On the Mixing Time of the SIS Markov Chain Model for Epidemic Spread
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Abstract— In this paper we study the mixing time of the Markov chain model for epidemic spread over a given complex network. Each node is either susceptible (healthy) or infected at any given time. In this setting the state of the system is one of \(2^n\) where \(n\) is the number of nodes. The Markov chain has a unique stationary distribution where all nodes are healthy with probability 1, and all initial probability distributions converge to the stationary distribution. In other words, epidemic eventually dies out after long enough time passes. Since the number of states, \(2^n\), increases exponentially as the number of nodes, \(n\), increases, it is difficult to analyze this model. We study the relationship between the Markov chain model and \(n\)-dimensional nonlinear dynamical system which approximates the evolution of the marginal probability that each node is infected. Our main result shows that this approximated model gives an upper bound on the true marginal probability as given by the Markov chain model. As an application of this, we show that when the origin, the all-healthy-state in the \(n\)-dimensional system, is globally stable then the Markov chain mixes fast, i.e. has an \(O(\log n)\) mixing time. We farther show that the linear system obtained from linearizing around the origin also provides the same upper bound on the mixing time. For this, we give an alternative proof using linear programming.

I. INTRODUCTION
Epidemic spread has 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 has a key role to prevent spread of the disease. Researchers have focused on various aspect of this problem such as immunization and minimizing the social cost [3], [9].

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-discrete-space can be understood as a differential equation defined on \([0,1]^n\) where \(n\) is the number of nodes [11], [12]. 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 [5], [6], [10]. 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 [2] 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 [4], [15]. Ahn et al. studied the dynamics of epidemic spread for a general networks [1]. Discrete-time-discrete-space is the Markov chain model defined on \(2^n\) states.

The nonlinear model proposed by Chakrabarti et al. and Wang et al. describes the dynamics of epidemics only with infection rate, recovery rate and the network topology [4], [15]. The nonlinear model is based on a Markov chain model which is hard to analyze because the size of the transition matrix, \(2^n\) grows exponentially as the number of nodes, \(n\) grows. Instead of probability distribution, the nonlinear model focuses on the marginal probability of infection for each node being infected at each time step. Chakrabarti et al.’s work suggests the epidemic threshold. Ganesh et al. studied continuous time version of the epidemic spread model [6]. Their work shows that the exponential decay condition of the nonlinear model is also a sufficient condition for a logarithmic fast recovery in continuous-time Markov chain model. The work also suggests sufficient conditions of exponentially slow recovery depending on the graph topology. This paper contributes to the understanding of the relation between the nonlinear model and the discrete-time Markov chain model. This paper shows that the nonlinear model gives an upper bound of the probability for epidemic survival in the discrete-time Markov chain model. By applying the upper bound, this paper also shows that the exponential decay condition in the nonlinear model guarantees the logarithmic fast recovery in discrete-time Markov chain model.

In the following section, we review both the Markov
chain model and the nonlinear model which focuses on the marginal probability of each node being infected. We prove that the nonlinear model 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 nonlinear model offers an upper bound on the transition matrix an order-preserving map. With that, we show that the nonlinear model offers an upper bound on the probability that the system is not in the absorbing state. To summarize this, the nonlinear model offers an upper bound on the probability that the system is not in the absorbing state. To summarize this, the nonlinear model offers an upper bound on the probability that the system is not in the absorbing state.

