0.21, 0.22],$$

respectively. The initial fraction of infected population is taken as 0.01 for all layers and nodes with no recovered population.

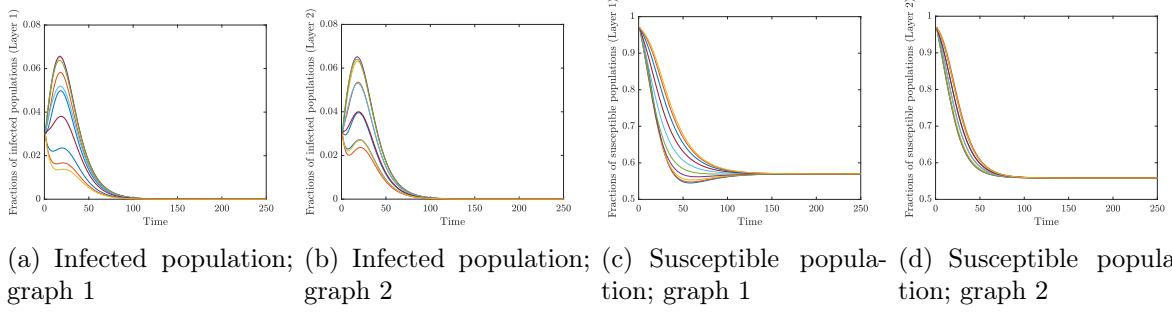


Figure 3.3: Simulation of deterministic model of SIR epidemic spread under 2 layer mobility, over Line-Ring graph structure. $n = 10$, $p_i(0) = 0.01$.

CHAPTER 4

SIS EPIDEMIC MODEL UNDER MOBILITY ON MULTI-LAYER NETWORKS: WEAKLY CONNECTED CASE

In this chapter, we relax the assumption that a layer need to be strongly connected. We characterize the stability of SIS model under mobility for a weakly connected multi-layer network.

4.1 SIS Model under Mobility with Non-strongly Connected Layers

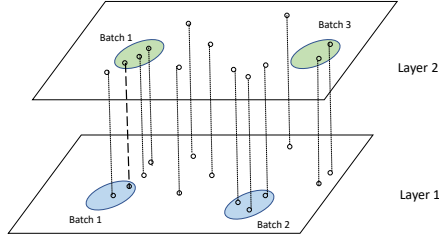


Figure 4.1: Non-strongly connected multilayer network with shaded sink components

In this section, we relax the Assumption 1, so that the digraph representing mobility on a layer need not be strongly connected. For each layer, at equilibrium, the entire population will be restricted to strongly connected sink components and hence we track infected population only among nodes belonging to these sink components. Furthermore, at equilibrium, the effect of nodes shared between different layers appears in the same fashion as before through mixing matrix F^* of the sink component nodes under consideration. Note that the matrix $BF^* - D - L^*$ considered for sink component nodes only, need not be strongly connected (as the inter-layer connections among restricted nodes shared between different layers need not be strongly connected) in contrast to the earlier case. Therefore, we can partition the total restricted nodes, comprised of strongly connected sink components on each layer, into different multi-layer network batches, which are strongly connected in themselves but at equilibrium disconnected from each other. Figure 4.1 shows the depiction. Note that there

may be nodes which do not belong to any of these batches. For any given batch, the effect of nodes outside that batch will be shown to be vanishing at equilibrium with ISS cascaded connection to that batch. We develop the formulation as below:

Consider a multi-layered population of n nodes comprising of m class. The dynamics of fraction of infected population for each class at each node is given by (2) reproduced below:

$$\dot{\mathbf{p}} = ((I - P)BF(\mathbf{x}) - D - L(\mathbf{x}))\mathbf{p} \quad (4.1a)$$

$$\dot{\mathbf{x}}^\alpha = (Q^\alpha)^\top \mathbf{x}^\alpha, \quad (4.1b)$$

Since the strongly connected sink components for all layers can be grouped into different batches, we consider a general batch comprising of $1 \leq l \leq m$ layers with class α contributing q_α strongly connected sink components. Stacking all the sink components of each layer one below the other and then such stacks one below the other gives $\mathbf{s} := [\mathbf{s}^1, \dots, \mathbf{s}^l]$ with $\mathbf{s}^k := [\mathbf{s}^{(k,1)}, \dots, \mathbf{s}^{(k,q_k)}]$. The dynamics is given by writing the dynamics of the concerned class of concerned nodes out of (4.1) and separating the contribution from the rest of the elements:

$$\begin{aligned} \dot{\mathbf{s}} &= ((I - S)\bar{B}F_1(\mathbf{x}) - \bar{D} - L_1(\mathbf{x}))\mathbf{s} \\ &\quad + (I - S)\bar{B}F_2(\mathbf{x})\mathbf{u} - L_2(\mathbf{x})\mathbf{u} \\ &= ((I - S)\bar{B}F_1(\mathbf{x}) - \bar{D} - L_1(\mathbf{x}))\mathbf{s} \\ &\quad + (I - S)\bar{B}\mathbf{c}_1 + \mathbf{c}_2 \end{aligned} \quad (4.2)$$

where, the elements of the matrix F and the matrix L for the concerned classes on concerned nodes are written as $F_1 + F_2$ and $L_1 + L_2$ with F_1 and L_1 being square matrices formed by retaining the rows i and columns i of the matrix F and L , F_2 and L_2 being rectangular formed by rows i and columns j where, p_i is a concerned element of the original vector $\mathbf{p}$, and p_j is not. It is clear from the definition of the matrix F_2 whose elements are 0

or $\frac{x_j^\alpha}{\sum_\alpha x_j^\alpha}$ and elements of matrix $-L_2$ with elements $q_{ji}^\alpha \frac{x_j^\alpha}{x_i^\alpha}$, that the elements (≥ 0) of these matrices are either identically zero or has globally asymptotically stable equilibrium at zero. Hence, $\mathbf{c}_1$ and $\mathbf{c}_2$ asymptotically go to zero. Note that at equilibrium the block diagonal matrix L_1^* comprises of strongly connected laplacian matrices as the diagonal blocks. Also, the matrix $\bar{B}F_1^* - \bar{D} - L_1^*$ now determines the existence and nature of equilibrium point as before. Unlike the strongly connected case, the block diagonal $\bar{D}^\alpha$ for a strongly connected sink component on a layer may be zero resulting in $\mathbf{s}^{*\alpha} = \mathbf{1}$. To avoid this situation here we assume each $\delta_i > 0$. We show the stability analysis as below:

