Epidemic threshold of the susceptible-infected-susceptible model on complex networks

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We demonstrate that the susceptible-infected-susceptible (SIS) model on complex networks can have an inactive Griffiths phase characterized by a slow relaxation dynamics. It contrasts with the mean-field theoretical prediction that the SIS model on complex networks is active at any nonzero infection rate. The dynamic fluctuation of infected nodes, ignored in the mean field approach, is responsible for the inactive phase. It is proposed that the question whether the epidemic threshold of the SIS model on complex networks is zero or not can be resolved by the percolation threshold in a model where nodes are occupied in degree-descending order. Our arguments are supported by the numerical studies on scale-free network models.

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Epidemic spreading is a common phenomenon in networked systems. Diseases spread from individual to individual through a contact network and computer viruses spread through the Internet. Since it has a huge impact on stability, epidemic spreading on complex networks has been attracting a lot of interest during the last decade [1]. Those studies have focused on both theoretical issues such as nonequilibrium critical phenomena [2] and practical issues such as searching for an efficient immunization strategy [3,4]. The SIS model is a paradigmatic epidemic spreading model where an infected individual becomes susceptible (or healthy) at a unit rate and infects its susceptible neighbor at a rate λ. We consider the SIS model on complex networks whose degree distribution $P(k)$ denoting the fraction of nodes with degree k is broad [5].

Pastor-Satorras and Vespignani proposed a so-called heterogeneous mean-field (HMF) theory for complex networks [6]. According to this theory, the epidemic threshold of the SIS model, above which the system is in an active phase with a finite density of infected nodes, is given by $\lambda_c = \langle k\rangle/\langle k^2\rangle$ with $\langle k^n\rangle = \int dk\, k^n P(k)$. Specifically, in scale-free networks characterized by $P(k) \sim k^{-\gamma}$ with a degree distribution exponent γ [5], $\lambda_c = 0$ for $\gamma \leqslant 3$ while $\lambda_c > 0$ otherwise [7]. The HMF theory, which becomes exact in the annealed network limit [8–11], turns out to be useful in studying various physical problems on complex networks [2].

Meanwhile, a mean-field theory on *quenched* networks has been developed in Ref. [12], which suggests a conclusion that the epidemic threshold of the SIS model vanishes ($\lambda_c = 0$) in any network with diverging maximum degree [13]. It implies that an epidemic spreading cannot be prevented on complex networks with an unbounded degree distribution. This study attracts much interest and is followed by a series of works [14–17]. The mean-field theory on quenched networks will be referred to as the quenched mean-field (QMF) theory. Due to its strong implication, the predicted null epidemic threshold by the QMF theory needs further investigation.

In this work, we complement the QMF theory by taking into account the dynamic fluctuation of infected nodes. This effect turns out to be crucial in determining whether the epidemic threshold of the SIS model on complex networks is zero or not. We find that the active phase predicted by the QMF theory near $\lambda = 0$ actually corresponds to the Griffiths phase [18–20] where the density of the infected nodes decays to zero more slowly than an exponential decay, unless the active nodes form a percolating cluster. It is proposed that a zero (nonzero) epidemic threshold of the SIS model is inherited from a zero (nonzero) percolation threshold in a model where nodes are occupied in degree-descending order. Such a specific percolation will be referred to as the degree-ordered percolation (DOP). Our argument is confirmed in the numerical studies on the (u,v)-flower model [21] for scale-free networks. We finally apply the DOP to survey whether λ_c of the SIS model should be zero or not on random scale-free networks, which remains unsettled in model simulations due to a strong finite-size effect [17].

We begin with a review on the QMF theory for the SIS model. Let $\rho_i(t)$ be the infection probability of node i at time t. Then the rate equation reads

$$\frac{d\rho_i(t)}{dt} = -\rho_i(t) + [1-\rho_i(t)]\sum_j a_{ij}\lambda\rho_j(t), \qquad (1)$$

where a_{ij} is an element of the adjacency matrix assigned with 1 if there is an edge between nodes i and j or 0 otherwise. The first term on the right-hand side of Eq. (1) is the recovery rate reducing the infection probability and the second term is the infection rate given by the product of the susceptible probability and the infection trial rate by infected neighbors.