II. 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 and undirected 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, $\xi(t) = (\xi_1(t), \ldots, \xi_n(t)) \in \{0, 1\}^n$ 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 $X, Y \in \{0, 1\}^n$,

$$\mathbb{P}[\xi(t+1) = Y | \xi(t) = X] = \prod_{i=1}^{n} \mathbb{P}[^{\xi_i(t+1)} = Y_i | \xi_i(t) = X_i]$$ (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 $\beta$. An infected node becomes healthy if it is recovered from disease with probability $\beta$ and is not infected from any of its neighbors. To summarize this,

$$\mathbb{P}[\xi_i(t+1) = Y_i | \xi_i(t) = X_i] = \begin{cases} (1-\beta)^m_i & \text{if } (X_i, Y_i) = (0, 0), |N_i \cap S(X)| = m_i, \\ 1 - (1-\beta)^m_i & \text{if } (X_i, Y_i) = (0, 1), |N_i \cap S(X)| = m_i, \\ 1 - \delta(1-\beta)^m_i & \text{if } (X_i, Y_i) = (1, 0), |N_i \cap S(X)| = m_i, \\ 1 - \delta(1-\beta)^m_i & \text{if } (X_i, Y_i) = (1, 1), |N_i \cap S(X)| = m_i, \end{cases}$$ (2)

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

Let $S$ be the transition matrix of this Markov Chain, $S_{X \to Y} = \mathbb{P}[\xi(t+1) = Y | \xi(t) = X]$. We assume that the Markov chain is time-homogeneous and write $S_{X \to Y} = \mathbb{P}[Y|X]$ for simplicity. The Markov chain has an absorbing state where all the nodes are healthy. 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.

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. $p_i(t) = \mathbb{P}[i \in I(t)]$.

$$p_i(t+1) = \mathbb{P}[i \in I(t+1)|i \in I(t)] \times p_i(t) + \mathbb{P}[i \notin I(t+1)|i \notin I(t)] \times (1 - p_i(t))$$ (3)

$$= (1 - \delta)(1 - \beta)^m_i p_i(t) + (1 - (1 - \beta)^m_i)(1 - p_i(t))$$

where $m_i = |N_i \cap I(t)|$

$$= \left(1 - \delta \left( \prod_{j \in N_i} 1 - \beta I_{I(t)}(j) \right) \right) p_i(t) + \left(1 - \prod_{j \in N_i} 1 - \beta I_{I(t)}(j) \right)(1 - p_i(t))$$ (5)

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

$$P_i(t+1) = \left(1 - \delta \left( \prod_{j \in N_i} 1 - \beta P_j(t) \right) \right) P_i(t) + \left(1 - \prod_{j \in N_i} 1 - \beta P_j(t) \right)(1 - P_i(t))$$ (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 computationally-demanding than $2^n$-dimensional discrete space. One of them was the nonlinear model studied by Chakrabarti and Wang [4], [15]. Ahn viewed the $n$-dimensional probability distribution at time $t + 1$ as image of the probability distribution at time $t$ mapped by $\Phi : [0, 1]^n \rightarrow [0, 1]^n$ [1]. The $i$-th component of the epidemic map, $\Phi_i$ is defined as follows:

$$\Phi_i(x) = (1 - \delta)x_i + (1 - (1 - \beta)x_i) \left(1 - \prod_{j \in N_i} (1 - \beta x_j) \right)$$ (7)

It is trivial to check that $P_i(t+1) = \Phi_i((P_i(t), \ldots, P_n(t))^T)$ in (6).

III. Partial Order

The mixing time of a Markov chain is defined as follows [8]:

$$t_{mix}(\varepsilon) = \min \{ t : \sup_{\mu} \left\| \mu S^t - \pi \right\|_1 \leq \varepsilon \}$$ (8)

$\mu$ is any initial probability distribution defined on the state space and $\pi$ is the stationary distribution in (8). 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 \(\mu\) which gives the supremum of \(\|\mu S - \pi\|_{TV}\) in (8).

