



# Epidemic spreading over quenched networks with local behavioral response



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## ABSTRACT

We discuss the impact of local information-based behavioral response on epidemic spreading in social networks. By using a pair quenched mean-field approach developed by Mata and Ferreira [Europhys. Lett. 103 (2013) 48003], we derive a dynamical model governing the epidemic spreading over a random network with a linear response function and density-dependent epidemic information. A deterministic relation between the epidemic threshold and the response parameter is derived according to a quasi-static approximation method. It is found that local behavioral response will induce the extinction of the disease via raising the epidemic threshold. Additionally, the theoretical result is supported by stochastic simulations on an Erdős–Rényi random network and a Barabási–Albert scale-free network. Simulations show that the pair quenched mean-field approach is more accurate than the classical quenched mean-field approach.

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## 1. Introduction

The theory of complex network involves the network itself (structure and its dynamics), dynamics on networks and coupled interactions between network and dynamics evolving over the network [1]. As a typical process occurring on the network [2], disease transmission dynamics have drawn a wide attention of researchers from mathematical, computer, physical and biological communities [3–6]. Recently, many researches focus on the coupled disease-behavior dynamics [7]. Generally speaking, individual behavioral response means that individual adjusts its adaptive behavior by changing contact numbers or contact objects [8,9], vaccination decision-Erdős–Rényimaking [10,11] and dynamical parameters [12–14].

In reality, the epidemic information (denoted by  $x$ ) can cause individuals to keep social distancing (by wearing protective masks, washing hands frequently, avoiding crowded public areas, or staying home from work or school or more creative precautions), which potentially results in the reduction of individual susceptibility (denoted by  $y$ ) [13,16]. For a node with  $k$  contact number and  $s$  infected neighbors, if the epidemic information obtained by a node is determined by the infection fraction in its neighborhood, then

$x = s/k$  and we say it is *density-dependent* [15–18]; if the information is only related to the number of infected neighbors, then  $x = s$  and it is *frequency-dependent* [19]. To incorporate the information effect into the transmission model, it is needed to define a response function  $y = \phi(x)$ , which satisfies  $\phi(0) = 0, 0 \leq \phi(x) \leq 1$ , and  $\phi'(x) < 0$ . It is relevant to investigate the effect of individual behavioral response on the epidemic spreading under the network framework with the spatial diffusion [20–22].

In [16], we studied the susceptible-infected-susceptible (SIS) model with a response function of linear form, i.e.,  $\phi(x) = 1 - \alpha x (1 \geq \alpha \geq 0)$ . Meanwhile, the epidemic information is density-dependent. By using the heterogeneous mean-field (HMF) approach, we obtained the epidemic threshold above which the epidemic spreads over the whole network, depending on the response parameter  $\alpha$ . Shang [17] analyzed the case of nonlinear form  $\phi(x) = 1 - \alpha (s/k)^m$  ( $m$  is a positive integer) and derived the epidemic threshold. Recently, Zhang et al. [19] proposed a response function of exponential form  $\phi(x) = (1 - \alpha)^x$  with the frequency-dependent epidemic information. Their theoretical analysis and simulations show that the epidemic threshold is strongly affected by individual response. So, the spread of an infectious disease over a network can be controlled by individual behavioral response. Compared to the immunization and quarantine, individual response is a very economic strategy.

All these researches are based on the HMF model, that has been shown to be exact only for the annealed network [23,24]. How to analyze this issue on the static or quenched network? [25] How to

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study the interplay between the network structure and the behavioral response?

For the SIS-type model, the microscopic Markov-chain (MMC) approach is frequently-used in the analysis of the epidemic spreading on the quenched network [26]. Van Mieghem et al. developed a continuous-time MMC approach and called it as the N-intertwined model [5], which is also referred to as the quenched mean-field (QMF) model [28]. Compared to the HMF modeling framework, the N-interwind model may be more adapted for the quenched network [24]. However, this model is not enough exact since it only applies one-order neighbor information. Therefore, a high-order mathematical formulation is required to provide a more exact threshold analysis [27]. Mata and Ferreira proposed a pair-type formulation of quenched mean-field model, referred to as the pair quenched mean-field model [28]. The pair QMF model makes use of the two-order neighbor information and gives a more exact prediction. More importantly, the epidemic threshold can be determined and analyzed by this model.