The QMF approach focuses on the linear stability analysis of the zero fixed point [$\rho_i(0) = 0$ for all i] of Eq. (1), which corresponds to a configuration of the inactive phase. It is easy to show that the fixed point becomes unstable as soon as $\lambda\Lambda_1 > 1$ for the largest eigenvalue Λ_1 of $\{a_{ij}\}$. This leads to the conclusion $\lambda_c^{\rm QMF} = 1/\Lambda_1$ for the epidemic threshold of the QMF theory [12]. Although appealing, it has some controversial points. Most of all, it predicts $\lambda_c = 0$ in any network with a diverging maximum degree. In an arbitrary graph with a maximum degree $k_{\rm max}$, the largest eigengenvalue satisfies an inequality $\sqrt{k_{\rm max}} \leqslant \Lambda_1 \leqslant k_{\rm max}$ [22]. This gives $\lambda_c^{\rm QMF} = 0$ in the $k_{\rm max} \to \infty$ limit. An alternative interpretation of $\lambda_c^{\rm QMF}$ follows recently in Ref. [16], which claims that a property of the eigenvector corresponding to Λ_1 plays an important role in epidemic prevalence.

As a counterexample to the QMF conclusion, it is instructive to consider a star graph consisting of a hub at the center and $k_{\rm max}$ linear chains of length L emanating from it. The total

number of nodes is $N = k_{\max}L + 1$. In use of the symmetry of the star graph with respect to the hub node, we find $\Lambda_1 \to k_{\max}/\sqrt{k_{\max}-1}$ for large L [23] [this is also obtainable by Eq. (10) of Ref [16]]. Hence, the QMF theory predicts $\lambda_c^{\rm QMF} = 1/\Lambda_1 = 0$ in the infinite $k_{\max}$ limit. Interestingly, on the other hand, the actual steady state solution of Eq. (1) gives a different result, as follows.

Let ρ_0 and ρ_r $(r = 1,2,\ldots,L)$ be the steady state solution at the hub and nodes at the distance r from the hub, respectively. Due to symmetry, the solution depends only on the distance r. Thus, Eq. (1) yields the recurrence relations

$$\begin{aligned} &\rho_r/(1-\rho_r) = \lambda(\rho_{r-1} + \rho_{r+1}) \quad \text{for} \quad r \geqslant 1, \\ &\rho_0/(1-\rho_0) = \lambda k_{\max}\rho_1. \end{aligned} \tag{2}$$

Equation (2) gives a self-consistent equation $\rho_s/(1-\rho_s) = 2\lambda\rho_s$ for $\rho_s \equiv \lim_{r\to\infty}\rho_r$. The nonzero $\rho_s = (2\lambda-1)/(2\lambda)$ appears when $2\lambda > 1$, while $\rho_s = 0$, otherwise.

When $\lambda < 1/\Lambda_1$, $\rho_r = 0$ for all $r = 0,1,2,\ldots,L$. In $1/\Lambda_1 \leqslant \lambda \leqslant 1/2$, the zero solution becomes unstable and a nonzero solution appears. Linearizing Eq. (2) in ρ_r, one can find that $\rho_r \propto [2\lambda/(1+\sqrt{1-4\lambda^2})]^r$ for $1 \ll r \ll L$. The solution decays exponentially with r. That is to say, the infection is localized around the hub. When $\lambda > 1/2$, the infection is extended with $\rho_r \approx \rho_s = (2\lambda-1)/(2\lambda)$ for $1 \ll r \ll L$. So the epidemic order parameter of the star graph, $\rho \equiv \lim_{L,k_{\max}\to\infty}\sum_i \rho_i/N$, is given by

$$\rho = \begin{cases} 0 & \text{for} \quad \lambda \leqslant 1/2 \\ (2\lambda-1)/(2\lambda) & \text{for} \quad \lambda > 1/2 \end{cases} \tag{3}$$

in the infinite size limit. Namely, the epidemic threshold is given by $\lambda_c = 1/2$. This example demonstrates that the linear stability analysis against the zero-fixed-point inactive state alone is not sufficient in determining the threshold of the SIS model on complex networks.