For two vectors \(X, Z\), \(X \preceq Z\) means that \(X_i \leq Z_i\) for all \(i\). We define \(\preceq_p\) on the set of probability vectors of \(\{0,1\}^n\) as follows.

\[
\mu \preceq_p \mu' \text{ iff } \sum_{X \preceq Z} \mu_X \geq \sum_{X \preceq Z} \mu'_X \quad \forall Z \in \{0,1\}^n \quad (9)
\]

The reader may note that \(\sum_{X \preceq Z} \mu_X\) represents the probability that each node of \(S(Z)\) is healthy. \(\mu \preceq_p \mu'\) means that the probability of some nodes being healthy is higher under \(\mu\) than under \(\mu'\), for any set of nodes. It is trivial to check that \(\preceq_p\) is a well-defined partial order. The \(X\)-th unit vector, denoted by \(e_X \in \mathbb{R}^n\), is the probability vector all of whose components are zero, except the \(X\)-th component. Denote \(\overline{0}, \overline{1} \in \{0,1\}^n\) as the state where everyone is healthy or infected, respectively. It’s obvious that \(e_{\overline{1}}\) is the greatest element and \(e_{\overline{0}}\) is the least element under \(\preceq_p\). Since 0, the all-healthy-state is an absorbing state of \(G\), \(e_{\overline{0}}\) which corresponds to all nodes being healthy with probability 1 is a unique stationary distribution.

\(\preceq_p\) is nice because it makes \(S\) an order-preserving map i.e. \(\mu \preceq_p \mu'\) implies \(\mu S \preceq_p \mu' S\). To prove this claim, we need an intermediate result.

**Lemma 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

\[
R_{X,Y} = \begin{cases} 
1 & \text{if } X \preceq Y, \\
0 & \text{otherwise}
\end{cases} \quad (10)
\]

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

\[
R'_{X,Y} = \begin{cases} 
(-1)^{|S(X)\cap S(Y)|} & \text{if } X \preceq Y, \\
0 & \text{otherwise}
\end{cases} \quad (11)
\]

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

\[
(R')_{X,Y} = \sum_Z R_{X,Z} R'_{Z,Y} = \sum_{X \preceq Y} 1_{S(Z)\cap S(Y)}(-1)^{|S(Z)\cap S(Y)|} = (1 - 1)^{|S(Y)\cap S(X)|} \quad (12)
\]

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

\[
(R^{-1}SR)_{X,Z} = \sum_{Y \preceq Z} (R^{-1})_{X,Y} R_{Y,Z} S_{Z,W} \\
= \sum_{Y \preceq Z} \sum_{W \preceq Z} (-1)^{|S(W - X)|} S_{W,Y} \quad (13)
\]

\[
= \sum_{W \preceq X} (-1)^{|S(W - X)|} \sum_{W \preceq Z} S_{W,Y} = \sum_{W \preceq X} (-1)^{|S(W - X)|} \prod_{i \in S(Z)} [\mathbb{P}[\xi_i(t + 1) = 0 | \xi_i(t) = W]] \quad (14)
\]

\[
= \sum_{W \preceq X} (-1)^{|S(W - X)|} \delta_{|S(W)| = |S(Z)|} (1 - \beta) \sum_{\nu \in S(Z)} |\nu|^{R_{SR}} \quad (15)
\]

By some algebra.

\[
\delta^{S(X)\cap S(Z)} (1 - \beta) - \sum_{\nu \in S(X)} |\nu|^{R_{SR}} (R^{-1}SR)_{X,Z} = \sum_{W \preceq X} (-1)^{|S(W - X)|} \delta^{|S(W)| = |S(Z)|} (1 - \beta) \sum_{\nu \in S(W - X)} |\nu|^{R_{SR}} \quad (16)
\]

\[
= \prod_{i \in S(Z)} \left(1 - (1 - \beta) |\nu_i|^{R_{SR}} \delta_1 \right) \quad (17)
\]

Define \(-X = \overline{1} - X\). Then, we simplify \((R^{-1}SR)_{X,Z}\) using \(-X\) and \(-Z\).

\[
(R^{-1}SR)_{X,Z} = \mathbb{P}[\xi(t + 1) = -X | \xi(t) = -Z] \geq 0 \quad (18)
\]

Now to the claim.