4.2 Stability Analysis

First, we use an ISS based approach to prove the stability of the SIS model over strongly connected multi-layer networks: Since, $(Q^\alpha)^\top$ has exactly one eigenvalue with multiplicity 1 at zero and all others in negative half plane, we can have a coordinate transformation $\mathbf{z}^\alpha = (V^\alpha)^{-1}\mathbf{x}$ such that $\mathbf{z}^\alpha = [N^\alpha, \mathbf{y}^\top]^\top$ with $\mathbf{y}^\alpha = \mathbf{0}$ (an $n - 1$ dimensional zero vector) and N^α is the total number of people in class α . It is easy to see that $\mathbf{y}^\alpha = \mathbf{0}$ is globally asymptotically stable. Defining $\mathbf{z} = [(\mathbf{z}^1)^\top, \dots, (\mathbf{z}^m)^\top]^\top$ and $\mathbf{y} = [(\mathbf{y}^1)^\top, \dots, (\mathbf{y}^m)^\top]^\top$, $\mathbf{y} = \mathbf{0}$ (an $m(n-1)$ dimensional zero vector) is globally asymptotically stable. Also, with a given population of each class, we can write $F(\mathbf{y})$ and $L(\mathbf{y})$ as functions of $\mathbf{y}$ alone and it can further be seen that $\|\tilde{F}(\mathbf{y})\|$ and $\|\tilde{L}(\mathbf{y})\|$ are positive definite functions of $\mathbf{y}$. Consider the cascaded system:

$$\dot{\mathbf{p}} = (BF^* - D - L^*)\mathbf{p} - PBF(\mathbf{y})\mathbf{p} + (B\tilde{F}(\mathbf{y}) - \tilde{L}(\mathbf{y}))\mathbf{p} \quad (4.3a)$$

$$\dot{\mathbf{y}} = A\mathbf{y}. \quad (4.3b)$$

Consider the Lyapunov function $V(\mathbf{p}) = \mathbf{p}^\top R \mathbf{p}$. Therefore,

$$\begin{aligned}
\dot{V} &= 2\mathbf{p}^\top R \dot{\mathbf{p}} \\
&= \mathbf{p}^\top (R(BF^* - D - L^*) + (BF^* - D - L^*)^\top R) \mathbf{p} \\
&\quad + 2\mathbf{p}^\top R(B\tilde{F} - \tilde{L})\mathbf{p} - 2\mathbf{p}^\top RPB(\tilde{F} + F^*)\mathbf{p} \\
&= -\mathbf{p}^\top K\mathbf{p} + 2\mathbf{p}^\top R(B(I - P)\tilde{F} - \tilde{L})\mathbf{p} - 2\mathbf{p}^\top RPBF^*\mathbf{p} \\
&\leq -2\mathbf{p}^\top RPBF^*\mathbf{p} + 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|), \quad k_1, b > 0 \\
&\leq -2(1 - \epsilon)\mathbf{p}^\top RPBF^*\mathbf{p} - 2\epsilon\mathbf{p}^\top RPBF^*\mathbf{p} \\
&\quad + 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|), \quad \forall 0 < \epsilon < 1 \\
&\leq -2(1 - \epsilon)\mathbf{p}^\top RPBF^*\mathbf{p} - k_2\|\mathbf{p}\|_\infty^3 + 2k_1(b\|\tilde{F}\| + \|\tilde{L}\|) \\
&\leq -2(1 - \epsilon)\mathbf{p}^\top RPBF^*\mathbf{p} - k_2\|\mathbf{p}\|_\infty^3 + \rho_1(\|\mathbf{y}\|_\infty) \\
&\leq -2(1 - \epsilon)\mathbf{p}^\top RPBF^*\mathbf{p}, \quad \|\mathbf{p}\|_\infty \geq \rho_2(\|\mathbf{y}\|_\infty)
\end{aligned} \tag{4.4}$$

Here, ρ_1 is a suitable class κ function as per [31, Lemma 4.3] and define $\rho_2 = \sqrt[3]{\frac{\rho_1}{k_2}}$, a class κ function of $\|\mathbf{y}\|_\infty$. Since the last term in (4.4) is a continuous negative definite function of $\mathbf{p}$ in $p_i \in [0, 1]$, it follows from [31, Theorem 4.19] that dynamics (4.3a) is ISS (Input to state stable) with respect to input $\mathbf{y}$. Note that (4.3b) has globally asymptotically stable equilibrium at origin. Further using [31, Lemma 4.7] over the cascaded system with $\mathbf{y}$ as input to dynamics for $\mathbf{p}$ implies that the cascaded system has globally asymptotically stable equilibrium at origin. Next, we modify this prove for the case of weakly connected networks as shown below:

Stability of epidemic equilibria: Consider the Lyapunov function $V(\mathbf{s}) = \mathbf{s}^\top R \mathbf{s}$. There-

fore,

$$\begin{aligned}
\dot{V} &= 2\mathbf{s}^\top R\dot{\mathbf{s}} \\
&= \mathbf{s}^\top (R(\bar{B}F_1^* - \bar{D} - L_1^*) + (\bar{B}F_1^* - \bar{D} - L_1^*)^\top R)\mathbf{s} \\
&\quad + 2\mathbf{s}^\top R(\bar{B}\tilde{F}_1 - \tilde{L}_1)\mathbf{s} - 2\mathbf{s}^\top RS\bar{B}(\tilde{F}_1 + F_1^*)\mathbf{s} \\
&\quad + 2\mathbf{s}^\top (I - S)\bar{B}\mathbf{c}_1 + 2\mathbf{s}^\top \mathbf{c}_2 \\
&= -\mathbf{s}^\top K\mathbf{s} + 2\mathbf{s}^\top R(B(I - S)\tilde{F}_1 - \tilde{L}_1)\mathbf{s} - 2\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s} \\
&\quad + 2\mathbf{s}^\top (I - S)\bar{B}\mathbf{c}_1 + 2\mathbf{s}^\top \mathbf{c}_2 \\
&\leq -2\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s} + 2k_1(b_1\|\tilde{F}_1\| + b_2\|\tilde{L}_1\| + b_3\|\mathbf{c}_1\| + \|\mathbf{c}_2\|) \\
&\quad , \quad k_1, b_1, b_2, b_3 > 0 \\
&\leq -2(1 - \epsilon)\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s} - 2\epsilon\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s} \\
&\quad + 2k_1(b_1\|\tilde{F}_1\| + b_2\|\tilde{L}_1\| + b_3\|\mathbf{c}_1\| + \|\mathbf{c}_2\|), \quad \forall 0 < \epsilon < 1 \\
&\leq -2(1 - \epsilon)\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s} - k_2\|\mathbf{s}\|_\infty^3 \\
&\quad + 2k_1(b_1\|\tilde{F}_1\| + b_2\|\tilde{L}_1\| + b_3\|\mathbf{c}_1\| + \|\mathbf{c}_2\|) \\
&\leq -2(1 - \epsilon)\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s} - k_2\|\mathbf{s}\|_\infty^3 + \rho_1(\|\mathbf{y}\|_\infty) \\
&\leq -2(1 - \epsilon)\mathbf{s}^\top RS\bar{B}F_1^*\mathbf{s}, \quad \|\mathbf{s}\|_\infty \geq \rho_2(\|\mathbf{y}\|_\infty) \tag{4.5}
\end{aligned}$$

Here, ρ_1 is a suitable class κ function as per [31, Lemma 4.3] and define $\rho_2 = \sqrt[3]{\frac{\rho_1}{k_2}}$, a class κ function of $\|\mathbf{y}\|_\infty$. Note, that a vector $\mathbf{y}$ can still be constructed as in (4.3b) for a weakly connected graph, where $\mathbf{c}_1(\mathbf{y})$, $\mathbf{c}_2(\mathbf{y})$, $\tilde{F}_1(\mathbf{y})$ and $\tilde{L}_1(\mathbf{y})$ are functions of $\mathbf{y}$ and $\mathbf{y}$ asymptotically goes to zero. Since the last term in (4.5) is a continuous negative definite function of $\mathbf{s}$ in $p_i \in [0, 1]$, it follows from [31, Theorem 4.19] that dynamics (4.2) is ISS (Input to state stable) with respect to input $\mathbf{y}$. The rest of the argument follows same as the ISS based epidemic equilibrium stability proof presented above.