In order to overcome the shortcomings of the previous QMF approach, we also take into account the other eigenvalues besides Λ_1. This approach was also taken in Ref. [16]. More importantly, we next incorporate the effect of an irreversible dynamic fluctuation due to stochasticity in dynamics, which is ignored in most mean-field approaches. As will be shown later, the fluctuation plays a crucial role.

For convenience, we label the nodes in degree-descending order: $k_1 \geqslant k_2 \geqslant \cdots \geqslant k_N$. Recent studies show that the nth largest eigenvalue of the adjacent matrix of a random network is $\Lambda_n \sim \sqrt{k_n}$ for large k_n [24] and the corresponding eigenvector is localized around the node n [25]. These findings imply that the steady state solution of Eq. (1) for small λ displays the local active domains around high-degree nodes: Each high-degree node n behaves like an independent local hub with its own activation threshold given by $\lambda_n = 1/\Lambda_n \sim 1/\sqrt{k_n}$ and the size of a local active domain is given by $\sim\lambda k_n$. Independence of the local active domains in the small λ limit is guaranteed only when higher degree nodes are distant enough from each other. A network with such a property will be referred to as an *unclustered* network. For $1/\Lambda_n < \lambda < 1/\Lambda_{n+1}$, local active domains of size $\sim\lambda k_i$ appear around all nodes $i \leqslant n$. Thus one may expect

$$\rho \sim \int_{1/\lambda^2}^{\infty} dk(\lambda k)P(k), \tag{4}$$

which yields $\rho \sim \lambda^{2\gamma-3}$ for a random scale-free network with a degree exponent γ. Note that the refined QMF theory still predicts that $\lambda_c = 0$ with order parameter exponent $\beta = 2\gamma - 3$ [23].

Numerical evidence, however, shows Eq. (4) is not valid. We have performed Monte Carlo simulations for the SIS model [26] on scale-free networks generated by the (u,v)-flower model [21]. This is a deterministic hierarchical model: One starts from two nodes connected with an edge (zeroth generation). Then, every link in a Gth generation is replaced with the two u- and v-link-long paths in the next $(G+1)$-th generation. The total number of nodes in a (u,v) flower of generation G is given by $N = [(u+v)^G(u+v-2)+(u+v)]/(u+v-1)$. It results in a scale-free network with $\gamma = 1 + \ln(u+v)/\ln 2$ in the $G \to \infty$ limit [21]. The (u,v)-flower model is particularly useful because one can generate an unclustered network easily. If $u > 1$ and $v > 1$, the degree of all nodes is doubled and the distance between them becomes farther after each iteration. We used the (3,3)-flower model in simulations. The numerical data shown in Fig. 1(a) strongly suggest a transition at nonzero λ_c. The threshold can be estimated from the peak positions of the susceptibility $\chi \equiv N(\langle\rho^2\rangle - \langle\rho\rangle^2)/\langle\rho\rangle$, where N is the total number of nodes [17]. The inset in Fig. 1 shows the peak position is extrapolated to $\lambda_c \simeq 0.65(5)$ in the infinite system size limit.

The origin of the inconsistency is an irreversible fluctuation of the local active domains, as follows. Consider a local active domain consisting of V nodes. Then, no matter how rare, there exists a moment when all nodes recover simultaneously by chance. This takes place after a characteristic time $\tau_V \sim e^{aV}$ for a certain $a > 0$. Once being recovered, the domain will remain inactive unless externally activated. Considering this effect of the irreversible fluctuation, Eq. (4) should be replaced by

$$\rho(t) \simeq \int_{1/\lambda^2}^{\infty} dk(\lambda k)P(k)e^{-t/\tau_{\lambda k}}. \tag{5}$$