**Lemma 3.2:** If \(\mu \succeq_p \mu'\), then \(\mu S \succeq_p \mu' S\).

**Proof:** By the definition of \(\mu \succeq_p \mu'\),

\[
((\mu - \mu')R)_{Y} = \sum_{X} (\mu - \mu')_{X} R_{X,Y} = \sum_{X \preceq Y} (\mu - \mu')_{X} \geq 0 \quad (23)
\]

\((\mu - \mu')R)_{Y} = 0\) if \(Y = \overline{1} = (1,1,\ldots,1)\) because both of \(\mu\) and \(\mu'\) are probability vectors whose 1-norm is 1.

Define a row vector \(v \in \mathbb{R}^{\{0,1\}^n}\) whose \(Y\)-th element is defined by \(v_Y = (\mu - \mu')R_Y\). \(v_Y \geq 0\) for all \(Y \in \{0,1\}^n\) by (23). \(v\) is a non-negative row vector, and \(v_{\overline{1}} = 0\). \(\mu - \mu' = vR^{-1}\). We can understand \(\mu - \mu'\) as a conical combination of all row vectors of \(R^{-1}\) but the \(1\)-th row vector. (23) also implies that \(\mu \succeq_p \mu'\) if and only if \((\mu - \mu')R\) is a vector all of whose entries are non-negative.

\(\mu S \succeq_p \mu' S\) if and only if \((\mu - \mu')SR\) is a non-negative vector. \(\mu - \mu' = vR^{-1}\) for non-negative \(v\) since \(\mu \succeq_p \mu'\). \((\mu - \mu')SR = vR^{-1}SR\) is non-negative since \(v\) is non-negative and \(R^{-1}SR\) is a matrix all of whose entries are non-negative by Lemma 3.1.

By Lemma 3.2, \(\sum_{\nu \in S(X)} (\mu S)_\nu = (\mu S)_{\overline{0}} = (e_1S)_{\overline{0}} \geq \sum_{\nu \in S(X)} (e_1S)_\nu\) for any probability vector \(\mu\) since \(\mu \succeq_p e_1\). Returning to the mixing time (8),

\[
\|\mu S - \pi\|_{TV} = \|\mu S - e_0\|_{TV} = 1 - (\mu S)_{\overline{0}} \quad (24)
\]

\[
\leq 1 - (e_1S)_{\overline{0}} = 1 - e_1S e_0^T \quad (25)
\]
Using the inequality above, we can now write
\[
t_{\text{mix}}(\varepsilon) = \min\{t : \sup_\mu \|\mu S^t - \pi\|_{TV} \leq \varepsilon\} \tag{26}
\]
\[
= \min\{t : 1 - e_1 S^T e_0 \leq \varepsilon\} \tag{27}
\]
\[
= \min\{t : e_1 S^T e_0 \geq 1 - \varepsilon\} \tag{28}
\]

IV. UPPER BOUND ON THE MIXING TIME

In this section, we prove that epidemic map \(\Phi(\cdot)\) defined as (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 \(e_1 S e_0^T\) to get an upper bound of \(t_{\text{mix}}(\varepsilon)\). Define a \(2^n\)-dimensional column vector \(u(r)\) for a given \(n\)-dimensional \(r = (r_1, \ldots, r_n)^T\) by \(u(r)_X = \prod_{i \in S(x)} (1 - r_i)\). We want to find an \(r' \in \mathbb{R}^n\) satisfying \(Su(r) \geq u(r')\).

Lemma 4.1: \(Su(r) \geq u(\Phi(r))\) for all \(r \in [0, 1]^n\).