Stability of endemic equilibria: The stability of endemic equilibrium can be shown by doing Lyapunov analysis similar to the strongly connected case and the extra terms can be incorporated into ISS terms similar to the previous proof.

CHAPTER 5

RESOURCE ALLOCATION

In this chapter, we formulate a resource allocation problem for the SIS epidemic model under mobility on single-layer and multi-layer network. We show that under certain assumptions the problem can be formulated as a geometric program. We give numerical illustrations to support our results.

5.1 Resource allocation

We formulate a resource allocation problem for the SIS model under markovian mobility where we allocate resources so as to have the disease free equilibrium (DFE) as the stable equilibrium. We consider two types of resources:

- i. Preventive resource: This can be used to change the infection rate such that $\beta_i \in [\underline{\beta}_i, \bar{\beta}_i]$. This resource is applied to a node with cost function $f_i(\beta_i)$.
- ii. Corrective resource: This can be used to change the recovery rate such that $\delta_i \in [\underline{\delta}_i, \bar{\delta}_i]$. The corresponding cost function is $g_i(\delta_i)$.

5.1.1 Single layer mobility

It is shown in Appendix A.3 that the matrix $B - D - L^*$ is similar to $B - D + Q^\top$, hence the condition for stability of DFE is given by:

$$\mu(B - D + Q^\top) \leq 0$$

Since $B - D + Q^\top$ is an irreducible Metzler matrix, μ is a real and simple eigenvalue referred to as λ_1 henceforth. We use the approach similar to the one in [32]. We use a lemma resulting from Perron-Frobenius theorem for irreducible non-negative matrix:

Lemma 3 *If M is an irreducible non-negative matrix, with $\lambda_1 = \mu(M)$ being its radial-abscissa, then $\lambda_1 = \inf\{\lambda \in \mathbb{R} : M\mathbf{u} \leq \lambda\mathbf{u} \text{ for } \mathbf{u} \gg \mathbf{0}\}$.*

By applying above lemma one can minimize $\lambda_1(M)$ by minimizing λ such that:

$$\frac{Mu_i}{\lambda u_i} \leq 1, \quad u_i > 0. \quad (5.1)$$

In order to maximize the decay rate of DFE, we minimize $\lambda_1(B - D + Q^\top)$ with a budget constraint over total resource cost. It can be seen that $\lambda_1(B - D + Q^\top) = \lambda_1(B + \hat{D} + \hat{Q}^\top) - \bar{\Delta} - 1 - \bar{\nu}$, where $\hat{D} = \text{diag}(\hat{\delta}_i)$, $\hat{\delta}_i = \bar{\Delta} + 1 - \delta_i$, $\bar{\Delta} = \max\{\bar{\delta}_i\}_{i=1}^n$, $\hat{Q}_{ij} = Q_{ij}$ for $i \neq j$, $\hat{Q}_{ii} = \hat{q}_{ii} = \bar{\nu} - \nu_i$, $\bar{\nu} = \max\{\nu_i\}_{i=1}^n$, where $\nu_i = \sum_{j \neq i} q_{ij}$. Note that minimising $\lambda_1(B - D + Q^\top)$ is same as minimising $\lambda_1(B + \hat{D} + \hat{Q}^\top)$, where latter corresponds to an irreducible non-negative matrix. To pose the optimization problem as a Geometric Program, we restrict ourselves to preventive and corrective resources only. Further, we assume the preventive cost $f(\beta_i)$ a posynomial and corrective cost $g(\delta_i) = \tilde{g}(\bar{\Delta} + 1 - \delta_i) = \tilde{g}(\hat{\delta}_i)$, with $\tilde{g}$ a posynomial. Consider a strongly connected digraph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$, where $\mathcal{V} = \{1, \dots, n\}$ is the node (patch) set and $\mathcal{E} \subset \mathcal{V} \times \mathcal{V}$ is the edge set. The generator matrix for mobility is Q , whose (i, j) -th entry is q_{ij} , where $q_{ij} > 0$ for $(i, j) \in \mathcal{E}$ and 0 otherwise. Utilising lemma 3, (5.1) on matrix $(B + \hat{D} + \hat{Q}^\top)$, the resource allocation problem [32] can be stated as a geometric programming problem:

$$\min_{\lambda, u_i, \beta_i, \hat{\delta}_i} \lambda \quad (5.2)$$

$$\text{s.t.} \quad \frac{\sum_{j=1:n} (B + \hat{D} + \hat{Q}^\top)_{ij} u_j}{\lambda u_i} \leq 1, \quad (5.3)$$

$$\sum_i [f_i(\beta_i) + \tilde{g}_i(\hat{\delta}_i)] \leq C, \quad (5.4)$$

$$\underline{\beta}_i \leq \beta_i \leq \bar{\beta}_i, \quad (5.5)$$

$$\bar{\Delta} + 1 - \bar{\delta}_i \leq \hat{\delta}_i \leq \bar{\Delta} + 1 - \underline{\delta}_i. \quad (5.6)$$

where $i \in [1, n]$.

5.1.2 Multilayer mobility

The condition for stability of DFE is given by:

$$\mu(BF^* - D - L^*) \leq 0$$

Since $BF^* - D - L^*$ is an irreducible Metzler matrix, μ is a real and simple eigenvalue referred to as λ_1 henceforth. We consider a variable transformation similar to the single layer case: $\lambda_1(BF^* - D - L^*) = \lambda_1(BF^* + \hat{D} + \hat{A}) - \bar{\Delta} - 1 - \bar{\nu}$, where $\hat{D} = \text{blkdiag}(\hat{D}^\alpha)$, $\hat{D}^\alpha = \text{diag}(\hat{\delta}_i)$, $\hat{\delta}_i = \bar{\Delta} + 1 - \delta_i$, $\bar{\Delta} = \max\{\bar{\delta}_i\}_{i=1}^n$, $\hat{A} = \text{blkdiag}(\hat{A}^\alpha)$, $\hat{A}_{ij}^\alpha = -L_{ij}^{\alpha*}$ for $i \neq j$, $\hat{A}_{ii}^\alpha = r_i^\alpha = \bar{\nu} - \nu_i^\alpha$, $\bar{\nu} = \max\{\nu_i^\alpha\}_{i=1, \alpha=1}^{n, m}$, where $\nu_i^\alpha = \sum_{j \neq i} q_{ij}^\alpha$. Note that minimising $\lambda_1(BF^* - D - L^*)$ is same as minimising $\lambda_1(BF^* + \hat{D} + \hat{A})$, where latter corresponds to an irreducible non-negative matrix. Similar to the single-layer case, restricting ourselves to posynomial costs $f(\beta_i)$ and $\tilde{g}(\hat{\delta}_i)$, the resource allocation problem can be stated as a geometric problem:

$$\min_{\lambda, u_i, \beta_i, \hat{\delta}_i} \lambda \tag{5.7}$$

$$\text{s.t. } \frac{\sum_{j=1:nm} (BF^* + \hat{D} + \hat{A})_{ij} u_j}{\lambda u_i} \leq 1, \quad \text{for } i = 1 \text{ to } nm, \tag{5.8}$$

$$\sum_i [f_i(\beta_i) + \tilde{g}_i(\hat{\delta}_i)] \leq C, \quad \text{for } i = 1 \text{ to } n, \tag{5.9}$$

$$\underline{\beta}_i \leq \beta_i \leq \bar{\beta}_i, \quad \text{for } i = 1 \text{ to } n, \tag{5.10}$$

$$\bar{\Delta} + 1 - \bar{\delta}_i \leq \hat{\delta}_i \leq \bar{\Delta} + 1 - \underline{\delta}_i, \quad \text{for } i = 1 \text{ to } n. \tag{5.11}$$

5.2 Numerical Illustration

We give numerical illustration for the budget constrained resource allocation problem for the case of multi-layer network. We take two layers: layer 1 as line graph and layer 2 as a ring graph. We use mobility transition rates as those obtained with the condition of equal outgoing rates to neighboring nodes with total outgoing transition rate fixed as 0.2. The

total number of individuals on layer 1 is taken as 300 whereas those on layer 2 as 500. The cost functions are taken as

$$f(\beta_i) = \frac{1}{\beta_i} - \frac{1}{\bar{\beta}_i},$$

$$g(\delta_i) = \frac{1}{\bar{\Delta} + 1 - \delta_i} - \frac{1}{\bar{\Delta} + 1 - \underline{\delta}_i} = \tilde{g}(\hat{\delta}_i) = \frac{1}{\hat{\delta}_i} - \frac{1}{\bar{\Delta} + 1 - \underline{\delta}_i}.$$

The bounds on the infection and curing rates are taken as

$$\underline{\beta}_i = 0.1, \quad \bar{\beta}_i = 0.4, \quad \underline{\delta}_i = 0.1, \quad \bar{\delta}_i = 0.4.$$

We solve the resulting geometric programming for minimisation of λ_1 corresponding to decay rate of disease-free equilibrium. Note that $\lambda = \lambda_1(BF^* + \hat{D} + \hat{A}) - 1 - \bar{\Delta} - \bar{\nu}$, where λ corresponds to the decay rate of disease-free equilibrium. Figure 5.1 shows the plot of obtained minimum λ against the maximum allowable cost (budget) C . As can be seen, λ is positive for very low values of budget implying unstable disease-free equilibrium. As the budget C increases λ saturates around a value of -0.3 . Note that the actual cost used is less than or equal to the budget and need not be equal to the budget C .

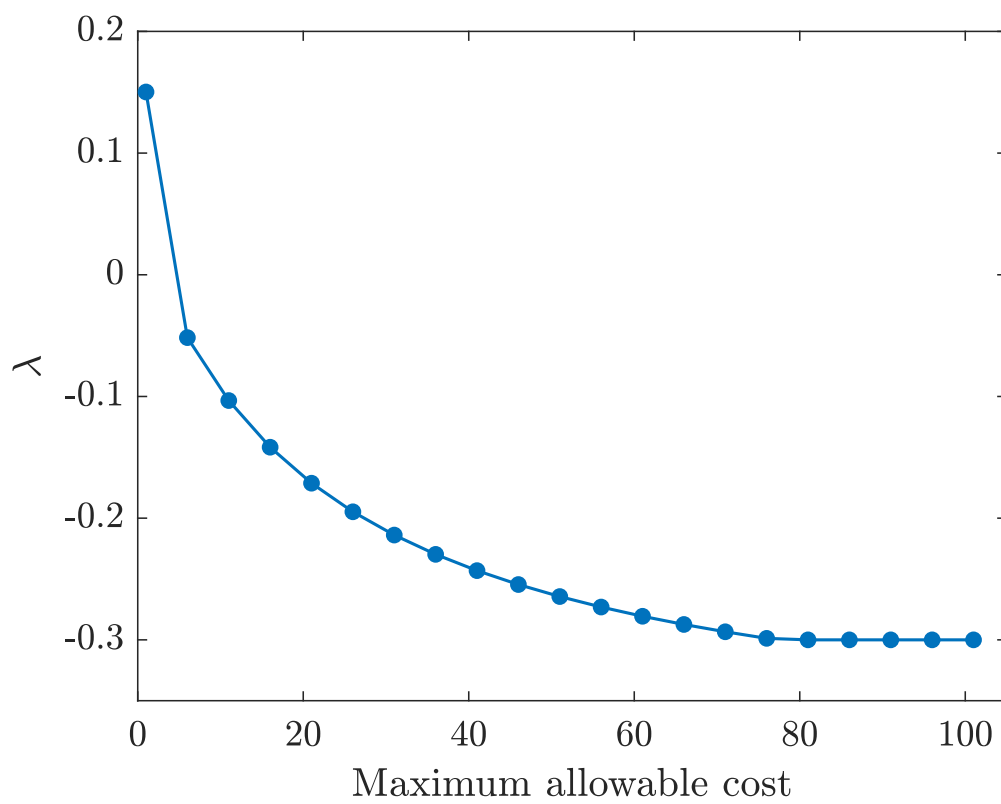


Figure 5.1: Decay rate λ against maximum allowable cost C . Graph1: Line, Graph 2: Ring, $n = 10$, $\nu_i = 0.2$.

CHAPTER 6

CONCLUSIONS

We derived a continuous-time model for epidemic propagation under Markovian mobility across a network of sub-populations. The epidemic spread within each node has been modeled as SIS and SIR population models. The derived models have been analysed to establish the existence, uniqueness 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. We extended the stability results for the SIS model to the case of non-strongly connected layers. Further, we formulated a budget constrained resource allocation problem as a geometric program and provided numerical illustrations.