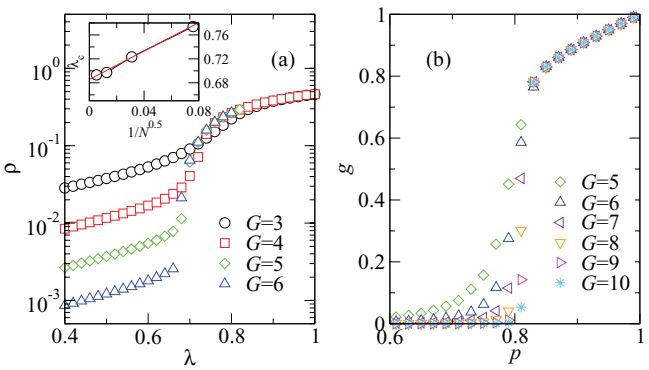

FIG. 1. (Color online) Density of infected nodes in the (3,3) flowers in (a). The largest cluster density in the DOP (see text) on the same flowers as in (b).

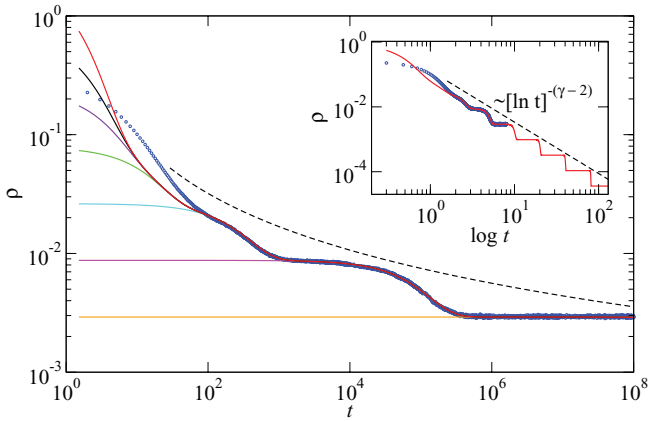

FIG. 2. (Color online) $\rho(t)$ in the (3,3) flower of $G = 8$. The data points are the SIS model simulation result. The solid curves are obtained from the direct integration of Eq. (5) with two fitting parameters $a_1 = 0.8$ and $a_2 = 0.325$ for $\tau_{\lambda k} = a_1 e^{a_2 \lambda k}$ and with the truncated degree distribution function; from bottom to top, $P(k)$ is truncated by $k \geqslant k_{\max}/2^n$ with $n = 1,2,\ldots,7$. The inset compares the long-time behavior predicted in our theory (red solid curve) with the currently available numerical data (blue dots).

Since it decays to zero eventually, the apparent active phase implied in Eq. (4) is in fact an inactive one. We note that the inactive phase is different from the usual one where the density decays exponentially in time. The density in Eq. (5) does not decay exponentially fast but extremely slow due to the broad distribution of relaxation times. For example, in scale-free networks with $P(k) \sim k^{-\gamma}$, one finds

$$\rho(t) \sim [\ln t]^{-(\gamma-2)}. \tag{6}$$

Equation (5) is numerically tested in the (3,3) flowers at $\lambda = 0.56 < \lambda_c$, which is shown in Fig. 2. It does not decay exponentially in time. Instead, the density is trapped in a plateau for a while and then decays to another plateau successively. Those plateaus are evidence for the existence of metastable local active domains. In the (u,v) flower, degrees of nodes are discretized as $k = 2^n$ with $n = 1,2,\ldots$. So the size $V_k \sim \lambda k$ of the local active domains and their lifetime $\tau_{\lambda k} \sim e^{a\lambda k}$ are also discrete. This discreteness results in the plateaus. As shown, the data in Fig. 2 are fitted to Eq. (5) very well for large $t \gtrsim 10^2$. The dashed curve therein represents the overall decay given by Eq. (6).

The slow dynamics given in Eqs. (5) and (6) is reminiscent of a relaxation dynamics in the Griffiths phase [18–20]. In a disordered system, disorder fluctuations may generate local domains which behave differently from the bulk. Denoting the probability that such a domain of size ξ is realized as $P(\xi)$ and the relaxation time therein as $\tau(\xi)$, a physical quantity f relaxes to its stationary value f_s as $\delta f(t) = f(t) - f_s \sim \int d\xi\, P(\xi) e^{-t/\tau(\xi)}$. In the Griffiths phase, the relaxation dynamics is dominated by rare events encoded in the tail of $P(\xi)$ with long characteristic time scales $\tau(\xi)$ [19]. In our case, the slow dynamics originates from the irreversible fluctuation near the hubs.