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

\[
(Su(r))_X = \sum_{Y \in \{0, 1\}^n} S_{X,Y} u(r)_Y \tag{29}
\]
\[
= \sum_{Y \in \{0, 1\}^n} \left(\prod_{i \in S(Y)} (1 - r_i)\right) \left(\prod_{j \in S(Y)} \mathbb{P}[Y_j = 0|X] \right) \tag{30}
\]
\[
= \prod_{i = 1}^n (1 - r_i)\mathbb{P}[Y_i = 1|X] = \mathbb{P}[Y_i = 0|X] \tag{31}
\]
Assume \(S(X) \cap S(Z) = \emptyset\) 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:

\[
\mathbb{P}[Y_k = 0|X + Z] = \mathbb{P}[Y_k = 0|X]\mathbb{P}[Y_k = 0|Z] \tag{33}
\]

For simplicity, we call \(q_{i_k} X = \mathbb{P}[Y_k = 0|X]\).

\[
(Su(r))_{X+Z} = \prod_{i = 1}^n (1 - r_i)\mathbb{P}[Y_i = 1|X + Z] + \mathbb{P}[Y_i = 0|X + Z] \tag{34}
\]
\[
= \prod_{i = 1}^n (1 - r_i)\mathbb{P}[Y_i = 1|X] + \mathbb{P}[Y_i = 0|X + Z] \tag{35}
\]
\[
= \prod_{i = 1}^n (1 - r_i)(1 - q_{i_k} X) + q_{i_k} X \tag{36}
\]
\[
= \prod_{i = 1}^n (1 - r_i)(1 - q_{i_k} X) + q_{i_k} X \tag{37}
\]
\[
\geq \prod_{i = 1}^n ((1 - r_i)(1 - q_{i_k} X))((1 - r_i)(1 - q_{i_k} Z) + q_{i_k} Z) \tag{38}
\]
\[
= (Su(r))_X (Su(r))_Z \tag{39}
\]
(38) holds by the following one for \(a, b, c \in [0, 1]\):

\[
(c(1 - ab) + ab) - (c(1 - a) + a)(c(1 - b) + b) = c(1 - c)(1 - a)(1 - b) \geq 0 \tag{40}
\]

Define \(i \in \{0, 1\}^n\) as the state where everyone is healthy but \(i\). The following inequality holds by (39).

\[
(Su(r))_X \geq \prod_{i \in S(X)} (Su_i(r)) \tag{41}
\]
\[
= \prod_{i \in S(X)} \prod_{j = 1}^n (1 - r_j + \mathbb{P}[Y_j = 0|\hat{i}]) \tag{42}
\]
\[
= \prod_{i \in S(X)} ((1 - r_i)(1 - \delta) + \delta \sum_{j = 1}^n (1 - r_j)\beta + 1 - \beta) \tag{43}
\]
\[
= \prod_{i \in S(X)} (1 - (1 - \delta) r_i) \prod_{j = 1}^n (1 - \beta r_j) \tag{44}
\]
\[
= \prod_{i \in S(X)} 1 - \Phi_i(r) \tag{45}
\]
\[
= u(\Phi(r))_X \tag{46}
\]

It’s obvious that \(e_1^T = u((1, 1, \ldots, 1)^T) = u(1_n)\). We distinguish \(1_n = (1, 1, \ldots, 1)^T \in [0, 1]^n\) from \(\hat{i} \in \{0, 1\}^n\) which is a state of infection. Since \(Su(r) \geq u(\Phi(r))\) by Lemma 4.1, and \(S\) is a matrix all of whose entries are non-negative,

\[
S e_0^T = S u(1_n) \geq u(\Phi(1_n)) \tag{47}
\]

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.

\[
\Phi_i(x) = (1 - \delta)x_i + (1 - (1 - \delta)x_i) \left(1 - \prod_{j = i}^n (1 - \beta x_j)\right) \tag{48}
\]
\[
\leq (1 - \delta)x_i + \left(1 - \prod_{j = i}^n (1 - \beta x_j)\right) \tag{49}
\]
\[
\leq (1 - \delta)x_i + \beta \left(\sum_{j \in N_i} x_j\right) = (Mx)_i \tag{50}
\]

We get an upper bound of \(\Phi\) with \(M. \Phi(\cdot) \leq Mx\). We can now give a practical result about mixing time under the condition that \(M\) is stable i.e. the spectral radius of \(M\) is less than 1.

