Random Propagation in Complex Systems : Nonlinear Matrix Recursions and Epidemic Spread

Thesis by

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To my family

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Abstract

This dissertation studies long-term behavior of random Riccati recursions and mathematical epidemic model. Riccati recursions are derived from Kalman filtering. The error covariance matrix of Kalman filtering satisfies Riccati recursions. Convergence condition of time-invariant Riccati recursions are well-studied by researchers. We focus on time-varying case, and assume that regressor matrix is random and identical and independently distributed according to given distribution whose probability distribution function is continuous, supported on whole space, and decaying faster than any polynomial. We study the geometric convergence of the probability distribution. We also study the global dynamics of the epidemic spread over complex networks for various models. For instance, in the discrete-time Markov chain model, each node is either healthy or infected at any given time. In this setting, the number of the state increases exponentially as the size of the network increases. The Markov chain has a unique stationary distribution where all the nodes are healthy with probability 1. Since the probability distribution of Markov chain defined on finite state converges to the stationary distribution, this Markov chain model concludes that epidemic disease dies out after long enough time. To analyze the Markov chain model, we study nonlinear epidemic model whose state at any given time is the vector obtained from the marginal probability of infection of each node in the network at that time. Convergence to the origin in the epidemic map implies the extinction of epidemics. The nonlinear model is upper-bounded by linearizing the model at the origin. As a result, the origin is the globally stable unique fixed point of the nonlinear model if the linear upper bound is stable. The nonlinear model has a second fixed point when the linear upper bound is unstable. We work on stability analysis of the second fixed point for both discrete-time and continuous-time models. Returning back to the Markov chain model, we claim that the stability of linear upper bound for nonlinear model is strongly related with the extinction time of the Markov chain. We show that stable linear upper bound is sufficient condition of fast extinction and the probability of survival is bounded by nonlinear epidemic map.

Contents

Chapter 1

Introduction

Mathematical models help us to understand and predict natural and social phenomena. Mathematical physics, modern economics, and meteorology are fields of science that frequently use such models. Of course, in these fields, a researcher faces a problem of choosing variables to take into account in her model. For instance, consider a spread of disease on a society. There are many factors that may affect the contagion; for example, genetics of the population and regional characteristics. Among many potential factors, a researcher could be interested in how a contagion depends on social network structures such as friendships, acquaintances, sexual relationships. In this case, to simplify her model, she may assume that all populations are homogeneous in other aspects. Another way to simplify the model is considering randomness of other characteristics. For instance, in the previous contagion model, the researcher may assume that each person's characteristics are drawn from a distribution. By this modeling, if the assumptions are appropriate, long-run behavior of the model would not depend on the assumptions. In this dissertation, we will study long-run behavior of models that are represented by nonlinear random matrix recursions, and epidemic spreads in complex networks.

1.1 Random Riccati Recursions

Estimation theory helps engineering and natural sciences for data analysis subject to random disturbances and decision makings under uncertain environments. Many estimation problems can be formulated as a minimum norm problem. There are different ways to formulate a problem of statistical estimation. The least square and the maximum likelihood estimations are frequently used techniques to find an optimal solution for given conditions.

1.1.1 Adaptive Filter

An adaptive filter is a computational device that models relationships between two signals iteratively. It is a powerful tool to model communications and statistical signal processing. An adaptive algorithm is useful when we analyze time-varying system with a little information. In those cases, the algorithm predicts future based on estimates, which are parameters of a model using a given data set and a statistical model. The algorithm performs better as more iterations are conducted.

An adaptive algorithm describes how the parameters are adjusted from a given time step to the next time step, and usually it is assumed to be linear. One of the most widely used linear adaptive filtering algorithm is the Least Mean Square (LMS) algorithm introduced by Widrow and Hoff [65]. LMS algorithm is operated by minimizing the cost function. To see more details, consider a zero-mean random variable d whose realizations are $\{d(0), d(1), \cdots\}$. d is the random variable which is to be estimated. Column vectors $u_0, u_1, \cdots$ are called regressors. Our goal is to find an optimal column vector w that minimizes error cost function

$$C_{LMS}(i) = \frac{1}{2}(d(i) - w(i-1)^T u(i))^2. \tag{1.1}$$

We can minimize the error cost $C_{LMS}(i)$ with the gradient vector

$$\frac{\partial}{\partial w(i-1)} C_{LMS}(i) = -(d(i) - w(i-1)^T u(i))u(i). \tag{1.2}$$

We update $w(i)$ by using a update rule

$$w(i) = w(i-1) + \mu(d(i) - w(i-1)^T u(i))u(i), \tag{1.3}$$

where μ is the step size. The LMS algorithm applies steepest gradient method to minimize error cost function at each time. It performs well when the step size μ is small enough, but a small μ may cause slow convergence.

The Recursive Least Square filter (RLS) algorithm is one of the most important linear adaptive filters. The RLS algorithm is similar to the LMS algorithm, but RLS uses a different cost function. At every iteration, the LMS algorithm minimizes the squared error of current state (1.1), however the RLS algorithm minimizes the sum of squared errors up to the current iteration. The error cost function of the RLS algorithm is defined as

$$C_{RLS}(i) = \sum_{j=1}^{i} (d(j) - w(i)^T u(j))^2. \tag{1.4}$$

The RLS update algorithm is given by

$$w(i) = w(i-1) + (d(i) - w(i-1)^T u(i))P(i)u(i) \tag{1.5}$$

$$P(i) = P(i-1) - \frac{P(i-1)u(i)u(i)^T P(i-1)}{1 + u(i)^T P(i-1)u(i)}. \tag{1.6}$$

The convergence rate of the RLS algorithms is much higher than the LMS algorithm, but it requires more computational complexity than the LMS algorithm. That is, the computational complexity of the LMS algorithm is proportional to the dimension of w; on the contrary, the computational complexity is proportional to the squared order of the dimension of w.

1.1.2 Kalman Filter and Riccati Equation

Linear time invariant models have been studied in the past decades, and the performance of estimation methods of linear time invariant models is well known. The Kalman filter, named after Rudolf E. Kálmán, was introduced in 1960, however it is still one of the most powerful algorithms today [31]. The Kalman filter has been successful because its computational requirement is not too cumbersome and the recursive properties are nice.

Consider the state space equation

$$\begin{cases} x_{i+1} = F_i x_i + G_i u_i \\ y_i = H_i x_i + v_i. \end{cases} \tag{1.7}$$

x_i is the true state at time i, which is not directly observable. y_i is an observation of x_i. u_i, v_i are i.i.d. random column vectors such that $u_i \sim N(0, Q_i)$ and $v_i \sim N(0, R_i)$. u_i and v_i represent process noise and observation noise, respectively. x_0 is a random column vector independent from $\{u_i, v_i\}$ for all i, and $x_0 \sim N(0, \Pi_0)$.

The Kalman filter suggests an optimal estimation algorithm based on the information at hand. $\hat{x}_{i|j}$ for $j \leq i$ is the best estimation based on $\{y_0, \cdots, y_j\}$. In other words,

$$\mathbb{E}[(\hat{x}_{i|j} - x_i) y_k^T] = 0 \quad \forall k \in \{0, 1, \cdots, j\}, \tag{1.8}$$

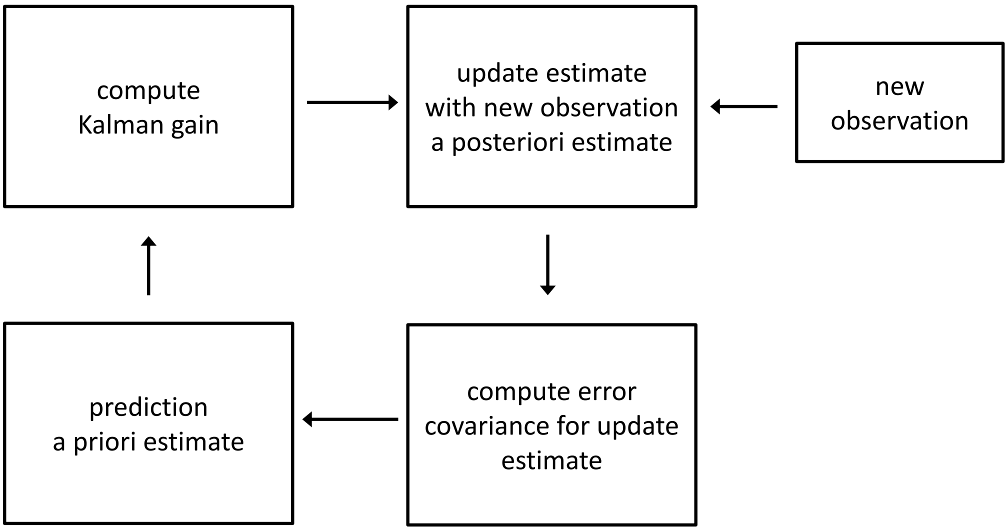

Figure 1.1: Schematic diagram of Kalman filter

$\hat{x}_{i|j}$ is the estimate that minimizes the mean-squared error covariance matrix

$$P_{i|j} = \mathbb{E}[(x_i - \hat{x}_{i|j})(x_i - \hat{x}_{i|j})^T], \tag{1.9}$$

based on the observations up to time j. We call $\hat{x}_{i+1|i}$ a priori estimate of x_{i+1} and $\hat{x}_{i+1|i+1}$ a posteriori state estimate of x_{i+1}.

$\mathbb{E}[u_i y_j^T] = 0$ for all $j \le i$ because u_i is independent to each v_k and u_j for all $j < i$. From this and the first equation of (1.7), we obtain the following a priori estimate and a priori state errors:

$$\hat{x}_{i+1|i} = F_i \hat{x}_{i|i}, \tag{1.10}$$

and

$$\begin{aligned} P_{i+1|i} &= \mathbb{E}[(x_{i+1} - \hat{x}_{i+1|i})(x_{i+1} - \hat{x}_{i+1|i})^T] && (1.11)\\ &= \mathbb{E}[(F_i x_i + G_i u_i - F_i \hat{x}_{i|i})(F_i x_i + G_i u_i - F_i \hat{x}_{i|i})^T] && (1.12)\\ &= F_i \mathbb{E}[(x_i - \hat{x}_{i|i})(x_i - \hat{x}_{i|i})^T] F_i^T + G_i \mathbb{E}[u_i u_i^T] G_i^T && (1.13)\\ &= F_i P_{i|i} F_i^T + G_i Q_i G_i^T. && (1.14) \end{aligned}$$

Having a priori estimate $\hat{x}_{i+1|i}$, suppose now that we have another observation y_{i+1}. To update a posteriori estimate with this observation, we assume that the estimate is the sum of a priori estimate and the new observation with linear weight:

$$\hat{x}_{i+1|i+1} = \hat{x}_{i+1|i} + K_{i+1}(y_{i+1} - \hat{y}_{i+1|i}). \tag{1.15}$$

$\hat{y}_{i+1|i}$ is the linear estimate of y_{i+1} based on the observations up to time i. $y_{i+1} - \hat{y}_{i+1|i}$ can be interpreted as the difference between the realized observation and the predicted observation. The linear weight of new observation, K_{i+1}, is called Kalman gain. From the second equation of (1.7) and the independence of v_i to all y_j for $j \leq i$,

$$\hat{y}_{i+1|i} = H_{i+1}\hat{x}_{i+1|i}. \tag{1.16}$$

The updated error covariance with new information follows:

$$\begin{aligned}
P_{i+1|i+1} &= \mathbb{E}[(x_{i+1} - \hat{x}_{i+1|i+1})(x_{i+1} - \hat{x}_{i+1|i+1})^T] && (1.17)\\
&= \mathbb{E}[(x_{i+1} - (\hat{x}_{i+1|i} + K_{i+1}(y_{i+1} - \hat{y}_{i+1|i})))(x_{i+1} - (\hat{x}_{i+1|i} + K_{i+1}(y_{i+1} - \hat{y}_{i+1|i})))^T] && (1.18)\\
&= \mathbb{E}[(I - K_{i+1}H_{i+1})(x_{i+1} - \hat{x}_{i+1|i})(x_{i+1} - \hat{x}_{i+1|i})^T(I - K_{i+1}H_{i+1})^T] \\
&\quad - \mathbb{E}[K_{i+1}v_{i+1}(x_{i+1} - \hat{x}_{i+1|i})^T(I - K_{i+1}H_{i+1})^T] \\
&\quad - \mathbb{E}[(I - K_{i+1}H_{i+1})(x_{i+1} - \hat{x}_{i+1|i})v_{i+1}^T K_{i+1}^T] + \mathbb{E}[K_{i+1}v_{i+1}v_{i+1}^T K_{i+1}^T]. && (1.19)
\end{aligned}$$

$\mathbb{E}[v_{i+1}x_{i+1}^T] = 0$ because v_{i+1} is independent with u_j for all j, which are the process noises that make x_{i+1} random vector. $\mathbb{E}[v_{i+1}\hat{x}_{i+1|i}^T] = 0$ because v_{i+1} is independent with y_j for $j \leq i$. (1.19) can be simplified by using $\mathbb{E}[v_{i+1}(x_{i+1} - \hat{x}_{i+1|i})^T] = 0$, $\mathbb{E}[(x_{i+1} - \hat{x}_{i+1|i})(x_{i+1} - \hat{x}_{i+1|i})^T] = P_{i+1|i}$, and $\mathbb{E}[v_{i+1}v_{i+1}^T] = R_{i+1}$ as follows:

$$\begin{aligned}
P_{i+1|i+1} &= (I - K_{i+1}H_{i+1})P_{i+1|i}(I - K_{i+1}H_{i+1})^T + K_{i+1}R_{i+1}K_{i+1}^T && (1.20)\\
&= K_{i+1}(H_{i+1}P_{i+1|i}H_{i+1}^T + R_{i+1})K_{i+1}^T - K_{i+1}H_{i+1}P_{i+1|i} - P_{i+1|i}H_{i+1}^T K_{i+1}^T + P_{i+1|i}. && (1.21)
\end{aligned}$$

Our goal is now to minimize (1.21) by choosing K_{i+1}, the optimal Kalman gain. Consider the following equation for known positive definite matrices A, C, a known matrix B, and an unknown matrix X:

$$XAX^T - XB - B^T X^T + C = (XA - B^T)A^{-1}(XA - B^T)^T - B^T A^{-1} B + C. \tag{1.22}$$

(1.22) is minimized when the positive semi-definite $(XA - B^T)A^{-1}(XA - B^T)^T$ is zero. By applying this to (1.21), we get K_{i+1} minimizing $P_{i+1|i+1}$:

$$K_{i+1} = P_{i+1|i} H_{i+1}^T (H_{i+1} P_{i+1|i} H_{i+1}^T + R_{i+1})^{-1}. \tag{1.23}$$

We focus on $\hat{x}_{i+1|i}$, a priori linear estimate and its error covariance matrix $P_{i+1|i}$. For simplicity, we remove $|i$ in the subscript, which represents the observation up to time i. The summarized update algorithm is

$$\hat{x}_{i+1} = F_i \hat{x}_i + F_i P_i H_i^T (H_i P_i H_i^T + R_i)^{-1} (y_i - H_i \hat{x}_i) \tag{1.24}$$

$$P_{i+1} = F_i P_i F_i^T - F_i P_i H_i^T (H_i P_i H_i^T + R_i)^{-1} H_i P_i F_i^T + G_i Q_i G_i^T. \tag{1.25}$$

Kalman showed that, when $F_i = F$, $G_i = G$, $H_i = H$, $R_i = R$ and $Q_i = Q$ for all i, the Riccati recursion (1.25) converges to a fixed point, which is a unique solution of Riccati equation:

$$P = FPF^T - FPH^T (HPH^T + R)^{-1} HPF^T + GQG^T, \tag{1.26}$$

if both detectability and stabilizability conditions are guaranteed. In Kalman filtering, the Riccati recursions represent evolution of the state error covariances. The result is powerful as it guarantees that the estimation error of the steady state is bounded.

The Riccati equation has received great interests in various fields. In particular, its application to control theory is prominent, from optimal control theory to robust and stochastic control theories. Even though time-invariant case is well-studied, there has been is no significant tool to analyze time-varying state space models. To study long-term properties, randomness and particular distribution is assumed in time-varying case. However, nonlinear structure of Riccati equation makes it hard to analyze.

1.1.3 Questions of Interest

Interesting problems in random Riccati recursions includes some additional random noises. Chen et al. studied linear stochastic systems with additive white Gaussian noise, where system matrices are random and adapted to the observation process [11]. The authors showed that in order for the standard Kalman filter to generate the conditional mean and conditional covariance of the conditionally Gaussian distributed state, it is sufficient for the random matrices to be finite with probability one at each time. Wang et al. provided a sufficient condition for stability of random Riccati equations [63]. The authors focused on L_r-stability of random Riccati equation, where $L_r\|A\| = \mathbb{E}[\|A\|^r]^{\frac{1}{r}}$ for random matrix A. Martins et al. studied the stabilizability of uncertain stochastic systems in the presence of finite capacity feedback [41]. Minero et al. studied the channel with the additional sources of non Gaussian randomness in control problems [44].

Researchers have been interested in models of a discrete-time system with random arrivals of observations. Sinopoli et al. studied the system beginning from the discrete Kalman filtering formulation. The authors modeled the arrival of the observation distributed according to Bernoulli distribution [59]. They studied statistical convergence properties of the estimation error covariance. Specifically, they proved existence of a critical value for the arrival rate of the observations. Kar et al. modeled the system of intermittent observations as a random dynamic system [32]. They studied asymptotic properties of the random Riccati equations. They showed that the sequence of random prediction error covariance matrices converges weakly to a unique invariant distribution whose support exhibits fractal behavior. Plarre et al. studied a critical probability of measurements for bounded covariance [54]. They investigated the system under the condition in which the system observation matrix restricted to the observable subspace is invertible.

Convergence and steady-state approximation of Riccati recursions with time-varying system matrices are interesting. Vakili et al. applied Stieltjes tranform to approximate eigendistribution of error covariance matrix of Riccati recursion when system matrices are time-varying and distributed according to a Gaussian distribution [60], [61]. The eigendistribution studied in the paper is the marginal distribution of one randomly selected eigenvalue of the matrix, i.e., $F_P(x) = \frac{1}{n}\sum_{i=1}^{n}\mathbb{P}[\lambda_i \leq x]$. In fact, the probability distribution function is the average of the probability distribution functions for all i-th largest eigenvalue of given random matrix. Their model assumed that the steady-state distribution of random Riccati recursions does exist and the steady-state eigendistribution also converges to a particular probability distribution as the size of the error covariance matrix increases.

Here is a short list of questions arising in Random Riccati recursions.

- How can we model the system if there is an additional noise?
- What is the dynamics of the system if the observation is arrived or not randomly?
- How can we prove the existence of steady-state of random Riccati recursions? Is there any way to describe its steady-state?

1.1.4 Contribution

One of the main questions in this dissertation is that :

- Can we determine whether the distribution of the error covariance matrix of random Riccati recursions converges in distribution? If so, does it converge geometrically fast?

We analyze time-varying Riccati recursions with random regressor matrix, H. We focus on geometric convergence of the probability distributions of error-covariance matrix. This strengthens results by Vakili et al. because Vakili et al. [60], [61] hastily assumed that the Riccati recursions converge to steady-state. Moreover, its geometric convergence promises that we can obtain a good estimated steady state distribution by a Monte Carlo simulation.

To see more details, we study the support of random Riccati recursion:

$$P^{(t+1)} = FP^{(t)}F^T - FP^{(t)}(H^{(t)})^T(R + H^{(t)}P^{(t)}(H^{(t)})^T)^{-1}H^{(t)}, P^{(t)}F^T + Q \tag{1.27}$$

where $P^{(t)}$ is the error covariance matrix at time t. $H^{(t)}$ is a time-varying regressor matrix which is assumed to be randomly distributed according to a particular probability distribution. We investigate the support of $P^{(t)}$ as a function of the initial error covariance matrix. The support of $P^{(t)}$ starting from a greater matrix has a bigger support beyond a finite time. In other words, the support of $P^{(t)}$ with $P^{(0)} = A$ is included the support of $P^{(t)}$ with $P^{(0)} = B$ after finite t if $B - A$ is positive definite. From a monotone property of Riccati equation, the maximal (minimal) element of support of $P^{(t)}$ with $P^{(0)} = B$ is greater than the maximal (minimal) element of support of $P^{(t)}$ with $P^{(0)} = A$. We will see that the minimal element of the support is identical after a finite t, and that it leads to that greater positive definite matrix has bigger support. The work on the support of Riccati recursions is a key result to understand the Riccari recursions because, to the best of our knowledge, the support of the Riccati recursions with time-varying regressor matrix has never appeared in the previous literature.

We compute the probability density function of the probability distribution of the error covariance matrix at a given time depending on an initial error covariance matrix. The matrix calculation is applied to do this. The regressor matrix, H, is the only factor that gives randomness to the Riccati recursions. If $P^{(0)}$, the initial error covariance matrix is fixed, $P^{(t)}$, the error covariance matrix at time t is determined by $H^{(0)}, H^{(1)}, \cdots, H^{(t-1)}$. We define a one-to-one map from the history of H, $H^{(0)}, H^{(1)}, \cdots, H^{(t-1)}$, to (L, O), a pair of a lower triangular matrix and an orthogonal matrix which simplifies the computation of the probability density function. Finding the map is a good application of the matrix calculation.

We also study the extension of the space of the positive definite matrices. Error covariance matrix of the Riccati equation is defined on the space of positive definite matrices. We extend the space by allowing zero and infinity as the eigenvalues of an error covariance matrix. By giving an extension on the space of positive definite matrices, we get a compact space.

To give a proof on geometric convergence of random Riccati recursions, we give a couple of intermediate results. The intermediate results include the support of the random Riccati recursions, computation of the probability density function, and extension on compact space. Each of them is meaningful as an independent result itself. The method used in this work can be applied to any random process to give a proof on the geometric convergence.

1.2 Epidemic Spread

Human beings are social creatures. We influence and are influenced by ourselves in the social network as part of it. In the past, we were only involved in small social networks such as a small village, or family-oriented relationships. By recent advances of related technologies, we are living in a world where a person's physical location does not matter to interact with others. For example, a researcher can discuss her ideas with other researchers via Skype. Furthermore, many social and economic decisions are influenced by existing social relationships. When a consumer is thinking of joining an online communication service (e.g., Skype or Google Talk), he considers how many of his friends and co-workers also have adopted the service.

One of the most critical phenomena that social networks matter is spread of diseases. A historical example is the Black Death. The Black Death was a devastating pandemic that results in the death of more than 100 million people in the middle of the 14th century. It is believed that the Black Death originated from central Asia and came to Europe along the Silk Road. After that, the Black Death peaked, as spreading throughout Europe. Of course, not all the infectious diseases spreads over a significant proportion of the population. We know that a number of people experience flu in the winter every year, but not the whole population.

Therefore, an interesting question is how does the social network structure affect disease transmissions. To understand and predict the dynamics of the spread of diseases is of obvious importance. The other half of this dissertation will pay attention to mathematical models of the spread of diseases through social networks.

1.2.1 Classical SIR Model

Researches on mathematical epidemic models began with classical papers by Kermack et al. [35]. Their seminal paper have contributed a lot on development of mathematical models for the spread of disease. In their paper, three epidemic states are assumed, which suggested a classical SIR model. The first state is “S”, which means susceptible. The people in the state S are healthy, but can get infected from others. The second state is “I”, which means infected. The people in the state I are infectious as well as infected. Susceptible people can get infected from other infected ones. The last state is “R”, which means recovered. The people in the state R are completely recovered and independent from the disease; that is, people in state R do not get infected any more because they have become immune to the disease. The model also assumed that each individual can reach at state R through state I, but not directly from S to R. Epidemics die out if no one is in state I. In the model, the population is constant. In other words, no birth or death from other reasons are admitted. This assumption is realistic if the life time span of disease is relatively shorter than the life time span of people.

We pay more attention to the works of classical SIR models because they have significantly influenced literature. Denote $S(t)$, $I(t)$ and $R(t)$ as the number of susceptible ones, infected ones and recovered ones, respectively. Since the number of people is constant, we have an equation on the sum of the number at each state:

$$S(t)+I(t)+R(t)=N, \tag{1.28}$$

where N is the number of people.

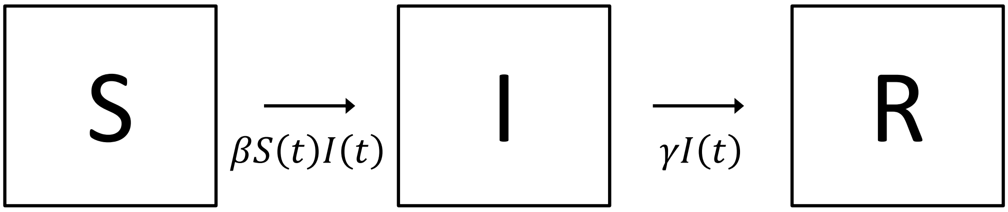

Figure 1.2: Flow diagram of SIR model

We assume that per unit time, an individual contacts with other individuals with rate of β_1, which is independent across the individuals. On a contact with an infected one, a susceptible one gets infected with probability β_2. Based on the two assumptions, we get a differential equation for $S(t)$:

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) \qquad \text{where} \qquad \beta = \beta_1\beta_2. \tag{1.29}$$

We also assume that the infected ones recover at rate γ per unit time. With this, the differential equations on $I(t)$ and $R(t)$ are defined.

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t) \tag{1.30}$$

$$\frac{dR(t)}{dt} = \gamma I(t) \tag{1.31}$$

Equipping with the above equations, we are now ready to analyze the spread of disease on the social network. The classical SIR model assumes that both the time and space which is the number of people in each state are continuous. The continuity assumption enables us to model this as a differential equation. This is a standard assumption in the literature.

The classical SIR model also assumes a well-mixed population, i.e., anyone can infect any other one. In fact, the homogeneous infection is not realistic. Instead of the homogeneous infection, many researchers assume heterogeneous interactions between individuals. The relationships between individuals are characterized by graphs consisting of a set of nodes representing individual people and edges representing the relationships between two individuals. The graph corresponds to a binary symmetric adjacency matrix. Each entry in the adjacency matrix is either 1 or 0 which represents that two particular nodes have relationship or not. In most of the cases the graph assumes no direction where the graph is undirected and corresponding adjacency matrix is symmetric. More complicated models are used to study epidemics on network. For example, weighted edge graph assigns real number to each edge which represents how deep the relationship between two nodes is. Directed graph assumes that the relationship between two nodes are not even.

There have been a lot of variations on the model. The SIR model with birth and death assumes that new nodes are added to the network with particular rates. The number of new coming nodes is proportional to the number of nodes in the network. Removal of nodes are also assumed, and it represents the death of nodes. Dynamics of differential equation and the long-run behavior is the main interests of the research [8], [34]. Besides the SIR model with birth and death process, a number of mathematical models have studied. The SIR model can be simplified to a SI model where recovery is not considered. In other words, once a node is infectious, then it can transmit disease forever. The SIS model admits infected nodes to get back to susceptibles.

1.2.2 Contact Process

Liggett studied SIS epidemic model called contact processes on graphs with countable nodes [39]. A contact process is a continuous time Markov chain defined on $\{0,1\}^S$ where S is a countable set having a graph structure. In the graph structure, $x \sim y$ for $x,y \in S$ means that two nodes x and y are connected by an edge. The degree of x is the number of $y \in S$ such that $y \sim x$. In the contact process, degree of node is assumed to be finitely bounded. For $\eta \in \{0,1\}^S$ and $u \in S$, $\eta(u) \in \{0,1\}$ represents u-th coordinates of η. Denote $\eta_x \in S$ as flipping x-th coordinate from η. In other words,

$$\eta_x(u) = \eta(u) \text{ if } u \neq x \quad \text{and} \quad \eta_x(u) = 1 - \eta(u) \text{ if } u = x. \tag{1.32}$$

For a given infection rate $\beta > 0$, the contact process is defined as

$$\eta \to \eta_x \text{ at rate } \begin{cases} 1 & \text{if } \eta(x) = 1, \\ \beta|\{y : y \sim x, \eta(y) = 1\}| & \text{if } \eta(x) = 0. \end{cases} \tag{1.33}$$

An interpretation is that an infected node x represented as $\eta(x) = 1$ recovers with rate 1, and a healthy node x represented as $\eta(x) = 0$ get infected from its infected neighbors at a rate proportional to the number of infected neighbors. It is clear that the distribution where all the nodes are healthy with probability 1 is invariant distribution, because there is no transmission of disease if all the nodes are healthy.

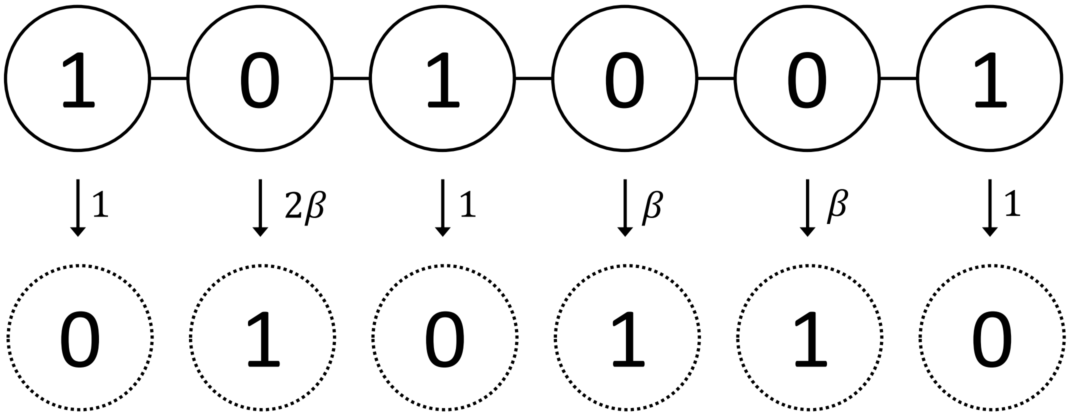

Figure 1.3: The contact process on a 1-dimensional lattice. Solid circles represent current state. Dotted circles represent possible change of the current state.

If S is finite, η eventually goes to all-zero state from the theory of finite state Markov chains. Liggett studied contact processes on the d-dimensional integer lattices. His results showed that there exists critical value β_c such that

- if $\beta \leq \beta_c$, all-healthy distribution is the only invariant distribution, and the probability distribution converges to it weakly for any initial distribution;
- if $\beta > \beta_c$, there exists another invariant probability distribution ν, and the probability distribution converges to ν weakly for any initial distribution.

One of the key differences of this contact process from classical model is that this process is defined on a discrete space $\{0,1\}^S$. Draief, Ganesh et al. and Mieghem et al. applied a continuous-time Markov chain to model epidemic dynamics [16], [23], [42]. Ganesh et al. studied contact processes on finite graphs, focusing on how extinction time is related to graph structures.

Furthermore, a contact process depends on the graph structure, which does not assume specific homogeneous interactions. Each node is directly influenced by its neighbors. Since heterogeneous interaction is considered, the graph structure of network plays a central role to construct epidemic dynamic system.

1.2.3 Random Networks

Diseases are transmitted from one individual to another by contact, and the pattern of contact forms network whose structure gives a lot of effect for the dynamics of epidemics. In classical models, each individual has an equal chance of contact with others. Probably it is an unnatural assumption, but it provides a remarkable tractability: it allows one to represents a diffusion of disease by a differential equation, which can be solved analytically or numerically. In fact, we can go beyond this restriction by incorporating a full network structure into the model. The random graphs provide a good basis for doing this.

In network analysis, Erdös-Rényi model is one of the most important random graph models [19]. In the $G(n, p)$ model, a graph is constructed by connecting n nodes randomly. Each edge is included in the graph with probability p, which is independent across the edges. An Erdös-Rényi random graph has a number of interesting properties as a model of a social network. For instance, the model shows a phase transition when $p(n)$, the probability of connecting each nodes, as a function of n, satisfies $p(n) = \dfrac{c}{n}$. A component is a subset of nodes in the social network that any two nodes are connected by a path consists of edges in the original social network. If c is small, we can expect that most nodes are disconnected from one another, and the size of each component is small, and vice versa. In fact, an Erdös-Rényi random graph has no components of size larger than $O(\log n)$ with high probability if $c < 1$. On the contrary, most nodes have higher chance to be connected to each other if c is large. If $c > 1$, the Erdös-Rényi random graph has a giant component whose size is $\Theta(n)$ with high probability. Another interesting phenomenon is connectivity of random graphs. Sharp threshold of connectivity on the Erdös-Rényi random graph is $p(n) = \frac{\log n}{n}$. The Erdös-Rényi random graph has a pair of disconnected nodes with high probability if $p(n) = \frac{c \log n}{n}$ for $c < 1$. Every pair of nodes is connected with high probability if $p(n) = \frac{c \log n}{n}$ for $c > 1$.

Random geometric graph model was devised to pay attention to the physical distance between nodes. Random geometric graphs are created by forming a link wherever the distance between any pair of nodes is less than a specified distance [52]. Specifically, a random geometric graph $G(n, r)$ is obtained by placing n nodes uniformly at random on a two-dimensional unit torus. Two nodes are connected if the Euclidean distance of between the nodes is smaller than r. The random geometric graph model is used successfully in applications where the physical distance between two nodes is an important factor of connectivity. The critical parameter for connectivity of random geometric graph model is similar to one of the Erdös-Rényi random graph model. Sharp threshold of connectivity on random geometric graph model satisfies $\pi r(n)^2 = \frac{c \log n}{n}$ with $c = 1$. The random geometric graph is connected with high probability when $c > 1$, and it is not connected with high probability when $c < 1$. However, the random graph has bigger probability of existence of edge if two nodes consisting the edge are connected to a same node. It is different from Erdös-Rényi random graph where the probability of existence for an edge is independent to each other.

With the comparison to real network model, a lot of random graph models describing real network have been proposed. One of them is “small-world” network. In the real networks, many pairs of people are actually connected by a short chain of acquaintance. In other words, even though two particular people live far from each other, they can reach to the other with the small number of intermediates in the real networks. Watts and Strogatz suggested small-world network where the required number of intermediates in the chain from any two particular nodes is relatively smaller than one of Erdös-Rényi model [64]. In the small-world network, diseases will spread through a community much faster than Erdös-Rényi model. One of the real-world effect which Erdös-Rényi model does not provide is peer-effect. If two nodes are related to a particular node, the probability that two nodes are related is higher than arbitrary two nodes. Roughly speaking, if two people know a particular person, it is more likely that the two people know each other. The small world network also provides peer-effect.

One of the most important random graph models describing real world was suggested by Barabási and Albert [4]. The random graph constructed by the model is scale-free network whose degree is distributed according to a power law. In a scale-free network, $P(k)$, the fraction of nodes connected to k other nodes satisfies $P(k) \sim k^{-\gamma}$ asymptotically for constant γ. This separates the Barabási-Albert model from other random graph families where $P(k)$ decreases exponentially as k increases. The Barabási-Albert model is constructed following preferential attachment condition. The graphs evolve over time in such a way that nodes with high degree are more likely to get additional edges than nodes with low degree. In fact, the models have the probability of attaching a new node to a particular previous node at a specific time point should be proportional to the degree of that node at that time. The model gives effect where rich nodes get richer than others. The Barabási-Albert model gets spotlight as it turns out that many kinds of computer networks, including the internet and World Wide Web is scale-free network.

1.2.4 Discrete Time Model

Continuous time model including classical SIR model and contact process assumes that the time period can be divided into infinitely small intervals. It is acceptable in various real world problems, however it is not in some situations. For example, consider a person living with family and working at company. He has more chance to contact with his family at night, but works at company and has more chance to contact with his colleagues during daytime. In this case, applying continuous time homogeneous model is not appropriate. Discrete time model is useful when dividing time interval into infinitely small pieces is not reasonable. Discrete time model is also useful when the interaction among the nodes are periodic. We can define unit interval as the period of the interaction.

A classic discrete time model of infectious disease transmission includes Reed-Frost model. In the classical Reed-Frost model, the disease is transferred directly from infected nodes to others. A susceptible node gets infected and is infectious to others only within the following time interval after contact with an infectious node. The contact probability between any two nodes are identical in the group within time interval. After a unit time interval, infectious nodes recover from the disease and become immune to the disease. Comparing to SIR model, a susceptible node in the class “S” gets infected after contact to infectious nodes. An infected node is in the class “I” and infectious to the susceptibles only within the unit time interval. After that, the infected node recovers and removed from epidemic dynamics in the class “R”.