The previous argument shows that the SIS model on an unclustered network can be in the inactive Griffiths phase for $\lambda_c^{\rm QMF} < \lambda < \lambda_c$ with a certain nonzero λ_c. It also provides a hint on the mechanism for the phase transition into an active phase. Inside the Griffiths phase, local active domains of size $\sim \lambda k$ are separated (unclustered network) and metastable. As λ increases, the size of the local domains grows and they begin to overlap each other. The active domains become globally stable when they form a percolating giant cluster above a certain threshold value of λ. That is to say, the epidemic transition is triggered by a percolation transition of the local active domains.

Note that the local active domains nucleate around high-degree nodes in degree-descending order. So the uncovered mechanism leads to the conjecture that the unclustered network with $\lambda_c \neq 0$ should have a nonzero percolation threshold in the DOP model. Recall that the DOP is suggested as a percolation model where nodes are occupied in degree-descending order [27]. A nonzero percolation threshold p_c (as the node-occupation ratio) implies that high-degree nodes are well separated from each other. Hence, in the context of the SIS model, one requires a nonzero value of λ for the local active domains (of size $\sim \lambda k$) to form a percolating cluster.

We provide numerical evidence of our claim. Figure 1(b) shows the percolation order parameter g, the density of nodes in the largest cluster, for the DOP in the same (3,3) flowers used in Fig. 1(a). The percolation threshold p_c is clearly nonzero, which is consistent with $\lambda_c \neq 0$ shown in Fig. 1(a). As another example, one may revisit the aforementioned $k_{\max}$-star graph case with diverging L. In this example, one can easily find $p_c \neq 0$ that supports our claim.

We also consider the opposite case with $p_c = 0$. It is achieved only when any finite fraction of occupied nodes in the DOP process are connected to form a percolation cluster. Those networks with $p_c = 0$ will be called the *clustered* network. In the context of the SIS model, the local active domains in the clustered network form a percolating cluster even in the limit $\lambda \to 0$. Therefore, we expect that the epidemic threshold is zero in the clustered network. The steady state density of the infected nodes can be expected to scale as

$$\rho \sim \int_{1/\lambda^2}^{\infty} dk\, P(k). \tag{7}$$

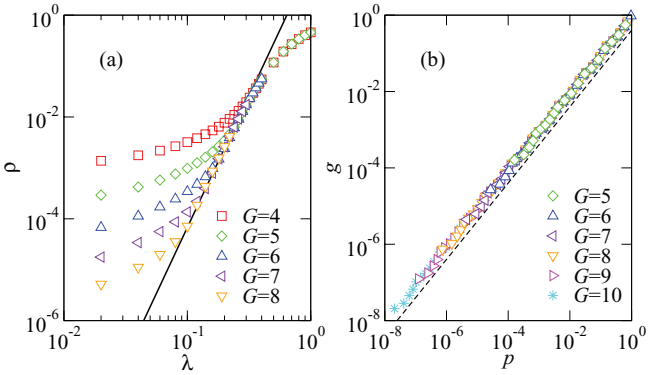

FIG. 3. (Color online) Density of infected nodes in the (1,5) flower in (a). The largest cluster density in the DOP on the same flower in (b). The solid lines in (a) have a slope $2 \ln 6/\ln 2 \simeq 5.19$, while the dashed line in (b) has a slope 1.