In the present work, we would like to give a rigorous derivation for the pair QMF model, and show that the pair QMF model is adapted for the static randomly connected network with no clustering [28]. In addition, we analyze the impact of local behavioral response on the epidemic spreading over the static network by using the pair QMF model, which is still challenging for us since it involves the relation between the contact structure and local behavioral response.

## 2. An analysis framework

We assume that an infectious disease follows SIS dynamics on a given network with a size  $N$ , denoted by  $G = (V, E)$ . Generally, the contact network is weighted [29] or directed [30]. For simplicity, we assume that  $G$  is a unweighted and undirected network and hence it is completely determined by its adjacency matrix  $A = (a_{ij})$ : if node  $i$  links to node  $j$  in  $G$ , then  $a_{ij} = 1$ ; otherwise  $a_{ij} = 0$ .

In this model, each node may stay in either susceptible (S) or infected (I) state. During a infinitesimal time interval  $(t, t + \Delta t)$ , an infected node transmits the infectious disease to its susceptible neighbor with probability  $\beta \Delta t$  and meanwhile, it recovers and becomes susceptible again with probability  $\gamma \Delta t$ . As usual, we define  $\lambda = \beta/\gamma$  be the effective spreading rate [4,25].

The mathematical model for the static contact network can be built by the microscopic Markov-chain approach [26,31]. This approach focuses on the dynamic of the probability of each node  $i$  to be infected at time  $t$ , denoted by  $\rho_i$ . Let  $X_i(t) \in \{0, 1\}$  denote the state of node  $i$  at time  $t$  [5]. If  $X_i(t) = 0$ , node  $i$  is susceptible; if  $X_i(t) = 1$ , node  $i$  is infectious. Then  $\rho_i = \mathbb{P}[X_i(t) = 1]$  and  $1 - \rho_i = \mathbb{P}[X_i(t) = 0]$ , where  $\mathbb{P}[A]$  represents the probability of event  $A$  occurring.

### 2.1. The pair quenched mean-field model

Mata and Ferreira [28] proposed a pair-type formulation of quenched mean-field model, i.e., the pair QMF model. In order to develop the pair QMF theory, they introduced a series of simple notations:  $[A_i] = \mathbb{P}[X_i(t) = A]$ , which is the probability that node  $i$  is in the state  $A$ ;  $[A_i, B_j] = \mathbb{P}[X_i(t) = A, X_j(t) = B]$ , which is the probability that nodes  $i$  and  $j$  are in states  $A$  and  $B$ , respectively;  $[A_i, B_j, C_l]$  is the extension to three nodes. In addition, they also defined specific pair-type variables:  $\omega_{ij} = [0_i, 0_j]$ ,  $\phi_{ij} = [0_i, 1_j]$ ,  $\bar{\phi}_{ij} = [1_i, 0_j]$ ,  $\psi_{ij} = [1_i, 1_j]$ . It is easy to know that pair-type variables must satisfy

$$\psi_{ij} = \rho_j - \phi_{ij}, \bar{\phi}_{ij} = \rho_i - \psi_{ij} = \rho_i - \rho_j + \phi_{ij}, \omega_{ij} = 1 - \rho_i - \phi_{ij}.$$

Within this perspective, they built a system describing the SIS epidemic dynamics on the network  $G$ , which takes the form

$$\begin{aligned} \frac{d}{dt} \rho_i &= -\gamma \rho_i + \beta \sum_{j=1}^N \phi_{ij} a_{ij} \\ \frac{d}{dt} \phi_{ij} &= -\gamma \phi_{ij} - \beta \phi_{ij} + \gamma \psi_{ij} \\ &\quad + \beta \sum_{\substack{l \in \mathcal{N}(j) \\ l \neq i}} [0_i, 0_j, 1_l] - \beta \sum_{\substack{l \in \mathcal{N}(i) \\ l \neq j}} [1_l, 0_i, 1_j] \end{aligned} \quad (1)$$

where  $\mathcal{N}(i)$  denotes the neighborhood of node  $i$ . In order to close the above equations, the authors used the standard approximation [28,32]

$$[A_i, B_j, C_l] \simeq \frac{[A_i, B_j][B_j, C_l]}{[B_j]}. \quad (2)$$

In Appendix A, we prove that this approximation holds for the random network with no clustering.