At each time t, the number of infected nodes is denoted as C_t, and the number of susceptibles is denoted as S_t. The basic Reed-Frost model assumes homogeneity of risk of infection in the network. Denote p as the probability of contact between any two nodes in the network, then $1-p$ is the probability that the two nodes do not have contact. A susceptible node does not get infected if the node does not have contact with any infected nodes during the unit interval of time. The model also assumes that the contact to each node is independent. We may use independence assumption to compute the probability of no contact to any of infected by multiplying the probabilities. We can then find the probability distribution of the number of infected nodes in the next generation.

$$\mathbb{P}[C_{t+1}=k|C_t,S_t]=\binom{S_t}{k}(1-(1-p)^{C_t})^k\left((1-p)^{C_t}\right)^{S_t-k} \tag{1.34}$$

S_{t+1}, the number of susceptibles in the next generation is decided by $S_{t+1}=S_t-C_{t+1}$.

The Reed-Frost model is widely studied because the model is simple and provides valuable insights. Abbey applied the Reed-Forest model to analyze various real-world data[1]. Ortega et al. applied fuzzy dynamical system to the Reed-Frost model for epidemic spreading taking into account uncertainties in the diagnostic of the infection[48].

The discrete time models also have been developed by admitting graph structure. Most of early works were conducted on the random graph model. Andersson studied stochastic process for exposing one or several given components of a random graph and applied the process to epidemic model[3]. Durrett studied how epidemic spread on networks commonly used in ecological models [17]. Chakrabarti et al. and Wang et al. suggested nonlinear epidemic map defined on fixed graph topology [10] [62]. Their research reveals that extinction and spread is deeply-related with the largest eigenvalue of adjacency matrix. Ahn et al. showed that the marginal probability of each node's infection for given closed network converges and the limit point depends on the largest eigenvalue of the network [2].

1.2.5 Applications and Questions of Interest

Epidemic models can be applied to the other field. For example, there is a basic similarity between the spread of information and the transmission of infectious disease between the individuals. Both are processes in which spread is based on the contact. Huang et al. and Jacquet et al. studied the propagation speed of information on the network [28], [29]. Effective modification of graph structure on given condition to improve propagation speed is one of the interesting problems. The research on this topic can be applied to effective establishment of computer network.

Applying SIR model to rumors spreading, “S” represents the state where each individual has no information about the rumors if the person is in the state S. “I” represents the state where each individual is exposed to the rumors and wants to transfer the rumors to acquaintances. “R” represents the state where each individual is not excited with the rumor any more. Each individual in the state R is tired from transferring the rumors and do not care any more. An interesting question on the size of people who are exposed to the rumors rises here. The size of eventual information holder distributes with particular probability distribution if probability model is admitted. The distribution depends on the topology of network, rate of converting each individual at the state S to the state I, and the rate from state I to R. Expected number of eventual information holder is well-defined if the probability on transition is defined. Asymptotic behavior of the expectation is an interesting question. Kenah et al. and Moore et al. applied percolation theory to study the infection of giant component in the graph [33], [45].

Vaccinations are one of the most effective ways to prevent disease with low cost. A random vaccination strategy vaccinates a fraction of the population randomly, using no knowledge of the network, however this is not an effective way. Cohen et al. and Madar et al. modified the random vaccination by vaccinating a higher degree nodes of randomly selected nodes [13], [40]. Miller et al. studied the effectiveness of targeted vaccination at preventing the spread of infectious disease by comparing vaccination strategies based on no information to complete information on the network [43]. Optimal vaccination strategy for given information is a topic many researchers are still working on.

On the contrary to the epidemic spread where one of the most important topic is how to prevent the disease to spread on the network, information diffusion focuses on how to spread the information. The idea is applied to viral marketing because a lot of people get information on goods from their friends or neighbors. The study to make the information on goods spread widely on the network. Phelps et al. and Richardson et al. studied viral marketing using epidmic model [53], [55].

Here is a short list of questions arising in epidemic spread.

- How the network topology affects the speed of information propagation? What is the effective way to modify network to improve the speed?
- What is the size of network exposed to the disease in the SIR model? Can we apply this to other epidemic models?
- How can we measure the effect of vaccination? What are the cost-effective vaccination algorithms?
- How can we apply epidemic model to the viral marketing? How can we measure the effect of the marketing?
- What is the dynamics of SIS epidemic models?

1.2.6 Contribution

The works on epidemic spreads in this thesis are conducted to answer the following questions :

- Can we study the global dynamics of the nonlinear epidemic model? Can we say what happens when the linearized model is unstable?
- Can we relate this to the “true” epidemic model which is a Markov chain with 2^n states?

In this dissertation, we analyze the various epidemic models. The main works are conducted on the discrete-time model. In the Chapter 3, we analyze the dynamics of the nonlinear epidemic map where domain represents each node's marginal probability of being infected. The dynamics of epidemic map is simple when the epidemics dies out. The origin which represents the extinction of epidemics are globally stable. On the contrary to the previous work which focuses on the extinction of epidemics or how to eradicate epidemics, we analyze the dynamics of epidemics when the epidemics do not die out. When the Jacobian matrix of the nonlinear map at the origin is not stable, the origin is an unstable fixed point of the nonlinear epidemic map. In the epidemic map proposed by Chakrabarti et al., there exists a unique nontrivial fixed point other than the origin. The nontrivial fixed point is globally stable, i.e., every point other than the origin converges to the nontrivial fixed point by time passes.

We also analyze the second model which admit immune effect. The immune-admitting model also has the unique nontrivial fixed point. However, the nontrivial fixed point in the immune-admitting model is not always stable. To analyze this, we give necessary and sufficient conditions for the nontrivial fixed point being locally stable. We apply the stability condition to the random graph families, and show that the nontrivial fixed point is locally stable with high probability if $\mathbb{P}[(d_{\min}^{(n)})^2 > a \cdot d_{\max}^{(n)}]$ goes to 1 as n goes to infinity for any fixed $a > 0$, where $d_{\min}^{(n)}$ and $d_{\max}^{(n)}$ are the minimum and the maximum degree of given random graph family with n vertices. The result can be applied to any random graph families. Since the degree distribution of Erdös-Rényi model is concentrated on the expected degree, the nontrivial fixed point is locally stable with high probability.

We propose a continuous time epidemic model. The continuous time model is based on the nonlinear epidemic map which is analyzed in the previous section. The origin is also an equilibrium point, and stability condition of the origin is same with one of the discrete time model. There also exists a unique nontrivial equilibrium point if the origin is unstable. The nontrivial fixed point is globally stable in the continuous time model even though the model is based on the immune-admitting model where stability of nontrivial fixed point is not guaranteed. To prove the stability, we suggest a Lyapunov function that is always decreasing except equilibrium points.

In the Chapter 4, we work on the Markov chain model on finite graph. In the Markov chain model each node is either healthy or infected, which gives 2^n possible states where n is the number of nodes in the network. The mass probability on all-the-healthy state is unique stationary distribution in the Markov chain model on finite graph because there is no more spread of disease. Since all the initial distribution on the Markov chain converges to the stationary distribution after long enough time, we study the “long enough time” which does not give any practical information. We give an upper bound of the probability that the epidemics does not die out until time t when the initial state is given.

To give a rigorous proof, we define a partial order which is defined on the set of the probability distributions on all the possible 2^n states. The upper bound is provided using the nonlinear epidemic map which is studied in the previous chapter. The nonlinear epidemic map is an approximation of the Markov chain model, and the upper bound shows that two models are closely related. With the upper bound, we provide a practical result that the mixing time is $O(\log n)$ if the origin is globally stable in the nonlinear epidemic map. The $O(\log n)$ mixing time can be proved without the partial order which is necessary to give an upper bound of the survival probability using the nonlinear epidemic map. The alternative proof for $O(\log n)$ mixing time uses linear programming method. We apply this result to show that the Markov chain model based on the immune-admitting nonlinear epidemic map also has $O(\log n)$ mixing time if the origin is stable in the discrete time model.

Finally, we study the special case of continuous time Markov chain model, where the underlying graph is fully connected. We show that the expect extinction time of disease is exponentially long if the origin is not stable in the nonlinear epidemic map. Since we cannot observe the epidemic extinction if the extinction time is exponentially long, it means that the epidemics do not die out practically.

Chapter 2

Random Riccati Equation

2.1 Introduction

In this chapter, we discuss geometric convergence of random Riccati recursions. We use superscript for time index in this chapter. Consider a linear time-varying state-space model of the form of

$$\begin{cases} x^{(t+1)} = F^{(t)}x^{(t)} + G^{(t)}u^{(t)} \\ y^{(t+1)} = H^{(t)}x^{(t)} + v^{(t)} \end{cases} \qquad \mathbb{E}\begin{bmatrix} u^{(t)} \\ v^{(t)} \end{bmatrix}\begin{bmatrix} (u^{(t)})^T & (v^{(t)})^T \end{bmatrix} = \begin{bmatrix} Q^{(t)} & 0 \\ 0 & R^{(t)} \end{bmatrix} \tag{2.1}$$

where $x^{(t)} \in \mathbb{R}^n$ is the unobserved state vector, $y^{(t)} \in \mathbb{R}^m$ is the m-dimensional observed measurement vector. $u^{(t)} \in \mathbb{R}^p$ and $v^{(t)} \in \mathbb{R}^m$ are zero-mean white noises which represent process and measurement noise respectively. $F^{(t)} \in \mathbb{R}^{n\times n}$, $G^{(t)} \in \mathbb{R}^{n\times p}$, and $H^{(t)} \in \mathbb{R}^{m\times n}$ are system matrices. The initial state of the system, $x^{(0)}$ is also considered to be zero-mean random vector which is independent from any of $u^{(t)}$ and $v^{(t)}$.

It is well-known that optimal estimate of $x^{(t)}$ can be recursively expressed as

$$\hat{x}^{(t+1)} = F^{(t)}\hat{x}^{(t)} + F^{(t)}P^{(t)}(H^{(t)})^T(R + H^{(t)}P^{(t)}(H^{(t)})^T)^{-1}(y^{(t)} - H^{(t)}\hat{x}^{(t)}) \tag{2.2}$$

In the time-invariant case, i.e.,

$$F^{(t)} = F, \quad G^{(t)} = G, \quad H^{(t)} = H, \quad Q^{(t)} = Q, \quad R^{(t)} = R \tag{2.3}$$

the problem is well-studied. The minimum mean square error recursive estimator of $x^{(t)}$ based on the $y^{(t)}$ is a Kalman filter. The estimation error covariance matrix $P^{(t)} = \mathbb{E}(x^{(t)} - \hat{x}^{(t)})(x^{(t)} - \hat{x}^{(t)})^T$

provided Kalman filter satisfies the following Riccati recursions :

$$P^{(t+1)} = FP^{(t)}F^T - FP^{(t)}H^T(R+HP^{(t)}H^T)^{-1}HP^{(t)}F^T + GQG^T \tag{2.4}$$

It is well-known that $P^{(t)}$ in (2.4) converges if (F,G) is stabilizable and (F,H) is detectable. The pair (F,G) is called stabilizable if and only if there is no left eigenvector of F, corresponding to an unstable eigenvalue of F, that is orthogonal to G. The pair $\{F,H\}$ is called detectable if and only if $\{F^T,H^T\}$ is stabilizable. [30]

We study the Riccati recursions when the regressor matrix $H^{(t)}$ is time-varying. We assume that $H^{(t)}$ is random matrix distributed according to a given distribution. Measuring average-eigenvalue distribution of $P^{(t)}$ was studied by Vakili et al. [60]. We focus on convergence of probability distribution of $P^{(t)}$. Specifically, we prove that the probability distribution of $P^{(t)}$ converges geometrically fast.

In the next section, we describe the random Riccati recursions and the probability distribution of $H^{(t)}$, the regressor matrix. We also describe the general property of geometric convergence defining the distance between two probability measures. To get geometric convergence, we need to verify that the maximum distance between measures at particular time is strictly less than 1, which is the convergence rate. We show that the distance between any two probability distributions of $P^{(t)}$ depending an initial point are strictly less than 1 after particular time depending on size of $H^{(t)}$. To prove this, we show that the probability distribution with any initial point has a common area of support which has strictly positive measure. We apply a well-known topological property that a continuous function defined in a compact space has a maximum. To apply this, we consider the probability distribution with an initial point as a map from an initial point to a measure space. We show that this is a continuous map. To get a compact space we compactify $\mathbb{S}^n_{++}$, the space of positive definite matrices by admitting 0 and ∞ as eigenvalues of matrices. The main result is obtained by combining all the intermediate results studied in this chapter.

2.2 Model Description

Let $\mathbb{S}^n$ denote family of $n \times n$ symmetric matrices, $\mathbb{S}^n_+$ denote family of n by n positive-semidefinite matrices, and $\mathbb{S}^n_{++}$ denote family of n by n positive definite matrices. The Riccati recursions with time-varying H is defined as follows.

$$P^{(t+1)} = FP^{(t)}F^T - FP^{(t)}(H^{(t)})^T(R + H^{(t)}P^{(t)}(H^{(t)})^T)^{-1}H^{(t)}P^{(t)}F^T + Q \tag{2.5}$$

$P^{(0)} \in \mathbb{S}^n_{++}, Q \in \mathbb{S}^n_{++}, R \in \mathbb{S}^m_{++}$, and $F \in \mathbb{R}^{n\times n}$ in (2.5). m by n random matrix $H^{(t)}$ is the only factor that generates randomness of the system. We assume that $H^{(t)}$ is independently and identically distributed according to a given probability density function. We further assume that the probability distribution of $H^{(t)}$ satisfies several conditions.

Definition 1 *p_H is a probability density function of H i.e., $\mathbb{P}[H^{(t)} \in E] = \int_E p_H(H)\mathrm{d}H$ for any measurable set $E \subset \mathbb{R}^{m\times n}$ satisfying the following conditions.*

(a) The support of p_H is $\mathbb{R}^{m\times n}$. That is, $\mathbb{P}[H^{(t)} \in E] > 0$ if E has positive Lebesgue measure.

(b) $p_H : \mathbb{R}^{m\times n} \to \mathbb{R}_+$ is continuous.

(c) It decays faster than any polynomial. For any $d > 0$, there exists M_d such that $p_H(H) < \|H\|_F^{-d}$ for all $\|H\|_F > M_d$ where $\|\cdot\|_F$ is Frobenius norm defined by square-root of all elements' square-sum.

Example 2.2.1 *A standard normal distribution $p_H(H) = (2\pi)^{-\frac{mn}{2}}\exp(-\frac{1}{2}\|H\|_F^2)$ is a distribution satisfying all the conditions in definition 1.*

We do not assume that each element of $H^{(t)}$ is independent to each other.

Lemma 2.2.2 *There are diagonal matrix $\widetilde{R}$ and random matrices $\widetilde{H}^{(t)}$ which gives the same probability distribution to the system with R and $H^{(t)}$.*

Proof: For fixed $\widetilde{O}$, define $\widetilde{R} = \widetilde{O}R\widetilde{O}^T$. We can rewrite (2.5) with $\widetilde{H}^{(t)} = \widetilde{O}H^{(t)}$

$$P^{(t+1)} = FP^{(t)}F^T - FP^{(t)}(\widetilde{H}^{(t)})^T(\widetilde{R} + \widetilde{H}^{(t)}P^{(t)}(\widetilde{H}^{(t)}))^T)^{-1}\widetilde{H}^{(t)}P^{(t)}F^T + Q \tag{2.6}$$

We can interpret that the probability distribution function of $\widetilde{H}^{(t)}$ is rotated from one of $H^{(t)}$ by multiplying the orthogonal matrix $\widetilde{O}$. It is easy to see that the probability density function of $\widetilde{H}^{(t)}$ also satisfies all the conditions in definition 1. Moreover, the system with $\widetilde{R}$, $\widetilde{H}^{(t)}$ and random Riccati recursion with R, $H^{(t)}$ have the same probability distribution. ■

We can assume that R is a diagonal matrix without loss of generality by Lemma 2.2.2. The assumption that R is diagonal simplifies the calculation of $P^{(t+1)}$ with $P^{(t)}$ and each column of $H^{(t)}$. It is convenient to verify the support of $P^{(t)}$ with a given initial point $P^{(0)}$.

Definition 2 *$\mu_P^{(t)}$ is a probability measure such that $\mu_P^{(t)}(E) = \mathbb{P}[P^{(t)} \in E | P^{(0)} = P]$.*

$\mu_P^{(t)}$ is the probability distribution of $P^{(t)}$ where its initial point is given as P. It is necessary to define a metric on the space of probability measures to show geometric convergence of the probability measure. We show that the distance between any two initial probability distributions converges geometrically fast using the metric. We use the total variation distance.

Definition 3 *For two measures μ, ν, $d_{TV}(\mu, \nu) = \sup_S |\mu(S) - \nu(S)|$.*

We define the support of $\mu_P^{(t)}$ depending on an initial point. The support of $P^{(t)}$ plays a central role in this chapter.

Definition 4 *$Supp_P^{(t)}$ is the support of $\mu_P^{(t)}$ when $P^{(0)} = P$. That is, $x \in Supp_P^{(t)}$ if and only if every open ball centered at x has positive measure under $\mu_P^{(t)}$. In other words,*

$$Supp_P^{(t)} = \{x \in \mathbb{S}_+^n : \forall B(x,\varepsilon), \mu_P^{(t)}(B(x,\varepsilon)) > 0\} \tag{2.7}$$

2.3 General Property for Geometric Convergence

In this section, we describe how total variation distance of two probability measures decays geometrically fast. The material in this section is not only for random Riccati recursions, but for any random process. We follow the notation from [15].

Definition 5 $\mathbb{P}^{(t)}(\zeta, E) = \mathbb{P}[P^{(t)} \in E | P^{(0)} = \zeta]$. $M_E^{(t)} = \sup_{\zeta} \mathbb{P}^{(t)}(\zeta, E)$, $m_E^{(t)} = \inf_{\zeta} \mathbb{P}^{(t)}(\zeta, E)$.

The following inequality shows that the supremum of probability measure on particular measurable set depending on an initial point decreases as time passes.

$$\begin{aligned} M_E^{(t+l)} &= \sup_{\alpha} \mathbb{P}^{(t+l)}(\alpha, E) && (2.8) \\ &= \sup_{\alpha} \int \mathbb{P}^{(l)}(\xi, E)(\mathbb{P}^{(t)}(\alpha, \mathrm{d}\xi)) && (2.9) \\ &\leq \sup_{\alpha} \int M_E^{(l)}(\mathbb{P}^{(t)}(\alpha, \mathrm{d}\xi)) = M_E^{(l)} && (2.10) \end{aligned}$$

Similarly, we can argue that $m_E^{(t+l)} \geq m_E^{(l)}$

$$\cdots \le m_E^{(t)} \le m_E^{(t+l)} \le \cdots \le M_E^{(t+l)} \le M_E^{(l)} \le \cdots \tag{2.11}$$

If $\lim_{t\to\infty} M_E^{(t)} = \lim_{t\to\infty} m_E^{(t)}$ for every measurable set E, the probability measure converges to a steady state. The steady state is also a probability measure whose value on E is a limit of $m_E^{(t)}$ and $M_E^{(t)}$.

$$M_E^{(t+l)} - m_E^{(t+l)} \tag{2.12}$$

$$= \sup_{\alpha,\beta} \mathbb{P}^{(t+l)}(\alpha,E) - \mathbb{P}^{(t+l)}(\beta,E) \tag{2.13}$$

$$= \sup_{\alpha,\beta} \int \mathbb{P}^{(l)}(\xi,E)(\mathbb{P}^{(t)}(\alpha,\mathrm{d}\xi) - \mathbb{P}^{(t)}(\beta,\mathrm{d}\xi)) \tag{2.14}$$

$$\le \sup_{\alpha,\beta,S} \int_S M_E^{(l)}(\mathbb{P}^{(t)}(\alpha,\mathrm{d}\xi) - \mathbb{P}^{(t)}(\beta,\mathrm{d}\xi)) + \int_{S^c} m_E^{(l)}(\mathbb{P}^{(t)}(\alpha,\mathrm{d}\xi) - \mathbb{P}^{(t)}(\beta,\mathrm{d}\xi)) \tag{2.15}$$

$$= \sup_{\alpha,\beta,S} \int_S (M_E^{(l)} - m_E^{(l)})(\mathbb{P}^{(t)}(\alpha,\mathrm{d}\xi) - \mathbb{P}^{(t)}(\beta,\mathrm{d}\xi)) \tag{2.16}$$

$$= \left(M_E^{(l)} - m_E^{(l)}\right)\left(\sup_{\alpha,\beta,S} \mathbb{P}^{(t)}(\alpha,S) - \mathbb{P}^{(t)}(\beta,S)\right) \tag{2.17}$$

Definition 6 $\pi^{(t)} = \sup_{\alpha,\beta} d_{TV}(\mu_\alpha^{(t)}, \mu_\beta^{(t)}) = \sup_{\alpha,\beta,S} \mathbb{P}^{(t)}(\alpha,S) - \mathbb{P}^{(t)}(\beta,S)$

We can interpret $\pi^{(t)}$ as the maximum distance of probability distributions from any initial point at time t. If $\pi^{(t)} < 1$ for particular t, then geometric convergence follows. It is obvious that $\pi^{(t)} \le 1$ for every t. However, in many mathematical problems proving that supremum of some set where every element is less than or equal to 1 is strictly less than 1 is challenging.

2.4 Common Area of Support

$\pi^{(t)} = 1$ if $Supp_\alpha^{(t)}$ and $Supp_\beta^{(t)}$ are disjoint for some α, β. As a result, the system does not converge geometrically fast if $Supp_\alpha^{(t)}$ and $Supp_\beta^{(t)}$ are disjoint for some α, β. We investigate particular t where $Supp_\alpha^{(t)}$ and $Supp_\beta^{(t)}$ have common area of the supports having positive probability measure. We study the support of $P^{(t)}$ for a given initial point. Specifically, we compare $Supp_A^{(t)}$ to $Supp_B^{(t)}$ when the matrix B is greater than A, i.e., $B - A \in \mathbb{S}_+^n$. It is well-known that Riccati equation is monotone.

$$\begin{aligned}&\left(FBF^T - FBH^T(R+HBH^T)^{-1}HBF^T\right) - \left(FAF^T - FAH^T(R+HAH^T)^{-1}HAF\right) \in \mathbb{S}^n_+\\&\text{if } B - A \in \mathbb{S}^n_+\end{aligned} \tag{2.18}$$

Since Riccati equation is monotone, the maximal elements in $Supp_B^{(t)}$ is greater than $Supp_A^{(t)}$ if B is greater than A i.e., $B - A \in \mathbb{S}^n_+$. It is easy to see that the maximal element of $Supp_A^{(1)}$ is $F^TAF + Q$. If F is nonsingular, monotonicity of the maximal element becomes strict. However, it is not trivial to check that whether the minimal element in $Supp_A^{(t)}$ is always strictly smaller than $Supp_B^{(t)}$. We show that the minimal element of $Supp_A^{(t)}$ is in $Supp_B^{(t)}$ after finite t. As a result, $Supp_B^{(t)}$ includes $Supp_A^{(t)}$ after that. To give a proof, we suggest an algorithm to choose regresor matrix $H^{(t)}$ to make $B^{(t)}$ equal to $A^{(t)}$ for given $A^{(t)}$.

$R = diag(r_0, \cdots, r_{m-1})$ without loss of generality by Lemma 2.2.2. For each row vector $(H^{(t)})_j$ such that $H^{(t)} = ((H^{(t)})_0^T \cdots (H^{(t)})_{m-1}^T)^T$,

$$\begin{aligned}&P^{(t)} - P^{(t)}(H^{(t)})^T(R + H^{(t)}P^{(t)}(H^{(t)})^T)^{-1}H^{(t)}P^{(t)}\\&= ((P^{(t)})^{-1} + H^{(t)}R^{-1}(H^{(t)})^T)^{-1} = \left((P^{(t)})^{-1} + \sum_{j=0}^{m-1} \frac{1}{r_j}(H^{(t)})_j^T(H^{(t)})_j\right)^{-1}\end{aligned} \tag{2.19}$$

Define A_k for $k = am + b$ with $b \in \{0, 1, \cdots, m-1\}$.

$$A_k = \begin{cases} A & \text{if} \quad k = 0,\\ A_{k-1} - \frac{A_{k-1}h_{k-1}h_{k-1}^TA_{k-1}}{r_{k-1}+h_{k-1}^TA_{k-1}h_{k-1}} & \text{if} \quad m \nmid k,\\ F\left(A_{k-1} - \frac{A_{k-1}h_{k-1}h_{k-1}^TA_{k-1}}{r_{k-1}+h_{k-1}^TA_{k-1}h_{k-1}}\right)F^T + Q & \text{if} \quad m \mid k,\ k > 0.\end{cases} \tag{2.20}$$

$A_{lm} = P^{(l)}$ by choosing $P^{(0)} = A$, and $r_k = r_b$, $h_k = (H^{(a)})_b^T$ for all $a \in \{0, \cdots, l-1\}$, $b \in \{0, \cdots, m-1\}$. h_k is a column vector while $(H^{(a)})_b$ is a row vector. This describes A_k when random H has a realization.

We apply the same idea to B. Define B_k for $k = am + b$ with $b \in \{0, 1, \cdots, m-1\}$. However, we suppose that realization of H for B_k is different from one for A_k.

$$B_k = \begin{cases} B \quad \text{if} \quad k=0, \\ B_{k-1} - \frac{B_{k-1}g_{k-1}g_{k-1}^T B_{k-1}}{r_{k-1}+g_{k-1}^T B_{k-1}g_{k-1}} \quad \text{if} \quad m \nmid k, \\ F\left(B_{k-1} - \frac{B_{k-1}g_{k-1}g_{k-1}^T B_{k-1}}{r_{k-1}+g_{k-1}^T B_{k-1}g_{k-1}}\right)F^T + Q \quad \text{if} \quad m \mid k,\ k>0. \end{cases} \tag{2.21}$$

We now claim that we can choose $g_0, g_1, \cdots, g_{n-1}$ to make $B_n = A_n$ for a given A_n with $B - A \in \mathbb{S}^n_{++}$.

We represent A_n as below for $n = cm + d$ with $d \in \{0, 1, 2, \cdots, m-1\}$.

$$A_n = F^c A (F^c)^T - \sum_{k=0}^{n-1} F^{\lceil c - \frac{k}{m} \rceil} \frac{A_k h_k h_k^T A_k}{r_k + h_k^T A_k h_k} (F^{\lceil c - \frac{k}{m} \rceil})^T + \sum_{a=0}^{c-1} F^a Q (F^a)^T \tag{2.22}$$

We can represent B_n similarly.

We give a lemma which is useful to compute rank of a positive semidefinite matrix in the algorithm which will be given later.

Lemma 2.4.1 *For $C \in \mathbb{S}^n_+$ and $v \in \mathbb{R}^n$ satisfying $v^T C v > 0$, the following statements hold.*

$$C - \frac{Cvv^T C}{v^T C v} \in \mathbb{S}^n_+ \quad \textit{and} \quad \operatorname{rank}\left(C - \frac{Cvv^T C}{v^T C v}\right) = \operatorname{rank}(C) - 1 \tag{2.23}$$

Proof: Define V_0 as null space of C. It is obvious that $v \notin V_0$ because $v^T C v > 0$. We can choose V_1 such that $v \in V_1$ and $\mathbb{R}^n = V_0 \oplus V_1$ (V_0 and V_1 don't have to be orthogonal.) Then, $< v_1, v_2 >= v_1^T C v_2$ is well-defined inner product on V_1.

$$(C - \frac{Cvv^T C}{v^T C v})v = Cv - Cv = 0 \tag{2.24}$$

The equation above guarantees that $\text{Null}(C - \frac{Cvv^T C}{v^T C v}) \supset \{v\}$. It is trivial to check that $\text{Null}(C - \frac{Cvv^T C}{v^T C v}) \supset \text{Null}(C)$. We get $\text{Null}(C - \frac{Cvv^T C}{v^T C v}) \supset \text{Null}(C) \oplus \{v\}$.

For any $u \in \mathbb{R}^n$, $u = u_0 + u_1$ such that $u_0 \in V_0, u_1 \in V_1$

$$u^T (C - \frac{Cvv^T C}{v^T C v})u = u_1^T (C - \frac{Cvv^T C}{v^T C v})u_1 = \frac{u_1^T C u_1 v^T C v - u_1^T C v v^T C u_1}{v^T C v} \geq 0 \tag{2.25}$$

The equality holds only for $u_1 = \alpha v$ with some scalar α by the equality condition of Cauchy-Schwarz. That means $u \in \text{Null}(C) \oplus \{v\}$ if $u \in \text{Null}(C - \frac{Cvv^T C}{v^T C v})$. $\text{Null}(C - \frac{Cvv^T C}{v^T C v}) \subset \text{Null}(C) \oplus \{v\}$.

From the discussion above, $\text{Null}(C - \frac{Cvv^TC}{v^TCv}) = \text{Null}(C) \oplus \{v\}$. It completes the proof. ■

We show that $Supp_B^{(t)}$ includes $Supp_A^{(t)}$ when $B - A \in \mathbb{S}^n_{++}$ by the following lemma. The lemma is based on the assumption that F is nonsingular.

Lemma 2.4.2 *Suppose that $F \in \mathbb{R}^{n\times n}$ is nonsingular. For given $A, B \in \mathbb{S}^n_{++}$ satisfying $B - A \in \mathbb{S}^n_+$ and $h_0, h_1, \cdots, h_{n-1}$, it's possible to find $g_0, g_1, \cdots, g_{n-1}$ such that $B_n = A_n$.*

Proof: Define a symmetric matrix C_k as below.

$$C_k = F^c(B-A)(F^c)^T + \sum_{j=0}^{n-1} F^{\lceil c-\frac{j}{m}\rceil} \frac{A_jh_jh_j^TA_j}{r_j + h_j^TA_jh_j}(F^{\lceil c-\frac{j}{m}\rceil})^T - \sum_{j=0}^{k-1} F^{\lceil c-\frac{j}{m}\rceil} \frac{B_jg_jg_j^TB_j}{r_j + g_j^TB_jg_j}(F^{\lceil c-\frac{j}{m}\rceil})^T \tag{2.26}$$

C_0 is decided by given condition A, B and $h_0, h_1, \cdots, h_{n-1}$. C_k for $k > 0$ is determined by choosing $g_0, g_1, \cdots, g_{k-1}$. From the definition of C_k, it's easy to verify that

$$C_k = F^{\lceil c-\frac{k}{m}\rceil}(B_k - A_k)(F^{\lceil c-\frac{k}{m}\rceil})^T + \sum_{j=k}^{n-1} F^{\lceil c-\frac{j}{m}\rceil} \frac{A_jh_jh_j^TA_j}{r_j + h_j^TA_jh_j}(F^{\lceil c-\frac{j}{m}\rceil})^T \tag{2.27}$$

We suggest an algorithm choosing $g_0, g_1, \cdots, g_{n-1}$.

Case 1. If $n - k - \text{rank}(C_k) > 0$, $g_k = h_k$.

Case 2. If $n - k - \text{rank}(C_k) = 0$, find g_k satisfying the equation below for some v such that $v^TC_kv > 0$.

$$F^{\lceil c-\frac{k}{m}\rceil} \frac{B_kg_kg_k^TB_k}{r_k + g_k^TB_kg_k}(F^{\lceil c-\frac{k}{m}\rceil})^T = \frac{C_kvv^TC_k}{v^TC_kv} \tag{2.28}$$

Before explaining how to find g_k satisfying (2.28), we claim that $C_k \in \mathbb{S}^n_+$ for every k by induction.

It is obvious that $C_0 \in \mathbb{S}^n_+$. Assume that $C_k \in \mathbb{S}^n_+$. If $n - j - \text{rank}(C_j) > 0$ for every $j \leq k$, then $g_j = h_j$ for all $j \leq k$ and it makes $B_{k+1} - A_{k+1} \in \mathbb{S}^n_+$ by the monotonicity of Riccati equation. $C_{k+1} \in \mathbb{S}^n_+$ by (2.27) and $\text{rank}(C_{k+1}) = \text{rank}(C_k) - 1$ or $\text{rank}(C_k)$ because C_{k+1} is just C_k or a positive semidefinite matrix whose rank is the same with C_k minus rank-one positive-semi-definite matrix by definition of C_k. Specifically,

$$\begin{aligned} C_{k+1} &= C_k - F^{\lceil c-\frac{k}{m}\rceil} \frac{A_kh_kh_k^TA_k}{r_k + h_k^TA_kh_k}(F^{\lceil c-\frac{k}{m}\rceil})^T \\ \text{or } C_{k+1} &= FC_kF^T - F^{\lceil c-\frac{k}{m}\rceil} \frac{A_kh_kh_k^TA_k}{r_k + h_k^TA_kh_k}(F^{\lceil c-\frac{k}{m}\rceil})^T \end{aligned} \tag{2.29}$$

If we find out g_k in Case 2, $C_{k+1} \in \mathbb{S}^n_+$ with $\text{rank}(C_{k+1}) = n - k - 1$ by the Lemma 2.4.1. It means that we also need to consider Case 2 for C_{k+1}. From both cases, $C_k \in \mathbb{S}^n_+$ for every k is true.

It is obvious that $n-k-\text{rank}(C_k) \leq 0$ at $k=n$. $n-k-\text{rank}(C_k)$ goes down by 1 or stays in Case 1 as k increases by 1. Since $n-k-\text{rank}(C_k)$ is non-positive at the end and it goes down by 1, $n-k-\text{rank}(C_k)$ should be zero at some particular k. It keeps staying at zero by Case 2 after that. Eventually, $n-k-\text{rank}(C_k)=0$ at $k=n$ and it's equivalent to $\text{rank}(C_n)=0$. It means that $C_n=0$. We find out $g_0, g_1, \cdots, g_{k-1}$ satisfying $B_n = A_n$.

It is enough to show that we can find out g_k in Case 2. We define C_k^+ as pseudo-inverse of C_k. (2.28) is satisfied if $C_k v = F^{\lceil c-\frac{k}{m}\rceil} B_k g_k$ and the following equation is true :

$$r_k + g_k^T B_k g_k = v^T C_k v = v^T C_k C_k^+ C_k v = g_k^T B_k (F^{\lceil c-\frac{k}{m}\rceil})^T C_k^+ F^{\lceil c-\frac{k}{m}\rceil} B_k g_k \tag{2.30}$$

If we can find $g_k \in \mathbb{R}^n$ such that

$$g_k^T (B_k (F^{\lceil c-\frac{k}{m}\rceil})^T C_k^+ F^{\lceil c-\frac{k}{m}\rceil} B_k - B_k) g_k > 0 \tag{2.31}$$

then we can make g_k satisfying (2.30) by multiplying proper scalar to g_k.

Define Z_k and D_k as below.

$$Z_k = B_k^{\frac{1}{2}} (F^{\lceil c-\frac{k}{m}\rceil})^T \qquad D_k = (Z_k^{-1})^T C_k Z_k^{-1} \in \mathbb{S}_+^n \tag{2.32}$$

$C_k^+ = Z_k^{-1} D_k^+ (Z_k^{-1})^T$ by property of pseudo-inverse matrix. (2.30) is equivalent to the following equation.

$$\begin{aligned} r_k &= g_k^T (B_k (F^{\lceil c-\frac{k}{m}\rceil})^T C_k^+ F^{\lceil c-\frac{k}{m}\rceil} B_k - B_k) g_k && (2.33) \\ &= ((F^{-\lceil c-\frac{k}{m}\rceil})^T g_k)^T (Z_k^T Z_k C_k^+ Z_k^T Z_k - Z_k^T Z_k)((F^{-\lceil c-\frac{k}{m}\rceil})^T g_k) && (2.34) \\ &= ((F^{-\lceil c-\frac{k}{m}\rceil})^T g_k)^T (Z_k^T (D_k^+ - I_n) Z_k)((F^{-\lceil c-\frac{k}{m}\rceil})^T g_k) && (2.35) \\ &= (B_k^{\frac{1}{2}} g_k)^T (D_k^+ - I_n)(B_k^{\frac{1}{2}} g_k) && (2.36) \end{aligned}$$

The subscript of I_n indicates that I_n is the n-dimensional identity matrix.