APPENDIX

A.1 Proof of Theorem 1 (iii), Chapter 2: Existence of an endemic equilibrium

We show below that in the case of $\mu(B - D - L^*) > 0$, there exists an endemic equilibrium $\mathbf{p}^*$, i.e.,

$$\dot{\mathbf{p}}|_{\mathbf{p}=\mathbf{p}^*} = (B - D - L^* - P^*B)\mathbf{p}^* = 0. \quad (1)$$

We use Brouwer's fixed point theorem, similar to the derivation in [9]. Rearranging the terms and writing the above as an equation in $\mathbf{p}$ to be satisfied at non-trivial equilibrium $\mathbf{p}^*$ leads to:

$$(L^* + D)((L^* + D)^{-1}B - I)\mathbf{p} = PB\mathbf{p}. \quad (2)$$

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 [33]. Rearranging (2) leads to

$$\mathbf{p} = H(\mathbf{p}) = (I + AP)^{-1}A\mathbf{p}. \quad (3)$$

Now we show that $H(\mathbf{p})$ as defined above is a monotonic function in the sense that $\mathbf{p}_2 \geq \mathbf{p}_1$ implies $H(\mathbf{p}_2) \geq H(\mathbf{p}_1)$. Define $\tilde{\mathbf{p}} := \mathbf{p}_2 - \mathbf{p}_1$ and $\tilde{P} := \text{diag}(\tilde{\mathbf{p}})$. Then,

$$\begin{aligned} & H(\mathbf{p}_2) - H(\mathbf{p}_1) \\ &= (A^{-1} + P_2)^{-1}\mathbf{p}_2 - (A^{-1} + P_1)^{-1}\mathbf{p}_1 \\ &= (A^{-1} + P_2)^{-1}(\mathbf{p}_2 - (A^{-1} + P_2)(A^{-1} + P_1)^{-1}\mathbf{p}_1) \\ &= (A^{-1} + P_2)^{-1}(\tilde{\mathbf{p}} - \tilde{P}(A^{-1} + P_1)^{-1}\mathbf{p}_1) \\ &= (A^{-1} + P_2)^{-1}(I - \text{diag}((A^{-1} + P_1)^{-1}\mathbf{p}_1))\tilde{\mathbf{p}}. \end{aligned} \quad (4)$$

Since $(A^{-1} + P_2) = B^{-1}(L^* + D) + P_2$ is an M-matrix its inverse and hence the first term

above is non-negative. The second term is shown to be non-negative as below:

$$\begin{aligned}
& (I - \text{diag}((A^{-1} + P_1)^{-1}\mathbf{p}_1)) \\
&= (I - \text{diag}((I + AP_1)^{-1}AP_1\mathbf{1}_n)) \\
&= \text{diag}((I - (I + AP_1)^{-1}AP_1)\mathbf{1}_n) \\
&= \text{diag}((I + AP_1)^{-1}\mathbf{1}_n) \\
&= \text{diag}((A^{-1} + P_1)^{-1}A^{-1}\mathbf{1}_n) \\
&\geq 0,
\end{aligned} \tag{5}$$

where we have used the identity:

$$(I + X)^{-1} = I - (I + X)^{-1}X, \tag{6}$$

in the second line. The last inequality in (5) holds as $A^{-1}\mathbf{1}_n = B^{-1}(L^* + D)\mathbf{1}_n = B^{-1}D\mathbf{1}_n \geq \mathbf{0}_n$ and $(A^{-1} + P_1)^{-1} \geq 0$ the inverse of an M-matrix. The last term in the last line of (4) is $\tilde{\mathbf{p}} \geq \mathbf{0}_n$. This implies that $H(\mathbf{p})$ is a monotonic function. Also, result in (5) implies that $H(\mathbf{p}) \leq \mathbf{1}_n$ for all $\mathbf{p} \in [0, 1]^n$. Therefore $H(\mathbf{1}_n) \leq \mathbf{1}_n$.

Convergent splitting property of irreducible M-matrices [33] implies $\mu(B - D - L^*) > 0$ if and only if $R_0 = \rho(A) = \rho((L^* + D)^{-1}B) > 1$. Here $\rho(A)$ is spectral radius of A . Since A is an irreducible non-negative matrix, Perron-Frobenius theorem implies $\rho(A)$ is a simple eigenvalue with right eigenvector $\mathbf{u}$ satisfying $A\mathbf{u} = \rho(A)\mathbf{u} = R_0\mathbf{u}$, with $\mathbf{u} \gg \mathbf{0}_n$. Define $U := \text{diag}(\mathbf{u})$ and $\gamma := \frac{R_0 - 1}{R_0}$. Now, we find a value of $\epsilon > 0$ such that $H(\epsilon\mathbf{u}) \geq \epsilon\mathbf{u}$ as below:

$$\begin{aligned}
H(\epsilon\mathbf{u}) - \epsilon\mathbf{u} &= (I + \epsilon AU)^{-1}A\epsilon\mathbf{u} - \epsilon\mathbf{u} \\
&= (I - (I + \epsilon AU)^{-1}\epsilon AU)\epsilon R_0\mathbf{u} - \epsilon\mathbf{u} \\
&= \epsilon R_0\left(\frac{R_0 - 1}{R_0}\mathbf{u} - (I + \epsilon AU)^{-1}\epsilon AU\mathbf{u}\right) \\
&= \epsilon R_0(\gamma\mathbf{u} - (I + \epsilon AU)^{-1}\epsilon AU\mathbf{u}).
\end{aligned} \tag{7}$$

Now, the expression in the brackets in the last line is a continuous function of ϵ and is equal to $\gamma \mathbf{u} \gg \mathbf{0}_n$ at $\epsilon = 0$. Therefore, there exists an $\epsilon > 0$ such that $H(\epsilon \mathbf{u}) - \epsilon \mathbf{u} \geq \mathbf{0}_n$ or equivalently, $H(\epsilon \mathbf{u}) \geq \epsilon \mathbf{u}$. Taking the closed compact set $K = [\epsilon \mathbf{u}, \mathbf{1}_n]$, $H : K \rightarrow K$ is a continuous function. Therefore, by Brouwer's fixed point theorem, there exists a fixed point in K . This proves the existence of a non-trivial equilibrium $\mathbf{p}^* \gg \mathbf{0}_n$ when $\mu(B - D - L^*) > 0$ or equivalently $R_0 > 1$. The uniqueness is further shown in the following proposition.

Proposition 4 *If the mapping H has a strictly positive fixed point, then it is unique.*

Proof: The proof is similar to the proof of [10, Proposition A.3] and is given below:

Assume there are two strictly positive fixed points: $\mathbf{p}^*$ and $\mathbf{q}^*$. Define

$$\eta := \max \frac{p_i^*}{q_i^*}, \quad k := \arg \max \frac{p_i^*}{q_i^*}$$

Therefore, $\mathbf{p}^* \leq \eta \mathbf{q}^*$. Lets assume $\eta > 1$. First we will show that $H(\eta \mathbf{q}^*) < \eta H(\mathbf{q}^*)$ as follows:

$$\begin{aligned} & H(\eta \mathbf{q}^*) - \eta H(\mathbf{q}^*) \\ &= (I + A\eta Q^*)^{-1} A\eta \mathbf{q}^* - \eta(I + AQ^*)^{-1} A\mathbf{q}^* \\ &= ((I + A\eta Q^*)^{-1} A - (I + AQ^*)^{-1} A)\eta \mathbf{q}^* \\ &= ((A^{-1} + \eta Q^*)^{-1} - (A^{-1} + Q^*)^{-1})\eta \mathbf{q}^* \\ &= (A^{-1} + \eta Q^*)^{-1} (I - (A^{-1} + \eta Q^*)(A^{-1} + Q^*)^{-1})\eta \mathbf{q}^* \\ &= (A^{-1} + \eta Q^*)^{-1} (-(\eta - 1)(A^{-1} + Q^*)^{-1})\eta \mathbf{q}^* \\ &< 0 \end{aligned} \tag{8}$$

where the last inequality uses result that inverse of a non-singular M-matrix is non-negative and non-singular, that $\eta > 1$ and, that $\mathbf{q}^* \gg \mathbf{0}$ by assumption. Consequently

$$p_k^* = H_k(\mathbf{p}^*) \leq H_k(\eta \mathbf{q}^*) < \eta H_k(\mathbf{q}^*) = \eta q_k^*, \tag{9}$$