After performing a quasi-static approximation for  $t \rightarrow \infty$ , the authors found that the epidemic threshold can be determined by the largest eigenvalue of the Jacobian matrix  $L$ , which is given by

$$L_{ij} = -\left(\gamma + \frac{\beta^2 k_i}{2\beta + 2\gamma}\right) \delta_{ij} + \frac{\beta(2\gamma + \beta)}{2\beta + 2\gamma} a_{ij}. \quad (3)$$

Here,  $\delta_{ij}$  is the Kronecker symbol and  $k_i$  is the degree of node  $i$ .

### 2.2. The derivation of the pair QMF equations

We will apply the total probability formula to derive the pair QMF equations for the SIS epidemic model (1). For the sake of the following analysis, we first present a lemma.

**Lemma 1.** For each a subset of nodes in  $G$ ,  $V^*$  (i.e.,  $V^* \subset V$ ), we assume that a probability of each node  $i \in V^*$  to be infected, denoted by  $\rho_i$  is given, then the number of infected nodes in this subset is a stochastic variable  $\xi \in [0, |V^*|]$  ( $|V^*|$  denotes the number of the elements in set  $V^*$ ) and its first and second order moment satisfy

$$\mathbb{E}[\xi] = \sum_{i \in V^*} \rho_i, \quad \mathbb{E}[\xi^2] = \sum_{i \in V^*} \rho_i + \sum_{i_1 \neq i_2} \rho_{i_1} \rho_{i_2},$$

respectively.

This lemma is easily proved by the mathematical induction. In fact, the first order moment formula has been proved in [31,33]. The second order formula can be justified by a simple example when  $|V^*| = 3$ . At this time,  $\mathbb{E}[\xi^2] = 1^2 \times [\rho_1(1 - \rho_2)(1 - \rho_3) + \rho_2(1 - \rho_1)(1 - \rho_3) + \rho_3(1 - \rho_1)(1 - \rho_2)] + 2^2 \times [\rho_1 \rho_2(1 - \rho_3) + \rho_1 \rho_3(1 - \rho_2) + \rho_2 \rho_3(1 - \rho_1)] + 3^2 \times \rho_1 \rho_2 \rho_3 = \rho_1 + \rho_2 + \rho_3 + 2(\rho_1 \rho_2 + \rho_2 \rho_3 + \rho_1 \rho_3)$ , which accords with the conclusion from Lemma 1.

In the following, we derive system (1). By the total probability formula, we have

$$\begin{aligned} \mathbb{P}[X_i(t + \Delta t) = 1] &= \mathbb{P}[X_i(t) = 1] \mathbb{P}[X_i(t + \Delta t) = 1 | X_i(t) = 1] \\ &\quad + \mathbb{P}[X_i(t) = 0] \mathbb{P}[X_i(t + \Delta t) = 1 | X_i(t) = 0]. \end{aligned} \quad (4)$$

Denote  $k_{\text{inf}}(i)$  be the number of infected nodes in the neighborhood of node  $i$ . Note that

$$\begin{aligned} \mathbb{P}[X_i(t) = 0] \mathbb{P}[X_i(t + \Delta t) = 1 | X_i(t) = 0] &= \mathbb{P}[X_i(t + \Delta t) = 1, X_i(t) = 0] \\ &= \sum_{s=0}^{k_i} \mathbb{P}[X_i(t + \Delta t) = 1, X_i(t) = 0, k_{\text{inf}}(i) = s] \\ &= \sum_{s=0}^{k_i} \mathbb{P}[X_i(t + \Delta t) = 1 | X_i(t) = 0, k_{\text{inf}}(i) = s] \end{aligned}$$

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