Define X_k as the following.

$$X_k = \sum_{j=k+1}^{n-1} F^{\lceil c-\frac{j}{m}\rceil - \lceil c-\frac{k}{m}\rceil} \frac{A_j h_j h_j^T A_j}{r_j + h_j^T A_j h_j} (F^{\lceil c-\frac{j}{m}\rceil - \lceil c-\frac{k}{m}\rceil})^T \tag{2.37}$$

$I_n - D_k$ is represented using X_k as the following.

$$I_n - D_k = (Z_k^{-1})^T F^{\lceil c-\frac{k}{m}\rceil}\left(A_k - \frac{A_k h_k h_k^T A_k}{r_k + h_k^T A_k h_k} - X_k\right)(F^{\lceil c-\frac{k}{m}\rceil})^T Z_k^{-1} \tag{2.38}$$

$$= B_k^{-\frac{1}{2}}\left(A_k - \frac{A_k h_k h_k^T A_k}{r_k + h_k^T A_k h_k} - X_k\right) B_k^{-\frac{1}{2}} \tag{2.39}$$

We know that $A_k - \dfrac{A_k h_k h_k^T A_k}{r_k + h_k^T A_k h_k} \in \mathbb{S}^n_{++}$. Define α_k as below.

$$\alpha_k = \left\|A_k^{-1} + \frac{1}{r_k} h_k h_k^T\right\|^{-1} \qquad \text{then} \qquad A_k - \frac{A_k h_k h_k^T A_k}{r_k + h_k^T A_k h_k} - \alpha_k I_n \in \mathbb{S}^n_{+} \tag{2.40}$$

Define W as null space of $B_k^{-\frac{1}{2}} X_k B_k^{-\frac{1}{2}}$. For all $w \in W$,

$$w^T(I_n - D_k)w = w^T B_k^{-\frac{1}{2}}\left(A_k - \frac{A_k h_k h_k^T A_k}{r_k + h_k^T A_k h_k}\right) B_k^{-\frac{1}{2}} w \tag{2.41}$$

$$\geq \alpha_k \|B_k^{-\frac{1}{2}} w\|^2 \tag{2.42}$$

$$\geq \alpha_k (\|B_k^{\frac{1}{2}}\|^{-1} \|w\|)^2 \tag{2.43}$$

$$= \frac{\alpha_k}{\|B_k\|}\|w\|^2 \tag{2.44}$$

$\dim(W) \geq k+1$ because X_k is summation of $n-k-1$ rank-one positive-semi-definite matrices by (2.37).

Define V as span of eigenvectors of D_k corresponding to positive eigenvalues. Then, $\dim(V) = \operatorname{rank}(D_k) = \operatorname{rank}(C_k) = n-k$ by assumption of Case 2.

There is nonzero $u \in W \cap V$.

$$\left(D_k^{\frac{1}{2}} u\right)^T (D_k^{+} - I_n)\left(D_k^{\frac{1}{2}} u\right) = u^T D_k^{\frac{1}{2}} (D_k^{+} - I_n) D_k^{\frac{1}{2}} u \tag{2.45}$$

$$= u^T u - u^T D_k u \tag{2.46}$$

$$= u^T (I_n - D_k) u \tag{2.47}$$

$$\geq \frac{\alpha_k}{\|B_k\|}\|u\|^2 > 0 \tag{2.48}$$

By choosing g_k as $B_k^{-\frac{1}{2}} D_k^{\frac{1}{2}} u$ with u of proper norm, (2.30) holds. It completes the proof. ■

We extend Lemma 2.4.2 to the singular F in the following theorem.

Theorem 2.4.3 *If $A,B \in \mathbb{S}^n_{++}$ satisfy $B-A \in \mathbb{S}^n_{+}$, then $Supp^{(t)}_A \subset Supp^{(t)}_B$ for $t \geq \frac{n}{m}$*

Proof: Since the support of p_H is $\mathbb{R}^{m\times n}$, B_{tm} with any $g_0,\cdots,g_{tm-1}$ is in the support, $Supp^{(t)}_B$. It is enough to show that we can find out $g_0,g_1,\cdots,g_{tm-1}$ such that $B_{tm}=A_{tm}$ for any given A_{tm}.

First, we claim that it's possible to find out $g_0,g_1,\cdots,g_{n-1}$ such that $B_n=A_n$ for given $A,B \in \mathbb{S}^n_{++}$ satisfying $B-A \in \mathbb{S}^n_{+}$ and $h_0,h_1,\cdots,h_{n-1}$. We already proved it for nonsingular F in Lemma 2.4.2.

For singular F, define $F_\varepsilon = F+\varepsilon I_n$. There is $\delta > 0$ such that F_ε is nonsingular for all $0 < \varepsilon < \delta$. For each $\{\varepsilon_l\}_{l=1}^{\infty}$ converging to 0, we can find $(g_0,g_1,\cdots,g_{n-1})$ which makes $B_n=A_n$. If $(g_0,g_1,\cdots,g_{n-1})$ corresponding to ε_l converges to some point, the limit point makes $B_n=A_n$ for F and it's exactly what we want.

If $(g_0,g_1,\cdots,g_{n-1})$ corresponding to ε_l is bounded independent to ε_l, then they are in compact space, and have convergent subsequence. The limit point of the subsequence is what we want.

We prove the claim by showing that $(g_0,g_1,\cdots,g_{n-1})$ of Lemma 2.4.2 has ε-independent upper bound. $g_k = B_k^{-\frac{1}{2}} D_k^{\frac{1}{2}} u$, then $u^T(I_n - D_k)u = r_k > 0$ by (2.36) and (2.47). u is also bounded since $u^T u \leq \dfrac{r_k \|B_k\|}{\alpha_k}$ by (2.48).

$$\begin{aligned}
\|g_k\|^2 = g_k^T g_k &= u^T D_k^{\frac{1}{2}} B_k^{-1} D_k^{\frac{1}{2}} u && (2.49)\\
&\leq \|B_k^{-1}\| \|D_k^{\frac{1}{2}} u\|^2 = \|B_k^{-1}\|(u^T D_k u) && (2.50)\\
&< \|B_k^{-1}\| \|u\|^2 && (2.51)\\
&\leq \frac{r_k \|B_k\| \|B_k^{-1}\|}{\alpha_k} && (2.52)
\end{aligned}$$

Since $\{\varepsilon_l\}_{l=1}^{\infty}$ is sequence which is in $(0,\delta)$, $\|F+\varepsilon_l I_n\|$ has upper bound depending only on $\|F\|$ and δ. With that, $\|B_k\|$ has an upper bound as below.

$$\|B_k\| \leq \left\| F_\varepsilon^{\lfloor \frac{k}{m} \rfloor} B (F_\varepsilon^{\lfloor \frac{k}{m} \rfloor})^T + \sum_{a=0}^{\lfloor \frac{k}{m} \rfloor -1} F_\varepsilon^a Q (F_\varepsilon^a)^T \right\| \tag{2.53}$$

For $k = am$, $\|A_k^{-1}\| \leq \|Q^{-1}\|$. For $k = am+b$ with $0<b<m$,

$$\|A_k^{-1}\| = \left\| A_{am}^{-1} + \sum_{j=0}^{b-1} \frac{1}{r_j} h_j h_j^T \right\| \leq \|Q^{-1}\| + \sum_{j=0}^{b-1} \frac{\|h_j\|^2}{r_j} \tag{2.54}$$

With that, $\frac{1}{\alpha_k}$ is upper bounded as below.

$$\frac{1}{\alpha_k} = \left\| A_k^{-1} + \frac{1}{r_k} h_k h_k^T \right\| \leq \|A_k^{-1}\| + \frac{\|h_k\|^2}{r_k} \tag{2.55}$$

In Case 1 of Lemma 2.4.2, g_k is bounded because $g_k = h_k$, and B_k is also bounded by similar inequality above.

We finish the proof by induction. It is obvious that $\|B_0\|, \|B_0^{-1}\|, \frac{1}{\alpha_0}$ are bounded because they are determined by the given condition. Then, g_0 also has ε-independent upper bound by (2.52). Assume that g_l and B_l^{-1} have ε-independent upper bound for all $l < k$. If $k = am$, $\|B_k^{-1}\| \leq \|Q^{-1}\|$ and g_k is also bounded by (2.52). For $k = am + b$ with $0 < b < m$,

$$\|B_k^{-1}\| = \left\| B_{am}^{-1} + \sum_{j=0}^{b-1} \frac{1}{r_j} g_j g_j^T \right\| \leq \|Q^{-1}\| + \sum_{j=0}^{b-1} \frac{\|g_j\|^2}{r_j} \tag{2.56}$$

g_k is also bounded by (2.52). It completes the proof of the claim.

Choosing $g_k = h_k$ for $n \leq k \leq tm - 1$ guarantee that $B_{tm} = A_{tm}$. It completes the proof of $Supp_A^{(t)} \subset Supp_B^{(t)}$. ■

It is obvious that $Supp_0^{(t)}$, the support of $P^{(t)}$ where an initial point is the zero-matrix, is same with $Supp_Q^{(t-1)}$. Since $Supp_A^{(t)} \supset Supp_0^{(t)}$ for any positive semidefinite matrix A, the following remark holds.

Remark 1 *$Supp_A^{(t)} \supset Supp_Q^{(t-1)}$ for any $A \in \mathbb{S}_+^n$ and $t > \frac{n}{m} + 1$*

$Supp_Q^{(t-1)}$ is the common area of support at time t with any initial point. Furthermore, $Supp_Q^{(t-1)}$ has nonzero probability measure for an initial point. The proof in this section requires the support of H to be the whole mn-dimensional space to choose regressor vectors of B everywhere.

2.5 Computation of Probability Density Function

In this section, we compute probability density function using matrix calculus. From this section, we suppose that $F \in \mathbb{R}^{n \times n}$ in (2.5) is nonsingular. We first study basic matrix calculus. We follow the notation of [46]

Definition 7 *$f^{(t)}(P,\cdot)$ is probability density function of measure $\mu_P^{(t)}(\cdot)$ i.e.,*

$$\mu_P^{(t)}(E) = \int_E f^{(t)}(P,C)\mathrm{d}C \tag{2.57}$$

If F is singular, $f^{(t)}(P,\cdot)$ is not defined. In this section, our goal is evaluating the actual value of $f^{(t)} : \mathbb{S}^n_{++} \times \mathbb{S}^n_{++} \to \mathbb{R}_+$. Roughly speaking, $f^{(t)}(P,C)$ is the probability density function of $P^{(t)} = C$ given $P^{(0)} = P$.

Definition 8 *For an arbitrary $n \times m$ matrix X, $\mathrm{d}X$ denotes the exterior product of the mn elements of $\mathrm{d}X$*

$$\mathrm{d}X = \bigwedge_{j=1}^{m} \bigwedge_{i=1}^{n} \mathrm{d}x_{ij} \tag{2.58}$$

For a symmetric n by n matrix S, $\mathrm{d}S$ denotes the exterior product of the $\frac{1}{2}n(n+1)$ distinct elements of $\mathrm{d}S$

$$\mathrm{d}S = \bigwedge_{1 \le i \le j \le n} \mathrm{d}s_{ij} \tag{2.59}$$

For a lower triangular n by n matrix L, $\mathrm{d}L$ denotes the exterior product of the $\frac{1}{2}n(n+1)$ lower triangular elements of $\mathrm{d}L$

$$\mathrm{d}L = \bigwedge_{1 \le j \le i \le n} \mathrm{d}l_{ij} \tag{2.60}$$

Lemma 2.5.1 *If $X = BY$ where X, Y are $n \times m$ matrices and B is a fixed nonsingular $n \times n$ matrix then*

$$(\mathrm{d}X) = (\det(B))^m(\mathrm{d}Y) \tag{2.61}$$

Proof: It is Theorem 2.1.4 of [46] ■

Lemma 2.5.2 *If S is an $n \times n$ positive definite matrix and $S = LL^T$ where L is lower-triangular with positive diagonal elements then,*

$$(\mathrm{d}S) = 2^n \prod_{i=1}^{n} l_{ii}^{n+1-i}(\mathrm{d}L) \tag{2.62}$$

Proof: It is Theorem 2.1.9 of [46] ■

Lemma 2.5.3 *Let Z be an $a \times b$ ($a \le b$) matrix of rank a and write $Z = LO$, where O is $a \times b$ matrix with $OO^T = I_a$ and L is an $a \times a$ lower-triangular matrix with positive diagonal elements. Then*

$$(\mathrm{d}Z) = 2^n \prod_{i=1}^{a} l_{ii}^{b-i}(\mathrm{d}L)(\mathrm{d}O) \tag{2.63}$$

where $\mathrm{d}O$ *is volume element of Stiefel manifold* $V_{a,b} = \{O \in \mathbb{R}^{a\times b} : OO^T = I_a\}$

Proof: It is Theorem 2.1.13 of [46] ∎

Remark 2

$$\mathrm{Vol}(V_{a,b}) = \int_{V_{a,b}} \mathrm{d}O = \frac{2^a \pi^{ab/2}}{\Gamma_a(b/2)} \qquad \textit{where} \qquad \Gamma_m(n) = \pi^{\frac{m(m-1)}{4}} \prod_{i=1}^{m} \Gamma(n - \frac{1}{2}(i-1)) \tag{2.64}$$

Definition 9 *For fixed* t *satisfying* $mt > n$, $\bar{H} = [(H^{(0)})^T\ (H^{(1)})^T\ \cdots\ (H^{(t-1)})^T] \in \mathbb{R}^{n\times mt}$. *We rewrite* $\bar{H} = [\bar{h}_0\ \bar{h}_1\ \cdots\ \bar{h}_{mt-1}]$.

$$\mu_P^{(t)}(E) = \int_{\{\bar{H}: P^{(0)}=P, P^{(t)}\in E\}} \bar{p}(\bar{H})\mathrm{d}\bar{H} \tag{2.65}$$

where $\bar{p}(\bar{H})$ is probability density function of $\bar{H}$. $\bar{p}(\bar{H}) = \prod_{l=0}^{t-1} p_H(H^{(l)})$ by definition of the first section that $H^{(l)}$ is i.i.d.

Define A_k as in the previous section.

$$A_k = \begin{cases} A \quad \text{if} \quad k = 0, \\ A_{k-1} - \frac{A_{k-1}\bar{h}_{k-1}\bar{h}_{k-1}^T A_{k-1}}{r_{k-1} + \bar{h}_{k-1}^T A_{k-1}\bar{h}_{k-1}} \quad \text{if} \quad m \nmid k, \\ F\left(A_{k-1} - \frac{A_{k-1}\bar{h}_{k-1}\bar{h}_{k-1}^T A_{k-1}}{r_{k-1} + \bar{h}_{k-1}^T A_{k-1}\bar{h}_{k-1}}\right)F^T + Q \quad \text{if} \quad m \mid k,\ k > 0. \end{cases} \tag{2.66}$$

It is obvious that $P^{(t)} = A_{tm}$ if $P^{(0)} = A$.

$$A_{tm} = F^t A (F^T)^t - \sum_{k=0}^{tm-1} F^{\lceil t - \frac{k}{m} \rceil} \frac{A_k \bar{h}_k \bar{h}_k^T A_k}{r_k + \bar{h}_k^T A_k \bar{h}_k} (F^T)^{\lceil t - \frac{k}{m} \rceil} + \sum_{l=0}^{t-1} F^l Q (F^T)^l \tag{2.67}$$

Definition 10 $\Psi_1 : \mathbb{R}^{n\times tm} \to \mathbb{R}^{n\times tm}$ *is defined by* $\Psi_1(\bar{H}) = \bar{G}$ *where*

$$\bar{g}_k = (\bar{G})_k = \frac{1}{\sqrt{r_k + \bar{h}_k^T A_k \bar{h}_k}} F^{\lceil t - \frac{k}{m} \rceil} A_k \bar{h}_k \tag{2.68}$$

Lemma 2.5.4 Ψ_1 *is one-to-one.*

Proof: Suppose that $\Psi_1(\bar{H}) = \bar{G} = \bar{G}' = \Psi_1(\bar{H}')$ for two $n \times mt$ matrices $\bar{H}, \bar{H}'$.

Assume that $\bar{h}_l = \bar{h}'_l$ for every $l \in \{0, \cdots, k-1\}$, then $A_k = A'_k$ and

$$\bar{g}_k = \bar{g}'_k \quad \Leftrightarrow \quad \frac{1}{\sqrt{r_k + \bar{h}_k^T A_k \bar{h}_k}} \bar{h}_k = \frac{1}{\sqrt{r_k + \bar{h}'^T_k A_k \bar{h}'_k}} \bar{h}'_k \tag{2.69}$$

$$\Leftrightarrow \quad \bar{h}'_k = \alpha \bar{h}_k \text{ such that } \frac{1}{\sqrt{r_k + \bar{h}_k^T A_k \bar{h}_k}} = \frac{\alpha}{\sqrt{r_k + \alpha^2 \bar{h}_k^T A_k \bar{h}_k}} \tag{2.70}$$

$$\Leftrightarrow \quad \bar{h}'_k = \alpha \bar{h}_k \text{ and } \alpha = 1 \tag{2.71}$$

The discussion above holds for $k = 0$. By induction, $\bar{h}_k = \bar{h}'_k$ for every k if $\Psi_1(\bar{H}) = \Psi_1(\bar{H}')$ ■

We can rewrite (2.67) with $\bar{G}$.

$$A_{tm} = F^t A (F^T)^t - \sum_{k=0}^{tm-1} \bar{g}_k \bar{g}_k^T + \sum_{l=0}^{t-1} F^l Q (F^T)^l = F^t A (F^T)^t - \bar{G}\bar{G}^T + \sum_{l=0}^{t-1} F^l Q (F^T)^l \tag{2.72}$$

Lemma 2.5.5 *$\Psi_1(\bar{H})$ is full-rank with probability 1*

Proof: $\bar{H}$ is full-rank with probability 1 because probability density function of $\bar{H}$ is continuous, and set of non-full-rank matrices is measure-zero. Since Ψ_1 is one-to-one by Lemma 2.5.4 and continuous, the range of $\Psi_1(\{\bar{H} : \bar{H} \text{ is full-rank}\})$ has measure 1. ■

Lemma 2.5.6 *If Z is $a \times b$ real matrix of rank a ($a \leq b$) then Z can be uniquely written as $Z = LO$, where O is $a \times b$ matrix with $OO^T = I_a$ and L is an $a \times a$ lower-triangular matrix with positive diagonal elements.*

Proof: It is well-known as QR-decomposition. ■

Definition 11 *For full-rank $\bar{G} \in \mathbb{R}^{n \times tm}$, $\Psi_2(\bar{G}) = (L, O)$ where L is lower-triangular $n \times n$ matrix with positive diagonal elements, $O \in V_{n,tm}$ and $LO = \bar{G}$.*

$\Psi_2(\bar{G})$ is well-defined with probability 1 and it's one-to-one in that case. It is enough to consider case of probability 1 on integration. We can rewrite (2.72) with (L, O).

$$A_{tm} = F^t A (F^T)^t - LOO^T L^T + \sum_{l=0}^{t-1} F^l Q (F^T)^l = F^t A (F^T)^t - LL^T + \sum_{l=0}^{t-1} F^l Q (F^T)^l \tag{2.73}$$

Lemma 2.5.7

$$\mathrm{d}\bar{G} = \left(\prod_{k=0}^{tm-1} (r_k + \bar{h}_k^T A_k \bar{h}_k)^{-\frac{n+2}{2}} \det(A_k) r_k \right) \det(F)^{\frac{mt(t+1)}{2}} \mathrm{d}\bar{H} \tag{2.74}$$

Proof: For arbitrary $X \in \mathbb{R}^{n\times m}$, define $\tilde{\mathrm{d}}X$ as $m \times n$ matrix whose (i,j) element is $\mathrm{d}x_{ij}$. It is different from $\mathrm{d}X = \bigwedge_{j=1}^{m}\bigwedge_{i=1}^{n}\mathrm{d}x_{ij}$

$$\tilde{\mathrm{d}}\bar{g}_0 = (r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{1}{2}}F^t A_0\tilde{\mathrm{d}}\bar{h}_k - \frac{1}{2}(r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{3}{2}}(\tilde{\mathrm{d}}\bar{h}_0^T A_0\bar{h}_0 + \bar{h}_0^T A_0\tilde{\mathrm{d}}\bar{h}_0)F^t A_0\bar{h}_0 \tag{2.75}$$

$$= (r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{1}{2}}\left(F^t A_0 - \frac{1}{r_0+\bar{h}_0^T A_0\bar{h}_0}F^t A_0\bar{h}_0^T\bar{h}_0 A_0\right)\tilde{\mathrm{d}}\bar{h}_0 \tag{2.76}$$

Applying Lemma 2.5.1 to the equation above,

$$\mathrm{d}\bar{g}_0 = \det\left((r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{1}{2}}\left(F^t A_0 - \frac{1}{r_0+\bar{h}_0^T A_0\bar{h}_0}F^t A_0\bar{h}_0^T\bar{h}_0 A_0\right)\right)\mathrm{d}\bar{h}_0 \tag{2.77}$$

$$= (r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{n}{2}}\det(F^t A_0)\det\left(I_n - \frac{1}{r_0+\bar{h}_0^T A_0\bar{h}_0}\bar{h}_0\bar{h}_0^T A_0\right)\mathrm{d}\bar{h}_0 \tag{2.78}$$

$$= (r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{n}{2}}\det(F^t A_0)\left(1 - \frac{\bar{h}_0^T A_0\bar{h}_0}{r_0+\bar{h}_0^T A_0\bar{h}_0}\right)\mathrm{d}\bar{h}_0 \tag{2.79}$$

$$= (r_0+\bar{h}_0^T A_0\bar{h}_0)^{-\frac{n+2}{2}}\det(F)^t\det(A_0)r_0\mathrm{d}\bar{h}_0 \tag{2.80}$$

For general k,

$$\tilde{\mathrm{d}}\bar{g}_k = (r_k+\bar{h}_k^T A_k\bar{h}_k)^{-\frac{1}{2}}\left(F^{\lceil t-\frac{k}{m}\rceil}A_k - \frac{1}{r_k+\bar{h}_k^T A_k\bar{h}_k}F^{\lceil t-\frac{k}{m}\rceil}A_k\bar{h}_k^T\bar{h}_k A_k\right)\tilde{\mathrm{d}}\bar{h}_k + \text{ some terms} \tag{2.81}$$

There are “some terms” in the equation above because A_k is not constant, but function of $\bar{h}_0,\cdots,\bar{h}_{k-1}$.

$$\mathrm{d}\bar{g}_k = (r_k+\bar{h}_k^T A_k\bar{h}_k)^{-\frac{n+2}{2}}\det(F)^{\lceil t-\frac{k}{m}\rceil}\det(A_k)r_k\mathrm{d}\bar{h}_k + \text{ some terms} \tag{2.82}$$

“Some terms” in the equation above are terms which contain $\mathrm{d}(\bar{H}_{il})$ for some $l<k$.

$$\mathrm{d}\bar{G} = \bigwedge_{j=1}^{tm}\bigwedge_{i=1}^{n}\mathrm{d}(\bar{G}_{ij}) = \bigwedge_{k=0}^{tm-1}\mathrm{d}\bar{g}_k \tag{2.83}$$

$$= \bigwedge_{k=0}^{tm-1}(r_k+\bar{h}_k^T A_k\bar{h}_k)^{-\frac{n+2}{2}}\det(F)^{\lceil t-\frac{k}{m}\rceil}\det(A_k)r_k\mathrm{d}\bar{h}_k + \text{ some terms} \tag{2.84}$$

$$= \bigwedge_{k=0}^{tm-1}(r_k+\bar{h}_k^T A_k\bar{h}_k)^{-\frac{n+2}{2}}\det(F)^{\lceil t-\frac{k}{m}\rceil}\det(A_k)r_k\mathrm{d}\bar{h}_k \tag{2.85}$$

$$= \left(\prod_{k=0}^{tm-1}(r_k+\bar{h}_k^T A_k\bar{h}_k)^{-\frac{n+2}{2}}\det(A_k)r_k\right)\det(F)^{\frac{mt(t+1)}{2}}\mathrm{d}\bar{H} \tag{2.86}$$

The equation above holds because wedge product of identical terms is canceled out. ■

Lemma 2.5.8

$$\mathrm{d}\bar{G} = 2^{-n}(\det(LL^T))^{\frac{mt-n-1}{2}}\mathrm{d}(LL^T)\mathrm{d}O \tag{2.87}$$

Proof: It is Theorem 2.1.14 of [46] ■

From the two lemmas above, we get

$$\mathrm{d}\bar{H} = \left(\prod_{k=0}^{tm-1}(r_k+\bar{h}_k^T A_k \bar{h}_k)^{\frac{n+2}{2}}\frac{1}{r_k\det(A_k)}\right)\det(F)^{-\frac{mt(t+1)}{2}}2^{-n}(\det(LL^T))^{\frac{mt-n-1}{2}}\mathrm{d}(LL^T)\mathrm{d}O \tag{2.88}$$

Write $O = [O_0\, O_1\, \cdots\, O_{tm-1}]$, then $\bar{g}_k = LO_k$. From the definition of $\bar{G}$, we get

$$\bar{h}_k = \left(\frac{r_k}{1-\bar{g}_k^T(F^T)^{-\lceil t-\frac{k}{m}\rceil}A_k^{-1}F^{-\lceil t-\frac{k}{m}\rceil}\bar{g}_k}\right)^{\frac{1}{2}}A_k^{-1}F^{-\lceil t-\frac{k}{m}\rceil}\bar{g}_k \tag{2.89}$$

$$= \left(\frac{r_k}{1-O_k^T L^T(F^T)^{-\lceil t-\frac{k}{m}\rceil}A_k^{-1}F^{-\lceil t-\frac{k}{m}\rceil}LO_k}\right)^{\frac{1}{2}}A_k^{-1}F^{-\lceil t-\frac{k}{m}\rceil}LO_k \tag{2.90}$$

$$r_k+\bar{h}_k^T A_k\bar{h}_k = \frac{r_k}{1-O_k^T L^T(F^T)^{-\lceil t-\frac{k}{m}\rceil}A_k^{-1}F^{-\lceil t-\frac{k}{m}\rceil}LO_k} \tag{2.91}$$

Since the left hand side of the equation above is always positive, there is a condition for O to be proper

$$O_k^T L^T(F^T)^{-\lceil t-\frac{k}{m}\rceil}A_k^{-1}F^{-\lceil t-\frac{k}{m}\rceil}LO_k < 1 \quad \text{for} \quad \forall k\in\{0,1,\cdots,tm-1\} \tag{2.92}$$

It is also possible to redefine A_k with (L,O) instead of $\bar{H}$

$$A_k = \begin{cases} A \quad \text{if} \quad k=0, \\ A_{k-1}-F^{-\lceil t-\frac{k-1}{m}\rceil}LO_{k-1}O_{k-1}^T L^T(F^T)^{-\lceil t-\frac{k-1}{m}\rceil} \quad \text{if} \quad m\nmid k, \\ F\left(A_{k-1}-F^{-\lceil t-\frac{k-1}{m}\rceil}LO_{k-1}O_{k-1}^T L^T(F^T)^{-\lceil t-\frac{k-1}{m}\rceil}\right)(F^T)+Q \quad \text{if} \quad m|k. \end{cases} \tag{2.93}$$

Domain of an integral can be properly redefined as the following because $(L,O) = (\Psi_2\circ\Psi_1)(\bar{H})$, and $\Psi_2\circ\Psi_1$ is one-to-one with probability 1.

$$\{\bar{H} : P^{(0)} = P, P^{(t)}\in E\} = \{(L,O) : F^tA(F^T)^t - LL^T + \sum_{l=0}^{t-1}F^lQ(F^T)^l \in E\} \tag{2.94}$$

Actually, one more condition is necessary for the equation above and it is (2.92). We can make $\bar{p}(\bar{H})$ well-defined for $\forall O \in V_{n,tm}$ by assigning zero for (L,O) that does not satisfy (2.92).

Finally, we are ready to compute $f^{(t)}(P,C)$. Define L as lower-triangular matrix with positive diagonal elements such that

$$LL^T = F^t P (F^T)^t + \sum_{l=0}^{t-1} F^l Q (F^T)^l - C \tag{2.95}$$

Then, it coincides with (2.73). We only need to think about the case where the right-hand side of the equation above is positive definite because it's out of support otherwise.
It is obvious that $\mathrm{d}(LL^T) = \mathrm{d}C$ if we ignore sign. We can get $f^{(t)}(P,C)$ by (2.88)

$$f^{(t)}(P,C) = \int_{V_{n,mt}} \left| 2^{-n} \det(F)^{-\frac{mt(t+1)}{2}} \left(\det(LL^T)\right)^{\frac{mt-n-1}{2}} \phi(P,C,O) \right| \mathrm{d}O \tag{2.96}$$

$\phi(P,C,O) = 0$ if (2.92) does not hold, it is defined as below otherwise

$$\phi(P,C,O) = \bar{p}(\bar{H}) \left(\prod_{k=0}^{tm-1} (r_k + \bar{h}_k^T A_k \bar{h}_k)^{\frac{n+2}{2}} \frac{1}{r_k \det(A_k)} \right) \tag{2.97}$$

For fixed initial condition including P, $\bar{H} = (\Psi_2 \circ \Psi_1)^{-1}(L,O)$ and well-defined because $\Psi_2 \circ \Psi_1$ is one-to-one. A_k with $A_0 = P$ are determined by P and (L,O) by (2.93). L is determined by P,C by (2.95). Therefore, terms inside the integral of (2.96) is well-defined function of (P,C,O).

2.6 Continuity of Probability Density Function

Even though we evaluate $f^{(t)}(P,C)$ in the previous section, it is not a closed form. In this section, we show that $f^{(t)} : \mathbb{S}^n_{++} \times \mathbb{S}^n_{++} \to \mathbb{R}_+$ is continuous by bounded convergence theorem.

We begin this section with simple recursive equation.

Definition 12 $w_k = A_k^{-\frac{1}{2}} F^{-\lceil t - \frac{k}{m} \rceil} L O_k$

It is obvious that $w_k^T w_k < 1$ by (2.92). Recall (2.93) in case of $m \nmid k$

$$\det(A_k) = \det\left(A_{k-1} - F^{-\lceil t-\frac{k-1}{m}\rceil} L O_{k-1} O_{k-1}^T L^T (F^T)^{-\lceil t-\frac{k-1}{m}\rceil}\right) \tag{2.98}$$

$$= \det(A_{k-1}) \det(I_n - w_{k-1} w_{k-1}^T) \tag{2.99}$$

$$= \det(A_{k-1})(1 - w_{k-1}^T w_{k-1}) \tag{2.100}$$

$$\det(A_k) = \det\left(A_{m\lfloor\frac{k}{m}\rfloor}\right) \prod_{j=m\lfloor\frac{k}{m}\rfloor}^{k-1} (1 - w_j^T w_j) \tag{2.101}$$

$$\prod_{k=am}^{(a+1)m-1} \det(A_k) = \det(A_{am})^m \prod_{k=am}^{(a+1)m-1} (1 - w_k^T w_k)^{(a+1)m-1-k} \tag{2.102}$$

$$\geq \det(A_{am})^m \left(\prod_{k=am}^{(a+1)m-1} (1 - w_k^T w_k) \right)^{m-1} \tag{2.103}$$

We also give an upper bound to $r_k + \bar{h}_k^T A_k \bar{h}_k$. From (2.91),

$$r_k + \bar{h}_k^T A_k \bar{h}_k = \frac{r_k}{1 - w_k^T w_k} = \frac{r_k w_k^T w_k}{1 - w_k^T w_k} + r_k \tag{2.104}$$

$$\leq r_k \|A_k\| \frac{w_k^T A_k^{-1} w_k}{1 - w_k^T w_k} + r_k \tag{2.105}$$

We know that $A_{m\lfloor\frac{k}{m}\rfloor} - A_k \in \mathbb{S}_+^n$ from (2.93). It implies that $\|A_{m\lfloor\frac{k}{m}\rfloor}\| \geq \|A_k\|$

$$\|A_{lm}\| = \left\| F^l A (F^T)^l - \sum_{k=0}^{lm-1} L O_k O_k^T L^T + \sum_{j=0}^{l-1} F^j Q (F^T)^j \right\| \leq \left\| F^l A (F^T)^l + \sum_{j=0}^{l-1} F^j Q (F^T)^j \right\| \tag{2.106}$$

Definition 13 $\alpha_t(A) = \max_{0 \leq l \leq t-1} \left\| F^l A (F^T)^l + \sum_{j=0}^{l-1} F^j Q (F^T)^j \right\|$

$\alpha_t(A)$ is independent from O. Using it,

$$r_k + \bar{h}_k^T A_k \bar{h}_k \leq r_k \alpha_t(A) \frac{w_k^T A_k^{-1} w_k}{1 - w_k^T w_k} + r_k \tag{2.107}$$

$$\leq r_k + \alpha_t(A) \sum_{j=\lfloor\frac{k}{m}\rfloor m}^{(\lfloor\frac{k}{m}\rfloor+1)m-1} r_j \frac{w_j^T A_j^{-1} w_j}{1 - w_j^T w_j} \tag{2.108}$$

$$= r_k + \alpha_t(A) \sum_{j=\lfloor\frac{k}{m}\rfloor m}^{(\lfloor\frac{k}{m}\rfloor+1)m-1} \bar{h}_j^T \bar{h}_j = r_k + \alpha_t(A) \|H^{(\lfloor\frac{k}{m}\rfloor)}\|_F^2 \tag{2.109}$$

$\phi(P,C,O)$ can be viewed as product of t continuous functions. Each of them is function of $H^{(0)},\cdots,H^{(t)}$ as below.

$$\phi(P,C,O)=\prod_{l=0}^{t-1}\left(p_H(H^{(l)})\prod_{k=lm}^{(l+1)m-1}(r_k+\bar{h}_k^TA_k\bar{h}_k)^{\frac{n+2}{2}}\frac{1}{r_k\det(A_k)}\right) \tag{2.110}$$

Let $r_{\max}=\max(r_0,\cdots,r_{m-1})$ and $r_{\min}=\min(r_0,\cdots,r_{m-1})$.

$$\begin{aligned}
&p_H(H^{(l)})\prod_{k=lm}^{(l+1)m-1}(r_k+\bar{h}_k^TA_k\bar{h}_k)^{\frac{n+2}{2}}\frac{1}{r_k\det(A_k)} && (2.111)\\
&\le\frac{p_H(H^{(l)})}{\det(A_{lm})^m}\prod_{k=lm}^{(l+1)m-1}\frac{1}{r_k(1-w_k^Tw_k)^{m-1}}(r_k+\bar{h}_k^TA_k\bar{h}_k)^{\frac{n+2}{2}} && (2.112)\\
&=\frac{p_H(H^{(l)})}{\det(A_{lm})^m}\prod_{k=lm}^{(l+1)m-1}r_k^{-m}(r_k+\bar{h}_k^TA_k\bar{h}_k)^{m+\frac{n}{2}} && (2.113)\\
&\le\frac{p_H(H^{(l)})}{r_{\min}^{m^2}\det(A_{lm})^m}(r_{\max}+\alpha_t(P)\|H^{(l)}\|_F^2)^{m^2+\frac{mn}{2}} && (2.114)
\end{aligned}$$

Returning back to $\phi(P,C,O)$,

$$\begin{aligned}
\phi(P,C,O)&\le\prod_{l=0}^{t-1}\frac{p_H(H^{(l)})}{r_{\min}^{m^2}\det(A_{lm})^m}(r_{\max}+\alpha_t(P)\|H^{(l)}\|_F^2)^{m^2+\frac{mn}{2}} && (2.115)\\
&\le\frac{1}{r_{\min}^{tm^2}\det(P)^m\det(Q)^{m(t-1)}}\prod_{l=0}^{t-1}p_H(H^{(l)})(r_{\max}+\alpha_t(P)\|H^{(l)}\|_F^2)^{m^2+\frac{mn}{2}} && (2.116)
\end{aligned}$$

By (c) of conditions for P_H, we can choose $M_d>0$ where

$$p_H(H)\le\|H\|_F^{-d}\quad\forall\|H\|_F>M_d \tag{2.117}$$

For $\|H^{(l)}\|_F>M_d>\left(\frac{r_{\max}}{\alpha_t(P)}\right)^{\frac{1}{2}}$,

$$\begin{aligned}
p_H(H^{(l)})(r_{\max}+\alpha_t(P)\|H^{(l)}\|_F^2)^{m^2+\frac{mn}{2}}&\le\|H^{(l)}\|_F^{-d}(r_{\max}+\alpha_t(P)\|H^{(l)}\|_F^2)^{m^2+\frac{mn}{2}} && (2.118)\\
&\le(2\alpha_t(P))^{m^2+\frac{mn}{2}}\|H^{(l)}\|_F^{2m^2+mn-d} && (2.119)
\end{aligned}$$

It is bounded above by choosing $d>2m^2+mn$. If $\|H^{(l)}\|_F\le M_d$, it is also bounded because a continuous function has a maximum inside a compact set. Condition (b) for p_H is necessary to guarantee that the right-hand side of (2.116) is continuous. The right-hand side of (2.116) depends only on P and other initial conditions. We call the maximum value of (2.116) as $\beta_t(P)$

Theorem 2.6.1 *$f^{(t)} : \mathbb{S}^n_{++} \times \mathbb{S}^n_{++} \to \mathbb{R}_+$ is continuous if $mt > n$*

Proof: For fixed P_* and C_*, define a sequence $\{(P_k, C_k)\}_{k=1}^{\infty}$ which converges to (P_*, C_*). Define a function $u_k : V_{n,mt} \to \mathbb{R}_+$ as below.

$$u_k(O) = \det\left(F^t P_k (F^T)^t + \sum_{l=0}^{t-1} F^l Q (F^T)^l - C_k\right)^{\frac{mt-n-1}{2}} \phi(P_k, C_k, O) \tag{2.120}$$

$$\text{then} \qquad f^{(t)}(P_k, C_k) = \int_{V_{n,mt}} 2^{-n} \det(F)^{-\frac{mt(t+1)}{2}} u_k(O) \mathrm{d}O \tag{2.121}$$

It is obvious that $u_k(O)$ goes to $u_*(O)$ as k goes to ∞ for fixed O

$$u_k(O) \leq \det\left(F^t P_k (F^T)^t + \sum_{l=0}^{t-1} F^l Q (F^T)^l - C_k\right)^{\frac{mt-n-1}{2}} \beta_t(P_k) \tag{2.122}$$

$$\leq (1+\varepsilon) \det\left(F^t P_* (F^T)^t + \sum_{l=0}^{t-1} F^l Q (F^T)^l - C_*\right)^{\frac{mt-n-1}{2}} \beta_t(P_*) \tag{2.123}$$

The second inequality holds for some $\varepsilon > 0$ because $\{(P_k, C_k)\}_{k=1}^{\infty}$ converges to (P_*, C_*) and right-hand side of the inequality is continuous function. By bounded convergence theorem,

$$\lim_{k \to \infty} \int_{V_{n,mt}} u_k(O) \mathrm{d}O = \int_{V_{n,mt}} u_*(O) \mathrm{d}O \tag{2.124}$$

It is straightforward that

$$\lim_{k \to \infty} f^{(t)}(P_k, C_k) = f^{(t)}(P_*, C_*) \tag{2.125}$$

■

2.7 Continuity of Measure

We show that $f^{(t)}$ is continuous in the previous section. We want to extend the continuity from function to measure. Specifically, we show that $\mu_P^{(t)}$ is continuous in topology defined by total variation distance under the assumption that $f^{(t)}$ is continuous function in this section.