Theorem 4.2: \(t_{\text{mix}}(\varepsilon) = O(\log n)\) if \(\|M\| < 1\).

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

\[
1 - \varepsilon \geq e_1 S e_0^T \tag{51}
\]
\[
\geq e_1 u(\Phi(1_n)) = \prod_{i = 1}^n (1 - \Phi_i(1_n)) \tag{52}
\]
\[
\geq 1 - \sum_{j = 1}^n \Phi_j(1_n) \tag{53}
\]
\[
\geq 1 - \frac{1}{n} \sum_{j = 1}^n (\Phi_j(1_n))^2 = 1 - \sqrt{n\|\Phi(1_n)\|} \tag{54}
\]
\[
\geq 1 - \sqrt{n\|M\|^\|1_n\|} \tag{55}
\]
\[
\geq 1 - \sqrt{n\|M\|^\|1_n\|} = 1 - n\|M\| \tag{56}
\]
\[
t \leq \frac{\log \frac{n}{\varepsilon}}{-\log\|M\|} \text{ for every } t \leq t_{\text{mix}}(\varepsilon) \text{ leads that } t_{\text{mix}}(\varepsilon) \leq \frac{\log \frac{n}{\varepsilon}}{-\log\|M\|}. \text{ The mixing time is } O(\log n). \tag{57}
\]
If $\|M\| > 1$, $\Phi^\tau(1n)$ converges to $x^*$, the unique nontrivial fixed point of $\Phi$ which is strictly greater than the origin as stated in [1]. The reason why this happen, even though the original Markov chain model always converges to the “all-healthy” state, is that the $i$-th component of $\Phi^\tau(1n)$ 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, $e_iS^\tau t e_0^\tau \geq e_i\mu(\Phi^\tau(1n)) = 1 - \Phi^\tau(1n)$ by (47),

$$
\Phi^\tau(1n) \geq 1 - e_iS^\tau t e_0^\tau = 1 - P[\xi(t) = 0 | \xi(0) = \hat{i}]
$$

In other words, if the origin is globally stable in the epidemic map $\Phi$, 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.

V. ALTERNATIVE PROOF USING LP

Our earlier result showed that the epidemic map $\Phi^\tau(\cdot)$ 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.

Denote $\mu(t) \in \mathbb{R}^n$ 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.

$$ p_i(t) = \sum_{X_k \in \{0, 1\}^n} \mu_X(t). $$

Write $p_0(t) = 1$ which represents sum of probability distribution i.e.

$$ p_0(t) = 1 = \sum_{X_k \in \{0, 1\}^n} \mu_X(t). $$

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.

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.

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

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.

\textbf{Lemma 5.1:} $p_i(t+1) \leq (1 - \delta)p_i(t) + \beta \sum_{j \in N_i} p_j(t)$

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

$$ \max_{\mu B = p^T, \mu \geq 0} p_i(t+1) = \max_{\mu B = p^T, \mu \geq 0} \mu SBf_i 
$$

$$ = \max_{\mu \geq 0} \min_{\lambda} \mu SBf_i - (\mu B - p^T)\lambda 
$$

$$ = \min_{\lambda} \max_{\mu \geq 0} \mu (SBf_i - B\lambda) + p^T\lambda 
$$

Therefore $\lambda^*$ is in feasible set.

$$ \max_{\mu B = p^T, \mu \geq 0} p_i(t+1) = \min_{\lambda \mu \geq 0} \mu SBf_i + p^T\lambda 
$$

By applying Lemma 5.1 to each node, $p(t+1) \leq ((1 - \delta)I_n + \beta A)p(t) = Mp(t)$

We also get the practical result that the mixing time is $O(\log n)$ by modifying Theorem 4.2.