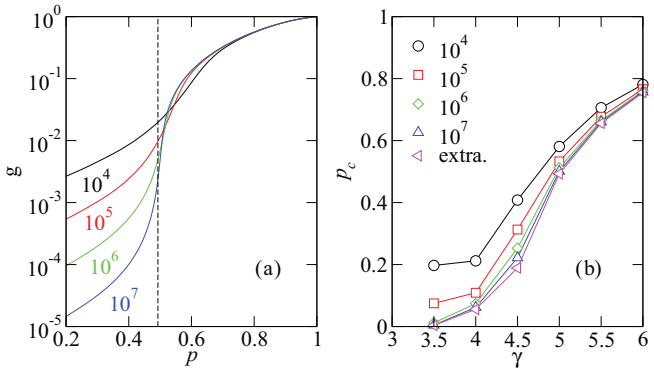

FIG. 4. (Color online) (a) The density of the largest DOP cluster in random scale-free networks of the configuration model with $\gamma = 5$. The dashed line denotes the percolation transition point. (b) Maximum cluster heterogeneity points and their extrapolated values. The system sizes are $N = 10^4, \ldots, 10^7$.

In comparison with Eq. (4), the factor (λk) is missing because high-degree nodes with $k \geqslant 1/\lambda^2$ are neighboring each other and compose the stable active domain. In scale-free networks with $P(k) \sim k^{-\gamma}$, one obtains $\rho \sim \lambda^{2\gamma-2}$. Note that the order parameter exponent $\beta = 2\gamma - 2$ is different from $\beta_{\rm QMF} = 1$ obtained from the simple QMF theory where only the largest eigenmode was taken into account [14].

A trivial example of the clustered network is the $k_{\rm max}$-star graph with $L = 1$. The density of the largest cluster is given by $g = p$ implying $p_c = 0$. Independently, $\lambda_c = 0$ obviously, as discussed in Ref. [13]. A nontrivial example is the (u,v) flowers with $u = 1$ (or $v = 1$). Recall that if two nodes are connected with an edge in a certain generation, then they remain connected afterward when $u = 1$ (or $v = 1$). So one can expect that high-degree nodes are clustered. In Fig. 3(a), we present the SIS model simulation results on the (1,5) flowers at several generations G. As G increases, the data approach the theoretical prediction $\rho \sim (\lambda - \lambda_c)^\beta$ with $\lambda_c = 0$ and $\beta = 2\gamma - 2 = 2 \ln 6/\ln 2$. The DOP property is presented in Fig. 3(b). The scaling of $g \sim p$ therein indicates $p_c = 0$.

What is the epidemic threshold in more interesting cases such as generic random scale-free networks? Recently, extensive Monte Carlo simulations were performed in random scale-free networks generated from the configuration model [17]. However, due to a strong finite-size effect, it still remains inconclusive whether $\lambda_c = 0$ or not even with simulations of system sizes up to $N = 3 \times 10^7$ at $\gamma = 3.5$.

Alternatively we investigate the DOP property of the configuration model networks. In Fig. 4(a), we present the percolation order parameter for the network with $\gamma = 5$. As in the (3,3) flower, the system undergoes a percolation transition at a finite threshold. In order to estimate the percolation threshold precisely, we make use of a so-called cluster heterogeneity which denotes the number of distinct cluster sizes [29]. It was shown [30] that $p_c(N)$ at which the cluster heterogeneity is maximum in networks of size N converges to the percolation threshold p_c in the infinite N limit. In Fig. 4(b), we present the numerical data for $p_c(N)$ at several values of γ and their extrapolated values. The percolation threshold is nonzero unless a small γ is considered. Thus, the random scale-free networks therein belong to the unclustered network class. It provides indirect evidence that the epidemic threshold could be nonzero on those scale-free networks.

In summary, we present a theoretical argument that the epidemic threshold of the SIS model on complex networks is nonzero in the unclustered network, while it is zero in the clustered network. This conclusion is drawn by taking into account the effect of the irreversible fluctuation which was ignored in the QMF theory. The fluctuation makes a local active domain unstable and leads to the Griffiths phase. Numerical simulations performed in the (u,v)-flower model support our argument. We suggest that the clustering property of a network can be determined by the DOP. By studying the DOP transition, the random scale-free networks are shown to belong to an unclustered network unless a small degree exponent is considered. It suggests the epidemic threshold in such scale-free networks is nonzero as opposed to the QMF prediction. Our work raises various interesting questions on the critical phenomenon associated with the epidemic transition and the DOP transition, which are left for future works.

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