Definition 14 *For two measures μ and ν with probability density functions p_μ and p_ν, $d_H(\mu, \nu)$ is*

Hellinger distance between two measures, i.e.,

$$d_H(\mu,\nu) = \left(\frac{1}{2}\int\left(\sqrt{p_\mu} - \sqrt{p_\nu}\right)^2\right)^{\frac{1}{2}} \tag{2.126}$$

Theorem 2.7.1 *For $mt > n$ and a sequence $\{P_k\}_{k=1}^{\infty}$ converging to P_*, $d_{TV}(\mu_{P_k}^{(t)}, \mu_{P_*}^{(t)})$ goes to zero as k goes to ∞*

Proof: It is well known that the topology defined by total variation distance is identical to the topology defined by Hellinger distance. It is enough to show that

$$d_H(\mu_{P_k}^{(t)}, \mu_{P_*}^{(t)}) \to 0 \qquad \text{as} \qquad k \to \infty \tag{2.127}$$

Define a set $E_\delta = \{C \in \mathbb{S}_{++}^n : f^{(t)}(P_*, C) \geq \delta\}$ and a function $\rho_\delta : \mathbb{S}_{++}^n \times E_\delta \to \mathbb{R}_+$ for this proof.

$$\rho_\delta(P,C) = \min\left(\sqrt{\frac{f^{(t)}(P,C)}{f^{(t)}(P_*,C)}}, 1\right) \tag{2.128}$$

Then, ρ_δ is well-defined because the denominator is greater than δ in the domain.

For given $\varepsilon > 0$, there exists $\delta > 0$ such that

$$\int_{E_\delta} f^{(t)}(P_*, C)\mathrm{d}C > 1 - \varepsilon \tag{2.129}$$

$$\begin{aligned} d_H(\mu_{P_k}^{(t)}, \mu_{P_*}^{(t)})^2 &= \frac{1}{2}\int_{\mathbb{S}_{++}^n}\left(\sqrt{f^{(t)}(P_k,C)} - \sqrt{f^{(t)}(P_*,C)}\right)^2 \mathrm{d}C && (2.130)\\ &= 1 - \int_{\mathbb{S}_{++}^n}\sqrt{f^{(t)}(P_k,C)f^{(t)}(P_*,C)}\mathrm{d}C && (2.131)\\ &\leq 1 - \int_{E_\delta}\sqrt{f^{(t)}(P_k,C)f^{(t)}(P_*,C)}\mathrm{d}C && (2.132)\\ &\leq 1 - \int_{E_\delta} f^{(t)}(P_*,C)\rho_\delta(P_k,C)\mathrm{d}C && (2.133) \end{aligned}$$

It is obvious that $\rho_\delta(P,C) = 1$ at $P = P_*$. We claim that

$$\inf_{C\in E_\delta}\rho_\delta(P,C) \to 1 \quad \text{as} \quad P \to P_* \tag{2.134}$$

The proof follows.

Assume that it's not true, then there exists $\eta > 0$ and a sequence $\{(\tilde{P}_i, \tilde{C}_i)\}_{i=1}^{\infty}$ such that

$$\rho_\delta(\tilde{P}_i, \tilde{C}_i) < 1 - \eta \quad \forall i \in \mathbb{N} \qquad \text{and} \qquad \lim_{i \to \infty} \tilde{P}_i = P_* \tag{2.135}$$

E_δ is closed because it is a preimage of continuous function $f^{(t)}(P_*, \cdot)$. It is also bounded because $E_\delta \subset Supp_{P_*}^{(t)}$ and $Supp_{P_*}^{(t)}$ is bounded. E_δ is compact because it is closed and bounded.

Since E_δ is compact in metric space, every sequence in E_δ has a convergent subsequence. Let $\{\tilde{C}_{i_j}\}_{j=1}^{\infty}$ denote the convergent subsequence of $\{\tilde{C}_i\}_{i=1}^{\infty}$ and C_* denote the limit point of the convergent subsequence. Then $\{(\tilde{P}_{i_j}, \tilde{C}_{i_j})\}_{j=1}^{\infty}$ converges to (P_*, C_*).

$\rho_\delta(\tilde{P}_{i_j}, \tilde{C}_{i_j}) \to \rho_\delta(P_*, C_*) = 1$ because ρ_δ is continuous. However, it contradicts that $\rho_\delta(\tilde{P}_i, \tilde{C}_i) < 1 - \eta \quad \forall i$. The previous assumption was wrong.

There exists K such that $\inf_{C \in E_\delta} \rho_\delta(P_k, C) > 1 - \varepsilon$ for all $k > K$. Returning back to (2.133)

$$d_H(\mu_{P_k}^{(t)}, \mu_{P_*}^{(t)})^2 \leq 1 - \int_{E_\delta} f^{(t)}(P_*, C) \rho_\delta(P_k, C) \mathrm{d}C \tag{2.136}$$

$$< 1 - \int_{E_\delta} f^{(t)}(P_*, C)(1 - \varepsilon) \mathrm{d}C \tag{2.137}$$

$$< 1 - (1 - \varepsilon)^2 < 2\varepsilon \tag{2.138}$$

$d_H(\mu_{P_k}^{(t)}, \mu_{P_*}^{(t)})$ goes to zero because ε is arbitrary. It completes the proof. ■

2.8 Extension on Compact Space

$\mu_{(\cdot)}^{(t)}$ can be interpreted as a map from the space of positive semidefinite matrices to the space of probability measures. We showed the continuity of map in the previous section. In this section, we extend the map to compact space including zero and infinity.

Lemma 2.8.1 *For two symmetric matrices $UDU^T, U'D'(U')^T \in \mathbb{S}^n$ where U, U' are orthogonal and D, D' are ordered-diagonal matrix, (i.e., $D = diag(d_1, \cdots, d_n)$ is ordered if $d_1 \leq \cdots \leq d_n$) $UDU^T = U'D(U')^T$ if and only if two statements below hold.*

(1) $D = D'$

(2) Suppose $D = D'$ has distinct eigenvalues $\{d_1, \cdots, d_a\}$ with $m_1, \cdots, m_a$ multiplicities and $u_{i,1}, \cdots, u_{i,m_i}$ are m_i column vectors of U corresponding to d_i. $u'_{i,1}, \cdots, u'_{i,m_i}$ can be defined similarly, then the

equation below holds for every i.

$$\sum_{j=1}^{m_i} u_{i,j}u_{i,j}^T = \sum_{j=1}^{m_i} u'_{i,j}(u'_{i,j})^T \tag{2.139}$$

Proof: The first condition requires both of eigenvalues to be same, and the second condition requires both of eigenspaces to be same. The remaining part is trivial to check. ■

With the lemma, we define extended space of $\mathbb{S}^n_{++}$.

Definition 15 *$\mathbb{X}^n = \{(U,D) : U \in V_{n,n}, D = diag(d_1,\cdots,d_n), 0 \leq d_1 \leq \cdots \leq d_n \leq \infty\}$ with equivalence relation $(U,D) \sim (U',D')$ if*

$$D = D' \qquad \textit{and} \qquad \sum_{d_i=d} u_i u_i^T = \sum_{d_i=d} u'_i(u'_i)^T \tag{2.140}$$

for every distinct diagonal element d

Remark 3 *$\mathbb{X}^n$ is homeomorphic to $\{(U,D) : U \in V_{n,n}, D = diag(d_1,\cdots,d_n), 0 \leq d_1 \leq \cdots \leq d_n \leq 1\}$. Therefore, there is a natural topology in $\mathbb{X}^n$, and it is possible to define convergence from that. It is also obvious that $\mathbb{X}^n$ is compact.*

The goal of this section is to define $\mu_P^{(t)}$ for all $P \in \mathbb{X}^n$. It is natural to define $\mu_P^{(t)}(E) = \lim_{k\to\infty} \mu_{P_k}^{(t)}(E)$ for the sequence $\{P_k\}_{k=1}^{\infty} \subset \mathbb{S}^n_{++}$ which converges to P. However, there is no guarantee that $\lim_{k\to\infty} \mu_{P_k}^{(t)}(E)$ exists.

Theorem 2.8.2 *For $P \in \mathbb{S}^n_+$ and $\{P_k\}_{k=1}^{\infty} \subset \mathbb{S}^n_{++}$ converging to P, $\lim\limits_{k\to\infty} \mu_{P_k}^{(t)}(E)$ exists if $t > \frac{n}{m} + 1$*

Proof: From the equation $P - PH^T(R + HPH^T)^{-1}HP = (P^{-1} + H^T R^{-1} H)^{-1}$,

$$\mu_{P_k}^{(t)}(E) = \int_{\mathbb{R}^{m\times n}} \mu^{(t-1)}_{F(P_k^{-1}+(H^{(0)})^T R^{-1} H^{(0)})^{-1}F^T+Q}(E)\, p(H^{(0)})\mathrm{d}H^{(0)} \tag{2.141}$$

$p(H^{(0)})$ is probability density function of Gaussian matrix $H^{(0)}$.

We can define $\mu_P^{(t)}(E)$ in similar way, then it is well-defined because $F(P_k^{-1} + (H^{(0)})^T R^{-1} H^{(0)})^{-1} F^T + Q \in \mathbb{S}^n_{++}$ by positivity of Q.

It is obvious that $\mu_{P_k}^{(t)}(E) \leq 1$.

$$\mu^{(t-1)}_{F(P_k^{-1}+(H^{(0)})^T R^{-1} H^{(0)})^{-1}F^T+Q}(E) \to \mu^{(t-1)}_{F(P^{-1}+(H^{(0)})^T R^{-1} H^{(0)})^{-1}F^T+Q}(E) \tag{2.142}$$

from the fact that $F(P_k^{-1}+(H^{(0)})^T R^{-1} H^{(0)})^{-1} F^T + Q \to F(P^{-1}+(H^{(0)})^T R^{-1} H^{(0)})^{-1} F^T + Q$ and continuity of $\mu_{(\cdot)}^{(t-1)}$ which is shown in the previous section.

By bounded convergence theorem, $\lim_{k\to\infty} \mu_{P_k}^{(t)}(E) = \mu_P^{(t)}(E)$ ■

It is possible to extend $\mu_P^{(t)}$ to the matrix which has zero as eigenvalue. The next step is to extend it to the matrix which has ∞ as eigenvalue.

We suggest a lemma used for the extension.

Lemma 2.8.3 *$\omega : Y \times Z \to X$ is a continuous function defined on $Y \times Z$. X, Z are Euclidean manifold. z is random variable on Z and ν is probability measure of it satisfying $\nu(\omega(y,\cdot)^{-1}(V)) = \nu(\omega(y,\cdot)^{-1}(\mathrm{cl}(V)))$ for every $y \in Y$ and every open $V \subset X$. Then $\mathbb{P}[\omega(y_k,z)\in E] \to \mathbb{P}[\omega(y_*,z)\in E]$ as $y_k \to y_*$.*

Proof: Let $\omega_k(\cdot)$ denote $\omega(y_k,\cdot)$, then ω_k is continuous and $\omega_k(z) \to \omega_*(z)$ for every z.

$$\nu(E) = \sup\{\nu(K) : K \subset E, K \text{ compact}\} = \inf\{\nu(W) : W \supset E, W \text{ open}\} \tag{2.143}$$

because ν is probability measure defined on Euclidean manifold and it's a Radon measure.

For any open set $V \subset X$, there is compact $K \subset \omega_*^{-1}(V)$ such that $\nu(K) > \nu(\omega_*^{-1}(V)) - \varepsilon_1$, then $\{y_*\} \times K$ is also compact in $Y \times Z$. Let $B((y_0,z_0);\delta) = \{(y,z) : d_Y(y,y_0) < \delta, d_Z(z,z_0) < \delta\}$ denote a ball in $Y \times Z$ where $d_Y(\cdot,\cdot)$ and $d_Z(\cdot,\cdot)$ are metric of Y and Z. Since $\{y_*\} \times K \subset \omega^{-1}(V)$, there is $\delta_z > 0$ for every $z \in K$ such that $B((y_*,z);\delta_z) \subset \omega^{-1}(V)$. Since $\{y_*\} \times K$ is compact, there is a finite subcover. We call δ_{min} as the smallest δ_z of the finite subcover. For all y_k such that $d_Y(y_k,y_*) < \delta_{min}$, $\{y_k\} \times K \subset \omega^{-1}(V)$ because it is contained in the subcover. That means $K \subset \omega_k^{-1}(V)$ and

$$\nu(\omega_k^{-1}(V)) \geq \nu(K) > \nu(\omega_*^{-1}(V)) - \varepsilon_1 \tag{2.144}$$

For open set $\mathrm{int}(X \setminus V)$, we can get a similar inequality for k large enough.

$$\nu(\omega_k^{-1}(X \setminus \mathrm{cl}(V))) = \nu(\omega_k^{-1}(\mathrm{int}(X \setminus V))) > \nu(\omega_*^{-1}(\mathrm{int}(X \setminus V))) - \varepsilon_2 = \nu(\omega_*^{-1}(X \setminus \mathrm{cl}(V))) - \varepsilon_2 \tag{2.145}$$

The equality above holds from the basic set theory algebra.

$$\nu(\omega_k^{-1}(\mathrm{cl}(V))) = 1 - \nu(\omega_k^{-1}(X \setminus \mathrm{cl}(V))) < 1 - \nu(\omega_*^{-1}(X \setminus \mathrm{cl}(V))) + \varepsilon_2 = \nu(\omega_*^{-1}(\mathrm{cl}(V))) + \varepsilon_2 \tag{2.146}$$

From the assumption that $\nu(\omega(y,\cdot)^{-1}(V)) = \nu(\omega(y,\cdot)^{-1}(\mathrm{cl}(V)))$,

$$\nu(\omega_k^{-1}(V)) = \nu(\omega_k^{-1}(\mathrm{cl}(V))) < \nu(\omega_*^{-1}(\mathrm{cl}(V))) + \varepsilon_2 = \nu(\omega_*^{-1}(V)) + \varepsilon_2 \tag{2.147}$$

Since $\varepsilon_1, \varepsilon_2$ is arbitrary,

$$\lim_{k\to\infty} \nu(\omega_k^{-1}(V)) = \nu(\omega_*^{-1}(V)) \tag{2.148}$$

For any compact set $J \subset X$, $X \setminus J$ is open and the equality below holds.

$$\lim_{k\to\infty} \nu(\omega_k^{-1}(J)) = 1 - \lim_{k\to\infty} \nu(\omega_k^{-1}(X\setminus J)) = 1 - \nu(\omega_*^{-1}(X\setminus J)) = \nu(\omega_*^{-1}(J)) \tag{2.149}$$

Let ν_* denote measure on X such that $\nu_*(E) = \nu(\omega_*^{-1}(E))$, then it is also a probability measure. For any measurable $E \in X$,

$$\nu_*(E) = \sup\{\nu_*(J) : J \subset E, J \text{ compact}\} = \inf\{\nu_*(V) : V \supset E, V \text{ open}\} \tag{2.150}$$

because ν_* is also probability measure defined on Euclidean manifold and it's a Radon measure.

Take compact J and open V such that $J \subset E \subset V$ and $\nu_*(V) - \varepsilon < \nu_*(E) < \nu_*(J) + \varepsilon$. There exists $M > 0$ such that

$$\nu(\omega_k^{-1}(V)) < \nu(\omega_*^{-1}(V)) + \varepsilon \qquad \textit{and} \qquad \nu(\omega_k^{-1}(J)) > \nu(\omega_*^{-1}(J)) - \varepsilon \qquad \forall k > M \tag{2.151}$$

For every $k > M$,

$$\nu(\omega_*^{-1}(E)) - 2\varepsilon < \nu(\omega_*^{-1}(J)) - \varepsilon < \nu(\omega_k^{-1}(J)) \le \nu(\omega_k^{-1}(E)) \tag{2.152}$$

$$\nu(\omega_k^{-1}(E)) \le \nu(\omega_k^{-1}(V)) < \nu(\omega_*^{-1}(V)) + \varepsilon < \nu(\omega_*^{-1}(E)) + 2\varepsilon \tag{2.153}$$

Since ε is arbitrary,

$$\lim_{k\to\infty} \mathbb{P}[\omega(y_k, z) \in E] = \lim_{k\to\infty} \nu(\omega_k^{-1}(E)) = \nu(\omega_*^{-1}(E)) = \mathbb{P}[\omega(y_*, z) \in E] \tag{2.154}$$

■

Returning back to discussion on $\mathbb{X}^n$

Definition 16 *τ is a function defined on $\mathbb{X}^n$. $\tau(A) = (FA^{-1}F^T + Q)^{-1}$.*

Lemma 2.8.4 *For all $A \in \mathbb{X}^n$, $\tau(A)$ is continuous and well-defined. Furthermore, its image is in $\mathbb{S}_+^n$.*

Proof: $\tau(0) = 0$ and Q^{-1} is upper bound of τ. Since τ is increasing function, it can be exteneded to $\mathbb{X}^n$. ■

Definition 17 $\bar{\tau}^{(t)} : \mathbb{S}_+^n \times (\mathbb{R}^{m\times n})^t \to \mathbb{S}_+^n$ *is defined by*

$$\bar{\tau}^{(t)}(A, H_0, \cdots, H_{t-1}) = \tau(\cdots \tau(\tau(A + H_0^T R^{-1} H_0) + H_1^T R^{-1} H_1) \cdots + H_{t-1}^T R^{-1} H_{t-1}) \tag{2.155}$$

Lemma 2.8.5 *For any $A \in \mathbb{S}_+^n$ and $t > \frac{n}{m} + 1$, Lebesgue measure of $\bar{\tau}^{(t)}(A, \cdot)^{-1}(E) \in (\mathbb{R}^{m\times n})^t$ is zero if $E \subset \mathbb{S}_+^n$ is measure-zero set.*

Proof: Since $\tau(\cdot)^{-1}$ is Riccati equation, it is possible to consider a Riccati equation rather than τ. The remaining part is trivial to check. ■

Previous lemma guarantees that

$$\int_{\bar{\tau}^{(t)}(A,\cdot)^{-1}(V)} \bar{p}(\bar{H}) \mathrm{d}\bar{H} = \int_{\bar{\tau}^{(t)}(A,\cdot)^{-1}(\mathrm{cl}(V))} \bar{p}(\bar{H}) \mathrm{d}\bar{H} \tag{2.156}$$

because $\bar{p}$ is continuous. We can apply Lemma 2.8.3 to the next theorem.

Theorem 2.8.6 *For $P \in \mathbb{X}^n$ and $\{P_k\}_{k=1}^{\infty} \subset \mathbb{S}_{++}^n$ converging to P, $\lim_{k\to\infty} \mu_{P_k}^{(t)}(E)$ exists if $t > \frac{n}{m} + 1$*

Proof: For given $P^{(0)} = P \in \mathbb{X}^n$ and $H^{(0)}$, $(P^{(1)})^{-1} = \tau(P^{-1} + (H^{(0)})^T R^{-1} H^{(0)}) \in \mathbb{S}_+^n$. We will deal with $(P^{(l)})^{-1}$ because its eigenvalues are finite.

$$\mu_P^{(t)}(E) = \mathbb{P}[\bar{\tau}^{(t-1)}(\tau(P^{-1} + (H^{(0)})^T R^{-1} H^{(0)}), H^{(1)}, \cdots, H^{(t-1)}) \in E^{-1}] \tag{2.157}$$

is well-defined where $E^{-1} = \{\frac{1}{x} : x \in E\}$ because it is computed on $\mathbb{S}_+^n$.

We know that $\tau(P_k^{-1} + (H^{(0)})^T R^{-1} H^{(0)}) \to \tau(P^{-1} + (H^{(0)})^T R^{-1} H^{(0)})$ from Lemma 2.8.4 and the equation below from Lemma 2.8.3

$$\lim_{k\to\infty} \mathbb{P}[\bar{\tau}^{(t-1)}(A, H^{(1)}, \cdots, H^{(t-1)}) \in E^{-1} | A = \tau(P_k^{-1} + (H^{(0)})^T R^{-1} H^{(0)})] \tag{2.158}$$

$$= \mathbb{P}[\bar{\tau}^{(t-1)}(A, H^{(1)}, \cdots, H^{(t-1)}) \in E^{-1} | A = \tau(P^{-1} + (H^{(0)})^T R^{-1} H^{(0)})] \tag{2.159}$$

$$\mu_{P_k}^{(t)}(E) = \int_{\mathbb{R}^{m\times n}} \mathbb{P}[\bar{\tau}^{(t-1)}(A, H^{(1)}, \cdots, H^{(t-1)}) \in E^{-1} | A = \tau(P_k^{-1} + (H^{(0)})^T R^{-1} H^{(0)})] p(H^{(0)}) \mathrm{d}H^{(0)} \tag{2.160}$$

It is also obvious that $\mathbb{P}[\bar{\tau}^{(t-1)}(A, H^{(1)}, \cdots, H^{(t-1)}) \in E^{-1} | A = \tau(P_k^{-1} + (H^{(0)})^T R^{-1} H^{(0)})] \leq 1$.

By bounded convergence theorem, $\lim_{k\to\infty} \mu_{P_k}^{(t)}(E) = \mu_P^{(t)}(E)$ ■

2.9 Main Result

We combine the results from previous sections to get main result here. The key point of the proof is showing that $\pi^{(t)} = \sup_{\alpha,\beta,S} \mathbb{P}^{(t)}(\alpha, S) - \mathbb{P}^{(t)}(\beta, S) < 1$. $\pi^{(t)} = 1$ if there are two initial points α, β where $Supp_\alpha^{(t)} \cap Supp_\beta^{(t)} = \emptyset$ at time t. We showed that every probability measure $\mu_{(\cdot)}^{(t)}$ at time t has common area with nonzero measure if t is large enough. Even though the distance between $\mu_\alpha^{(t)}$ and $\mu_\beta^{(t)}$ is strictly less than 1 for every $\alpha, \beta \in \mathbb{S}_{++}^n$, it is still questionable whether the supremum of the total variation distance, $\pi^{(t)} = \sup_{\alpha,\beta} d_{TV}(\mu_\alpha^{(t)}, \mu_\beta^{(t)})$ is strictly less than 1. We overcome this by applying the topological property that every continuous map has the maximum in compact set. The possible continuous map is $d_{TV}(\mu_{(\cdot)}^{(t)}, \mu_{(\cdot)}^{(t)}) : \mathbb{S}_{++}^n \times \mathbb{S}_{++}^n \to \mathbb{R}_+$. To show that $d_{TV}(\mu_{(\cdot)}^{(t)}, \mu_{(\cdot)}^{(t)})$ is actually continuous, we needed several intermediate results. We evaluated probability density function of $\mu_P^{(t)}$ applying matrix calculation technique. By evaluating the probability density function, we showed that the probability density function is continuous. The continuity of the probability density function was necessary to show that $\mu_{(\cdot)}^{(t)}$ is a continuous map from the space of positive semidefinite matrices to the space of probability measures. Finally, we extended $\mathbb{S}_{++}^n$ to admit 0 and ∞ to eigenvalues. The following is the main result of this section.

Theorem 2.9.1 *There exists a measure μ_* and constants $\kappa > 0, \gamma < 1$ independent from P, the initial point, satisfying*

$$d_{TV}(\mu_*, \mu_P^{(t)}) < \kappa\gamma^t \tag{2.161}$$

Proof: First, we show that $\pi^{(t)} < 1$ for $t > \frac{n}{m} + 1$.
$d : \mathbb{X}^n \times \mathbb{X}^n \to \mathbb{R}_+$ defined by $d(P_1, P_2) = d_{TV}(\mu_{P_1}^{(t)}, \mu_{P_2}^{(t)})$ is well-defined from Theorem 2.8.2 and Theorem 2.8.6. It is also continuous from Theorem 2.7.1.
Since $d(\cdot,\cdot)$ is continuous on compact space $\mathbb{X}^n \times \mathbb{X}^n$, it has maximum. Suppose that $d_{max} =$

$d_{TV}(\mu_{P_1}^{(t)}, \mu_{P_2}^{(t)})$ for some $P_1, P_2 \in \mathbb{X}^n$.

$$\begin{aligned} d_{TV}(\mu_{P_1}^{(t)}, \mu_{P_2}^{(t)}) &= \sup_S \left| \mu_{P_1}^{(t)}(S) - \mu_{P_2}^{(t)}(S) \right| && (2.162) \\ &= 1 - \int_{Supp_{P_1}^{(t)} \cap Supp_{P_2}^{(t)}} \min\left(f^{(t)}(P_1, C), f^{(t)}(P_2, C) \right) \mathrm{d}C && (2.163) \end{aligned}$$

$Supp_{P_1}^{(t)} \cap Supp_{P_2}^{(t)}$ and has nonempty interior because $Supp_{P_1}^{(t)}, Supp_{P_2}^{(t)} \supset Supp_0^{(t)} = Supp_Q^{(t-1)}$ from Theorem 2.4.3. $f^{(t)}(P_1, C), f^{(t)}(P_2, C) > 0$ on the support of each probability density function.

We can conclude that

$$\pi^{(t)} = d_{max} = 1 - \int_{Supp_{P_1}^{(t)} \cap Supp_{P_2}^{(t)}} \min\left(f^{(t)}(P_1, C), f^{(t)}(P_2, C) \right) \mathrm{d}C < 1 \tag{2.164}$$

Since $\pi^{(t)} < 1$, we can define $\mu_*(E)$ as limit of $M_E^{(t)}$ and $m_E^{(t)}$.

$$\left| \mu_*(E) - \mu_P^{(tl)}(E) \right| \leq M_E^{(tl)} - m_E^{(tl)} \leq (\pi^{(t)})^l \tag{2.165}$$

for all P guarantees the exsitence of $\kappa > 0, \gamma < 1$ which is independent from P. ■

Chapter 3

Nonlinear Epidemic Model

3.1 Introduction

Modeling the spread of an infectious disease on a complex network is a topic of increasing interest. The classical epidemic models include the susceptible-infected-susceptible (SIS) model. In the SIS model, each node of the network exists in one of two different states. In the susceptible state, the node is healthy, but it may be infected if it is exposed to disease. The node is exposed to disease if any of its neighbors in the network are infected. The probability for being infected from a susceptible state depends on the number of infected neighbors. From an infected state, the node may become healthy with some probability, after which it returns to a susceptible state.

Early work in the SIS model has been conducted using random graph approach [49], [50]. In the random graph model, the number of infected neighbors depend on both of the degree distribution and rate of infected nodes. The work is focused on high-probability behavior of steady state and convergence of various random graph models.

The other approach is fixed graph one. We can model this process as Markov chain with 2^n states where n is the number of nodes in the network when underlying graph is given [16], [23], [42]. At each time, the state of the Markov chain represents the joint probability of the all the nodes being in either susceptible or infected states. Since the joint probability distribution at any given time only depends on the joint probability distribution at the previous time this is a Markov chain. The transition matrix of the Markov chain is closely related to the adjacency matrix of the underlying graph. When the underlying graph is connected, Perron-Frobenius theory implies that the Markov chain has a unique absorbing state, which is the state where all the nodes in the network are susceptible. The reason being that if all the nodes are susceptible, no node will be exposed to disease, and therefore they will always stay healthy. It is therefore clear that, in the Markov chain model, if one waits long enough, the epidemic will die out and all nodes will be healthy. However, this result is not very informative since depending on the mixing time of the Markov chain, it may take a very long time, in fact exponentially long in the number of nodes, for steady state to be achieved. In this situation, the dying out of the epidemic may not be observed in practice.

As a result of this, we study approximate models which have a much smaller number of states. Once such model has been introduced by Wang et al. and Chakrabarti et al. [62], [10] and some more work has been conducted based on the model [20], [25]. In what follows we shall study this and two other models (a discrete-time model similar to the Chakrabarti model, as well as a continuous-time model). The main result is that, when the origin (corresponding to the all susceptible states) is not stable, the epidemic model has a unique second fixed point. For the continuous-time model, and Chakrabarti model, we show that the second fixed point attracts *all* non-origin points. For the other discrete-time model, we show that this is not necessarily the case, and give conditions under which the second fixed point is stable.

This chapter organizes as follows. In the following section, we describe the nonlinear epidemic map suggested by [10] which focuses on the marginal probability of each node being infected. In the next section, we describe linear upper bound of the nonlinear map, which is actually Jacobian matrix of the nonlinear map at the origin. We analyze the case where linear upper bound is not stable. The main result of this section is that, when the origin (corresponding to the all-healthy states) is not stable, the epidemic model has a unique second fixed point other than the origin and it is globally stable. In the next section, we mention another model which admits immune-effect where a node does not get infected from its neighbors after recovering from the disease at the same time. The immune-admitting model has similar properties to the nonlinear model described at the previous section, but different in stability of the second fixed point. We focus more on the stability analysis and conclude that the second fixed point is stable with high probability in some random graph family including Erdös-Rényi graphs. Finally, we suggest continuous-time model and analyze the stability of the equilibrium point.

3.2 Model Description

In this section, we describe our model for epidemic spread. We do not assume homogeneous connectivity. Each node has its own connectivity with other nodes in the given network. The connectivity is represented as the graph. For a given connected undirected graph G with n nodes, let N_i be the neighborhood of node i.

Each node can be in a state of health, represented by “0”, or a state of infection, represented by “1”. Two possible states for each node lead 2^n states for the given network. We assume an identical infection rate β for each edge connected to an infected node and a recovery rate δ for each infected node. We can view β as a virus transfer rate and δ as a virus death rate if we consider the epidemics as the propagation of virus on the network. We do not assume coming of new nodes which is a birth of a baby in a real network or deletion of nodes which is a death of person.

The model works for time interval. During each time interval, infected node transfer disease to its neighbors with probability β, the infection rate. At same time, an infected node tries to recover from disease. The recovery happens with probability δ, the recovery rate. We assume that the infection from each node is independent to each other. This process can be modeled as a Markov chain with 2^n states. All the states of the Markov chain corresponds to $\{0,1\}^n$. The epidemic states of each node at time $t+1$ only depends on ones at time t.

However, the number of states for the Markov chain model increases exponentially as the number of nodes increases. Huge number of the states make it hard to analyze the Markov chain. Instead of analyzing Markov chain model, we study the approximated nonlinear dynamical model in this chapter. The nonlinear dynamical model focuses on the marginal probability of each node being infected. Denote $P(t) = (P_1(t), \cdots, P_n(t))^{\mathrm{T}}$ as the epidemic probability vector where $P_i(t)$ is the probability that the node i is infected at time t.

We clarify the infection and recovery rule before going on.

- If node i is healthy, i may get infected from its infected neighbors. The infection from each neighbor is independent. i is infected at the next time step if i gets infected from any of its neighbors. In other words, i stays healthy if i does not get infected from any of its neighbors.
- If node i is infected, i may recover from the disease. i can get infected from its infected neighbors at same time step in which it recovers. i is healthy at the next time step if it is recovered from disease, and it does not get infected from any of its neighbors at same time.

The recovery rule above assumes that there is no effect of immune. We analyze the immune-admitting model which ban the recovery and the instant infection at same time. Denote Ξ_i as the probability that i gets infected from its neighbors.

$$1 - P_i(t+1) = (1-\Xi_i)(1-P_i(t)) + \delta(1-\Xi_i)P_i(t) \tag{3.1}$$

To represent Ξ_i only by $P(t) = (P_1(t), \cdots, P_n(t))^{\mathrm{T}}$, we apply independent infection.

$$\Xi_i = 1 - \prod_{j \in N_i} (1 - \beta P_j(t)) \tag{3.2}$$

Ξ_i will be generalized and redefined in the next section. Applying (3.2) to (3.1), we get the nonlinear epidemic map Φ which is suggested by Chakrabarti et al. [10].

$$\Phi_i(x) = (1-\delta)x_i + (1-(1-\delta)x_i)\left(1 - \prod_{j \in N_i}(1-\beta x_j)\right) \tag{3.3}$$

It is trivial to check that $P_i(t+1) = \Phi_i((P_1(t), \cdots, P_n(t))^T)$ from (3.3)

3.3 Dynamics of Epidemic Map

We study epidemic map suggested by Chakrabarti in this section. $P_i(t+1) = \Phi_i((P_1(t), \cdots, P_n(t))^T)$ where $\Phi : [0,1]^n \to [0,1]^n$ is defined as (3.3) is an epidemic map on n-dimensional probability space. To understand the behavior of this model, we obtain the following upper bound of Φ:

$$\Phi_i(x) = (1-\delta)x_i + (1-(1-\delta)x_i)\left(1 - \prod_{j \in N_i}(1-\beta x_j)\right) \tag{3.4}$$

$$\leq (1-\delta)x_i + \left(1 - \prod_{j \in N_i}(1-\beta x_j)\right) \tag{3.5}$$

$$\leq (1-\delta)x_i + \beta\left(\sum_{j \in N_i} x_j\right) \tag{3.6}$$

(3.6) can be regarded as a linear approximation of (3.3) for small β. It is nice approximation around the origin because it is a Jacobian matrix of Φ at the origin. Note that this linearization gives an upper bound on the nonlinear model.

For two real-valued column vectors $u = (u_1, \cdots, u_n)^{\mathrm{T}}, v = (v_1, \cdots, v_n)^{\mathrm{T}} \in \mathbb{R}^n$, we say $u \preceq v$ if $u_i \leq v_i$ for all $i \in \{1, \cdots, n\}$ and $u \prec v$ if $u_i < v_i$ for all $i \in \{1, \cdots, n\}$. For $P(t) = (P_1(t), \cdots, P_n(t))^{\mathrm{T}}$

$$P(t+1) = \Phi(P(t)) \preceq ((1-\delta)I_n + \beta A)P(t) \tag{3.7}$$

It is obvious that $P(t)$ converges to the origin for both of (3.3) and (3.6) if $\lambda_{max}((1-\delta)I_n + \beta A) < 1$. In other words, the origin is a unique fixed point of (3.3) which is globally stable if the largest eigenvalue of $(1-\delta)I_n+\beta A$ is less than 1. The reason is that this happens for the linearized upper bound which is actually Jacobian matrix of (3.3) at the origin. We will therefore focus on the dynamics of the system when $\lambda_{max}((1-\delta)I_n+\beta A)>1$.

Wang et al. [62] and Chakrabarti et al. [10] focus on staying healthy by defining the probability that a node receives no infection from its neighborhood. We focus on *infection* rather than staying healthy.