VI. 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. To summarize this,
\[
\mathbb{P}[\xi(t+1) = Y|\xi(t) = X] = \begin{cases} 
1 - (1-\beta)^{m_i} & \text{if } (X,Y) = (0,0), |N_i \cap S(X)| = m_i, \\
1 - (1-\beta)^{m_k} & \text{if } (X,Y) = (0,1), |N_i \cap S(X)| = m_i, \\
\delta & \text{if } (X,Y) = (1,0), \\
1 - \delta & \text{if } (X,Y) = (1,1). 
\end{cases}
\]
(72)

Transition matrix is defined in a similar way. In this model which is described as (72), the probability that a node becomes healthy from infected is \(\delta\) which is larger than \(\delta(1-\beta)^{m_i}\), the probability for immune-not-admitting model which is described as (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 give just sketch of the proof because most of the formal proof is very similar to the one for immune-not-admitting model. It can be proven using linear programming as in the previous section. The only difference is (64), which is written as follows:
\[
\mathbb{P}[Y_i = 1|X] = \begin{cases} 
1 - (1-\beta)^{m_i} & \text{if } X_i = 0, \\
1 - \delta & \text{if } X_i = 1. 
\end{cases}
\]
(73)

It is trivial to check that \(\lambda^* = (\lambda^*_0, \lambda^*_1, \ldots, \lambda^*_n)^T\) defined by \(\lambda^*_0 = 0, \lambda^*_j = 1 - \delta, \lambda^*_j = \beta\) for \(j \in N_i\) and \(\lambda^*_j = 0\) for \(j \notin N_i\) is also in feasible set for immune-admitting model. The system matrix, \(M = (1-\delta)I_n + \beta A\) is the same here, and we get the upper bound of mixing time.

VII. SIMULATION RESULTS

We compare two simulation results. Epidemics dies out in the first case as \((1-\delta) + \beta|A| < 1\). In the second case epidemic spreads as \((1-\delta) + \beta|A| > 1\).

Fig. 1 and Fig. 2 show the simulation results of epidemic spread on Erdős-Rényi graphs with \(n = 2000\) nodes. After generating an Erdős-Rényi graph we set \(\beta\) and \(\delta\) to satisfy given condition. 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 dying-out of epidemics by Theorem 4.2. Fig. 1 shows that the number of infected nodes decays fast as \(\frac{\beta|A|}{\delta} = 0.999 < 1\). \(\frac{\beta|A|}{\delta} > 1\) is necessary condition for epidemic spread. Fig. 2 shows that the number of infected nodes does not decay fast i.e. epidemic spreads as \(\frac{\beta|A|}{\delta} = 1.009 > 1\). 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 4.2 and the epidemic dies out at an exponential rate. However, when it is larger than one the epidemic persists and does not die out in any reasonable time.

VIII. CONCLUSIONS

In this paper we have studied when the epidemic die out fast by analyzing the discrete-time Markov chain model based on the classical SIS model. We have reviewed the nonlinear model proposed by Chakrabarti et al. [4] and have studied how it is related to the discrete-time Markov chain model. The nonlinear model is not only an approximation of the discrete-time Markov chain model but an upper bound when the marginal probability from the nonlinear model is compared to the probability for epidemic survival in the discrete-time Markov chain model. By applying this result, we get a practical result that the mixing time of the discrete-time Markov chain model is logarithmically fast in the size of a given network. The figures in the section VII representing simulation result suggests that the condition is tight.

Ganesh et al.’s work shows that the tightness of necessary and sufficient conditions in the continuous-time Markov chain depends on the network topology. It suggests the directions of study on the epidemic model. Mixing time
depending on the network topology is an interesting problem of the discrete-time Markov chain model. Especially, a sufficient condition of exponentially slow mixing time attracts attention. A newly envisioned direction is modeling the epidemic spread on time-varying networks. Both the Markov chain model and the nonlinear model are based on the fixed network topology. Time-varying network problem would be useful to the study on the real human network where weekdays and weekend have different networks.

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