Since, $\eta q_k^* = p_k^*$ by definition, if $\eta > 1$, we have from above $p_k^* < p_k^*$, a contradiction. Hence, $\eta \leq 1$ which implies $\mathbf{p}^* \leq \mathbf{q}^*$. By switching the roles of $\mathbf{p}^*$ and $\mathbf{q}^*$ and repeating the above argument we can show $\mathbf{q}^* \leq \mathbf{p}^*$. Thus $\mathbf{p}^* = \mathbf{q}^*$ and hence there is a unique strictly positive fixed point. $\square$

A.2 Proof of Theorem 2 (iii), Chapter 3: Existence of an endemic equilibrium: Multi-layer Case

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

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

Theorem 4 (*Properties of M-matrix*, [33]) *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 $\mathbf{x} \gg \mathbf{0}$ such that $A\mathbf{x} \gg \mathbf{0}$;*

vi. **Modified semi-positivity:** there exists $\mathbf{x} \gg \mathbf{0}$ such that $\mathbf{y} = A\mathbf{x} > \mathbf{0}$ and matrix $\hat{A}$ 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 4 (vi) is that an irreducible Laplacian matrix perturbed with a non-negative diagonal matrix with atleast one positive element is a non-singular M-matrix (take $\mathbf{x} = \mathbf{1} \gg \mathbf{0}$). 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 atleast 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 $\mathbf{p}^* \gg 0$, i.e.,

$$\dot{\mathbf{p}}|_{\mathbf{p}=\mathbf{p}^*} = (BF^* - D - L^* - P^*BF^*)\mathbf{p}^* = 0. \quad (10)$$

We use Brouwer's fixed point theorem, similar to the derivation in [9]. 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 $\mathbf{p}$ to be satisfied at $\mathbf{p}^*$ leads to

$$\begin{aligned} (L^* + D)((L^* + D)^{-1}B - I)\mathbf{p} &= (PB + (I - P)BM)\mathbf{p} \\ &= B(P + (I - P)M)\mathbf{p}. \end{aligned} \quad (11)$$

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 [33]. Rearranging (11) leads to

$$\mathbf{p} = H(\mathbf{p}) = (I + A(P + (I - P)M))^{-1}A\mathbf{p}. \quad (12)$$

Now we show that $H(\mathbf{p})$ as defined above is a monotonic function in the sense that $\mathbf{p}_2 \geq \mathbf{p}_1$ implies $H(\mathbf{p}_2) \geq H(\mathbf{p}_1)$. Define $\tilde{\mathbf{p}} := \mathbf{p}_2 - \mathbf{p}_1$ and $\tilde{P} := \text{diag}(\tilde{\mathbf{p}})$. Then,

$$\begin{aligned}
& H(\mathbf{p}_2) - H(\mathbf{p}_1) \\
&= \left(A^{-1} + P_2 + (I - P_2)M \right)^{-1} \mathbf{p}_2 \\
&\quad - \left(A^{-1} + P_1 + (I - P_1)M \right)^{-1} \mathbf{p}_1 \\
&= \left(A^{-1} + P_2 + (I - P_2)M \right)^{-1} \left(\mathbf{p}_2 - \right. \\
&\quad \left. \left(A^{-1} + P_2 + (I - P_2)M \right) \left(A^{-1} + P_1 + (I - P_1)M \right)^{-1} \mathbf{p}_1 \right) \quad (13) \\
&= \left(A^{-1} + P_2 + (I - P_2)M \right)^{-1} \left(\tilde{\mathbf{p}} \right. \\
&\quad \left. - \tilde{P}(I - M) \left(A^{-1} + P_1 + (I - P_1)M \right)^{-1} \mathbf{p}_1 \right) \\
&= (A^{-1} + P_2 + (I - P_2)M)^{-1} \left(I \right. \\
&\quad \left. - \text{diag} \left((I - M)(A^{-1} + P_1 + (I - P_1)M)^{-1} \mathbf{p}_1 \right) \right) \tilde{\mathbf{p}}
\end{aligned}$$

Since $(A^{-1} + P_2 + (I - P_2)M) = B^{-1}(L^* + D) + P_2 + (I - P_2)M$ is a non-singular M-matrix (consider theorem 4 (vi) with $\mathbf{x} = \mathbf{1} \gg \mathbf{0}$), its inverse and hence the first term

above is non-negative. The second term is shown to be non-negative as below

$$\begin{aligned}
& \left(I - \text{diag} \left((I - M)(A^{-1} + P_1 + (I - P_1)M)^{-1} \mathbf{p}_1 \right) \right) \\
&= \left(I - \text{diag} \left((I - M)(A^{-1} + P_1 + (I - P_1)M)^{-1} P_1 \mathbf{1} \right) \right) \\
&= \text{diag} \left(\left(I - (I - M)(I + AP_1 + A(I - P_1)M)^{-1} AP_1 \right) \mathbf{1} \right) \\
&= \text{diag} \left((I - M - (I - M)(I + AP_1 + A(I - P_1)M)^{-1} \right. \\
&\quad \left. (AP_1 + A(I - P_1)M)) \mathbf{1} \right) \\
&= \text{diag} \left((I - M)(I - (I + AP_1 + A(I - P_1)M)^{-1} \right. \\
&\quad \left. (AP_1 + A(I - P_1)M)) \mathbf{1} \right) \\
&= \text{diag} \left((I - M)(I + AP_1 + A(I - P_1)M)^{-1} \mathbf{1} \right) \\
&= \text{diag} \left(F^* (A^{-1} + P_1 + (I - P_1)M)^{-1} A^{-1} \mathbf{1} \right) \\
&\geq 0,
\end{aligned} \tag{14}$$

where we have used the identity

$$(I + X)^{-1} = I - (I + X)^{-1} X, \tag{15}$$

and $M\mathbf{1} = \mathbf{0}$, as M is a Laplacian matrix. The last inequality in (14) holds as $A^{-1}\mathbf{1} = B^{-1}(L^* + D)\mathbf{1} = B^{-1}D\mathbf{1} \geq \mathbf{0}$ and $(A^{-1} + P_1 + (I - P_1)M)^{-1} \geq \mathbf{0}$, since it is the inverse of an M-matrix. The last term in the last line of (13) is $\tilde{\mathbf{p}} \geq \mathbf{0}$. This implies that $H(\mathbf{p})$ is a monotonic function. Also, argument similar to above can be used to show that $H(\mathbf{p}) \leq \mathbf{1}$ for all $\mathbf{0} \leq \mathbf{p} \leq \mathbf{1}$. Therefore, $H(\mathbf{1}) \leq \mathbf{1}$.