Let $\Xi:[0,1]^n\to[0,1]^n$ with $\Xi=(\Xi_1,\cdots,\Xi_n)^{\mathrm{T}}$ be a map associated with network G satisfying the three properties below.

(a) $\Xi_i(x)=0$ and $\dfrac{\partial\Xi_i}{\partial x_j}=\beta A_{i,j}$ at the origin.

(b) $\dfrac{\partial\Xi_i}{\partial x_j}>0$ if $i\in N_j$ in G, and $\dfrac{\partial\Xi_i}{\partial x_j}=0$ if $i\notin N_j$ in G.

(c) For any $i,j,k\in\{1,\cdots,n\}$, $\dfrac{\partial^2\Xi_i}{\partial x_j\partial x_k}\le 0$.

Ξ_i represents the probability that i get infected from its infected neighbors in the next time step when i is healthy. It is obvious that $\Xi_i(x)=\left(1-\prod_{j\in N_i}(1-\beta x_j)\right)$ satisfies all the conditions above. The sum of infection rate $\beta\sum\limits_{j\in N_i}x_j$ also satisfies all three conditions above. However, we do not apply the sum of infection rates in the discrete time model because it is not well-defined if β is small enough. In other words, Ξ_i can be greater than 1 if β is not small.

We define another map here. Let $\omega:[0,1]\to\mathbb{R}_+$ be a function which also satisfies three properties below.

(d) $\omega(0)=0$, $\omega(1)\ge 1$

(e) $\omega'(0)=\delta$, $\omega'(s)>0$ for all $s\in(0,1)$

(f) $\dfrac{\omega(s_1)}{s_1}<\dfrac{\omega(s_2)}{s_2}$ if $s_1<s_2$

It is also obvious that $\omega(s)=\dfrac{\delta s}{1-(1-\delta)s}$ satisfies all three conditions above. By defining $\Xi(\cdot)$ and $\omega(\cdot)$ here, the analysis can be applied directly to the immune-admitting model which will be described later.

We can view (3.3) as

$$P_i(t+1)=P_i(t)+(1-(1-\delta)P_i(t))(\Xi_i(P(t))-\omega(P_i(t))) \tag{3.8}$$

We close this section by giving a lemma which is useful in the next section.

Lemma 3.3.1 *Let $h_{i,u,v}:s\to\Xi_i(u+sv)$ be a function defined on subset of nonnegative real numbers for given $i\in\{1,\cdots,n\}$, $u,v\in[0,1]^n$. Then $\dfrac{h_{i,u,v}(s)-h_{i,u,v}(0)}{s}$ is a decreasing function of s.*

Proof: $h_{i,u,v}(s)$ is concave by property (c).

$$\begin{aligned}
&\frac{d}{ds}\left(\frac{h_{i,u,v}(s)-h_{i,u,v}(0)}{s}\right) \\
&=\frac{1}{s}\left(h'_{i,u,v}(s)-\frac{h_{i,u,v}(s)-h_{i,u,v}(0)}{s}\right) &(3.9)\\
&=\frac{1}{s}\left(h'_{i,u,v}(s)-h'_{i,u,v}(s^*)\right)\leq 0 &(3.10)
\end{aligned}$$

$\frac{h_{i,u,v}(s)-h_{i,u,v}(0)}{s}=h'_{i,u,v}(s^*)$ for some $s^*\in(0,s)$ by the mean value theorem. ■

3.3.1 Existence and Uniqueness of Nontrivial Fixed Point

The origin, the trivial fixed point of the system equation is unstable if $\lambda_{max}((1-\delta)I_n+\beta A)>1$. However, it is unknown whether the system has another fixed point or not. In this section, we prove that there actually exists a nontrivial fixed point of (3.8). We also prove that the nontrivial fixed point is unique.

Lemma 3.3.2 *$\lambda_{max}((1-\delta)I_n+\beta A)>1$ if and only if there exists $v\succ(0,\cdots,0)^{\mathrm{T}}=0_n$ such that $(\beta A-\delta I_n)v\succ 0_n$*

Proof: Suppose that $\lambda_{max}((1-\delta)I_n+\beta A)>1$ and w as an eigenvector corresponding to the maximum eigenvalue. $(1-\delta)I_n+\beta A$ is nonnegative and irreducible (a nonnegative matrix X is irreducible if there exists $m(i,j)\in\mathbb{N}$ for each pair of indices i,j such that $(X^{m(i,j)})_{i,j}$ is nonzero because A is the adjacency matrix of a connected graph G. Every entry of w is positive by Perron-Frobenius theorem for irreducible matrices, and $(\beta A-\delta I_n)w\succ 0_n$ because the eigenvalue corresponding to w is greater than unity.

Suppose that there exists $v\succ 0_n$ such that $(\beta A-\delta I_n)v\succ 0_n$. Then, $((1-\delta)I_n+\beta A)v\succ v$

$$\begin{aligned}
\lambda_{max}((1-\delta)I_n+\beta A)&=\sup_{u\in\mathbb{R}^n}\frac{\|((1-\delta)I_n+\beta A)u\|_2}{\|u\|_2} &(3.11)\\
&\geq\frac{\|((1-\delta)I_n+\beta A)v\|_2}{\|v\|_2}>1 &(3.12)
\end{aligned}$$

■

The main theorem of this section which guarantees the existence and uniqueness of nontrivial fixed point of (3.8) follows.

Theorem 3.3.3 *Define a map* $\Psi : [0,1]^n \to \mathbb{R}^n$ *with* Ξ *and* ω *satisfying the conditions (a)-(f) above. Define*

$$\Psi_i(x) = \Xi_i(x) - \omega(x_i) \; . \tag{3.13}$$

Then $\Psi = (\Psi_1, \cdots, \Psi_n)$ *has a unique nontrivial (other than the origin) zero if* $\lambda_{max}((1-\delta)I_n + \beta A) > 1$.

Proof: U_i and U are defined by Ψ as below.

$$U_i = \{x \in [0,1]^n : \Psi_i(x) \geq 0\} \qquad U = \bigcap_{i=1}^{n} U_i \tag{3.14}$$

By the lemma above, there exists $v \succ 0_n$ such that $(\beta A - \delta I_n)v \succ 0_n$. There is a small $\varepsilon > 0$ such that $\varepsilon v \in U$ because the Jacobian of $\Psi = (\Psi_1, \cdots, \Psi_n)^{\mathrm{T}}$ is equal to $\beta A - \delta I_n$ at the origin and $\Psi(0) = 0$ by property (a) of Ξ and (d) of ω.

Define $\max(x,y) = (\max(x_1,y_1), \cdots, \max(x_n,y_n))$. We claim that $\max(x,y) \in U$ if $x, y \in S$. The proof follows.

$\max(x_i,y_i) = x_i$ without loss of generality for $x, y \in U$.

$$\Psi_i(\max(x,y)) = \Xi_i(\max(x,y)) - \omega(x_i) \geq \Xi_i(x) - \omega(x_i) \geq 0 \tag{3.15}$$

The first inequality holds by property (b), and the second inequality holds because $x \in U$. Therefore $\max(x,y) \in U_i$ for every i and it completes the proof of the claim.

This leads to the existence of a unique maximal point $x^* \in U$ such that $x^* \succeq x$ for all $x \in U$. $\varepsilon v \in U$ and the maximality of x^* guarantees that x^* has positive entries.

We claim that $\Psi_i(x^*) = 0$ for all $i \in \{1, \cdots, n\}$. Assume that $\Psi_i(x^*) \neq 0$ for some i. Then, $\Psi_i(x^*) > 0$ since $x^* \in U$. There exists $z_i > x_i^*$ such that

$$\Psi_i(x^*) = \Xi_i(x^*) - \omega(x_i^*) > \Xi_i(x^*) - \omega(z_i) \geq 0 \tag{3.16}$$

Define $z = (z_1, \cdots, z_n)^{\mathrm{T}}$ with $z_j = x_j^*$ for $j \neq i$. For every $k \in \{1, \cdots, n\}$,

$$\Psi_k(z) = \Xi_k(z) - \omega(z_k) \geq \Xi_k(x^*) - \omega(z_k) \geq 0 \tag{3.17}$$

The first inequality of (3.17) holds by property (b). The second inequality of (3.17) holds by (3.16) if $k = i$ and the inequality holds by definition of z if $k \neq i$. (3.17) guarantees that $z \in U$. $z_i > x_i^*$ and $z_j = x_j^*$ for $j \neq i$ contradict that x^* is the maximal point of U. The assumption was therefore wrong, $\Psi_i(x^*) = 0$ for all $i \in \{1, \cdots, n\}$, and there exists a nontrivial zero of Ψ.

The next step is showing that x^* is the unique nontrivial zero of Ψ. Assume that y^* is another nontrivial zero. Then $y^* \in U$ and $\Psi(y^*) = 0_n$.

We claim that every entry of y^* is positive. Define K_0 and K_+ where $y_i^* = 0$ if $i \in K_0$ and $y_i^* > 0$ if $i \in K_+$. Then, $K_0 \cup K_+ = \{1, \cdots, n\}$. K_0 and K_+ are separation of vertex set of the system. Assume that K_0 is a non-empty set. There exists $j \in K_+$ such that j is connected to a node in K_0 because G is connected. Denote $k \in K_0$ as a node which is connected to j.

$$\Psi_k(y^*) = \Xi_k(y^*) - \omega(y_k^*) = \Xi_k(y^*) > 0 \tag{3.18}$$

The inequality above is strict by property (b) since $k \in N_j$ and $y_j^* > 0$. It contradicts that $\Psi(y^*) = 0$. K_0 is the empty set.

We get the following inequality by Lemma 3.3.1 for $u = 0_n, v = x^*$ and $s \leq 1$.

$$\frac{\Xi_i(sx^*)}{s} = \frac{h_{i,u,v}(s) - h_{i,u,v}(0)}{s} \geq h_{i,u,v}(1) - h_{i,u,v}(0) = \Xi_i(x^*) \tag{3.19}$$

There exists $\alpha \in (0,1)$ such that $y^* \succeq \alpha x^*$ and $y_j^* = \alpha x_j^*$ for some $j \in \{1, \cdots, n\}$.

$$\begin{align} \Psi_j(y^*) &= \Xi_j(y^*) - \omega(\alpha x_j^*) \tag{3.20}\\ &\geq \Xi_j(\alpha x^*) - \omega(\alpha x_j^*) \tag{3.21}\\ &\geq \alpha \Xi_j(x^*) - \omega(\alpha x_j^*) \tag{3.22}\\ &> \alpha\left(\Xi_j(x^*) - \omega(x_j^*)\right) = 0 \tag{3.23}\end{align}$$

(3.21) and (3.22) are guaranteed by property (b) and (3.19). (3.23) also holds because $\dfrac{\alpha\omega(x_j^*)}{\alpha x_j^*} > \dfrac{\omega(\alpha x_j^*)}{\alpha x_j^*}$ by $\alpha \in (0,1)$, $x_j^* > 0$ and property (f).

This contradicts that $\Psi_i(y^*) = 0$ for all i. Therefore, x^* is the unique nontrivial zero of Ψ. ■

We remark that x^* in the above proof is also the unique nontrivial fixed point of (3.8). This theorem guarantees that we do not need to consider lots of complex dynamical system where a number of fixed points exist and some points are stable and the others are not. Even though epidemic spreads, there is a unique fixed point other than the origin.

3.3.2 Global Stability of Nontrivial Fixed Point

The origin, the trivial fixed point of the system is globally stable if $\lambda_{max}((1-\delta)I_n+\beta A)<1$. The next issue is whether the nontrivial fixed point is also stable if $\lambda_{max}((1-\delta)I_n+\beta A)>1$.

Theorem 3.3.4 *Suppose that* $\lambda_{max}((1-\delta)I_n+\beta A)>1$, *then* $P(t+1)=\Phi(P(t))$ *defined by* (3.3) *converges to* x^* *which is a nontrivial fixed point of* (3.3) *as* t *increases if* $P(0)$ *is not the origin.*

Proof: It is trivial to check that $\dfrac{\partial \Phi_i}{\partial x_j}\geq 0$ for any $i,j\in\{1,\cdots,n\}$.

Suppose that $\Phi(x)\preceq x$. Then, $\Phi(\Phi(x))\preceq\Phi(x)$ since Φ is increasing. Similarly, $\Phi(\Phi(x))\succeq\Phi(x)$ if $\Phi(x)\succeq x$.

Define a sequence $y^{(0)}=1_n=(1,1,\cdots,1)^{\mathrm{T}}$ and $y^{(k+1)}=\Phi(y^{(k)})$.

$$y^{(1)}=(1-\delta)1_n+\delta\Xi(1_n)\preceq 1_n=y^{(0)} \tag{3.24}$$

The equation above implies that $y^{(k+1)}\preceq y^{(k)}$ for every $k\in\mathbb{N}$. The sequence $\{y^{(k)}\}_{k=0}^{\infty}\subset[0,1]^n$ has a limit point because it is decreasing, and bounded from below. Denote y^* as a limit point of the sequence, then $\Phi(y^*)=y^*$. There are two candidates for y^* because Φ has only two fixed points.

Since Φ is an increasing map, and $y^{(0)}\succeq x$ for every $x\in[0,1]^n$, $y^{(k)}\succeq\Phi^k(x)$. $y^{(k)}\succeq\Phi^k(x^*)=x^*$ for every k implies that $y^*\succeq x^*$. It also implies that $y^*=x^*$. For any $P(0)\in[0,1]^n$, an upper bound of $P(t)$ is $y^{(t)}$ and it goes to x^* as t goes to infinity.

Suppose that all the entries of $P(0)$ are positive. This is reasonable since there exists m such that all the entries of $P(m)$ are positive if $P(0)$ is not the origin. There exists $\alpha\in(0,1)$ such that $\alpha x^*\preceq P(0)$. Define a sequence $z^{(0)}=\alpha x^*$ and $z^{(k+1)}=\Phi(z^{(k)})$.

$$\begin{aligned} z_i^{(1)} &= z_i^{(0)}+(1-(1-\delta)z_i^{(0)})\left(\Xi_i(\alpha x^*)-\frac{\delta\alpha x_i^*}{1-(1-\delta)\alpha x_i^*}\right) && (3.25)\\ &> z_i^{(0)}+\alpha(1-(1-\delta)z_i^{(0)})\left(\Xi_i(x^*)-\frac{\delta x_i^*}{1-(1-\delta)x_i^*}\right) && (3.26)\\ &= z_i^{(0)} && (3.27)\end{aligned}$$

The inequality above holds by (3.21), (3.22) and (3.23). It implies that $z^{(k+1)}\succeq z^{(k)}$ for every $k\in\mathbb{N}$, and $z^{(k)}$ gives a lower bound for $P(k)$. Since $z^{(0)}=\alpha x^*\preceq x^*$, $z^{(k)}\preceq\Phi^k(x^*)=x^*$. $\{z^{(k)}\}_{k=0}^{\infty}\subset[0,1]^n$

has a limit point because it is increasing, and bounded from above. x^* is the only possible limit point of $\{z^{(k)}\}_{k=0}^{\infty}$. The lower bound of $P(t)$ is $z^{(t)}$ and it goes to x^* as t goes to infinity.

Both the upper and lower bounds of $P(t)$ go to x^* which implies that $P(t)$ converges to x^*. ■

3.3.3 Generalized Epidemics

We consider a fully connected network where the infection rate and recovery rate are not identical in this section. β is described as $\beta_{i,j} \in [0,1]$ which depends on the edge (i,j) in the network. We can understand two nodes i and j are so close that they are more likely to transfer disease if $\beta_{i,j}$ are large. We also assume that each node i has its own recovery rate δ_i. The infection and recovery rules in this section are the same as the ones in the previous section. If node i is susceptible, it becomes infected by each of its infected neighbors independently. The probability that i is infected from j is $\beta_{i,j}$ if j is infected. The probability that i is infected from j is obviously 0 if j is not infected. If node i is infected, it recovers with probability δ_i. It can be infected in the same time-step in which it recovers. In other words, the probability that node i is susceptible at the next time interval is the probability that it recovers and it is not infected from any of its infected neighbors. If recovery and no-infection does not happen at same time, the node stays infected at the next time interval.

Considering $P_i(t)$, the marginal probability of infection for node i at time t as in the previous section, we can suggest the following equation.

$$1 - P_i(t+1) = \left(\prod_{j \neq i}(1 - \beta_{i,j}P_j(t))\right)(1 - P_i(t)) + \delta_i \left(\prod_{j \neq i}(1 - \beta_{i,j}P_j(t))\right) P_i(t) \tag{3.28}$$

We approximate the probability that i get infected from j as $\beta_{i,j}P_j(t)$ in the (3.28). By simple algebra, we get

$$P_i(t+1) = (1-\delta_i)P_i(t) + (1-(1-\delta_i)P_i(t))\left(1 - \prod_{j \neq i}(1 - \beta_{i,j}P_j(t))\right) \tag{3.29}$$

We define the epidemic map $\Phi : [0,1]^n \to [0,1]^n$ satisfying $P(t+1) = \Phi(P(t))$. Φ_i is defined as

$$\Phi_i(x) = (1-\delta_i)x_i + (1-(1-\delta_i)x_i)\left(\prod_{j \neq i}(1 - \beta_{i,j}x_j)\right) \tag{3.30}$$

Define $M = (m_{i,j}) \in \mathbb{R}^{n \times n}$, the system matrix of the generalized epidemics.

$$m_{i,j} = \begin{cases} \beta_{i,j} & \text{if } i \neq j, \\ 1 - \delta_i & \text{if } i = j. \end{cases} \tag{3.31}$$

We give similar results even though the recovery rate and the infection rate are not identical, i.e.,each node has its own recovery rate and each edge has its own infection rate. We represent the epidemic map $\Phi^{(M)}$ in this section to focus that the epidemic map is associated with the system matrix M.

Theorem 3.3.5 *Consider generalized epidemic map $\Phi^{(M)}$ defined by* (3.30) *and its system matrix M defined by* (3.31). *If $\lambda_{\max}(M) < 1$, the origin is the unique fixed point of $\Phi^{(M)}$ and it is globally stable. If $\lambda_{\max}(M) > 1$, there is the second fixed point which is different from the origin. The second nontrivial fixed point is globally stable in the space excluding the origin.*

Proof: We begin the proof by simplifying $\Phi^{(M)}$.

$$\Phi_i^{(M)}(x) = m_{i,i}x_i + (1 - m_{i,i}x_i)\left(\prod_{j\neq i}(1 - m_{i,j}x_j)\right) \tag{3.32}$$

$$= 1 - \prod_{j=1}^{n}(1 - m_{i,j}x_j) \tag{3.33}$$

It is trivial to check that

$$\Phi_i^{(M)}(x) \leq \sum_{j=1}^{n} m_{i,j}x_j = (Mx)_i \tag{3.34}$$

Applying (3.34) to each node, we get $\Phi^{(M)}(x) \preceq Mx$. The origin is the unique fixed point which is globally stable if the largest eigenvalue of M is smaller than 1 since $(\Phi^{(M)})^t(x) \preceq M^t x$ for every nonnegative integer t.

We analyze the case where the largest eigenvalue of M is greater than 1. Define U_i, the set $\Phi_i^{(M)}$ is greater than x_i and U, intersection of all U_i.

$$U_i = \{x \in [0,1]^n : \Phi_i^{(M)}(x) \geq x_i\} \qquad U = \bigcap_{i=1}^{n} U_i \tag{3.35}$$

We first claim that U has a nonempty interior. Denote v as the eigenvector of M corresponding to $\lambda_{\max}(M)$, the largest eigenvalue of M. By Perron-Frobenius theorem, v has strictly positive entries if M is irreducible. We assume that M is irreducible because M has more than one component if M is not irreducible.

Since M is the Jacobian matrix of $\Phi^{(M)}$ at the origin, $\Phi^{(M)}$ is close to M around the origin. For small $\varepsilon > 0$,

$$\Phi^{(M)}(\varepsilon v) \approx M(\varepsilon v) = \lambda_{\max}(M)(\varepsilon v) = (\lambda_{\max}(M) - 1)(\varepsilon v) + (\varepsilon v) \tag{3.36}$$

Since $\lambda_{\max}(M)$ is strictly greater than 1, all the entries of $\Phi^{(M)}(\varepsilon v)$ is strictly greater than ones of (εv) for small enough ε. $v \in U$ and it's obvious that small open set containing v is also included in U. We conclude that U has a nonempty interior.

We also claim that $x, y \in U$ implies that $\max(x,y) \in U$ where $\max(x,y)$ entrywise maximum of two n-dimensional vectors x and y, i.e., $\max(x,y)_i = \max(x_i, y_i)$. Consider i-th entry of $\max(x,y)$. We can assume that $\max(x,y)_i = x_i$ without loss of generality. Since $\Phi_i^{(M)}$ is increasing function for each x_j,

$$\Phi_i^{(M)}(\max(x,y)) \geq \Phi_i^{(M)}(x)) \geq x_i = \max(x,y)_i \tag{3.37}$$

The equation above guarantees that $\max(x,y) \in U_i$. Since i is arbitrary $\max(x,y) \in U$.

Denote $x^* = \sup\{x : x \in U\}$. Since U is closed set, the supremum of U is actually the maximum of the set. The next step is showing that x^* is a fixed point of $\Phi^{(M)}$. The short proof goes by contradiction. The basic idea is showing that it's possible to find the element in U which is greater than x^* if x^* is not a fixed point of $\Phi^{(M)}$. Assume that x^* is not a fixed point of $\Phi^{(M)}$. Since $x^* \in U$, there exists an index i such that $\Phi_i^{(M)}(x^*) > x_i^*$. Consider $x' \in [0,1]^n$ where $x'_j = x_j^*$ for all $j \neq i$ and $x'_i = x_i^* + \varepsilon$ for small $\varepsilon > 0$. We can choose $\varepsilon > 0$ small enough to satisfy that $\Phi_i^{(M)}(x') > x'$ because the inequality holds for $\varepsilon = 0$ where $x' = x^*$ at that time, and $\Phi_i^{(M)}$ is continuous function. $x' \in U_i$ for small enough ε. For $j \neq i$,

$$\Phi_j^{(M)}(x') \geq \Phi_j^{(M)}(x^*) \geq x_j^* = x'_j \tag{3.38}$$

The equation above guarantees that $x' \in U_j$ for all $j \neq i$. $x' \in U$, however it contradicts that x^* is the maximal element of U. x^* is a fixed point of $\Phi^{(M)}$ and it is different from the origin because x^* is the maximum element of U, and U has nonempty interior. x^* is greater than the origin.

The next step is showing that x^* is a unique nontrivial fixed point of $\Phi^{(M)}$. We call x^* nontrivial because the origin is the fixed point of $\Phi^{(M)}$ even though the largest eigenvalue of M is big. We call the origin the trivial fixed point and x^* as the nontrivial fixed point if there is no other fixed point different from the origin.

The short proof of uniqueness also goes by contradiction. Assume that y^* is another fixed point of $\Phi^{(M)}$ which is not the origin. $y^* \in U$ by definition of U and $y^* \preceq x^*$. All the entries of y^* are strictly positive by the connectivity of the network. If y^* has indices where the entries of y^* for given indices are zero, the set of indices for zero-entries and the set of indices for nonzero-entries are not connected. Since each entry of y^* is strictly positive, we can find $\alpha \in (0,1)$ such that $y^* \succeq \alpha x^*$ and $y^*_k = \alpha x^*_k$ for some index $k \in \{1,2,\cdots,n\}$.

Before going on we define function $f_i : \mathbb{R}_+ \to \mathbb{R}$ where $f_i(r) = \Phi_i^{(M)}(rx^*) - rx_i^*$.

$$\begin{aligned}\frac{d^2 f_i}{dr^2} &= \frac{d^2}{dr^2}\left(\Phi_i^{(M)} - rx_i^*\right) && (3.39)\\ &= \frac{d^2}{dr^2}\left(1 - \prod_{j=1}^{n}(1 - m_{i,j}rx_j^*) - rx_i^*\right) && (3.40)\\ &= \frac{d}{dr}\left(\sum_{j=1}^{n} m_{i,j}x_j^* \prod_{l\neq j}(1 - m_{i,l}rx_l^*) - x_i^*\right) && (3.41)\\ &= -\sum_{j=1}^{n}\sum_{l\neq j} m_{i,j}m_{i,l}x_j^*x_l^* \prod_{h\neq j, h\neq l}(1 - m_{i,h}rx_h^*) \leq 0 && (3.42)\end{aligned}$$

Since $f_i(0) = f_i(1) = 0$, $f_i(r) > 0$ for $r \in (0,1)$.

$$\Phi_i^{(M)}(rx^*) > rx_i^* \quad \forall r \in (0,1) \tag{3.43}$$

Returning back to the discussion of y^*,

$$\alpha x_k^* = y_k^* = \Phi_k^{(M)}(y^*) \geq \Phi_k^{(M)}(\alpha x^*) > \alpha x_k^* \tag{3.44}$$

The last inequality holds (3.43). By the contradiction, we conclude that there is no other nontrivial fixed point than x^*.

The last claim is that x^* is globally stable in the space excluding the origin. In other words, any initial point other than the origin converges to x^* as time passes. We can easily check that $\dfrac{\partial \Phi_i^{(M)}}{\partial x_j} \geq 0$ for any $i,j \in \{1,2,\cdots,n\}$. The positiveness of partial derivative guarantees that $\Phi^{(M)}(x) \preceq \Phi^{(M)}(y)$ if $x \preceq y$. Since $\Phi^{(M)}(1_n) \preceq 1_n$. The sequence $\{y^{(t)}\}_{t=0}^{\infty}$ defined as $y^{(t)} = (\Phi^{(M)})^t(1_n)$ is decreasing because all the entries of first term are smaller than ones of the zero-th term. Since $\{y^{(t)}\}_{t=0}^{\infty}$ is decreasing and the origin is its lower bound, it has a limit point. Actually the limit point is a fixed point of $\Phi^{(M)}$ and it means that the limit point is either the origin or x^*. $x^* \preceq 1_n$ implies that $(\Phi^{(M)})^t(x^*) \preceq (\Phi^{(M)})^t(1_n)$. Since the limit point of the recursive sequence whose initial point is x^*

is still x^*, the limit point of $\{y^{(t)}\}_{t=0}^{\infty}$ is greater than x^*. x^* is the limit point of $\{y^{(t)}\}_{t=0}^{\infty}$ because the origin cannot be the limit point. Similarly, define the sequence $\{z^{(t)}\}_{t=0}^{\infty}$ whose initial point εv where v is the eigenvector of M corresponding to the largest eigenvalue of M with arbitrary small $\varepsilon > 0$. $\{z^{(t)}\}_{t=0}^{\infty}$ is increasing in this case because $\Phi^{(M)}(\varepsilon v) \succeq \varepsilon v$ which is commented before. Since $\{z^{(t)}\}_{t=0}^{\infty}$ has an upper bound 1_n, it has limit point. The only possible candidate is x^* with the same reason for $\{y^{(t)}\}_{t=0}^{\infty}$. All the initial points other than origin converges to the nontrivial fixed point x^* by the epidemic map $\Phi^{(M)}$. ■

3.4 Immune-admitting Model

In this section, we study the immune-admitting model. The model is the same as that of the previous section except that in a single time interval a node cannot go from infected to healthy back to infected. In other words, a node is not infected from its neighbors if it just has recovered from the disease. We also study an epidemic map of immune-admitting model which is defined as

$$\widetilde{\Phi}_i(x) = (1-\delta)x_i + (1-x_i)\left(1 - \prod_{j\in N_i}(1-\beta x_j)\right) \tag{3.45}$$

$\widetilde{\Phi} : [0,1]^n \to [0,1]^n$ of (3.45) has similar properties with $\Phi(\cdot)$ of (3.3). $\widetilde{\Phi}(\cdot)$ and $\Phi(\cdot)$ have same Jacobian matrix at the origin which is linear upper bound of both nonlinear epidemic maps. Analysis of $\Phi(\cdot)$ is modified to analyze $\widetilde{\Phi}(\cdot)$ here. We represent $\widetilde{\Phi}(\cdot)$ using $\Xi(\cdot)$ and $\omega(\cdot)$ as we did in (3.8). We can view

$$\widetilde{\Phi}_i(x) = x_i + (1-x_i)(\Xi_i(x) - \omega(x_i)) \tag{3.46}$$

where $\Xi_i(x) = \left(1 - \prod_{j\in N_i}(1-\beta x_j)\right)$ and $\omega(s) = \dfrac{\delta s}{1-s}$. It's trivial to check that $\widetilde{\Phi}(\cdot)$ and $\omega(\cdot)$ and satisfy all the conditions (a) - (f). By doing this, we can apply Theorem 3.3.3 to show that $\widetilde{\Phi}(\cdot)$ has unique nontrivial fixed point if the largest eigenvalue of the Jacobian matrix at the origin is greater than 1.

The origin, the trivial fixed point of the system is globally stable if $\lambda_{max}((1-\delta)I_n + \beta A) < 1$. The next issue is whether the unique nontrivial fixed point is also stable if $\lambda_{max}((1-\delta)I_n + \beta A) > 1$.

This is not true in general for $\widetilde{\Phi}(\cdot)$. The following is an example of an unstable nontrivial fixed point.

$$\mathbf{A} = \begin{pmatrix} 0 & 1 & 1 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \end{pmatrix} \qquad \delta = 0.9 \quad \beta = 0.9 \tag{3.47}$$

The nontrivial fixed point of the system above is $x^* = (0.286, 0.222, 0.222)^{\mathrm{T}}$. The Jacobian matrix of $\widetilde{\Phi}$ at x^* is

$$J_{\widetilde{\Phi}(x^*)} = \begin{pmatrix} -0.260 & 0.514 & 0.514 \\ 0.700 & -0.157 & 0 \\ 0.700 & 0 & -0.157 \end{pmatrix} \tag{3.48}$$

The eigenvalue with largest absolute value in the above Jacobian matrix is -1.059 whose absolute value is greater than 1. However, $P(t) = \widetilde{\Phi}^t(P(0))$ converges to a cycle rather than a nontrivial fixed point x^*.

The biggest difference of (3.45) and (3.3) is that $\dfrac{\partial \Phi_i}{\partial x_j} \geq 0$ for any $i, j \in \{1, \cdots, n\}$ in (3.3) while it does not hold for $\widetilde{\Phi}(\cdot)$ in (3.45). The proof of Theorem 3.3.4 can be applied to $\widetilde{\Phi}(\cdot)$ if $\dfrac{\partial \widetilde{\Phi}_i}{\partial x_j} \geq 0$ for any $i, j \in \{1, \cdots, n\}$ in (3.45).

3.4.1 Random Graphs

Even though the nontrivial fixed point of $\widetilde{\Phi}(\cdot)$ is not stable generally, we shall show that it is stable with high probability for random Erdös-Rényi graphs. To study the stability of the nontrivial fixed point with high probability, we will begin with the following lemma that demonstrates that the Jacobian matrix at x^* has no eigenvalue greater than or equal to unity for any values of β and δ and for any connected graph.

Lemma 3.4.1 *Suppose that x^* is a unique nontrivial fixed point of $\widetilde{\Phi} : [0,1]^n \to [0,1]^n$ with Ξ satisfying the conditions (a),(b) and (c) when $\lambda_{max}((1-\delta)I_n + \beta A) > 1$. Then the Jacobian matrix of $\widetilde{\Phi}$ at x^* has no eigenvalue which is greater than or equal to* 1.

Proof: The i-th component of $\widetilde{\Phi}$ is written as $\widetilde{\Phi}_i(x) = (1-\delta)x_i + (1-x_i)\Xi_i(x)$

$$J_{\widetilde{\Phi}} = (1-\delta)I_n - \operatorname{diag}(\Xi) + \operatorname{diag}(1_n - x)J_{\Xi} \tag{3.49}$$

$J_{\widetilde{\Phi}} + \delta I_n$ is a nonnegative matrix by some properties of Ξ. By the Perron-Frobenius theorem of irreducible aperiodic matrices, $J_{\widetilde{\Phi}} + \delta I_n$ has an eigenvector v with eigenvalue μ whose components are all positive, and any other eigenvalues of $J_{\widetilde{\Phi}} + \delta I_n$ is strictly smaller than μ in absolute value.

For each eigenvalue λ of $J_{\widetilde{\Phi}}$, there is λ' which is an eigenvalue of $J_{\widetilde{\Phi}} + \delta I_n$ and $\lambda' = \lambda + \delta$. Furthermore, the eigenvectors corresponding to λ and λ' are the same.

$J_{\widetilde{\Phi}}$ has the largest eigenvalue $\kappa = \mu - \delta$ corresponding to eigenvector v. All the entries of v are strictly positive.

Fix $\omega(s) = \dfrac{\delta s}{1-s}$ in this section, and define a map $\Omega : [0,1]^n \to \mathbb{R}^n_+$ by $\Omega(x_1, \cdots, x_n) = (\omega(x_1), \cdots, \omega(x_n))^{\mathrm{T}}$.

$$\delta + \Xi_i(x^*) = \delta + \frac{\delta x_i^*}{1-x_i^*} = \frac{\delta}{1-x_i^*} = (1-x_i^*)\omega'(x_i^*) \tag{3.50}$$

By applying (3.50) to (3.49),

$$J_{\widetilde{\Phi}(x^*)} = I_n + \operatorname{diag}(1_n - x^*)\left(J_{\Xi(x^*)} - J_{\Omega(x^*)}\right) \tag{3.51}$$

Assume that $\kappa > 1$.

$$\kappa v = J_{\widetilde{\Phi}(x^*)} v = v + \operatorname{diag}(1_n - x^*)\left(J_{\Xi(x^*)} - J_{\Omega(x^*)}\right) v \tag{3.52}$$

For simplicity, apply $\Psi(x) = \Xi(x) - \Omega(x)$.

$$J_{\Psi(x^*)} v = \left(J_{\Xi(x^*)} - J_{\Omega(x^*)}\right) v = (\kappa - 1)\left(\operatorname{diag}(1_n - x^*)\right)^{-1} v \succ 0_n \tag{3.53}$$

$$\Psi(x^* + v) \approx \Psi(x^*) + J_{\Psi(x^*)} v \succ 0_n \tag{3.54}$$

There is an $\varepsilon > 0$ which is small enough and $\Psi(x^* + \varepsilon v) \succ 0_n$. However, it contradicts that x^* is the maximal element in $U = \{x \in [0,1]^n : \Psi_i(x) \geq 0 \text{ for all } i = 1, 2, \cdots, n\}$ which has a key role in the proof of Theorem 3.3.3. Therefore the assumption was wrong.

Assume now that $\kappa = 1$.

$$J_{\Psi(x^*)} v = \left(J_{\Xi(x^*)} - J_{\Omega(x^*)}\right) v = (\kappa - 1)\left(\operatorname{diag}(1_n - x^*)\right)^{-1} v = 0_n \tag{3.55}$$

By property (c) of Ξ and $\omega''(s) = \dfrac{\delta}{(1-s)^3} > 0$, the Hessian matrix of Ψ_i is a non-positive matrix. Furthermore, $(H_{\Psi_i(x^*)})_{i,i} = -\omega''(x_i^*) = -\dfrac{\delta}{(1-x_i^*)^3} < 0$,

$$\Psi_i(x^*+v) \approx \Psi_i(x^*) + \text{grad}(\Psi_i(x^*))v + \frac{1}{2}v^T H_{\Psi_i(x^*)} v < 0 \tag{3.56}$$

Since the inequality above holds for every $i \in \{1, \cdots, n\}$, there exists $\varepsilon > 0$ which is small and such that the entries of $\Psi(x^* - \varepsilon v)$ are all negative. There is $\alpha \in (0,1)$ such that $x^* - \varepsilon v \succeq \alpha x^*$ and $(x^* - \varepsilon v)_j = \alpha x_j^*$ for some $j \in \{1, \cdots, n\}$. Just substitute $x^* - \varepsilon v$ for y^* in (3.22). Then, $\Psi_j(x^* - \varepsilon v)$ is positive, however it contradicts that $\Psi(x^* - \varepsilon v)$ has all negative entries. Therefore the assumption was wrong. ■

Even though $J_{\tilde{\Phi}}$ has no eigenvalue which is greater than or equal to 1, the fixed point x^* still has a chance to be unstable if there is an eigenvalue which is greater than or equal to 1 in absolute value. We now show that x^* is stable with high probability when we consider a certain family of random graphs and the number of vertices is large. We will later show that this family of random graphs includes Erdös-Rényi graphs.

