Second-order moment-closure for tighter epidemic thresholds

Masaki Ogura [a],*, Victor M. Preciado [b]

[a] Graduate School of Information Science, Nara Institute of Science and Technology, Ikoma, Nara 630-0192, Japan
[b] Department of Electrical and Systems Engineering, University of Pennsylvania, Philadelphia, PA 19104-6314, USA

ABSTRACT

In this paper, we study the dynamics of contagious spreading processes taking place in complex contact networks. We specifically present a lower-bound on the decay rate of the number of nodes infected by a susceptible–infected–susceptible (SIS) stochastic spreading process. A precise quantification of this decay rate is crucial for designing efficient strategies to contain epidemic outbreaks. However, existing lower-bounds on the decay rate based on first-order mean-field approximations are often accompanied by a large error resulting in inefficient containment strategies. To overcome this deficiency, we derive a lower-bound based on a second-order moment-closure of the stochastic SIS processes. The proposed second-order bound is theoretically guaranteed to be tighter than existing first-order bounds. We also present various numerical simulations to illustrate how our lower-bound drastically improves the performance of existing first-order lower-bounds in practical scenarios, resulting in more efficient strategies for epidemic containment.

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1. Introduction

Understanding the dynamics of spreading processes taking place in complex networks is one of the central questions in the field of network science, with applications in information propagation in social networks [1], epidemiology [2], and cyber-security [3]. Among various quantities characterizing the asymptotic behaviors of spreading processes, the *decay rate* (see, e.g., [4,5]) of the spreading size (i.e., the number of nodes affected by the spread) is of fundamental importance. Besides quantifying the impact of contagious spreading processes over networks [6,7], the decay rate has been used to measure the performance of containment strategies to control epidemic outbreaks [8]. In this direction, the authors in [9] presented an optimization-based approach for distributing a limited amount of resources to efficiently contain spreading processes by maximizing their decay rate towards the disease-free equilibrium. This framework was later extended to the cases where the underlying network in which the spreading process is taking place is uncertain [10], temporal [11,12], and adaptively changing [13,14]. Recently, the authors in [15] presented an approach for achieving an optimal resource allocation in order to maximize the decay rate under sparsity constraints.

However, finding the decay rate of a spreading process is, in general, a computationally hard problem. Even for the case of the susceptible–infected–susceptible (SIS) model [2], which is one of the simplest models of spread, the exact decay rate is given in terms of the eigenvalues of a matrix whose size grows *exponentially* fast with respect to the number of nodes in the networks [4]. In order to avoid this computational difficulty, it is common in the literature [9,10,15] to use a lower-bound on the decay rate based on first-order mean-field approximations of the spreading processes. However, this first-order approximation is not necessarily accurate; in other words, its approximation error can be significantly large for several important social and biological networks, as we will demonstrate later in this paper. Therefore, the design of strategies for epidemic containment based on mean-field approximations can result in inefficient control policies.

The aim of this paper is to present a tighter lower-bound on the decay rate of the stochastic SIS process based on a second-order moment closure. Specifically, we show that the decay rate is bounded from below by the maximum real eigenvalue of a Metzler matrix whose size grows quadratically with respect to the number of nodes in the network. In order to derive our lower-bound, we describe the stochastic dynamics of the SIS process using a system of stochastic differential equations with Poisson jumps. This approach allows us to conveniently evaluate the dynamics of the first and the *second*-order moments of random variables relevant for the spreading processes. Furthermore, we prove theoretically and illustrate numerically that our lower-bound strictly improves the one based on first-order approximations.

We remark that, although improved decay rates for the discrete-time SIS model were presented using second-order analysis in [16], their bounds are applicable only to the special case

where the transmission and recovery rates of nodes are homogeneous and, furthermore, satisfy restrictive algebraic conditions in terms of nonnegativity of infinitely many matrices. Likewise, the second-order analysis of the continuous-time SIS model by the authors in [17] uses mean-field approximations and, hence, it is not clear how the analysis relates to the dynamics of the original stochastic SIS process. Moreover, their analysis is valid only when a dominant eigenvalue of a certain matrix (i.e., an eigenvalue having the maximum real part) is real. In contrast with these limitations of the results in the literature, our framework applies to the heterogeneous SIS model without any restrictions, and is supported by rigorous proofs instead of approximations.