Applying the converse of Theorem 4 (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 $AF^* = [(A^1)^\top \bar{F}^\top(\mathbf{x}^*), \dots, (A^m)^\top \bar{F}^\top(\mathbf{x}^*)]^\top$.

Since $A^\alpha > 0$ and $\bar{F}^* \geq 0$ 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 $AF^*\mathbf{u} = \rho(AF^*)\mathbf{u} = R_0\mathbf{u}$ with $\mathbf{u} \gg \mathbf{0}$. Using $F^* = I - M$ implies:

$$\begin{aligned} A\mathbf{u} &= R_0\mathbf{u} + AM\mathbf{u} \\ &= (R_0 - 1)\mathbf{u} + (I + AM)\mathbf{u}. \end{aligned} \tag{16}$$

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

$$\begin{aligned} &H(\epsilon\mathbf{u}) - \epsilon\mathbf{u} \\ &= (I + \epsilon AU + A(I - \epsilon U)M)^{-1}A\epsilon\mathbf{u} - \epsilon\mathbf{u} \\ &= \epsilon \left((I + \epsilon AU + A(I - \epsilon U)M)^{-1}(R_0 - 1)\mathbf{u} \right. \\ &\quad \left. + (I + \epsilon AU + A(I - \epsilon U)M)^{-1}(I + AM)\mathbf{u} - \mathbf{u} \right) \\ &\equiv \epsilon K(\epsilon). \end{aligned} \tag{17}$$

Now we evaluate $K(\epsilon)$ at $\epsilon = 0$:

$$\begin{aligned} &K(0) \\ &= (I + AM)^{-1}(R_0 - 1)\mathbf{u} + (I + AM)^{-1}(I + AM)\mathbf{u} - \mathbf{u} \\ &= (I + AM)^{-1}(R_0 - 1)\mathbf{u} \\ &= (R_0 - 1)(A^{-1} + M)^{-1}A^{-1}\mathbf{u} \\ &= \frac{(R_0 - 1)}{R_0}(A^{-1} + M)^{-1}F^*\mathbf{u} \\ &= \gamma(A^{-1} + M)^{-1}F^*\mathbf{u} \\ &\gg \mathbf{0}. \end{aligned} \tag{18}$$

The last inequality follows as γ and $\mathbf{u}$ are both positive, and $(A^{-1} + M)^{-1}F^* = (B^{-1}(L + D) + M)^{-1}F^* > 0$ 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 ϵ , $\exists \epsilon_0$ such that $\epsilon_0 > \epsilon > 0$ implies $K(\epsilon) \gg \mathbf{0}$ and therefore, $H(\epsilon \mathbf{u}) \geq \epsilon \mathbf{u}$. Therefore there exists an $\epsilon > 0$ such that $H(\epsilon \mathbf{u}) - \epsilon \mathbf{u} \geq \mathbf{0}$ or equivalently, $H(\epsilon \mathbf{u}) \geq \epsilon \mathbf{u}$. Taking the closed compact set $J = [\epsilon \mathbf{u}, \mathbf{1}]$, $H(\mathbf{p}) : J \rightarrow J$ is a continuous function of $\mathbf{p}$. Brouwer's fixed point theorem implies there exists a fixed point of H in J . This proves the existence of an endemic equilibrium $\mathbf{p}^* \gg \mathbf{0}$ when $\mu(BF^* - D - L^*) > 0$ or equivalently $R_0 > 1$. The uniqueness is further shown in the following proposition.

Proposition 5 *If the mapping H has a strictly positive fixed point, then it is unique.*

Proof: Assume there are two strictly positive fixed points: $\mathbf{0} \ll \mathbf{p}^* \ll \mathbf{1}$ and $\mathbf{0} \ll \mathbf{q}^* \ll \mathbf{1}$. Strict inequality compared to $\mathbf{1}$ is assumed which can be easily proved for any equilibrium point using (2.4) under Assumptions 1 and 3. Define

$$\eta := \max \frac{p_i^*}{q_i^*}, \quad k := \arg \max \frac{p_i^*}{q_i^*}, \quad z_i = \min(\eta q_i^*, 1)$$

Therefore, $\mathbf{p}^* \leq \mathbf{z} \leq \eta \mathbf{q}^*$. Lets assume $\eta > 1$, which implies $\mathbf{q}^* \ll \mathbf{z}$. First we will show that $H(\mathbf{z}) \ll \eta H(\mathbf{q}^*)$ as follows:

$$\begin{aligned} & H(\mathbf{z}) - \eta H(\mathbf{q}^*) \\ &= (A^{-1} + Z + (I - Z)M)^{-1} \mathbf{z} \\ &\quad - \eta (A^{-1} + Q^* + (I - Q^*)M)^{-1} \mathbf{q}^* \\ &\leq (A^{-1} + Z + (I - Z)M)^{-1} \\ &\quad (I - (A^{-1} + Z + (I - Z)M)(A^{-1} + Q^* + (I - Q^*)M)^{-1}) \eta \mathbf{q}^* \\ &= W^{-1} (I - I - ((Z - Q^*) - (Z - Q^*)M)) (A^{-1} + Q^* + (I - Q^*)M)^{-1} \eta \mathbf{q}^* \\ &= -W^{-1} (Z - Q^*) (I - M) (A^{-1} + Q^* + (I - Q^*)M)^{-1} \eta \mathbf{q}^* \\ &= -W^{-1} (Z - Q^*) F^* (A^{-1} + Q^* + (I - Q^*)M)^{-1} \eta \mathbf{q}^* \\ &\ll \mathbf{0} \end{aligned} \tag{19}$$

where the last inequality uses result that, W^{-1} and $(A^{-1} + Q^* + (I - Q^*)M)^{-1}$ inverse of non-singular M-matrices are non-negative and non-singular (hence with no zero rows), that F^* is non-negative with no zero rows, that $Z - Q^*$ has all elements positive and, that $\mathbf{q}^* \gg \mathbf{0}$ by assumption. Consequently

$$p_k^* = H_k(\mathbf{p}^*) \leq H_k(\mathbf{z}) < \eta H_k(\mathbf{q}^*) = \eta q_k^*, \quad (20)$$

Since, $\eta q_k^* = p_k^*$ by definition, if $\eta > 1$, we have from above $p_k^* < p_k^*$, a contradiction. Hence, $\eta \leq 1$ which implies $\mathbf{p}^* \leq \mathbf{q}^*$. By switching the roles of $\mathbf{p}^*$ and $\mathbf{q}^*$ and repeating the above argument we can show $\mathbf{q}^* \leq \mathbf{p}^*$. Thus $\mathbf{p}^* = \mathbf{q}^*$ and hence there is a unique strictly positive fixed point. $\square$

A.3 Similarity of $B - D - L^*$ and $B - D + Q^\top$

Using definition of L^* it can be seen that:

$$\begin{aligned} L_{ii}^* &= \sum_{j \neq i} q_{ji} \frac{x_j^*}{x_i^*}, \\ &= -q_{ii} \frac{x_i^*}{x_i^*}, \quad (Q^\top \mathbf{x}^* = 0) \\ &= -q_{ii} \end{aligned}$$

Also, $L_{ij} = -q_{ji} \frac{x_j^*}{x_i^*}$. This implies:

$$\begin{aligned} L^* &= -(X^*)^{-1} Q^\top X^*, \\ B - D - L^* &= (X^*)^{-1} (B - D + Q^\top) X^* \end{aligned}$$

Here we have used the fact that B and D are diagonal matrices.