We fix $\Xi_i(x) = \left(1 - \prod_{j \in N_i}(1 - \beta x_j)\right)$ from now on.

$$\frac{\partial \Xi_i}{\partial x_j} = \beta \prod_{k \in N_i \setminus \{j\}} (1 - \beta x_k) = \beta \frac{1 - \Xi_i}{1 - \beta x_j} \text{ if } i \in N_j \text{ in } G \tag{3.57}$$

$$J_\Xi = \beta \,\text{diag}(1_n - \Xi) A \,\text{diag}(1_n - \beta x)^{-1} \tag{3.58}$$

Lemma 3.4.2 *Suppose that $G^{(n)}$ is a random graph with n vertices and let $d_{\min}^{(n)}$ and $d_{\max}^{(n)}$ denote the minimum and maximum degree of $G^{(n)}$. If $\mathbb{P}[(d_{\min}^{(n)})^2 > a \cdot d_{\max}^{(n)}]$ goes to 1 as n goes to infinity for any fixed $a > 0$, then the system is unstable at the origin and locally stable at the nontrivial fixed point x^* with high probability as n grows, for any fixed β and δ.*

Proof: First note that $\lambda_{max}\left((1-\delta)I_n + \beta A\right) \geq (1-\delta) + \beta d_{min}^{(n)}$. Since $\mathbb{P}[(d_{\min}^{(n)})^2 > a \cdot d_{\max}^{(n)}]$ goes to 1 as n goes to infinity, this means $\mathbb{P}[d_{\min}^{(n)} > a]$ goes to 1 as n goes to infinity, for any a, which further means that λ_{max} exceeds one with high probability. Thus, the origin is unstable.

$$J_{\tilde{\Phi}} = (1-\delta)I_n - \text{diag}(\Xi) + \text{diag}(1_n - x)J_\Xi \tag{3.59}$$

$$\simeq (1-\delta)I_n - \text{diag}(\Xi) + \beta D^{\frac{1}{2}} A D^{\frac{1}{2}} \tag{3.60}$$

where D is a diagonal matrix whose $i-$th diagonal element is $\dfrac{(1-x_i)(1-\Xi_i)}{1-\beta x_i}$ and $\simeq$ refers to similarity.

All the eigenvalues of $J_{\widetilde{\Phi}}$ are real because it is similar to a symmetric matrix by (3.60). Since Lemma 3.4.1 shows that all the eigenvalue of $J_{\widetilde{\Phi}(x^*)}$ are strictly less than 1, we need to show that all the eigenvalues of $J_{\widetilde{\Phi}(x^*)}+I_n$ are positive to show the system is locally stable at x^*.

By applying (3.50) to (3.60),

$$J_{\widetilde{\Phi}(x^*)}+I_n \simeq 2I_n-\delta\,\mathrm{diag}(1_n-x^*)^{-1}+\beta D^{\frac{1}{2}}AD^{\frac{1}{2}} \tag{3.61}$$

Since the right hand side of (3.61) is symmetric, it is positive definite if all the eigenvalues of $J_{\widetilde{\Phi}(x^*)}+I_n$ are strictly positive.

With simple algebra, we can show that the right hand side of (3.61) is positive definite if and only if $E+A$ is positive definite where $E=\dfrac{1}{\beta}D^{-\frac{1}{2}}(2I_n-\delta\,\mathrm{diag}(1_n-x^*)^{-1})D^{-\frac{1}{2}}$ is a diagonal matrix whose $i-$th diagonal entry is defined as below.

$$\begin{aligned} E_{ii} &= \frac{2}{\beta}\cdot\frac{\left(1-\frac{\delta}{2}-x_i^*\right)(1-\beta x_i^*)}{(1-(1+\delta)x_i^*)(1-x_i^*)} \qquad (3.62)\\ &= \frac{2(1-\beta x_i^*)}{\beta(1+\delta)(1-x_i^*)}\cdot\left(1+\frac{\delta(1-\delta)}{2(1-(1+\delta)x_i^*)}\right) \qquad (3.63)\end{aligned}$$

We will give a lower bound on E_{ii} because the smallest eigenvalue of $E+A$ is what we are interested in.

$$\frac{1-(1+\delta)x_i^*}{1-x_i^*}=1-\frac{\delta x_i^*}{1-x_i^*}=1-\Xi_i(x^*)=\prod_{j\in N_i}(1-\beta x_j^*) \tag{3.64}$$

Let $x_m^*=\min\{x_1^*,\cdots,x_n^*\}$ and denote by d_m the degree of the m-th node.

$$1-(1+\delta)x_m^*=(1-x_m^*)\prod_{j\in N_m}(1-\beta x_j^*)\leq(1-\beta x_m^*)^{d_m} \tag{3.65}$$

If $y > 0$ satisfies $1-(1+\delta)y = (1-\beta y)^{d_m}$, then $x_m^* > y$. For $1-(1+\delta)y = \eta$,

$$\eta = \left(1 - \frac{\beta}{1+\delta}(1-\eta)\right)^{d_m} \tag{3.66}$$

$$\Leftrightarrow \qquad 1-\eta^{\frac{1}{d_m}} = \frac{\beta}{1+\delta}(1-\eta) \tag{3.67}$$

$$\Leftrightarrow \qquad \frac{1+\delta}{\beta} = \sum_{k=0}^{d_m-1} \eta^{\frac{k}{d_m}} \geq 1+(d_m-1)\eta^{\frac{1}{2}} \tag{3.68}$$

$$\Rightarrow \qquad \eta \leq \left(\frac{1-\beta+\delta}{\beta(d_m-1)}\right)^2 \leq \left(\frac{1-\beta+\delta}{\beta(d_{\min}-1)}\right)^2 \tag{3.69}$$

d_m and $d_{\min}$ are generally different. d_m is the degree of the m-th node and $d_{\min}$ is a minimum degree of the network.

$$E_{ii} \geq \frac{2}{\beta(1+\delta)} \cdot \left(1 + \frac{\delta(1-\delta)}{2} \cdot \frac{1}{1-(1+\delta)x_i^*}\right) \tag{3.70}$$

$$\geq \frac{2}{\beta(1+\delta)} \cdot \left(1 + \frac{\delta(1-\delta)}{2} \cdot \frac{1}{\eta}\right) \tag{3.71}$$

$$\geq \frac{2}{\beta(1+\delta)} \cdot \left(1 + \frac{\delta(1-\delta)}{2} \cdot \left(\frac{\beta(d_{\min}-1)}{1-\beta+\delta}\right)^2\right) \tag{3.72}$$

Since $\lambda_{\min}(A) \geq -\lambda_{\max}(A) \geq -d_{\max}$,

$$\lambda_{\min}(E+A) \geq \frac{2}{\beta(1+\delta)} + \frac{\delta(1-\delta)}{\beta(1+\delta)} \cdot \left(\frac{\beta(d_{\min}-1)}{1-\beta+\delta}\right)^2 - d_{\max} \tag{3.73}$$

(3.73) guarantees that the smallest eigenvalue of $E+A$ is positive and the system is locally stable at the nontrivial fixed point with high probability if $d_{\min}^2$ grows faster than $d_{\max}$ as the size of graph grows. ■

We can think of several random graph models that satisfy the condition of Lemma 3.4.2. For example, if the random graph has uniform degree then the minimum degree and maximum degree are identical and as long as the degree grows with n, the ratio $\frac{d_{\min}^2}{d_{\max}} = d$ will grow with any n and exceed a with high probability. Similarly, for random graphs where the degree distribution of each node is identical and the degree distribution "concentrates", so that we can expect that the maximum degree and the minimum degree are proportional to the expected degree, in which case $\frac{d_{\min}^2}{d_{\max}}$ grows if the expected degree increases unbounded with n.

3.4.1.1 Erdös-Rényi Graphs

The Erdös-Rényi random graph, $G^{(n)} = G(n, p(n))$ has identical degree distribution.

Theorem 3.4.3 *Consider an Erdös-Rényi random graph* $G^{(n)} = G(n, p(n))$ *with* $p(n) = c\dfrac{\log n}{n}$ *where* $c > 1$ *is a constant. Then* $\widetilde{\Phi}(\cdot)$ *is locally unstable at the origin and has a locally stable nontrivial fixed point with high probability for any fixed* β *and* δ*.*

Proof: The proof of instability of the origin is similar to the proof of Lemma 3.4.2. For the remaining, it is enough to show that $\mathbb{P}[(d_{\min}^{(n)})^2 > a \cdot d_{\max}^{(n)}]$ goes to 1 as n goes to infinity for any $a > 0$. The degree of random Erdös-Rényi graphs is studied in [7]. In particular, there exists two constants $\eta_\Delta > 0$ and $\eta_\delta \in (-1, 0)$ such that

$$d_{\max}^{(n)} \sim (1 + \eta_\Delta) c \log n \qquad d_{\min}^{(n)} \sim (1 + \eta_\delta) c \log n \tag{3.74}$$

It is straightforward to see that $\mathbb{P}[(d_{\min}^{(n)})^2 > a \cdot d_{\max}^{(n)}]$ goes to 1 as n goes to infinity for any $a > 0$. ■

Since $p = c\dfrac{\log n}{n}$ for $c = 1$ is also the threshold for connectivity, we can say that connected Erdös-Rényi graphs have a nontrivial stable fixed point with high probability.

We also consider the case for β which is not fixed. It's reasonable to assume that δ is fixed because the recovering from infected state does not depend on neighbors since δ is defined as the probability that an infected node is recovered when there is no infected neighbors at a given time. However, β is the probability that the disease is transmitted by a neighbor and it's also reasonable that β decreases when the expected number of neighbors increases because the chance to interact with a particular neighbor decreases when the number of neighbors increases. We assume that $\beta = \beta(n)$.

Suppose that $np(n)\beta(n) \ll 1$. Asymptotic behavior of the largest eigenvalue of Erdös-Rényi graphs is studied in [36]. $G(n, p)$ satisfies almost surely $\lambda_{max}(A) = (1 + o(1)) \max\left(\sqrt{d_{\max}}, np\right)$. By connectivity of the underlying graph, $p(n) = \Omega(\dfrac{\log n}{n})$ and the asymptotic order of $p(n)$ guarantees $d_{\max} = \Theta(np(n))$.

$$\beta(n)\lambda_{max}(A) = (1 + o(1)) np(n)\beta(n) \ll 1 \tag{3.75}$$

Since $\delta \in (0, 1)$ is fixed by assumption, $(1 - \delta) + \beta(n)\lambda_{max}(A) < 1$ with high probability. In this case, the system does not have nontrivial fixed point, and the origin is unique fixed point which is globally stable.

Suppose that $np(n)\beta(n) \gg 1$. Connectivity of the underlying graph also guarantees that $p(n) = \Omega(\frac{\log n}{n})$. $(1-\delta)+\beta(n)\lambda_{max}(A) > 1$ with high probability by

$$\beta(n)\lambda_{max}(A) = (1+o(1))np(n)\beta(n) \gg 1 \tag{3.76}$$

$p(n) = \Omega(\frac{\log n}{n})$ guarantees both $d_{\max} = \Theta(np(n))$ and $d_{\min} = \Theta(np(n))$. It implies that $\frac{d_{\max}^{(n)}}{d_{\min}^{(n)}}$ is bounded by constant with probability 1 as n grows up when the underlying Erdös-Rényi graphs are connected with high probability. Since $np(n)\beta(n) \gg 1$, $(\beta(d_{\min}^{(n)}-1))^2$ is far greater than $\beta d_{\max}^{(n)}$. (3.73) is positive with high probability as n increases, and it guarantees that the nontrivial fixed point is locally stable with high probability.

The only remaining case is $\beta(n) = \frac{c}{np(n)}$ for some constant c. It is reasonable to assume that $c > \delta$ to satisfy $\beta\lambda_{max}(A) > \delta$ which guarantees the existence of the nontrivial fixed point.

Theorem 3.4.4 *Suppose that* $\frac{np(n)}{\log n} \to \infty$ *and* $np(n)\beta(n) \to c > \delta$ *as* $n \to \infty$. $\widetilde{\Phi}(\cdot)$ *whose underlying graph is Erdös-Rényi random graph* $G^{(n)} = G(n, p(n))$ *with* $\beta(n)$, δ *is locally unstable at the origin. However, it has a locally stable nontrivial fixed point with high probability*

Proof: It is obvious that $\beta\lambda_{\min}(A) > \delta$ with high probability. Define Laplacian matrix $L = D-A$ of graph G where A is adjacency matrix of G and D is a diagonal matrix whose i-th entry is degree of i. In other words,

$$L_{i,j} = \begin{cases} \sum_{k=1}^{n} A_{i,k} & \text{if } i = j, \\ -A_{i,j} & \text{if } i \neq j. \end{cases} \tag{3.77}$$

The largest eigenvalue of L is studied in [14]. $\frac{\lambda_{\max}(L)}{np(n)} \to 1$ if $p(n) \gg \frac{\log n}{n}$.

$$0 \geq \lambda_{\min}(A) \geq \lambda_{\min}(D) - \lambda_{\max}(L) = (1+o(1))np(n) - (1+o(1))np(n) = o(np(n)) \tag{3.78}$$

Since $\lambda_{\min}(A) = o(np(n))$ with high probability, the following inequality also holds with high probability. We can give a lower bound $E_{i,i} \geq \frac{1}{\beta}$ from (3.72).

$$\lambda_{\min}(E+A) \geq \lambda_{\min}(E) + \lambda_{\min}(A) \geq \frac{1}{\beta} + \lambda_{\min}(A) \geq np(n)(\frac{1}{c}+o(1)) > 0 \tag{3.79}$$

The nontrivial fixed point is locally stable since $E+A$ is positive definite. ■

The Random *geometric* graph $G^{(n)} = G(n, r(n))$ also has identical degree distribution if each node is distributed uniformly. As studied in [52], such random graphs have maximum and minimum degree which are proportional to the expected degree with high probability if $r(n)$ is smaller than the threshold of connectivity. Like Erdös-Rényi graphs, it has a high probability of having a nontrivial stable fixed point if the degree grows with n.

On the other hand, the minimum degree of the Barabási-Albert model is fixed as the size of the graph increases. In this case, we cannot generally argue that the nontrivial fixed point is stable.

3.4.2 Stability of the Nontrivial Fixed Point for Given Network Topology

From the (3.47), we found out the nontrivial fixed point is not always stable. However, random graph approach shows that the nontrivial fixed point is stable with high probability. We question whether there exists β and δ which makes the nontrivial fixed point unstable for given network topology. Here are some results for that.

Theorem 3.4.5 *For any connected graph G which is not a complete graph, there exist β and δ such that the nontrivial fixed point is unstable. The nontrivial fixed point is always locally stable if G is a complete graph.*

Proof: Applying E defined as (3.63) to the stability of the nontrivial fixed point, the nontrivial fixed point is locally stable if and only if $E + A$ is positive definite as mentioned in the proof of Lemma 3.4.2. It is enough to show that there exists $w \in \mathbb{R}^n$ such that $w^T(E + A)w < 0$.

x^* depends only on β and δ for fixed G. Suppose that β and δ are close to 1. It's obvious that the origin is unstable since $\lambda_{max}((1-\delta)I + \beta A) \approx \lambda_{max}(A) > 1$. We can also observe what happens to E when both β and δ are close to 1

$$\lim_{(\beta,\delta)\to(1,1)} E_{ii} = \lim_{(\beta,\delta)\to(1,1)} \frac{2(1-\beta x_i^*)}{\beta(1+\delta)(1-x_i^*)} \cdot \left(1 + \frac{\delta(1-\delta)}{2(1-(1+\delta)x_i^*)}\right) = 1 \tag{3.80}$$

E is close to the n-dimensional identity matrix, I_n when β and δ are close to 1.

Since G is connected, but not fully connected, we can find three vertices j, k, l such that $l \sim j, l \sim k$ and $j \nsim k$. Define $u \in \mathbb{R}^n$ such that $u_j = u_k = 1$, $u_l = -1$ and $u_i = 0$ otherwise.

$$u^T(I + A)u = u_j^2 + u_k^2 + u_l^2 + 2u_j u_l + 2u_k u_l = -1 < 0 \tag{3.81}$$

Since E only depends on β and δ, $u^T(E + A)u < 0$ when both β and δ are close to 1.

If G is a complete graph,

$$E_{ii} = \frac{2(1-\beta x_i^*)}{\beta(1+\delta)(1-x_i^*)} \cdot \left(1 + \frac{\delta(1-\delta)}{2(1-(1+\delta)x_i^*)}\right) \geq \frac{2(1-\beta x_i^*)}{\beta(1+\delta)(1-x_i^*)} \geq 1 \tag{3.82}$$

For complete graph G, its adjacency matrix is represented by $A = 1_n 1_n^T - I_n$ where 1_n is n-dimensional column vector all whose entries are 1. It can be easily checked that x_i^* is identical for all nodes i if G is a complete graph. $E = cI_n$ for some constant c which is greater than 1 by (3.82).

$$E + A = cI_n + 1_n 1_n^T - I_n = (c-1)I_n + 1_n 1_n^T \tag{3.83}$$

The equation above guarantees that the $E+A$ is positive definite, and it also guarantees that the nontrivial fixed point is locally stable for any β and δ. ■

It gives an interesting result. For any not-fully-connected graph, there exists β and δ which makes the nontrivial fixed point unstable, however, for any fixed β and δ, the nontrivial fixed point is locally stable with high probability.

3.5 Continuous Time Model

The discrete time model may give an unstable nontrivial fixed point as in (3.47). However, in the continuous-time model the nontrivial fixed point is globally stable if Ξ and ω satisfy all the properties from (a) to (f).

Consider a differential equation.

$$\frac{dx_i}{dt} = \frac{1}{\Delta t}\left((1-x_i)\Xi_i(x_1, \cdots, x_n) - \delta x_i\right) = \frac{1-x_i}{\Delta t}\left(\Xi_i(x) - \omega(x_i)\right) \tag{3.84}$$

Then, (3.46) is just the forward Euler method of (3.84) with Δt as step size for time. The origin is a trivial equilibrium point of (3.84). The origin is unstable if, and only if, $-\delta I_n + \beta A$ has an eigenvalue in the RHP, i.e., one or more eigenvalues of $-\delta I_n + \beta A$ have positive real parts. Since A is symmetric and by Perron-Frobenius theorem its largest eigenvalue in absolute value is positive, unstableness of the origin is equivalent to $\lambda_{max}((1-\delta)I_n + \beta A) > 1$. By Theorem 3.3.3, we know that (3.84) has a nontrivial fixed point x^* under this condition.

Theorem 3.5.1 *Suppose that* $\lambda_{max}((1-\delta)I_n+\beta A)>1$*, then* $x(t)$ *defined by* (3.84) *converges to* x^* *as* t *goes to infinity unless* $x(0)=0_n$.

Proof: We will suggest a Lyapunov function that is strictly decreasing for all initial points except $x(0)=0_n$:

$$V(x)=\max_{1\le i\le n}\left\{\frac{|x_i-x_i^*|}{x_i^*}\right\} \tag{3.85}$$

It's obvious that $V(x^*)=0$ and $V(x)>0$ for all $x\in[0,1]^n\setminus\{x^*\}$. Suppose that $V(x)=r>0$. Then, $x_j\in[(1-r)x_j^*,(1+r)x_j^*]$ for all $j\in\{1,\cdots,n\}$. There is i such that $x_i=(1-r)x_i^*$ or $(1+r)x_i^*$.

In the case of $x_i=(1+r)x_i^*$, $0_n\preceq\max(x,x^*)-x^*\preceq rx^*$, we obtain the following equation by Lemma 3.3.1 for $u=x^*-\dfrac{\max(x,x^*)-x^*}{r}$, $v=\dfrac{\max(x,x^*)-x^*}{r}$.

$$\begin{align}
\Xi_i(x) &\le \Xi_i(\max(x,x^*))=\Xi_i(u+(1+r)v) \tag{3.86}\\
&=(1+r)\left(\frac{h_{i,u,v}(1+r)-h_{i,u,v}(0)}{1+r}\right)+h_{i,u,v}(0) \tag{3.87}\\
&\le(1+r)\left(h_{i,u,v}(1)-h_{i,u,v}(0)\right)+h_{i,u,v}(0) \tag{3.88}\\
&=(1+r)\Xi_i(u+v)-r\Xi_i(u) \tag{3.89}\\
&\le(1+r)\Xi_i(u+v)=(1+r)\Xi_i(x^*) \tag{3.90}
\end{align}$$

The equation above is necessary to prove following inequality:

$$\begin{align}
\frac{dx_i}{dt} &= \frac{1-x_i}{\Delta t}\left(\Xi_i(x)-\omega(x_i)\right) \tag{3.91}\\
&= \frac{1-(1+r)x_i^*}{\Delta t}\left(\Xi_i(x)-\omega((1+r)x_i^*)\right) \tag{3.92}\\
&\le \frac{1-(1+r)x_i^*}{\Delta t}\left((1+r)\Xi_i(x^*)-\omega((1+r)x_i^*)\right) \tag{3.93}\\
&< \frac{(1+r)(1-(1+r)x_i^*)}{\Delta t}\left(\Xi_i(x^*)-\omega(x_i^*)\right)=0 \tag{3.94}
\end{align}$$

Hence, $\dfrac{|x_i(t)-x_i^*|}{x_i^*}=\dfrac{x_i(t)-x_i^*}{x_i^*}$ is strictly decreasing.

Otherwise, $x_i = (1-r)x_i^*$. If $r < 1$,

$$\begin{aligned}
\frac{dx_i}{dt} &= \frac{1-x_i}{\Delta t}\left(\Xi_i(x) - \omega(x_i)\right) && (3.95)\\
&= \frac{1-(1-r)x_i^*}{\Delta t}\left(\Xi_i(x) - \omega((1-r)x_i^*)\right) && (3.96)\\
&\geq \frac{1-(1-r)x_i^*}{\Delta t}\left(\Xi_i((1-r)x^*) - \omega((1-r)x_i^*)\right) && (3.97)\\
&\geq \frac{1-(1-r)x_i^*}{\Delta t}\left((1-r)\Xi_i(x^*) - \omega((1-r)x_i^*)\right) && (3.98)\\
&> \frac{(1-r)(1-(1-r)x_i^*)}{\Delta t}\left(\Xi_i(x^*) - \omega(x_i^*)\right) = 0 && (3.99)
\end{aligned}$$

$\frac{|x_i(t) - x_i^*|}{x_i^*} = \frac{x_i^* - x_i(t)}{x_i^*}$ is strictly decreasing. If $r = 1$, all the entries of $x(t)$ are positive after short time unless $x(t)$ is the origin.

Since $\frac{d}{dt}\left(\frac{|x_i(t)-x_i^*|}{x_i^*}\right) < 0$ for all i such that $\frac{|x_i(t)-x_i^*|}{x_i^*} = V(x)$, $\frac{d}{dt}V(x(t)) < 0$. $V(x)$ is a Lyapunov function of this system and it completes the proof. ■

We focused on $\Xi_i(x) = \left(1 - \prod_{j\in N_i}(1-\beta x_j)\right)$ for discrete-time epidemic maps because the sum of infection rate multiplied by marginal probability of each node $\beta \sum_{j\in N_i} x_j$ makes the epidemic map not-well-defined if β is big. However, it does not happen in continuous-time model. Theorem 3.5.1 holds for all Ξ satisfying the conditions (a) - (c).

We finally remark that, even though the continuous-time and discrete-time models are related through the forward Euler method and that the discrete-time model can be viewed as a discretization of the continuous-time model, it does not mean that continuous-time model is approximation to the true underlying epidemic spread. There are certain applications, such as the interaction of humans over a social network, say, where the discrete-time model appears to be more appropriate. In either case, whether to use a continuous-time model or a discrete-time model (and in the latter case whether to use Immune-admitting or the Chakrabarti model) depends on the application at hand.

Chapter 4

Markov Chain Model

4.1 Introduction

Epidemic spread threatened mankind for a long time. Ancient Greek historians described the Plague of Athens which took lives of many people during the second year of the Peloponnesian War (430 BC). The Black Death was one of the most devastating epidemic spreads of all time, which killed around 100 million people in 14th century Europe. Modeling epidemic spread plays a key role to preventing the spread of the disease. Researchers have focused on various aspects of this problem such as immunization and minimizing the social cost [5], [40].

We analyze the classical susceptible-infected-susceptible (SIS) model here. In the SIS model, each node in the network is in one of two different states : susceptible (healthy) or infected. A healthy node has a chance of getting infected if it has infected neighbors in the network. The probability of getting infected increases as the number of infected neighbors increases. An infected node also has a chance of recovering after which it still has a chance of getting infected by its neighbors.

There are four SIS models depending on the continuity of time and space. For the discrete space, two possible states are “0” and “1” which represent healthy and infected, respectively. Continuous space admits real numbers between 0 and 1, which can be understood as the probability for being infected or the rate of infection. Continuous-time-continuous-space can be understood as a differential equation defined on $[0,1]^n$ where n is the number of nodes [49], [50]. Continuous-time-discrete-space is a random process, called a continuous-time Markov chain. Draief, Ganesh et al. and Mieghem et al. have applied continuous-time Markov chains to model epidemic dynamics [16], [23], [42]. Discrete-time-continuous-space is studied as an iterative map where the mapping represents the dynamics of the epidemic after a unit time step. Some work has been conducted on random graph models where the graph topology is distributed according to a particular distribution. Barabási-Albert model [4] is one of the most preferred network models describing real network. Chakrabarti et al. and Wang et al. suggested nonlinear epidemic map defined on fixed graph topology [10], [62]. Ahn et al. studied the dynamics of epidemic spread for general networks [2]. Discrete-time-discrete-space is the Markov chain model defined on 2^n states.

The discrete-time Markov chain model is hard to analyze because the size of the transition matrix, 2^n grows exponentially as the number of nodes, n grows. In this paper, we shall study the dynamics of nonlinear epidemic map suggested by [10] and how the epidemic map is related to the discrete-time Markov chain model. The main contributions of this paper is existence and stability analysis of continuous-space models and upper bound of extinction probability in discrete-space model a.k.a the Markov chain model using the nonlinear epidemic model. The continuous-time Markov chain model also gives fast extinction of epidemics when the largest eigenvalue of linearized upper bound of nonlinear epidemic map at the origin is stable [23]. This paper contributes that same result holds for discrete-time Markov model.

In the following section, we describe both the Markov chain model and the epidemic map which focuses on the marginal probability of each node being infected. In the next section, we prove that the epidemic map gives an upper bound on the probability that the system is not in the absorbing state. To give a rigorous proof, we define a partial order which makes the transition matrix an order-preserving map. With that, we show that the epidemic map offers an upper bound on the mixing time and gives a practical result that the mixing time of the Markov chain is $O(\log n)$ when the origin is globally stable in the epidemic map. We also give the same result under the condition that the linear map is stable by applying linear programming. In fact, stability of the origin in the epidemic map has the pivotal role to achieve this result. We describe generalized contact model in the following section. Generalized contact model admits each node's own recovery rate and infection rate. We mention another model which admits immune-effect where a node does not get infected from its neighbors after recovering from the disease at the same time. We describe continuous-time Markov chain model and shows that the expected extinction time is exponentially big when the origin is not a stable fixed point of the epidemic map. Finally, we give simulation results which shows that the marginal probability for each node's infection is close to the nontrivial fixed point of the epidemic map.

4.2 Model Description

We will consider a discrete-time Markov chain model for epidemic spread, referred to as the SIS (susceptible-infected-susceptible) model. For a given connected network G with n nodes, let N_i be the neighborhood of node i. Let A be the adjacency matrix of G. Each node can be in a state of health, represented by "0", or a state of infection, represented by "1". Consequently, $\xi(t) = (\xi_1(t), \cdots, \xi_n(t)) \in \{0,1\}^n$ is a binary n-tuple and each of its entries represents the state of each node at time t, i.e., i is infected if $\xi_i(t) = 1$ and it's healthy if $\xi_i(t) = 0$.

We assume that probability of infection of each node given the current state $\xi(t)$ is independent. In other words, for any two state vectors $X, Y \in \{0,1\}^n$,

$$\mathbb{P}[\xi(t+1) = Y | \xi(t) = X] = \prod_{i=1}^{n} \mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X] \tag{4.1}$$

A healthy node remains healthy if all its neighbors are healthy. A healthy node can become infected by any of its infected neighbors independently with probability β. An infected node becomes healthy if it is recovered from disease with probability δ and is not infected from any of its neighbors. To summarize this,

$$\mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X] = \begin{cases} (1-\beta)^{m_i} & \text{if } (X_i, Y_i) = (0,0),\ |N_i \cap \mathbb{S}(X)| = m_i, \\ 1-(1-\beta)^{m_i} & \text{if } (X_i, Y_i) = (0,1),\ |N_i \cap \mathbb{S}(X)| = m_i, \\ \delta(1-\beta)^{m_i} & \text{if } (X_i, Y_i) = (1,0), |N_i \cap \mathbb{S}(X)| = m_i, \\ 1-\delta(1-\beta)^{m_i} & \text{if } (X_i, Y_i) = (1,1), |N_i \cap \mathbb{S}(X)| = m_i. \end{cases} \tag{4.2}$$

where $\mathbb{S}(X)$ is the support of $X \in \{0,1\}^n$, i.e., $\mathbb{S}(X) = \{i : X_i = 1\}$.

Let S be the transition matrix of this Markov Chain, $S_{X,Y} = \mathbb{P}[\xi(t+1) = Y | \xi(t) = X]$. We assume that the Markov chain is time-homogeneous and write $S_{X,Y} = \mathbb{P}[Y|X]$ for simplicity.

The Markov chain has a unique stationary distribution, which is the state where all the nodes in the network are healthy with probability 1. If all the nodes are healthy, no node will be exposed to disease, and therefore they will always stay healthy since the occurrence of new disease is not considered in this model. Therefore the probability distribution on the states, $\{0,1\}^n$ goes to the all-healthy-state as time progresses. In other words, the disease will die out if we wait long enough. However, this result is not practical since it may take a very long time especially if the mixing time of the Markov chain is exponentially big. It is difficult to analyze the dynamics of the Markov chain as the number of nodes increases.

Comparing the discrete-time Markov chain model to the continuous-time Markov chain model described in [23], continuous-time Markov chain model allows only one flip of each node's epidemic state at each moment. However, the discrete-time model allows change of epidemic states for more than one node at the same time. The reason being that change of epidemic state for two or more nodes can occur at the same time interval even though they do not happen at the same moment. The transition matrix of the embedded Markov chain of continuous-time model has nonzero entry only for the Hamming distance of row coordinate and column coordinate is 1. In other words, the statement that the number of different digits for $X,Y \in \{0,1\}^n$ is 1 is necessary for the entry of the X-th row and the Y-th column is nonzero. However, the transition matrix of discrete-time Markov chain model can have nonzero entries everywhere except the row of absorbing state.

Denote $I(t)$ as the set of infected nodes at time t. Define $p_i(t)$ as the probability that node i is infected at time t, i.e., $p_i(t) = \mathbb{P}[i \in I(t)]$.

$$\begin{aligned} p_i(t+1) &= \mathbb{P}[i \in I(t+1) | i \in I(t)] \times p_i(t) \\ &\qquad + \mathbb{P}[i \in I(t+1) | i \notin I(t)] \times (1 - p_i(t)) && (4.3) \\ &= (1 - \delta(1-\beta)^{m_i}) p_i(t) + (1 - (1-\beta)^{m_i})(1 - p_i(t)) \\ &\qquad \text{where } m_i = |N_i \cap I(t)| && (4.4) \\ &= \left(1 - \delta \left(\prod_{j \in N_i} 1 - \beta \mathbb{1}_{I(t)}(j)\right)\right) p_i(t) + \left(1 - \prod_{j \in N_i} 1 - \beta \mathbb{1}_{I(t)}(j)\right)(1 - p_i(t)) && (4.5) \end{aligned}$$

We approximate $\prod_{j \in N_i} 1 - \beta \mathbb{1}_{I(t)}(j)$ by using expectation $\mathbb{E}[1 - \beta \mathbb{1}_{I(t)}(j)] = 1 - \beta p_j(t)$ and the assumption that each event is independent of each other.

$$P_i(t+1) = \left(1 - \delta \left(\prod_{j \in N_i} 1 - \beta P_j(t)\right)\right) P_i(t) + \left(1 - \prod_{j \in N_i} 1 - \beta P_j(t)\right)(1 - P_i(t)) \tag{4.6}$$

We use $P_i(t)$ instead of $p_i(t)$ because we want to distinguish $P_i(t)$, the approximated probability from $p_i(t)$, the exact probability of the Markov chain model.

Approximated model is studied on $[0,1]^n$, the n-dimensional probability space which is less computation-demanding than 2^n-dimensional discrete space. One of them was studied by Chakrabarti and Wang [10], [62]. Ahn viewed the n-dimensional probability distribution at time $t+1$ as image of the probability distribution at time t mapped by $\Phi : [0,1]^n \to [0,1]^n$ [2]. The i-th component of the epidemic map, Φ is defined as follows:

$$\Phi_i(x) = (1-\delta)x_i + (1-(1-\delta)x_i)\left(1 - \prod_{j\in N_i}(1-\beta x_j)\right) \tag{4.7}$$

It is trivial to check that $P_i(t+1) = \Phi_i((P_1(t),\cdots,P_n(t))^T)$ in (4.6).

4.3 Partial Order

Returning back to the Markov chain model, we study the mixing time of Markov chain and how it is related with the epidemic map $\Phi(\cdot)$ described in previous section. The mixing time of a Markov chain is defined as follows [38]:

$$t_{mix}(\varepsilon) = \min\{t : \sup_{\mu} \|\mu S^t - \pi\|_{TV} \le \varepsilon\} \tag{4.8}$$

μ is any initial probability distribution defined on the state space and π is the stationary distribution in (4.8). $\|\cdot\|_{TV}$ is total variation distance which measures the distance of two probability distributions. Total variation distance of two probability measure μ and μ' are defined by

$$\|\mu - \mu'\|_{TV} = \frac{1}{2}\sum_x |\mu(x) - \mu'(x)| \tag{4.9}$$

where x is any possible state in the probability space. $t_{mix}(\varepsilon)$ is the smallest time where distance between the stationary distribution and probability distribution at time t from any initial distribution is smaller than or equal to ε. Roughly speaking, the mixing time measures how fast initial distribution converges to the limit distribution. In this section, we give a partial order on the set of probability vectors of $\{0,1\}^n$. By giving a partial order, we can find a particular μ which gives the supremum of $\|\mu S^t - \pi\|_{TV}$ in (4.8).

For two vectors X, Z, $X \preceq Z$ means that $X_i \le Z_i$ for all i. We define $\le_{st}$ on the set of probability vectors of $\{0,1\}^n$ as follows.

$$\mu \le_{st} \mu' \quad \text{iff} \quad \sum_{X\preceq Z} \mu_X \ge \sum_{X\preceq Z} \mu'_X \quad \forall Z \in \{0,1\}^n \tag{4.10}$$

The reader may note that $\sum_{X\preceq Z}\mu_X$ represents the probability that each node of $\mathbb{S}(Z)^c$ is healthy under probability distribution μ. $\mu \le_{st} \mu'$ means that the probability of some nodes being healthy is higher under μ than under μ', for any set of nodes. Roughly speaking, infection probability under μ' stochastically dominates one under μ. It is trivial to check that $\leq_{st}$ is a well-defined partial order. The X-th unit vector, denoted by $e_X \in \mathbb{R}^{2^n}$, is the probability vector all of whose components are zero, except the X-th component. Denote $\bar{0}, \bar{1} \in \{0,1\}^n$ as the state where everyone is healthy or infected, respectively. It's obvious that $e_{\bar{1}}$ is the greatest element and $e_{\bar{0}}$ is the least element under $\leq_{st}$. Since G, the underlying graph is connected, the Markov chain is irreducible and it is not hard to see that the stationary distribution is $e_{\bar{0}}$, which corresponds to all nodes being healthy with probability 1. If all the nodes in the network are healthy, there is no infection and they always stay healthy in this model.

$\leq_{st}$ is nice because it makes S an order-preserving map, i.e., $\mu \leq_{st} \mu'$ implies $\mu S \leq_{st} \mu' S$. To prove this claim, we need an intermediate result.