This paper is organized as follows. In Section 2, we state the problem studied in this paper. In Section 3, we present our lower-bound on the decay rate, and show that this bound strictly improves the one based on first-order approximations. The effectiveness of our lower-bound is numerically illustrated in Section 4.

1.1. Mathematical preliminaries

We denote the identity and the zero matrices by I and O, respectively. For a vector u, we denote by $u_{\setminus\{i\}}$ the vector that is obtained after removing the ith element from u. Likewise, for a matrix A, we let $A_{i,\setminus\{j\}}$ denote the row vector that is obtained after removing the jth element from the ith row of A. We say that a square matrix A is irreducible if no similarity transformation by a permutation matrix transforms A into a block upper-triangular matrix. The block-diagonal matrix containing matrices $A_1, \ldots, A_n$ as its diagonal blocks is denoted by $\bigoplus_{i=1}^{n} A_i$. If the matrices $A_1, \ldots, A_n$ have the same number of columns, then the matrix obtained by stacking $A_1, \ldots, A_n$ in vertical is denoted by $\mathrm{col}_{1 \leq i \leq n} A_i$.

A directed graph is defined as the pair $\mathcal{G} = (\mathcal{V}, \mathcal{E})$, where $\mathcal{V}$ is a finite ordered set of nodes and $\mathcal{E} \subset \mathcal{V} \times \mathcal{V}$ is a set of directed edges. By convention, if $(v, v') \in \mathcal{E}$, we understand that there is an edge from v pointing towards v', in which case v is said to be an in-neighbor of v'. A directed path from v to v' in $\mathcal{G}$ is an ordered set of nodes $(v_0, \ldots, v_\ell)$ such that $v_0 = v$, $v_\ell = v'$, and $(v_k, v_{k+1}) \in \mathcal{E}$ for $k = 0, \ldots, \ell - 1$. We say that $\mathcal{G}$ is strongly connected if there exists a directed path from v to v' for all $v, v' \in \mathcal{V}$. The adjacency matrix of $\mathcal{G}$ is defined as the square matrix, having the same dimension as the number of the nodes, such that its (i, j)th entry equals 1 if the jth node is an in-neighbor of the ith node, and equals 0 otherwise. It is well known that a directed graph is strongly connected if and only if its adjacency matrix is irreducible.

A real matrix A (or a vector as its special case) is said to be nonnegative, denoted by $A \geq 0$, if all the entries of A are nonnegative. Likewise, if all the entries of A are positive, then A is said to be positive. For another matrix B having the same dimensions as A, the notation $A \leq B$ implies $B - A \geq 0$. If $A \leq B$ and $A \neq B$, we write $A \lneq B$. For a square matrix A, we say that A is Metzler [18] if the off-diagonal entries of A are nonnegative. It is easy to see that $e^{At} \geq 0$ if A is Metzler and $t \geq 0$ (see, e.g., [18]). For a Metzler matrix A, the maximum real part of the eigenvalues of A is denoted by $\lambda_{\max}(A)$. In this paper, we use the following basic properties of Metzler matrices:

Lemma 1. *The following statements hold for a Metzler matrix A:*

1. *$\lambda_{\max}(A)$ is an eigenvalue of A. Moreover, if A is irreducible, then there exists a positive eigenvector corresponding to the eigenvalue $\lambda_{\max}(A)$.*
2. *If $A \leq B$, then $\lambda_{\max}(A) \leq \lambda_{\max}(B)$. Furthermore, if A is irreducible and $A \neq B$, then $\lambda_{\max}(A) < \lambda_{\max}(B)$.*
3. *Assume that A is irreducible. If there exist a positive vector u and a positive constant ρ such that $Au \lneq \rho u$, then $\lambda_{\max}(A) < \rho$.*