BIBLIOGRAPHY

BIBLIOGRAPHY

- [1] Roy M Anderson and Robert M May. *Infectious Diseases of Humans: Dynamics and Control*. Oxford University Press, 1992.
- [2] D. Easley and J. Kleinberg. *Networks, Crowds, and Markets: Reasoning About a Highly Connected World*. Cambridge University Press, 2010.
- [3] Jon Kleinberg. The wireless epidemic. *Nature*, 449(7160):287, 2007.
- [4] Pu Wang, Marta C González, César A Hidalgo, and Albert-László Barabási. Understanding the spreading patterns of mobile phone viruses. *Science*, 324(5930):1071–1076, 2009.
- [5] Xiaolan Zhang, Giovanni Neglia, Jim Kurose, and Don Towsley. Performance modeling of epidemic routing. *Computer Networks*, 51(10):2867–2891, 2007.
- [6] Fang Jin, Edward Dougherty, Parang Saraf, Yang Cao, and Naren Ramakrishnan. Epidemiological modeling of news and rumors on twitter. In *Proceedings of the Workshop on Social Network Mining and Analysis*, page 8. ACM, 2013.
- [7] C. Nowzari, V. M. Preciado, and G. J. Pappas. Analysis and control of epidemics: A survey of spreading processes on complex networks. *IEEE Control Systems Magazine*, 36(1):26–46, Feb 2016.
- [8] Wenjun Mei, Shadi Mohagheghi, Sandro Zampieri, and Francesco Bullo. On the dynamics of deterministic epidemic propagation over networks. *Annual Reviews in Control*, 44:116–128, 2017.
- [9] A Fall, Abderrahman Iggidr, Gauthier Sallet, and Jean-Jules Tewa. Epidemiological models and Lyapunov functions. *Mathematical Modelling of Natural Phenomena*, 2(1):62–83, 2007.
- [10] Ali Khanafer, Tamer Başar, and Bahman Ghahsifard. Stability of epidemic models over directed graphs: A positive systems approach. *Automatica*, 74:126–134, 2016.
- [11] Hyoungh Jun Ahn and Babak Hassibi. Global dynamics of epidemic spread over complex networks. In *52nd IEEE Conference on Decision and Control*, pages 4579–4585. IEEE, 2013.
- [12] Navid Azizan Ruhi and Babak Hassibi. SIRS epidemics on complex networks: Concurrency of exact Markov chain and approximated models. In *2015 54th IEEE Conference on Decision and Control (CDC)*, pages 2919–2926. IEEE, 2015.
- [13] Mehran Mesbahi and Magnus Egerstedt. *Graph Theoretic Methods in Multiagent Networks*, volume 33. Princeton University Press, 2010.

- [14] Jesús Gómez-Gardeñes, Alessandro S de Barros, Suani TR Pinho, and Roberto FS Andrade. Abrupt transitions from reinfections in social contagions. *Europhysics Letters*, 110(5):58006, 2015.
- [15] Renato Pagliara, Biswadip Dey, and Naomi Ehrich Leonard. Bistability and resurgent epidemics in reinfection models. *IEEE Control Systems Letters*, 2(2):290–295, 2018.
- [16] VS Bokharaie, O Mason, and F Wirth. Spread of epidemics in time-dependent networks. In *Proceedings of the 19th International Symposium on Mathematical Theory of Networks and Systems–MTNS*, volume 5, 2010.
- [17] M. Ogura and V. M. Preciado. Stability of spreading processes over time-varying large-scale networks. *IEEE Transactions on Network Science and Engineering*, 3(1):44–57, Jan 2016.
- [18] P. E. Paré, C. L. Beck, and A. Nedić. Epidemic processes over time-varying networks. *IEEE Transactions on Control of Network Systems*, 5(3):1322–1334, Sep. 2018.
- [19] Vittoria Colizza and Alessandro Vespignani. Epidemic modeling in metapopulation systems with heterogeneous coupling pattern: Theory and simulations. *Journal of Theoretical Biology*, 251(3):450–467, 2008.
- [20] Joan Saldaña. Continuous-time formulation of reaction-diffusion processes on heterogeneous metapopulations. *Phys. Rev. E*, 78:012902, Jul 2008.
- [21] Wendi Wang and Xiao-Qiang Zhao. An epidemic model in a patchy environment. *Mathematical biosciences*, 190(1):97–112, 2004.
- [22] Yu Jin and Wendi Wang. The effect of population dispersal on the spread of a disease. *Journal of mathematical analysis and applications*, 308(1):343–364, 2005.
- [23] Michael Y Li and Zhisheng Shuai. Global stability of an epidemic model in a patchy environment. *Canadian Applied Mathematics Quarterly*, 17(1):175–187, 2009.
- [24] D Soriano-Paños, L Lotero, A Arenas, and J Gómez-Gardeñes. Spreading processes in multiplex metapopulations containing different mobility networks. *Physical Review X*, 8(3):031039, 2018.
- [25] Julien Arino, Jonathan R Davis, David Hartley, Richard Jordan, Joy M Miller, and P Van Den Driessche. A multi-species epidemic model with spatial dynamics. *Mathematical Medicine and Biology*, 22(2):129–142, 2005.
- [26] Lewi Stone, Frank Hilker, and Guy Katriel. SIR models. In *Encyclopedia of Theoretical Ecology*, pages 648–658. University of California Press, 2012.
- [27] F. Bullo. *Lectures on Network Systems*. CreateSpace, 1 edition, 2018. With contributions by J. Cortes, F. Dorfler, and S. Martinez.
- [28] Jean-Jacques E Slotine and Weiping Li. *Applied Nonlinear Control*, volume 199. Prentice Hall Englewood Cliffs, NJ, 1991.

- [29] Chai Wah Wu. On bounds of extremal eigenvalues of irreducible and m-reducible matrices. *Linear Algebra and its Applications*, 402:29–45, 2005.
- [30] W. K. Hastings. Monte carlo sampling methods using markov chains and their applications. *Biometrika*, 57(1):97–109, 1970.
- [31] H. K. Khalil. *Nonlinear Systems*. Prentice Hall, third edition, 2002.
- [32] Cameron Nowzari, Victor M Preciado, and George J Pappas. Optimal resource allocation for control of networked epidemic models. *IEEE Transactions on Control of Network Systems*, 4(2):159–169, 2015.
- [33] Abraham Berman and Robert J Plemmons. *Nonnegative Matrices in the Mathematical Sciences*, volume 9. Siam, 1994.