Lemma 4.3.1 *$R^{-1}SR$ is a 2^n by 2^n matrix all of whose entries are non-negative where $R \in \mathbb{R}^{\{0,1\}^n \times \{0,1\}^n}$ is defined as*

$$R_{X,Y} = \begin{cases} 1 & \text{if } X \preceq Y, \\ 0 & \text{otherwise} \end{cases} \tag{4.11}$$

Proof: We want to compute the inverse matrix of R first. Define a matrix R'.

$$R'_{X,Y} = \begin{cases} (-1)^{|\mathbb{S}(Y-X)|} & \text{if } X \preceq Y, \\ 0 & \text{otherwise} \end{cases} \tag{4.12}$$

$|\mathbb{S}(Y-X)|$ represents the number of nodes which are infected in Y, but not in X. We claim that $R' = R^{-1}$. If $X \npreceq Y$, then $X \npreceq Z$ or $Z \npreceq Y$ holds for every $Z \in \{0,1\}^n$. By the definition of R and R', $R_{X,Z} = 0$ or $R'_{Z,Y} = 0$ if $X \npreceq Y$. It is straightforward that $(RR')_{X,Y} = 0$ if $X \npreceq Y$. It's enough to consider the case $X \preceq Y$.

$$\begin{aligned} (RR')_{X,Y} &= \sum_Z R_{X,Z} R'_{Z,Y} = \sum_{X \preceq Z \preceq Y} 1^{|\mathbb{S}(Z-X)|} (-1)^{|\mathbb{S}(Y-Z)|} \\ &= (1-1)^{|\mathbb{S}(Y-X)|} \end{aligned} \tag{4.13}$$

$(RR')_{X,Y} = 1$ if $|\mathbb{S}(Y-X)| = 0$ and $(RR')_{X,Y} = 0$ otherwise. It leads that RR' is an identity matrix of size 2^n and $R' = R^{-1}$.

$$
\begin{aligned}
&(R^{-1}SR)_{X,Z} && (4.14)\\
&= \sum_{Y \preceq Z} (R^{-1}S)_{X,Y} = \sum_{Y \preceq Z} \sum_{W} R^{-1}_{X,W} S_{W,Y} && (4.15)\\
&= \sum_{Y \preceq Z} \sum_{W \succeq X} (-1)^{|\mathbb{S}(W-X)|} S_{W,Y} && (4.16)\\
&= \sum_{W \succeq X} (-1)^{|\mathbb{S}(W-X)|} \prod_{i \in \mathbb{S}(Z)^c} \mathbb{P}[\xi_i(t+1) = 0 | \xi(t) = W] && (4.17)\\
&= \sum_{W \succeq X} (-1)^{|\mathbb{S}(W-X)|} \delta^{|\mathbb{S}(W) \cap \mathbb{S}(Z)^c|} (1-\beta)^{\sum_{i \in \mathbb{S}(Z)^c} |N_i \cap \mathbb{S}(W)|} && (4.18)\\
&= \sum_{W \succeq X} (-1)^{|\mathbb{S}(W-X)|} \delta^{|\mathbb{S}(W) \cap \mathbb{S}(Z)^c|} (1-\beta)^{\sum_{i \in \mathbb{S}(W)} |N_i \cap \mathbb{S}(Z)^c|} && (4.19)
\end{aligned}
$$

By some algebra,

$$
\begin{aligned}
&\delta^{-|\mathbb{S}(X) \cap \mathbb{S}(Z)^c|} (1-\beta)^{-\sum_{i \in \mathbb{S}(X)} |N_i \cap \mathbb{S}(Z)^c|} (R^{-1}SR)_{X,Z} && (4.20)\\
&= \sum_{W \succeq X} (-1)^{|\mathbb{S}(W-X)|} \delta^{|\mathbb{S}(W-X) \cap \mathbb{S}(Z)^c|} (1-\beta)^{\sum_{i \in \mathbb{S}(W-X)} |N_i \cap \mathbb{S}(Z)^c|} && (4.21)\\
&= \prod_{i \in \mathbb{S}(X)^c} \left(1 - (1-\beta)^{|N_i \cap \mathbb{S}(Z)^c|} \delta^{1_{\{i \in \mathbb{S}(Z)^c\}}}\right) && (4.22)
\end{aligned}
$$

Define $\neg X = \bar{1} - X$. $\neg X$ is an opposite state of X where each node is healthy in $\neg X$ if it is infected in X and vice versa. From (4.19) and (4.22), we simplify $(R^{-1}SR)_{X,Z}$ using $\neg X$ and $\neg Z$.

$$(R^{-1}SR)_{X,Z} = \mathbb{P}[\xi(t+1) = \neg X | \xi(t) = \neg Z] \geq 0 \tag{4.23}$$

■

Now to the claim.

Lemma 4.3.2 *If $\mu \leq_{st} \mu'$, then $\mu S \leq_{st} \mu' S$.*

Proof: We defined 2^n-dimensional square matrix R from Lemma 4.3.1 because we can represent $\mu \leq_{st} \mu'$ using R. By definition of $\mu \leq_{st} \mu'$,

$$((\mu - \mu')R)_Y = \sum_X (\mu - \mu')_X R_{X,Y} = \sum_{X \preceq Y} (\mu - \mu')_X \geq 0 \tag{4.24}$$

$\mu \leq_{st} \mu'$ if and only if all of $(\mu - \mu')R$'s entries are nonnegative. $((\mu - \mu')R)_Y = 0$ if $Y = \bar{1} =$

$(1,1,,\cdots,1)$ because both of μ and μ' are probability vectors whose 1-norm is 1.

Define a row vector $\nu \in \mathbb{R}^{\{0,1\}^n}$ whose Y-th element is defined by $\nu_Y = ((\mu-\mu')R)_Y$. $\nu_Y \geq 0$ for all $Y \in \{0,1\}^n$ by (4.24). ν is a non-negative row vector, and $\nu_{\bar{1}} = 0$. $\mu - \mu' = \nu R^{-1}$. We can understand $\mu - \mu'$ as a conical combination of all row vectors of R^{-1}, but the $\bar{1}$-th row vector.

$\mu S \leq_{st} \mu' S$ if and only if $(\mu-\mu')SR$ is a non-negative vector. $\mu - \mu' = \nu R^{-1}$ for non-negative ν since $\mu \leq_{st} \mu'$. $(\mu-\mu')SR = \nu R^{-1}SR$ is non-negative since ν is non-negative and $R^{-1}SR$ is a matrix all of whose entries are non-negative by Lemma 4.3.1. ■

By Lemma 4.3.2, $\sum_{X\preceq\bar{0}}(\mu S^t)_X = (\mu S^t)_{\bar{0}} \geq (e_{\bar{1}}S^t)_{\bar{0}} = \sum_{X\preceq\bar{0}}(e_{\bar{1}}S^t)_X$ for any probability vector μ since $\mu \leq_{st} e_{\bar{1}}$. Returning to the mixing time (4.8),

$$\|\mu S^t - \pi\|_{TV} = \|\mu S^t - e_{\bar{0}}\|_{TV} = 1 - (\mu S^t)_{\bar{0}} \tag{4.25}$$

$$\leq 1 - (e_{\bar{1}}S^t)_{\bar{0}} = 1 - e_{\bar{1}}S^t e_{\bar{0}}^T \tag{4.26}$$

Using the inequality above, we can now write

$$t_{mix}(\varepsilon) = \min\{t : \sup_{\mu} \|\mu S^t - \pi\|_{TV} \leq \varepsilon\} \tag{4.27}$$

$$= \min\{t : 1 - e_{\bar{1}}S^t e_{\bar{0}}^T \leq \varepsilon\} \tag{4.28}$$

$$= \min\{t : e_{\bar{1}}S^t e_{\bar{0}}^T \geq 1 - \varepsilon\} \tag{4.29}$$

By defining the partial order, we only need to consider $e_{\bar{1}}$, the all-infected-state for initial distribution to compute the mixing time of the Markov chain model.

4.4 Upper Bound on the Mixing Time

In this section, we prove that epidemic map $\Phi(\cdot)$ defined as (4.7) gives an upper bound on the mixing time of the Markov chain model and apply it to get a practical result.

We want a lower bound $e_{\bar{1}}S^t e_{\bar{0}}^T$ to get an upper bound of $t_{mix}(\varepsilon)$. Define a 2^n-dimensional column vector $u(r)$ for a given n-dimensional $r = (r_1,\cdots,r_n)^T$ by $u(r)_X = \prod_{i\in\mathbb{S}(X)}(1-r_i)$. We want to find an $r' \in \mathbb{R}^n$ satisfying $Su(r) \succeq u(r')$.

Lemma 4.4.1 *$Su(r) \succeq u(\Phi(r))$ for all $r \in [0,1]^n$.*

Proof: We begin the proof of this lemma by evaluating each entry of $Su(r)$.

$$
\begin{aligned}
&(Su(r))_X && (4.30)\\
&= \sum_{Y\in\{0,1\}^n} S_{X,Y}u(r)_Y && (4.31)\\
&= \sum_{Y\in\{0,1\}^n} \left(\prod_{i\in\mathbb{S}(Y)} (1-r_i)\mathbb{P}[Y_i=1|X]\right)\left(\prod_{i\notin\mathbb{S}(Y)} \mathbb{P}[Y_i=0|X]\right) && (4.32)\\
&= \prod_{i=1}^{n}(1-r_i)\mathbb{P}[Y_i=1|X]+\mathbb{P}[Y_i=0|X] && (4.33)
\end{aligned}
$$

Assume $\mathbb{S}(X)\cap\mathbb{S}(Z)=\emptyset$ for two states $X,Z\in\{0,1\}^n$, i.e., there is no common infected node in the two states X and Z. It's trivial to check that the following is true:

$$\mathbb{P}[Y_k=0|X+Z]=\mathbb{P}[Y_k=0|X]\mathbb{P}[Y_k=0|Z] \tag{4.34}$$

For simplicity, we call $q_{k,X}=\mathbb{P}[Y_k=0|X]$.

$$
\begin{aligned}
&(Su(r))_{X+Z} && (4.35)\\
&= \prod_{i=1}^{n}(1-r_i)\mathbb{P}[Y_i=1|X+Z]+\mathbb{P}[Y_i=0|X+Z] && (4.36)\\
&= \prod_{i=1}^{n}(1-r_i)(1-q_{i,X+Z})+q_{i,X+Z} && (4.37)\\
&= \prod_{i=1}^{n}(1-r_i)(1-q_{i,X}q_{i,Z})+q_{i,X}q_{i,Z} && (4.38)\\
&\geq \prod_{i=1}^{n}((1-r_i)(1-q_{i,X})+q_{i,X})((1-r_i)(1-q_{i,Z})+q_{i,Z}) && (4.39)\\
&= (Su(r))_X(Su(r))_Z && (4.40)
\end{aligned}
$$

(4.39) holds by the following one for $r,b,c\in[0,1]$:

$$
\begin{aligned}
&((1-r)(1-ab)+ab)-((1-r)(1-a)+a)((1-r)(1-b)+b)\\
&= r(1-r)(1-a)(1-b)\geq 0 && (4.41)
\end{aligned}
$$

Define $\hat{i}\in\{0,1\}^n$ as the state where everyone is healthy, but i. The following inequality holds by (4.40).

$$\begin{aligned}
(Su(r))_X &\geq \prod_{i\in\mathbb{S}(X)} (Su(r))_{\hat{i}} && (4.42)\\
&= \prod_{i\in\mathbb{S}(X)} \prod_{j=1}^{n} (1-r_j)\mathbb{P}[Y_j=1|\hat{i}] + \mathbb{P}[Y_j=0|\hat{i}] && (4.43)\\
&= \prod_{i\in\mathbb{S}(X)} ((1-r_i)(1-\delta)+\delta)\prod_{j\sim i}((1-r_j)\beta+1-\beta) && (4.44)\\
&= \prod_{i\in\mathbb{S}(X)} (1-(1-\delta)r_i)\prod_{j\sim i}(1-\beta r_j) && (4.45)\\
&= \prod_{i\in\mathbb{S}(X)} 1-\Phi_i(r) && (4.46)\\
&= u(\Phi(r))_X && (4.47)
\end{aligned}$$

■

It's obvious that $e_{\bar{0}}^T = u((1,1,\cdots,1)^T) = u(1_n)$. We distinguish $1_n = (1,1,\cdots,1)^T \in [0,1]^n$ from $\bar{1} \in \{0,1\}^n$ which is a state of infection. Since $Su(r) \succeq u(\Phi(r))$ by Lemma 4.4.1, and S is a matrix all of whose entries are non-negative,

$$S^t e_{\bar{0}}^T = S^t u(1_n) \succeq u(\Phi^t(1_n)) \tag{4.48}$$

Denote $M = (1-\delta)I_n + \beta A$ as the system matrix of linear model, which is the Jacobian matrix of $\Phi(\cdot)$ at the origin.

$$\begin{aligned}
\Phi_i(x) &= (1-\delta)x_i + (1-(1-\delta)x_i)\left(1-\prod_{j\sim i}(1-\beta x_j)\right) && (4.49)\\
&\leq (1-\delta)x_i + \left(1-\prod_{j\sim i}(1-\beta x_j)\right) && (4.50)\\
&\leq (1-\delta)x_i + \beta\left(\sum_{j\in N_i} x_j\right) = (Mx)_i && (4.51)
\end{aligned}$$

We get an upper bound of Φ with M. $\Phi(x) \preceq Mx$. We can now give a practical result about mixing time.

Theorem 4.4.2 *$t_{mix}(\varepsilon) = O(\log n)$ if $\|M\| < 1$*

Proof: Suppose that $t \leq t_{mix}(\varepsilon)$.

$$
\begin{aligned}
1-\varepsilon &\geq e_{\bar{1}} S^t e_{\bar{0}}^T && (4.52)\\
&\geq e_{\bar{1}} u(\Phi^t(1_n)) = \prod_{j=1}^{n} (1-\Phi_j^t(1_n)) && (4.53)\\
&\geq 1-\sum_{j=1}^{n} \Phi_j^t(1_n) && (4.54)\\
&\geq 1-n\sqrt{\frac{1}{n}\sum_{j=1}^{n}(\Phi_j^t(1_n))^2} = 1-\sqrt{n}\|\Phi^t(1_n)\| && (4.55)\\
&\geq 1-\sqrt{n}\|M^t 1_n\| && (4.56)\\
&\geq 1-\sqrt{n}\|M\|^t\|1_n\| = 1-n\|M\|^t && (4.57)
\end{aligned}
$$

$t \leq \dfrac{\log\frac{n}{\varepsilon}}{-\log\|M\|}$ for every $t \leq t_{mix}(\varepsilon)$ leads that $t_{mix}(\varepsilon) \leq \dfrac{\log\frac{n}{\varepsilon}}{-\log\|M\|}$. The mixing time is $O(\log n)$. ■

If $\|M\| > 1$, $\Phi^t(1_n)$ converges to x^*, the unique nontrivial fixed point of Φ which is strictly greater than the origin as stated in [2]. The reason why this happens, even though the original Markov chain model always converges to the "all-healthy" state, is that the i-th component of $\Phi^t(1_n)$ provides an upper bound on the probability that the current state is not the steady state when i is the only infected node with probability 1 in the initial probability distribution. More specifically, $e_{\hat{i}} S^t e_{\bar{0}}^T \geq e_{\hat{i}} u(\Phi^t(1_n)) = 1-\Phi_i^t(1_n)$ by (4.48),

$$
\begin{aligned}
\Phi_i^t(1_n) &\geq 1-e_{\hat{i}} S^t e_{\bar{0}}^T = 1-\mathbb{P}[\xi(t)=\bar{0}|\xi(0)=\hat{i}] && (4.58)\\
&= \mathbb{P}[\xi(t)\neq\bar{0}|\xi(0)=\hat{i}] && (4.59)
\end{aligned}
$$

Similarly, the probability that the epidemic state at time t is not "all-healthy" state given the initial epidemic state is X is bounded above by the entries of $\Phi^t(1_n)$.

$$
\begin{aligned}
\mathbb{P}[\xi(t)\neq\bar{0}|\xi(0)=X] = 1-\mathbb{P}[\xi(t)=\bar{0}|\xi(0)=X] &= 1-e_X S^t e_{\bar{0}}^T && (4.60)\\
&\leq 1-u(\Phi^t(1_n))_X && (4.61)\\
&= 1-\prod_{i\in\mathbb{S}(X)}\left(1-\Phi_i^t(1_n)\right) && (4.62)
\end{aligned}
$$

In other words, if the origin is globally stable in the epidemic map Φ, we can infer that the Markov chain model mixes fast. However, if the origin in the epidemic map is unstable, we cannot infer anything about mixing time.

Figure 4.1 and Figure 4.2 give the simulation results of epidemic spread on Erdös-Rényi graphs with 2000 nodes. The horizontal and vertical axes represent time (number of iterations) and the number of infected nodes, respectively. At $t = 0$, half of the whole nodes, 1000, are infected. $\frac{\beta\|A\|}{\delta} < 1$ is equivalent to $(1-\delta)+\beta\|A\| < 1$ and it guarantees the fast extinction of epidemics by Theorem 4.4.2. Figure 4.1 shows that the number of infected nodes decays fast as $\frac{\beta\|A\|}{\delta} = .999 < 1$. The epidemics die out in 100 iterations.

$\frac{\beta\|A\|}{\delta} > 1$ is necessary condition for epidemic spread. Figure 4.2 shows that the number of infected nodes does not decay fast, i.e., epidemic spreads as $\frac{\beta\|A\|}{\delta} = 1.01 > 1$. We cannot observe extinction of epidemics until given time, 10000, in this case. Although we have not been able to prove this, the simulations suggest that a phase transition occurs at $\frac{\beta\|A\|}{\delta}$. When this value is less than unity we have fast mixing by Theorem 4.4.2 and the epidemic dies out at an exponential rate. However, when it is larger than unity the epidemic persists and does not die out in any reasonable time. The horizontal thick red line between 200 and 300 represents the number of infected nodes at the nontrivial fixed point obtained by $\Phi(\cdot)$ of (4.7). In the approximated nonlinear map, $\Phi(\cdot)$, the marginal probability of each node's infection converges to the unique nontrivial fixed point if $\frac{\beta\|A\|}{\delta} > 1$. Figure 4.2 shows that the number of infected nodes oscillates around the sum of entries of x^* which is a nontrivial fixed point of $\Phi(\cdot)$.

4.5 Alternative Proof Using LP

Our earlier result showed that the epidemic map $\Phi(\cdot)$ provides an upper bound on the probability that the i-th node in the Markov chain model is infected. However, to prove that the mixing time is $O(\log n)$, we only needed to show the weaker result that the system matrix is an upper bound. It turns out that one can give a simpler proof using linear programming for it, which we write below.

$\mu(t) \in \mathbb{R}^{2^n}$ is a probability row vector of $\{0,1\}^n$ at time t. $p_i(t)$ is the probability that node i is infected at time t as defined in the previous section. This is simply the marginal probability of $\mu(t)$, i.e., $p_i(t) = \sum_{X_i=1} \mu_X(t)$. Write $p_0(t) = 1$ which represents sum of probability distribution, i.e., $p_0(t) = 1 = \sum \mu_X(t)$. Define now the column vector $p(t) = (p_0(t), p_1(t), \cdots, p_n(t))^T$. We can understand $p(t)$ as observable data and $\mu(t)$ as hidden complete data at time t. We give an upper bound of $p(t+1)$, observable data at the next time step, using only current observable information.

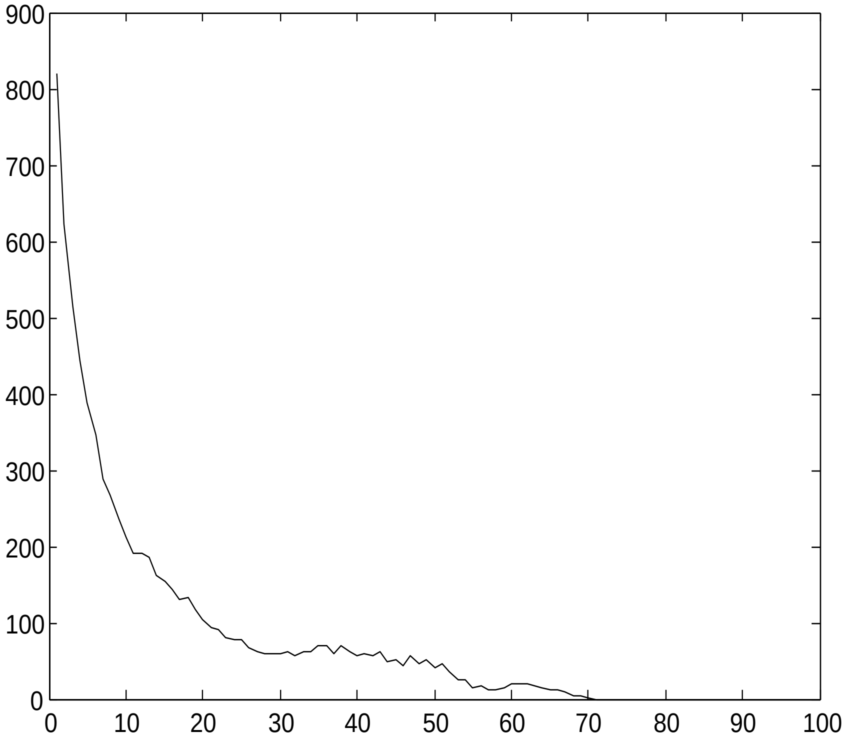

Figure 4.1: Epidemic Extinction

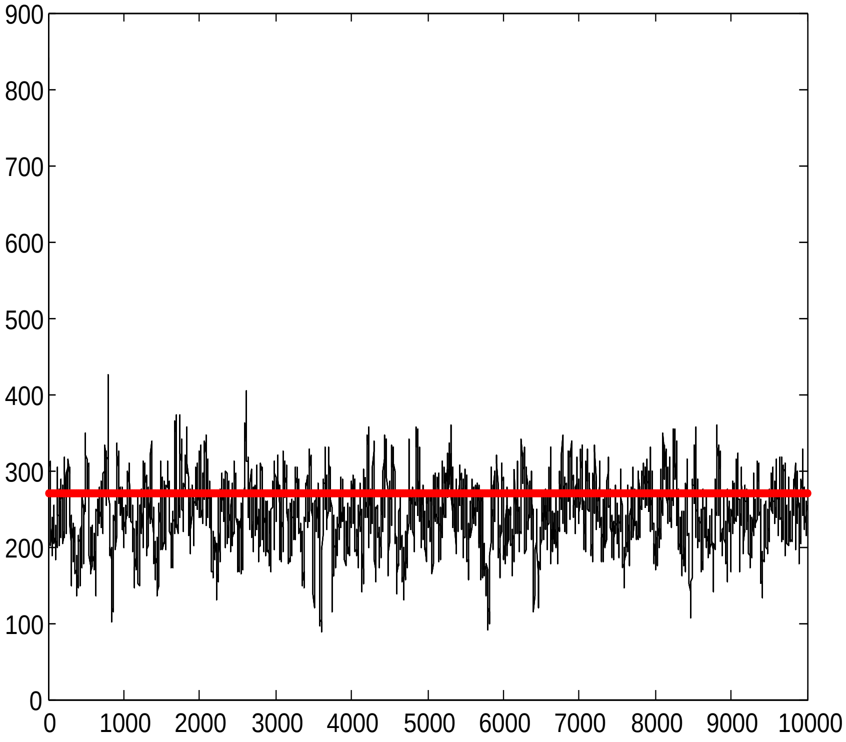

Figure 4.2: Epidemic Spread

Let $f_i \in \mathbb{R}^{n+1}$ be the i-th unit column vector. S is transition matrix of the Markov chain defined before. $B \in \mathbb{R}^{2^n \times (n+1)}$ is a matrix representing complete information to observable information, which consists all-1 column vector and truth table. Formal definition of B follows.

$$B_{X,k} = \begin{cases} 1 & \text{if } k = 0, \\ X_k & \text{if } k \in \{1, 2, \cdots, n\}. \end{cases} \tag{4.63}$$

We would like to maximize $p_i(t+1)$ for particular node i with given $p_1(t), \cdots, p_n(t)$. This leads to the following result.

Lemma 4.5.1 $p_i(t+1) \leq (1-\delta)p_i(t) + \beta \sum_{j \in N_i} p_j(t)$

Proof: We drop time index t for simplicity and mark time index only for $t+1$ in this proof from now on.

$$\max_{\mu B = p^T, \mu \succeq 0} p_i(t+1) = \max_{\mu B = p^T, \mu \succeq 0} \mu S B f_i \tag{4.64}$$

$$= \max_{\mu \succeq 0} \min_{\lambda} \mu S B f_i - (\mu B - p^T)\lambda \tag{4.65}$$

$$= \min_{\lambda} \max_{\mu \succeq 0} \mu (S B f_i - B\lambda) + p^T \lambda \tag{4.66}$$

$\max_{\mu \succeq 0} \mu(SBf_i - B\lambda) = +\infty$ if any entry of $(SBf_i - B\lambda)$ is strictly positive. It leads that $SBf_i - B\lambda \preceq 0$. Evaluation of SBf_i and $B\lambda$ follows.

$$(SBf_i)_X = (SB)_{X,i} = \sum_{Y \in \{0,1\}^n} S_{X,Y} B_{Y,i} = \sum_{Y \in \{0,1\}^n} S_{X,Y} Y_i \tag{4.67}$$

$$= \mathbb{P}[Y_i = 1 | X] = \begin{cases} 1 - (1-\beta)^m & \text{if } X_i = 0, \\ 1 - \delta(1-\beta)^m & \text{if } X_i = 1. \end{cases} \tag{4.68}$$

$\mathbb{P}[Y_i = 1|X]$ follows (4.2) and m is the number of infected neighbors of i as stated before.

$$(B\lambda)_X = \lambda_0 + \sum_{k=1}^{n} B_{X,k} \lambda_k = \lambda_0 + \sum_{k=1}^{n} \lambda_k X_k \tag{4.69}$$

We try several X for (4.68), (4.69) and $SBf_i - B\lambda \preceq 0$ to get feasible λ.

$$\begin{cases} X = \bar{0} & ,\lambda_0 \geq 0 \\ X = \hat{i} & ,\lambda_0 + \lambda_i \geq 1 - \delta \\ X = \hat{j}, j \in N_i & ,\lambda_0 + \lambda_j \geq \beta \\ X = \hat{j}, j \notin N_i & ,\lambda_0 + \lambda_j \geq 0 \end{cases} \tag{4.70}$$

We claim that $\lambda^* = (\lambda_0^*, \lambda_1^*, \cdots, \lambda_n^*)^T$ defined by $\lambda_0^* = 0$, $\lambda_i^* = 1 - \delta$, $\lambda_j^* = \beta$ for $j \in N_i$ and $\lambda_j^* = 0$ for $j \notin N_i$ is in feasible set.

For $X_i = 0$, $|N_i \cap \mathbb{S}(X)| = m$

$$\mathbb{P}[Y_i = 1|X] = 1 - (1-\beta)^m \leq m\beta = \lambda_0^* + \sum_{k=1}^{n} \lambda_k^* X_k \tag{4.71}$$

For $X_i = 1$, $|N_i \cap \mathbb{S}(X)| = m$

$$\mathbb{P}[Y_i = 1|X] = 1 - \delta(1-\beta)^m \leq 1 - \delta + m\beta = \lambda_0^* + \sum_{k=1}^{n} \lambda_k^* X_k \tag{4.72}$$

Therefore λ^* is in feasible set.

$$\max_{\mu B = p^T, \mu \succeq 0} p_i(t+1) = \min_{\lambda} \max_{\mu \succeq 0} \mu(SBf_i - B\lambda) + p^T\lambda \tag{4.73}$$

$$\leq p^T\lambda^* = (1-\delta)p_i + \beta \sum_{j \in N_i} p_j \tag{4.74}$$

■

By applying Lemma 4.5.1 to each node,

$$p(t+1) \preceq ((1-\delta)I_n + \beta A)p(t) = Mp(t) \tag{4.75}$$

We also get the practical result that the mixing time is $O(\log n)$ by modifying Theorem 4.4.2.

4.6 Generalized Infection Model

In this section, we suggest generalized infection model. In the previous model, everyone has the same recovery rate δ and infection rate β. One of the main result is that the epidemic dies out if the largest eigenvalue of $M = (1-\delta)I_n + \beta A$ is smaller than 1. M is defined by β, the infection rate, δ, the recovery rate, and A, the adjacency matrix.

We begin the discussion by defining M, the generalized infection matrix first. Define $M = (m_{i,j})$ as an infection matrix where $m_{i,j} \in [0,1]$ represent the infection probability that i is infected at time $t+1$ when j is the only infected node at time t. In this setting, each diagonal entry $m_{i,i}$ represents self-infection rate. In other words, $1 - m_{i,i}$ is recovery rate of node i and $m_{i,i}$ is the probability that i stays infected when there is no other infected nodes in the network. We also assume that probability of infection of each node given the current state $\xi(t)$ is independent. More precisely, for any two state vectors $X, Y \in \{0,1\}^n$,

$$\mathbb{P}[\xi(t+1) = Y | \xi(t) = X] = \prod_{i=1}^{n} \mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X] \tag{4.76}$$

Probability transition from given state is defined by M.

$$\mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X] = \begin{cases} \displaystyle\prod_{j \in \mathbb{S}(X)} (1 - m_{i,j}) & \text{if } Y_i = 0, \\ 1 - \displaystyle\prod_{j \in \mathbb{S}(X)} (1 - m_{i,j}) & \text{if } Y_i = 1, \end{cases} \tag{4.77}$$

We define the transition matrix, $S^{(M)} \in \mathbb{R}^{\{0,1\}^n \times \{0,1\}^n}$ by $S^{(M)}_{X,Y} = \mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X]$ in the equation above. It is also trivial to check that all the nodes are healthy with probability 1 at the stationary distribution because there is no disease transition if all the nodes in the network are healthy.

We also define partial order in the same manner. Two probability distributions μ and μ' which are defined in $\{0,1\}^n$, μ is stochastically dominated by μ' and written as $\mu \leq_{st} \mu'$ if any subset of nodes are more likely to be healthy under μ rather than under μ'. More precisely,

$$\mu \leq_{st} \mu' \quad \text{iff} \quad \sum_{X \preceq Z} \mu_X \geq \sum_{X \preceq Z} \mu'_X \quad \forall Z \in \{0,1\}^n \tag{4.78}$$

We prove that $S^{(M)}$ is an order-preserving map.

Lemma 4.6.1 *If $\mu \leq_{st} \mu'$, then $\mu S^{(M)} \leq_{st} \mu' S^{(M)}$.*

Proof: We first show that $R^{-1} S^{(M)} R$ is the matrix whose entries are all nonnegative. R is defined by

$$R_{X,Y} = \begin{cases} 1 & \text{if } X \preceq Y, \\ 0 & \text{otherwise} \end{cases} \tag{4.79}$$

It is not hard to check that R^{-1} is verified as

$$R^{-1}_{X,Y} = \begin{cases} (-1)^{|\mathbb{S}(Y-X)|} & \text{if } X \preceq Y, \\ 0 & \text{otherwise} \end{cases} \tag{4.80}$$

$|\mathbb{S}(Y-X)|$ represents the number of nodes which are infected in Y, but not in X. The 2^n-dimensional matrix R is important to the partial order $\leq_{st}$ because $\mu \leq_{st} \mu'$ is equivalent to the statement that all the entries of $(\mu - \mu')R$ are nonnegative. After verifying that all the entries of $R^{-1}S^{(M)}R$ is nonnegative, we show that $S^{(M)}$ preserves the partial order $\leq_{st}$.

$$(R^{-1}S^{(M)}R)_{X,Z} \tag{4.81}$$

$$= \sum_{Y\preceq Z} (R^{-1}S^{(M)})_{X,Y} = \sum_{Y\preceq Z}\sum_{W} R^{-1}_{X,W} S^{(M)}_{W,Y} \tag{4.82}$$

$$= \sum_{Y\preceq Z}\sum_{W\succeq X} (-1)^{|\mathbb{S}(W-X)|} S^{(M)}_{W,Y} \tag{4.83}$$

$$= \sum_{W\succeq X} (-1)^{|\mathbb{S}(W-X)|} \prod_{i\in\mathbb{S}(Z)^c} \mathbb{P}[\xi_i(t+1)=0|\xi(t)=W] \tag{4.84}$$

$$= \sum_{W\succeq X} (-1)^{|\mathbb{S}(W-X)|} \prod_{i\in\mathbb{S}(Z)^c}\prod_{j\in\mathbb{S}(W)} (1-m_{i,j}) \tag{4.85}$$

$$= \left(\prod_{i\in\mathbb{S}(Z)^c}\prod_{j\in\mathbb{S}(X)} (1-m_{i,j})\right)\left(\sum_{W\succeq X} (-1)^{|\mathbb{S}(W-X)|} \prod_{j\in\mathbb{S}(W-X)}\prod_{i\in\mathbb{S}(Z)^c} (1-m_{i,j})\right) \tag{4.86}$$

$$= \left(\prod_{i\in\mathbb{S}(Z)^c}\prod_{j\in\mathbb{S}(X)} (1-m_{i,j})\right)\left(\prod_{j\in\mathbb{S}(X)^c}\left(1-\prod_{i\in\mathbb{S}(Z)^c}(1-m_{i,j})\right)\right) \geq 0 \tag{4.87}$$

The inequality of (4.87) is true because $m_{i,j} \in [0,1]$ for all i, j.

$\mu \leq_{st} \mu'$ is equivalent to that $(\mu-\mu')R$ has nonnegative entries. $(\mu-\mu')S^{(M)}R$ also has nonnegative entries because $(\mu-\mu')S^{(M)}R = (\mu-\mu')R \times R^{-1}S^{(M)}R$ and all the entries of $(\mu-\mu')R$ and $R^{-1}S^{(M)}R$ are nonnegative. Nonnegativity of $(\mu-\mu')S^{(M)}R$ also means that $\mu S^{(M)} \leq_{st} \mu' S^{(M)}$. It completes the proof. ■

By Lemma 4.6.1, $(\mu(S^{(M)})^t)_{\bar{0}} = \sum_{X\preceq\bar{0}}(\mu(S^{(M)})^t)_X \geq \sum_{X\preceq\bar{0}}(e_{\bar{1}}(S^{(M)})^t)_X = (e_{\bar{1}}(S^{(M)})^t)_{\bar{0}}$ for any probability vector μ since $\mu \leq_{st} e_{\bar{1}}$. Returning to the mixing time,

$$\|\mu(S^{(M)})^t - \pi\|_{TV} = \|\mu(S^{(M)})^t - e_{\bar{0}}\|_{TV} = 1 - (\mu(S^{(M)})^t)_{\bar{0}} \tag{4.88}$$

$$\leq 1 - (e_{\bar{1}}(S^{(M)})^t)_{\bar{0}} = 1 - e_{\bar{1}}(S^{(M)})^t e_{\bar{0}}^T \tag{4.89}$$

Using the inequality above, we can now write

$$t_{mix}(\varepsilon) = \min\{t : \sup_{\mu} \|\mu(S^{(M)})^t - \pi\|_{TV} \leq \varepsilon\} \tag{4.90}$$

$$= \min\{t : 1 - e_{\bar{1}}(S^{(M)})^t e_{\bar{0}}^T \leq \varepsilon\} \tag{4.91}$$

$$= \min\{t : e_{\bar{1}}(S^{(M)})^t e_{\bar{0}}^T \geq 1 - \varepsilon\} \tag{4.92}$$

The next step is giving an lower bound of $(S^{(M)})^t e_{\bar{0}}^T$ using the epidemic map associated with M. The epidemic map associated with M is defined by $\Phi^{(M)} : [0,1]^n \to [0,1]^n$ is defined by $\Phi_i^{(M)}(x) = 1 - \prod_{j=1}^{n}(1 - m_{i,j}x_j)$ where $\Phi^{(M)} = (\Phi_1^{(M)}, \Phi_2^{(M)}, \cdots, \Phi_n^{(M)})$. M is Jacobian matrix of $\Phi^{(M)}(\cdot)$ at the origin which gives an upper bound, i.e., $\Phi^{(M)}(x) \preceq Mx$. The origin is unique fixed point which is globally stable if the largest eigenvalue of M is smaller than 1. We give an upper bound of extinction probability of epidemics at time t. We give an upper bound using 2^n-dimensional column vector $u(r)$ which is defined for a given n-dimensional $r = (r_1, \cdots, r_n)^T$. The X-th entry of $u(r)$ is defined as $u(r)_X = \prod_{i \in \mathbb{S}(X)} (1 - r_i)$. The following lemma shows that $S^{(M)}u(r) \succeq u(\Phi^{(M)})(r)$.