Proof. The first claim is part of the Perron–Frobenius theorem for Metzler matrices (see, e.g., [18, Theorems 11 and 17]). The second claim follows from the Perron–Frobenius theory and the monotonicity of the maximum real eigenvalue of nonnegative matrices [19, Section 8.4]. To prove the last statement, let $\epsilon = \rho u - Au$ and define $A' = A + \bigoplus(\epsilon_1/u_1, \ldots, \epsilon_n/u_n)$, where n is the length of the vector u. Since $A'u = Au + \epsilon = \rho u$, A' is irreducible, and v is positive, it follows that $\lambda_{\max}(A') = \rho$ from the Perron–Frobenius theorem for irreducible Metzler matrices [18, Theorem 17]. Since A is irreducible and $A \lneq A'$, the second statement of the lemma shows that $\lambda_{\max}(A) < \lambda_{\max}(A') = \rho$. $\square$

2. Problem statement

We start by giving a brief overview of the SIS model [2]. Let $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ be a strongly connected directed graph with nodes $v_1, \ldots, v_n$. In the SIS model, at a given (continuous) time $t \geq 0$, each node can be in one of two possible states: *susceptible* or *infected*. When a node v_i is infected, it can randomly transition to the susceptible state with an instantaneous rate $\delta_i > 0$, called the *recovery rate* of node v_i. On the other hand, if an in-neighbor of node v_i is in the infected state, then the in-neighbor can infect node v_i with an instantaneous rate β_i, where $\beta_i > 0$ is called the *infection rate* of node v_i. It is easy to see that the SIS model is a continuous-time Markov process and has a unique absorbing state at which all the nodes are susceptible. Since this absorbing state is reachable from any other state, the SIS model reaches this infection-free absorbing state in a finite time with probability one. The aim of this paper is to study the stability of this infection-free absorbing state, defined as follows:

Definition 2. Let $\epsilon > 0$ and define the probability

$p_i(t) = \mathrm{Pr}(v_i \text{ is infected at time } t)$.

We say that the SIS model is ϵ-*exponentially mean stable* if there exists a constant $C > 0$ such that, for all nodes v_i and $t \geq 0$, we have $p_i(t) \leq Ce^{-\epsilon t}$ for any set of initially infected nodes at time $t = 0$. Then, we define the *decay rate* of the SIS model as

$\rho = \sup\{\epsilon : \text{SIS model is } \epsilon\text{-exponentially stable}\}$.

The notion of the decay rate was studied in, e.g., [4] and [5] for the cases of continuous- and discrete-time problem settings, respectively, and is closely related to other important quantities on spreading processes such as epidemic thresholds [4] and mean-time-to-absorption [7]. Specifically, a basic argument from the theory of Markov processes shows that the SIS model is ϵ-exponentially mean stable for a sufficiently small $\epsilon > 0$ (with a possibly large C) and, therefore, it always has a positive decay rate. However, exact computation of the decay rate is hard in practice. Even in the homogeneous case, where all nodes share the same infection and recovery rates, the decay rate equals the modulus of the largest real-part of the non-zero eigenvalues of a $2^n \times 2^n$ matrix representing the infinitesimal generator of the SIS model [4]. An alternative approach for analyzing the decay rate is via upper bounds on the dynamics of the SIS model based on first-order mean-field approximations. An example of such a first-order upper bound is described below. Let us define the vector $p(t) = \mathrm{col}_{1 \leq i \leq n} p_i(t)$ containing the infection probabilities of the nodes. Also, let A be the adjacency matrix of $\mathcal{G}$ and define the diagonal matrices $B = \bigoplus(\beta_1, \ldots, \beta_n)$ and $D = \bigoplus(\delta_1, \ldots, \delta_n)$. Then, we can show [9] the inequality $p(t) \leq e^{(BA-D)t}p(0)$, which gives the following lower-bound on the decay rate:

$$\rho \geq \rho_1 = -\lambda_{\max}(BA - D). \tag{1}$$