

The infinitesimal generator of Markovian SIS epidemics on a graph

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Abstract

A brief description and motivation is given to study the large infinitesimal generator matrix of a Markov chain for SIS epidemics on a fixed graph.

1 Introduction

We consider epidemic spread in a contact graph G that represents a set \mathcal{N} of N individuals as nodes and specifies the L contacts between all pairs of individuals as links [4]. We assume that the graph G , characterized [6] by a symmetric adjacency matrix A , is fixed and does not change over time. Epidemic spread on a graph is one of the simplest, non-trivial diffusion processes in networks that not only models biological disease spread (e.g. Covid) and digital computer viruses and malware in the Internet, but also social contagion in on-line social platforms (e.g. Twitter and Facebook), rumor spread, cascades of failures in infrastructural networks as the Internet and power grids and brain anomalies such as epileptic seizures and other real-world diffusion applications in graphs.

The class of Susceptible-Infected-Susceptible (SIS) epidemics is the simplest compartmental model of a disease spread with re-infections in a population, in which individuals are either infectious (I) or healthy, but susceptible (S). Other compartmental models can be described, both stochastically and deterministically (after a mean-field approximation), similarly [5] as SIS epidemic.

2 Markovian SIS epidemics on a graph

The viral state of a node i at time t is specified by a Bernoulli random variable $X_i(t) \in \{0, 1\}$: $X_i(t) = 0$ for a healthy node and $X_i(t) = 1$ for an infected node. A node i at time t can be in one of the two states: *infected*, with probability $w_i(t) = \Pr[X_i(t) = 1]$ or *healthy*, with probability $1 - w_i(t)$, but susceptible to the virus. We assume that the curing process per node i is a Poisson process with rate δ and that the infection process per link is a Poisson process with rate β . The effective infection rate is $\tau = \frac{\beta}{\delta}$. Obviously, only when a node is infected, it can infect its direct neighbors, that are still healthy. Both the curing and infection Poisson process are independent. This is the general continuous-time description of the simplest type of a Susceptible-Infected-Susceptible (SIS)

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virus process on a network. Occasionally, a third, independent self-infection process with self-infection rate ε is considered, which describes background or indirect infections. Infections may happen either through direct contact or indirectly, for example, after touching infected surfaces or inhaling air in a closed room previously contaminated by an infected individual. The Markovian ε -SIS model consists of three, independent Poisson processes: (i) the curing process with rate δ , (ii) infection process with rate β and (iii) self-infection process with rate ε .

A description of the ε -SIS epidemic process is as follows. Let I denote the set of infected nodes in the graph G and let a_{ij} be the element of the adjacency matrix A . Then, the Markov transitions

$$\begin{cases} \text{for } j \notin I: & I \mapsto I \cup \{j\} & \text{at rate } \beta \sum_{k \in I} a_{kj} + \varepsilon \\ \text{for } i \in I: & I \mapsto I \setminus \{i\} & \text{at rate } \delta \end{cases} \quad (1)$$

detail the dynamics between the infected subgraph I and its complement $I^c = G \setminus I$.

The time-dependent ε -SIS process can be described as a continuous-time Markov chain with 2^N states [9],[8]. Computationally, enumerating the subgraphs I in G leads to the governing equation (2). Indeed, representing the Markov state i as $i = \sum_{k=1}^N x_k(i) 2^{k-1}$, where the binary k -th digit $x_k(i)$ represents the infectious state of a node k in the network, the time dependence of the probability state vector $s(t)$ in ε -SIS epidemics, with components

$$s_i(t) = \Pr[X_1(t) = x_1(i), X_2(t) = x_2(i), \dots, X_N(t) = x_N(i)]$$

and normalization $\sum_{i=0}^{2^N-1} s_i(t) = 1$, obeys the differential equation

$$\frac{ds(t)}{dt} = -Qs(t) \quad (2)$$

where the $2^N \times 2^N$ infinitesimal generator $-Q$ is specified in [9] and [8]. The solution of the matrix differential equation is

$$s(t) = e^{-Qt} s(0) \quad (3)$$

and, for self-infection rate $\varepsilon > 0$, a non-trivial¹ $2^N \times 1$ steady-state vector s_∞ exists, that obeys $Qs_\infty = 0$ and which is the right-eigenvector belonging to zero eigenvalue of Q . Exact analyses for the complete graph are presented in [1] and [7] and for the star in [2].

Although exact, the solution (3) is hardly computable for a large size N of the contact graph. However, all details about the phase transition of the ε -SIS process around the epidemic threshold² are embedded in the huge $2^N \times 2^N$ matrix Q , still waiting to be unraveled. Analogous to crystallization of matter from the liquid to the solid phase, understanding the formation of ‘‘epidemic cohesion’’ in a graph when sweeping the effective infection rate τ from below to above the epidemic threshold τ_c is a major motivation to compute the $2^N \times 1$ probability state vector $s(t)$ for large³ N .

¹If $\varepsilon = 0$, then the Markov graph possesses an absorbing state (i.e. the overall healthy state in which there is no virus anymore). That absorbing state is also the steady-state vector.

²The epidemic threshold lies approximately in a region of the effective infection rate $\tau \in (\frac{1}{\lambda_1}, \frac{1}{\lambda_1} + c)$, where λ_1 is the largest eigenvalue of the adjacency matrix A of the graph G and c is a yet unknown, positive real number.

³The larger the size N of the graph, the faster quantities change around the phase transition. When $N \rightarrow \infty$, a zero-one transition occurs at a single point, which defines the phase transition sharply. If N is finite, there is always an interval in which the transition happens.

3 Open problem

The $2^N \times 2^N$ infinitesimal generator matrix Q is minus a weighted Laplacian matrix. All Laplacian matrices on graphs are positive semi-definite, with a zero eigenvalue of multiplicity 1 if the graph is connected. Moreover, as shown in [9, Fig. 2 & 3] and [8, Fig. 2], the matrix Q contains structure and is sparse. Via nodal relabelling, which interchanges rows and columns in Q , an other structure may be found (see e.g. [3]). Commercial software such as Matlab and Mathematica are able to provide the solution (3) of the probability state vector roughly up to $N = 12$ (i.e. solving linear equations in matrices up to ca. 4000×4000).

Can we find a numerical computation method of the $2^N \times 1$ probability state vector $s(t)$ as a function of time t for graphs larger than $N = 12$ with about 3 digits accurate (i.e. the numerical computation $s_i^*(t)$ for all $1 \leq i \leq 2^N$ satisfies $|s_i(t) - s_i^*(t)| < 10^{-a}$ with $a = 3$)? What is the maximal size N of the contact graph for which the $2^N \times 1$ probability state vector $s(t)$ can be computed?

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