Lemma 4.6.2 *$S^{(M)}u(r) \succeq u(\Phi^{(M)})(r)$ for all $r \in [0,1]^n$.*

Proof: We begin the proof of this lemma by evaluating each entry of $S^{(M)}u(r)$.

$$(S^{(M)}u(r))_X \tag{4.93}$$

$$= \sum_{Y \in \{0,1\}^n} S_{X,Y}^{(M)} u(r)_Y \tag{4.94}$$

$$= \sum_{Y \in \{0,1\}^n} \left(\prod_{i \in \mathbb{S}(Y)} (1 - r_i)\mathbb{P}[Y_i = 1|X] \right) \left(\prod_{i \notin \mathbb{S}(Y)} \mathbb{P}[Y_i = 0|X] \right) \tag{4.95}$$

$$= \prod_{i=1}^{n} (1 - r_i)\mathbb{P}[Y_i = 1|X] + \mathbb{P}[Y_i = 0|X] \tag{4.96}$$

Assume $\mathbb{S}(X) \cap \mathbb{S}(Z) = \emptyset$ for two states $X, Z \in \{0,1\}^n$, i.e., there is no common infected node in the two states X and Z. It's trivial to check that the following is true:

$$\mathbb{P}[Y_k = 0|X+Z] = \mathbb{P}[Y_k = 0|X]\mathbb{P}[Y_k = 0|Z] \tag{4.97}$$

For simplicity, we call $q_{k,X} = \mathbb{P}[Y_k = 0|X]$.

$$\begin{aligned}
&(S^{(M)}u(r))_{X+Z} && (4.98)\\
&= \prod_{i=1}^{n}(1-r_i)\mathbb{P}[Y_i = 1|X+Z] + \mathbb{P}[Y_i = 0|X+Z] && (4.99)\\
&= \prod_{i=1}^{n}(1-r_i)(1-q_{i,X+Z}) + q_{i,X+Z} && (4.100)\\
&= \prod_{i=1}^{n}(1-r_i)(1-q_{i,X}q_{i,Z}) + q_{i,X}q_{i,Z} && (4.101)\\
&\geq \prod_{i=1}^{n}((1-r_i)(1-q_{i,X}) + q_{i,X})((1-r_i)(1-q_{i,Z}) + q_{i,Z}) && (4.102)\\
&= (S^{(M)}u(r))_X(S^{(M)}u(r))_Z && (4.103)
\end{aligned}$$

(4.102) holds by the following one for $r, b, c \in [0,1]$:

$$\begin{aligned}
&((1-r)(1-ab)+ab) - ((1-r)(1-a)+a)((1-r)(1-b)+b)\\
&= r(1-r)(1-a)(1-b) \geq 0 && (4.104)
\end{aligned}$$

Define $\hat{i} \in \{0,1\}^n$ as the state where everyone is healthy, but i. The following inequality holds by (4.103).

$$\begin{aligned}
(S^{(M)}u(r))_X &\geq \prod_{i\in\mathbb{S}(X)} (S^{(M)}u(r))_{\hat{i}} && (4.105)\\
&= \prod_{i\in\mathbb{S}(X)}\prod_{j=1}^{n}(1-r_j)\mathbb{P}[Y_j = 1|\hat{i}] + \mathbb{P}[Y_j = 0|\hat{i}] && (4.106)\\
&= \prod_{i\in\mathbb{S}(X)}\prod_{j=1}^{n}(1-r_j)m_{i,j} + 1 - m_{i,j} && (4.107)\\
&= \prod_{i\in\mathbb{S}(X)}\prod_{j=1}^{n}1 - m_{i,j}r_j && (4.108)\\
&= \prod_{i\in\mathbb{S}(X)} 1 - \Phi_i^{(M)}(r) && (4.109)\\
&= u(\Phi^{(M)}(r))_X && (4.110)
\end{aligned}$$

■

It's obvious that $e_{\bar{0}}^T = u((1,1,\cdots,1)^T) = u(1_n)$. Since $S^{(M)}u(r) \succeq u(\Phi^{(M)}(r))$ by Lemma 4.6.2, and $S^{(M)}$ is a matrix all of whose entries are non-negative,

$$(S^{(M)})^t e_{\bar{0}}^T = (S^{(M)})^t u(1_n) \succeq u((\Phi^{(M)})^t(1_n)) \tag{4.111}$$

We can show that the mixing time of the generalized epidemic Markov chain model is $O(\log n)$ by applying Theorem 4.4.2 in the previous section. Similarly, the probability that the epidemics is not extinct at time t for given initial epidemic state X is bounded above by the entries of $(\Phi^{(M)})^t(1_n)$.

$$\begin{aligned} \mathbb{P}[\xi(t) \neq \bar{0} | \xi(0) = X] &= 1 - \mathbb{P}[\xi(t) = \bar{0} | \xi(0) = X] = 1 - e_X (S^{(M)})^t e_{\bar{0}}^T && (4.112) \\ &\leq 1 - u(\Phi^t(1_n))_X && (4.113) \\ &= 1 - \prod_{i \in \mathbb{S}(X)} \left(1 - (\Phi^{(M)})_i^t(1_n)\right) && (4.114) \end{aligned}$$

By adopting infection rate and recovery rate which are not identical, we can model the epidemic spread in the network which is closer to the real world.

4.7 Immune-admitting Model

In this section, we study the immune-admitting model. The model is the same as that of the previous section except that in a single time interval a node cannot go from infected to healthy back to infected. In other words, a node is not infected from its neighbors if it has just recovered from the disease. To summarize this,

$$\mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X] = \begin{cases} (1-\beta)^{m_i} & \text{if } (X_i, Y_i) = (0,0),\ |N_i \cap \mathbb{S}(X)| = m_i, \\ 1 - (1-\beta)^{m_i} & \text{if } (X_i, Y_i) = (0,1),\ |N_i \cap \mathbb{S}(X)| = m_i, \\ \delta & \text{if } (X_i, Y_i) = (1,0), \\ 1 - \delta & \text{if } (X_i, Y_i) = (1,1). \end{cases} \tag{4.115}$$

Transition matrix is defined in a similar way. By assuming independence of infection to the each node,

$$\widetilde{S}_{X,Y} = \mathbb{P}[\xi(t+1) = Y | \xi(t) = X] = \prod_{i=1}^{n} \mathbb{P}[\xi_i(t+1) = Y_i | \xi(t) = X] \tag{4.116}$$

$\widetilde{S}$ is a transition matrix of the immune-admitting-model. In this model which is described as (4.115), the probability that a node becomes healthy from infected is δ which is larger than $\delta(1-\beta)^{m_i}$, the probability for immune-not-admitting model which is described as (4.2). Roughly speaking, the immune-admitting model is more likely to go to steady state than the immune-not-admitting model and it leads smaller mixing time. The mixing time of this model is also $O(\log n)$. We apply linear programming to give a result.

Theorem 4.7.1 *The mixing time of Markov chain whose transition matrix $\widetilde{S}$ is defined by* (4.115) *and* (4.116) *has steady state where all nodes are healthy with probability 1. The mixing time of this Markov chain is $O(\log n)$ if $1-\delta+\beta\lambda_{\max}(A)<1$.*

Proof: We show that $p_i(t+1) \le (1-\delta)p_i(t) + \beta \sum_{j\in N_i} p_j(t)$ first. We drop time index t for simplicity and mark time index only for $t+1$ in this proof from now on.

$$\max_{\mu B = p^T, \mu \succeq 0} p_i(t+1) = \max_{\mu B = p^T, \mu \succeq 0} \mu S B f_i \tag{4.117}$$

$$= \max_{\mu \succeq 0} \min_{\lambda} \mu S B f_i - (\mu B - p^T)\lambda \tag{4.118}$$

$$= \min_{\lambda} \max_{\mu \succeq 0} \mu(SBf_i - B\lambda) + p^T\lambda \tag{4.119}$$

$\max_{\mu\succeq 0} \mu(SBf_i - B\lambda) = +\infty$ if any entry of $(SBf_i - B\lambda)$ is strictly positive. It leads that $SBf_i - B\lambda \preceq 0$. Evaluation of SBf_i and $B\lambda$ follows.

$$(SBf_i)_X = (SB)_{X,i} = \sum_{Y\in\{0,1\}^n} S_{X,Y} B_{Y,i} = \sum_{Y\in\{0,1\}^n} S_{X,Y} Y_i \tag{4.120}$$

$$= \mathbb{P}[Y_i = 1|X] = \begin{cases} 1-(1-\beta)^{m_i} & \text{if } X_i = 0, \\ 1-\delta & \text{if } X_i = 1. \end{cases} \tag{4.121}$$

$\mathbb{P}[Y_i = 1|X]$ follows (4.115) and m is the number of infected neighbors of i as stated before.

$$(B\lambda)_X = \lambda_0 + \sum_{k=1}^{n} B_{X,k}\lambda_k = \lambda_0 + \sum_{k=1}^{n} \lambda_k X_k \tag{4.122}$$

We try several X for (4.121), (4.122) and $SBf_i - B\lambda \preceq 0$ to get feasible λ.

$$\begin{cases} X = \bar{0} & ,\lambda_0 \geq 0 \\ X = \hat{i} & ,\lambda_0 + \lambda_i \geq 1 - \delta \\ X = \hat{j}, j \in N_i & ,\lambda_0 + \lambda_j \geq \beta \\ X = \hat{j}, j \notin N_i & ,\lambda_0 + \lambda_j \geq 0 \end{cases} \tag{4.123}$$

We claim that $\lambda^* = (\lambda_0^*, \lambda_1^*, \cdots, \lambda_n^*)^T$ defined by $\lambda_0^* = 0$, $\lambda_i^* = 1 - \delta$, $\lambda_j^* = \beta$ for $j \in N_i$ and $\lambda_j^* = 0$ for $j \notin N_i$ is in feasible set.

For $X_i = 0$, $|N_i \cap \mathbb{S}(X)| = m$

$$\mathbb{P}[Y_i = 1|X] = 1 - (1-\beta)^m \leq m\beta = \lambda_0^* + \sum_{k=1}^{n} \lambda_k^* X_k \tag{4.124}$$

For $X_i = 1$, $|N_i \cap \mathbb{S}(X)| = m$

$$\mathbb{P}[Y_i = 1|X] = 1 - \delta(1-\beta)^m \leq 1 - \delta + m\beta = \lambda_0^* + \sum_{k=1}^{n} \lambda_k^* X_k \tag{4.125}$$

Therefore λ^* is in feasible set.

$$\max_{\mu B = p^T, \mu \succeq 0} p_i(t+1) = \min_{\lambda} \max_{\mu \succeq 0} \mu(SBf_i - B\lambda) + p^T\lambda \tag{4.126}$$

$$\leq p^T\lambda^* = (1-\delta)p_i + \beta \sum_{j \in N_i} p_j \tag{4.127}$$

By applying (4.127) to each node, we get

$$p(t+1) \preceq ((1-\delta)I_n + \beta A)p(t) = Mp(t) \tag{4.128}$$

Suppose that $t \leq t_{mix}(\varepsilon)$.

$$\begin{aligned}
\varepsilon &\leq 1 - \mathbb{P}[\text{ all the nodes are healthy at time } t] && (4.129)\\
&= \mathbb{P}[\text{ there exists an infected node at time } t] && (4.130)\\
&\leq \sum_{i=1}^{n} p_i(t) = 1_n^T p(t) && (4.131)\\
&\leq 1_n^T M^t p(0) && (4.132)\\
&\leq 1_n^T M^t 1_n && (4.133)\\
&\leq \|1_n\|^2 \|M\|^t && (4.134)\\
&= n\|M\|^t && (4.135)
\end{aligned}$$

$t \leq \dfrac{\log \frac{n}{\varepsilon}}{-\log \|M\|}$ for every $t \leq t_{mix}(\varepsilon)$ leads that $t_{mix}(\varepsilon) \leq \dfrac{\log \frac{n}{\varepsilon}}{-\log \|M\|}$. The mixing time is $O(\log n)$.
■

4.8 Continuous Time Markov Chain on Complete Graph

We showed that epidemics dies out fast if $1 - \delta + \beta\lambda_{\max}(A) < 1$. However, it is the sufficient condition for the discrete-time Markov chain model even though it is epidemic threshold for continuous space model such as epidemic map or epidemic differential equation. We have two questions here. The first one is that how long is the mixing time if the mixing time is not $O(\log n)$. It can be linear with n, n^2 or any polynomial of n with fixed degree. There is also possibility that the mixing time is exponentially long if it's not so short. The second one is whether the sufficient condition is a tight condition for epidemic.

To give an answer to the two questions above, we introduce a continuous-time Markov chain model and analyze a special case for complete graph in this section. First, we define the continuous time Markov chain in general networks and consider special case.

$G = (V,E)$ is connected undirected graph with n nodes. $V = \{1,2,\cdots,n\}$ and $E \in\subseteq V^2$. $i \sim j$ means that node i is connected to node j. Define $X(t) = (X_1(t),\cdots,X_n(t))$ as epidemic state at time t. Node i is infected at time t if $X_i(t) = 1$. Node i is healthy at time t if $X_i(t) = 0$. Assume the infected nodes transfer diseases to their neighbors at rate β and they recover at rate δ. This defines a Markov process with transition rates:

$$X_i : 0 \to 1 \text{ at rate } \beta \sum_{j\sim i} X_j \qquad\qquad X_i : 1 \to 0 \text{ at rate } \delta \tag{4.136}$$

We suppose that underlying graph is complete. Define now a Markov process Z which represents the number of infected nodes, i.e., $Z(t) = \sum X_i(t)$ on $\{0, 1, \cdots, n\}$, with transition rates:

$$m \to m+1 \text{ at rate } \beta m(n-m) \qquad\qquad m \to m-1 \text{ at rate } \delta m \tag{4.137}$$

Consider the embedded discrete time Markov chain associated with Z, which tracks the successive states visited by Z. We denote it by Y_k where $k \in \mathbb{N}$. The transition matrix P is tridiagonal matrix whose terms are:

$$P_{m,m+1} = \frac{\beta(n-m)}{\beta(n-m)+\delta} \qquad P_{m,m-1} = \frac{\delta}{\beta(n-m)+\delta} \qquad P_{0,0} = 1$$

It is easy to check that 0 is the absorbing state. Define T_m as the expected steps to 0 when $Y_0 = m$.

$$T_m = \frac{\beta(n-m)}{\beta(n-m)+\delta} T_{m+1} + \frac{\delta}{\beta(n-m)+\delta} T_{m-1} + 1 \tag{4.138}$$

$$\Rightarrow \quad T_m - T_{m-1} - \frac{\beta(n-m)}{\delta}(T_{m+1} - T_m) = \frac{\beta(n-m)}{\delta} + 1 \tag{4.139}$$

$$\Rightarrow \quad T_m - T_{m-1} = 2\left(\sum_{k=1}^{n-m} \left(\frac{\beta}{\delta}\right)^k \frac{(n-m)!}{(n-m-k)!}\right) + 1 \tag{4.140}$$

$$\Rightarrow \quad T_n = 2\left(\sum_{k=1}^{n-1} \left(\frac{\beta}{\delta}\right)^k k! \binom{n}{k+1}\right) + n \tag{4.141}$$

$$\Rightarrow \quad T_n \geq 2 \max_{1\leq k\leq n-1} \left\{ \left(\frac{\beta}{\delta}\right)^k k! \binom{n}{k+1} \right\} + n \tag{4.142}$$

Assume that $\frac{\delta}{\beta} = \frac{1+\varepsilon}{n-1}$ for $\varepsilon > 0$. By simple algebra, we can check that $k^* = \frac{\varepsilon}{1+\varepsilon}(n-1)$ maximizes (4.142).

$$
\begin{aligned}
T_n &\geq 2\left(\frac{\beta}{\delta}\right)^{k^*}\frac{n}{k^*+1}(n-1)(n-2)\cdots(n-k^*) && (4.143)\\
&= \frac{2n}{k^*+1}(1+\varepsilon)^{k^*}\left(1-\frac{1}{n-1}\right)\left(1-\frac{2}{n-1}\right)\cdots\left(1-\frac{k^*-1}{n-1}\right) && (4.144)\\
&= \frac{2n}{k^*+1}(1+\varepsilon)^{k^*}\exp\left(\sum_{j=0}^{k^*-1}\log\left(1-\frac{j}{k^*}\frac{\varepsilon}{1+\varepsilon}\right)\right) && (4.145)\\
&\geq \frac{2n}{k^*+1}(1+\varepsilon)^{k^*}\exp\left(\frac{k^*(1+\varepsilon)}{\varepsilon}\int_{\frac{1}{1+\varepsilon}}^{1}\log x\mathrm{d}x\right) && (4.146)\\
&= \frac{2n}{k^*+1}(1+\varepsilon)^{k^*}\exp\left((n-1)\left(\frac{\log(1+\varepsilon)}{1+\varepsilon}-\frac{\varepsilon}{1+\varepsilon}\right)\right) && (4.147)\\
&= \frac{2n}{k^*+1}\exp\left((n-1)\left(\log(1+\varepsilon)-\frac{\varepsilon}{1+\varepsilon}\right)\right) && (4.148)
\end{aligned}
$$

$\log(1+\varepsilon)-\dfrac{\varepsilon}{1+\varepsilon}\geq\dfrac{1}{2}\left(\dfrac{\varepsilon}{1+\varepsilon}\right)^2$ guarantees that T_n is exponentially large when $\varepsilon>0$.

Returning back to continuous-time Markov process, denote T as the expected time to absorbing state.

$$
\mathbb{E}[T]\geq\frac{T_n}{\min_m\{\delta m+\beta m(n-m)\}}\geq\frac{T_n}{\delta n+\beta n^2} \tag{4.149}
$$

Expected time to absorbing state is exponentially long if $1-\delta+\beta\lambda_{\max}(A)>1$ on the fully-connected network in continuous time model. However, it is a special case where the exact expected time to the absorbing state can be computed. We can say that the sufficient condition for fast extinction of epidemics is tight in a special case, and the mixing time is exponentially long in that case.

Ganesh et al. studied this continuous-time Markov chain model in the finite graph [23]. The research showed that the sufficient condition for fast extinction of epidemics in continuous-time Markov chain is $1-\delta+\beta\lambda_{\max}(A)<1$, which is also the sufficient condition for fast extinction in discrete-time Markov chain. Ganesh et al. also proved that the expected time to the absorbing state is exponentially long, $\Omega(e^{n^{\alpha}})$ for some $\alpha<1$ in various cases. The complete graph is a case which has the exponentially long expected absorbing time. The contribution of this section is that the expected absorbing time on the complete graph can be computed almost exactly since

$$
T_n=2\left(\sum_{k=1}^{n-1}\left(\frac{\beta}{\delta}\right)^k k!\binom{n}{k+1}\right)+n\leq 2n\max_{1\leq k\leq n-1}\left\{\left(\frac{\beta}{\delta}\right)^k k!\binom{n}{k+1}\right\}+n \tag{4.150}
$$

(4.142) gives lower bound, and the upper bound from the equation above is same with lower bound multiplied by n. However, the multiplication does not give big difference because the lower bound is exponentially big. This section also contributes that the expected absorbing time is exponential to n, not n^{α} for some $\alpha < 1$.

Chapter 5

Future Work

We have investigated random propagation in complex systems, especially nonlinear random matrix recursions and epidemic spreads in complex networks. In this chapter, we discuss the future directions.

5.1 Random Riccati Recursions

Researches on random Riccati recursions have been conducted under a couple of assumptions. We now consider the cases where those assumptions are changed.

We have viewed the $\mu_P^{(t)}$, the probability measure of error covariance matrix on Riccari recursion at time t, i.e., $\mu_P^{(t)}(E) = \mathbb{P}[P^{(t)} \in E | P^{(0)} = P]$, as a map from $\mathbb{S}_{++}^n$, the space of positive definite matrices, to the space of the probability measures on $\mathbb{S}_{++}^n$. One of important steps of the chapter is showing that the map $P \to \mu_P^{(t)}$ is continuous at any given time t. We have considered continuity of the map $\mu_{(\cdot)}^{(t)}$ according to the usual topology on the space of matrices and the metric topology defined by total variation distance on the measure space. It requires a lot of analytic and topological skills to prove continuity of the map. One of them is evaluating the probability density function from the initial error covariance matrix to the error covariance matrix at a given time according to Riccati recursion.

We have assumed that the state transition matrix F of following Riccari recursion is nonsingular:

$$P^{(t+1)} = FP^{(t)}F^T - FP^{(t)}(H^{(t)})^T(R + H^{(t)}P^{(t)}(H^{(t)})^T)^{-1}H^{(t)}P^{(t)}F^T + Q. \tag{5.1}$$

Assumption about nonsingularity of F is essential to evaluating the probability density function $f^{(t)}$

on $\mathbb{S}^n_{++} \times \mathbb{S}^n_{++}$ satisfying

$$\mathbb{P}[P^{(t)} \in E | P^{(0)} = P] = \mu_P^{(t)}(E) = \int_E f^{(t)}(P, C) \mathrm{d}C. \tag{5.2}$$

Note that the following part of the Riccati recursion is a lower-dimensional manifold of $\mathbb{S}^n_{++}$:

$$F\left(P^{(t-1)} - P^{(t-1)}(H^{(t-1)})^T(R + H^{(t-1)}P^{(t-1)}(H^{(t-1)})^T)^{-1}H^{(t-1)}P^{(t-1)}\right)F^T. \tag{5.3}$$

Thus, the support of $P^{(t)}$ is a measure-zero set of $\mathbb{S}^n_{++}$ if F is singular.

If F is singular, then $f^{(t)}$ is not well-defined on $\mathbb{S}^n_{++} \times \mathbb{S}^n_{++}$. For this reason, continuity of $\mu_{(\cdot)}^{(t)}$ relies on the continuity assumption of $f^{(t)}$ in our approach. In addition, we need to consider a measure without a probability density function $f^{(t)}$ to study singular cases. Measure theory may enable us to overcome this problem, but this is out of scope this paper.

We assumed three conditions on the probability distribution of H, the random regressor matrix. Gaussian distributions of a multi-dimensional matrix are important distributions satisfying all the required conditions of p_H. The first condition is “whole-space-support condition”, which assumes that $H^{(t)}$ is distributed on the whole space, i.e., $\mathbb{P}[H^{(t)} \in E] > 0$ if $E \subset \mathbb{R}^{m \times n}$ has a positive Lebesgue measure. This condition guarantees that independent of the initial matrix, the common area of supports is not measure zero. The second condition of p_H, “continuous probability distribution function condition”, is necessary to prove that $f^{(t)} : \mathbb{S}^n_{++} \times \mathbb{S}^n_{++} \to \mathbb{R}_+$, the probability distribution function for the error covariance matrix at time t, is continuous. The third condition of p_H, “fast decaying condition”, is essential to show that $f^{(t)} : \mathbb{S}^n_{++} \times \mathbb{S}^n_{++} \to \mathbb{R}_+$ is continuous. This condition can be changed by a less strict condition if we can find a way to prove the continuity of $\mu_{(\cdot)}^{(t)}$ without considering the probability density function of the measure.

Even though we prove the geometric convergence of random Riccati recursions defined on arbitrary dimension, we do not know how big the convergence rate is. If the convergence rate is close to 1, the probability distribution converges to the steady state slowly. The analysis on the convergence rate, as a function of n and the distribution of $H^{(t)}$, is an interesting topic to study.

Considering both continuous and discrete distributions of $H^{(t)}$ is also worth studying. We can view constant $H^{(t)}$ as a random regressor whose probability distribution is atomic. The convergence condition is well-studied by previous researchers for time-constant $H^{(t)}$. One may extend our study to analyze the convergence condition of the system for various probability distributions mixed by both continuous and discrete measures.

Finally, the proof of geometric convergence does depend on a specific metric and shows the distance defined by the metric goes to zero at a geometric rate. We have used the total variation distance as the metric on the probability measure space. Another metric defined on the probability measure space may require a weaker assumption of the distributions of $H^{(t)}$; however it may require a totally different approach from the current work.

5.2 Epidemic Spread

There are a number of issues on the study of epidemic spreads. We have studied SIS model, the model considers only healthy and infected state. Of course, modeling the epidemics with other states could be interesting. The epidemic model concerning incubation period would be appropriate to study spreads of certain diseases such as AIDS.

Returning back to the SIS model, a nontrivial fixed point of the nonlinear epidemic map exists if and only if the ratio of β and δ, the infection rate and the recovery rate, is greater than the largest eigenvalue of the adjacency matrix of a given network. The nontrivial fixed point is globally stable in the Chakrabarti's immune-free model; however it is may not stable in the immune-admitting model. From a random graph approach, the nontrivial fixed point is locally stable with high probability in the family of Erdös-Rényi random graphs. A natural question to ask at this point is whether the nontrivial fixed point is globally stable if it is local stable. In general, local stability does not necessarily imply global stability. The immune-admitting epidemic map has only two fixed points. The origin, the first trivial fixed point, is not stable. Even though an initial point is very close to the origin, it goes away from the origin as time passes. x^*, the second nontrivial fixed point, is locally stable if and only if the Jacobian matrix of the nonlinear epidemic map at the nontrivial fixed point is stable. Since there is no more fixed point, stable manifolds are concerned as attractor if x^* is not globally stable. Actually, oscillation between two points is observed when x^* is not locally stable. Another possible scenario is whether a chaotic movement arises. However, globally stability of x^* is observed in many simulations when local stability is assumed. A rigorous proof on global stability based on local stability could be interesting in the literature.

For epidemic Markov chain models, finding a sufficient condition for a slow mixing time is an open question. This thesis shows that the Markov chain mixes fast if the origin, the state where everyone is healthy, is the stable fixed point of the nonlinear epidemic map. This result is salient because the nonlinear epidemic map and the Markov chain model have the same sufficient condition for epidemic extinction. The difference is that the sufficient condition is also the necessary condition of the nonlinear epidemic model, but it is not necessarily true in the Markov chain model. Figure 4.1 and Figure 4.2 suggest that the phase transition phenomenon arises in the Markov chain when the phase transition phenomenon is observed in the nonlinear epidemic map. Analysis on the role of the nontrivial fixed point in the nonlinear epidemic map is interesting.

Figure 4.2 suggests that the number of infected nodes can oscillate around the sum of entries of the nontrivial fixed point. Moreover, another simulation results show that each node's marginal probability for being infected derived from the Markov chain's eigenvector corresponding to the second largest eigenvalue is close to the nontrivial fixed point. The second largest eigenvalue of the Markov chain is responsible for the convergence rate of the Markov chain. A rigorous analysis requires more mathematical tools to describe how close the couple of marginal probabilities are. A metric that defines a distance between two marginal probabilities is one of the tools. The study on the nontrivial fixed point in the nonlinear epidemic model and the marginal probability of each node from the eigenvector corresponding to the second largest eigenvalue would be the starting point to investigate the how well the nonlinear model approximates the true Markov chain model.

It might be more realistic to introduce a time-varying network in the literature on epidemics on complex networks. We have studied the epidemic dynamics on a fixed network topology; however, admitting a time-varying network could be more appropriate. For example, consider a businessman who works with office-mates during weekdays but spends with families and friends on weekends. This means that the network during weekdays and the one on weekends are different; that is, the network periodically changes. The periodic change of the network between two given networks is a simple variation of the existing model that captures the idea of time-varying networks.

Bibliography

[1] H. Abbey. “An examination of the Reed-Frost theory of epidemics”. Hum. Biol. 1952.

[2] H. J. Ahn and B. Hassibi. “Global Dynamics of Epidemic Spread over Complex Networks” IEEE CDC, 2013.

[3] H. Andersson. “Limit Theorems for a Random Graph Epidemic Model” The Annals of Applied Probability, 1998.

[4] A. L. Barabási and R. Albert. “Emergence of Scaling in Random Networks” Science, 1999.

[5] E. Bodine-Baron, S. Bose, B. Hassibi and A. Wierman. “Minimizing the social cost of an epidemic” Proceedings of ICST Gamenets, 2011.

[6] V. S. Bokharaie, O. Mason and F. Wirth. “Spread of epidemics in time-dependent networks”. Proceedings of the 19th International Symposium on Mathematical Theory of Networks and Systems, 2010.

[7] B. Bollobás. “Random Graph”. Academic Press, 1985.

[8] J. V. D. Broek, H. Heesterbeek. “Nonhomogeneous birth and death models for epidemic outbreak data”. Biostatistics, 2007.

[9] M. Cha, A. Mislove, and K.P. Gummadi. “A measurement-driven analysis of information propagation in the flickr social network”. Proc. 18th WWW Conf., 2009.

[10] D. Chakrabarti, Y. Wang, C. Wang, J. Leskovec and C. Faloutsos. ”Epidemic thresholds in real networks” ACM Trans. on Info. and System Security (TISSEC),10(4), 2008.

[11] H. Chen, P. Kumar, and J. van Schuppen. “On Kalman filtering for conditionally Gaussian systems with random matrices”. Systems & Control Letters, 1989.

[12] I. Chueshov. “Monotone random systems”. Springer, 2002.

[13] R. Cohen, S. Havlin, D. ben-Avraham. “Efcient immunization strategies for computer networks and populations”. Phys. Rev. Lett. 2003.

[14] X. Ding and T. Jiang. “Spectral distributions of adjacency and Laplacian matrices of random graphs”. Annals of Applied Probabability. Volume 20, Number 6. 2010.

[15] J. L. Doob. “Stochastic Processes”. John Wiley and Sons, New York, 1953.

[16] M. Draief. ”Epidemic processes on complex networks”. Physica A: Statistical Mechanics and its Applications, 2006.

[17] R. Durrett. “Some features of the spread of epidemics and information on a random graph”. Proc. Natl. Acad. Sci. 2010.

[18] E. Eleftheriou and D. Falconer. “Tracking properties and steady-state performance of RLS adaptive filter algorithms”. IEEE Transactions on Acoustics, Speech and Signal Processing, 1986.

[19] P. Erdös and A. Rényi. “On random graphs”. Publicationes Mathematicae 6, 1959.

[20] E. Estrada, F. Kalala-Mutombo and A. Valverde-Colmeiro. “Epidemic spreading in networks with nonrandom long-range interactions”. PHYSICAL REVIEW E 84, 2011.

[21] E. Eweda. “Comparison of RLS, LMS, and sign algorithms for tracking randomly time-varying channels”. IEEE Transactions on Signal Processing, 1994.

[22] A. Fall, A. Iggidr, G. Sallet and J. J. Tewa. “Epidemiological models and Lyapunov functions”. Math. Model. Nat. Phenom, 2007.

[23] A. Ganesh, L. Massoulie and D. Towsley. “The effect of network topology on the spread of epidemics”. in Proc. IEEE INFOCOM 2005.

[24] D. Godard. “Channel equalization using a Kalman filter for fast data transmission”. IBM Journal of Research and Development, 1974.

[25] S. Gomez, A. Arenas, J. Borge-Holthoefer1, S. Meloni and Y. Moreno. “Discrete-time Markov chain approach to contact-based disease spreading in complex networks” EPL(Europhysics Letter), 2010.

[26] B. Hassibi, A. H. Sayed, and T. Kailath. “Indefinite-Quadratic Estimation and Control: A United Approach to H^2 and H^∞ Theories”. SIAM, 1999.

[27] S. Haykin. “Adaptive Filter Theory”. Academic Press, 2001.

[28] L. Huang, K. Park, and Y. C. Lai. “Information propagation on modular networks”. Phys. Rev. E, 2006.

[29] P. Jacquet, B. Mans, and G. Rodolakis. “Information propagation speed in mobile and delay tolerant networks”. IEEE Trans. on Info. Theory, 2010.

[30] T. Kailath, A. H. Sayed, and B. Hassibi. “Linear Estimation”. Prentice Hall, 2000.

[31] R. E. Kalman. “A new approach to linear filtering and prediction problems”. Transactions of the ASME - Journal of Basic Engineering on Automatic Control, 1960.

[32] S. Kar, B. Sinopoli, and J. M. F. Moura. “Kalman filtering with intermittent observations: Weak convergence to a stationary distribution”. Automatic Control, IEEE Transactions on, 2009.

[33] E. Kenah and James M. Robins. “Second look at the spread of epidemics on networks”. Physical Review E (Statistical, Nonlinear, and Soft Matter Physics), 2007.

[34] D. G. Kendall. “On the generalized birth-and-death process”. Annals of Mathematical Statistics 19, 1948.

[35] W.O. Kermack and A.G. McKendrick. “A contribution to the mathematical theory of epidemics”. Proc. Roy. Soc. Lond. A, 1927.

[36] M. Krivelevich and B. Sudakov. “The Largest Eigenvalue of Sparse Random Graphs”. Combinatorics, Probability and Computing, 2003.

[37] P. Lancaster and L. Rodman. “Algebraic Riccati Equations”. Oxford University Press, 1995.

[38] D. A. Levin, Y. Peres and E. L. Wilmer. “Markov Chains and Mixing Times” Amer. Math. Soc., Providence, RI. 2008.

[39] T. M. Liggett. “Interacting Particle Systems”. Springer, New York, 1985.

[40] N. Madar, T. Kalisky, R. Cohen, D. Ben-Avraham and S. Havlin. “Immunization and epidemic dynamics in complex networks” The European Physical Journal B - Condensed Matter and Complex Systems, 2004.

[41] N. Martins, M. Daleh, and N. Elia. “Feedback stabilization of uncertain systems in the presence of a direct link”. IEEE Transactions on Automatic Control, 2006.

[42] V. Mieghem, P. Omic and J. Kooij. “Virus spread in networks” IEEE/ACM Trans Network, 2009.

[43] J. Miller and J. Hyman. “Effective vaccination strategies for realistic social networks”. Physica A: Statistical Mechanics and its Applications, 2007.

[44] P. Minero, M. Franceschetti, S. Dey, and G. Nair. “Data rate theorem for stabilization over time-varying feedback channels”. IEEE Transactions on Automatic Control, 2009.

[45] C. Moore and M. E. J. Newman. “Epidemics and percolation in small-world networks”. Physical Review E, 2000.

[46] R.J. Muirhead. “Aspects of Multivariate Statistical Theory”. John Wiley and Sons, New York, 1982.

[47] M. E. J. Newman. “Spread of epidemic disease on networks”. Physical Review E, 2002.

[48] N. R. Ortega, F. S. Santos, D. M. Zanetta, and E. Massad. “A fuzzy reed-frost model for epidemic spreading”. Bull. Math. Biol. 2008.

[49] R. Pastor-Satorras and A. Vespignani. “Epidemic dynamics and endemic states in complex networks”. Physical Review E 63, 2001.

[50] R. Pastor-Satorras and A. Vespignani. “Epidemic spreading in scale-free networks” Physical Review E 86, 2001.

[51] C. Penga, X. Jina and M. Shic. “Epidemic threshold and immunization on generalized networks” Physica A: Statistical Mechanics and its Applications, 2010.

[52] M. Penrose. ”Random Geometric Graph”. Oxford University Press, 2003.

[53] J. Phelps, R. Lewis, L. Mobilio, D. Perry, and N. Raman. “Viral marketing or electronic word-of-mouth advertising: Examining consumer responses and motivations to pass along email”. Journal of Advertising Research, 2004.

[54] K. Plarre and F. Bullo. “On Kalman Filtering for Detectable Systems with Intermittent Observations”. IEEE Transactions on Automatic Control, 2009.

[55] M. Richardson and P. Domingos. “Mining knowledge-sharing sites for viral marketing”. Proc. 8th ACM SIGKDD, 2002.

[56] F. D. Sahneh and C. Scoglio. “Epidemic Spread in Human Networks”. Decision and Control and European Control Conference (CDC-ECC), 2011.

[57] A. H. Sayed. “Fundamentals of Adaptive Filtering”. Wiley-IEEE, 2003.

[58] A. H. Sayed and T. Kailath. “A state-space approach to adaptive RLS filtering”. Signal Processing Magazine IEEE, 1994.

[59] B. Sinopoli, L. Schenato, M. Franceschetti, K. Poolla, M. Jordan, and S. Sastry. “Kalman filtering with intermittent observations”. IEEE Transactions of Automatic Control, 2004.

[60] A. Vakili and B. Hassibi. “A Stieltjes transform approach for analyzing the RLS adaptive filter”. In Proceedings of 46th annual Allerton Conference on Communication, Control and Computing, 2008.

[61] A. Vakili and B. Hassibi. “On the eigendistribution of the steady-state error covariance matrix for the extended RLS algorithm”. In Proceedings of 34th International Conference on Acoustics, Speech, and Signal Processing, 2009.

[62] Y. Wang, D. Chakrabarti, C. Wang and C. Faloutsos. “Epidemic spreading in real networks: An eigenvalue viewpoint” Proc. Symp. Reliable Dist. Systems, 2003.

[63] Y. Wang and L. Guo. “On stability of random Riccati equations”. Science in China Series E: Technological Sciences, 1999.

[64] D. J. Watts and S. H. Strogatz. “Collective dynamics of small-world networks”. Nature, 1998.

[65] B. Widrow and M. E. Hoff. “Adaptve switching circuits”. In IRE WESCON Convention Record, 1960.