Different thresholds of bond percolation in scale-free networks with identical degree sequence

Zhongzhi Zhang,[1,2,*] Shuigeng Zhou,[1,2,†] Tao Zou,[1,2] Lichao Chen,[1,2] and Jihong Guan[3,‡]
[1]*School of Computer Science, Fudan University, Shanghai 200433, China*
[2]*Shanghai Key Laboratory of Intelligent Information Processing, Fudan University, Shanghai 200433, China*
[3]*Department of Computer Science and Technology, Tongji University, 4800 Cao'an Road, Shanghai 201804, China*
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Generally, the threshold of percolation in complex networks depends on the underlying structural characterization. However, what topological property plays a predominant role is still unknown, despite the speculation of some authors that degree distribution is a key ingredient. The purpose of this paper is to show that power-law degree distribution itself is not sufficient to characterize the threshold of bond percolation in scale-free networks. To achieve this goal, we first propose a family of scale-free networks with the same degree sequence and obtain by analytical or numerical means several topological features of the networks. Then, by making use of the renormalization-group technique we determine the threshold of bond percolation in our networks. We find an existence of nonzero thresholds and demonstrate that these thresholds can be quite different, which implies that power-law degree distribution does not suffice to characterize the percolation threshold in scale-free networks.

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I. INTRODUCTION

As one of the best studied problems in statistical physics, percolation [1] is nowadays also the subject of intense research in the field of complex networks [2]. In a network, if a fraction of its vertices (nodes, sites) or edges (links, bonds) is chosen independently with a probability p to be "occupied," it may undergo a percolation phase transition: when p is above a threshold value p_c, called percolation threshold, the network possesses a giant component consisting of a finite fraction of interconnected nodes; otherwise, the giant component disappears and all nodes disintegrate into small clusters. So far, percolation in complex networks has received considerable attention in the community of statistical physics [3], because it is not only of high theoretical interest, but also relevant to many aspects of networks, including network security [4–7], disease spread on networks [8–12], etc.

Since global physical properties of random media alter substantially at the percolation threshold, which is central to understanding and applying this process, thus the precise knowledge of percolation threshold is extremely important [13]. The issue of determining or calculating the percolation threshold has been the subject of intense study since the introduction of the model over half a century ago [14,15]. Despite decades of effort, there is still no general method for computing the percolation threshold of arbitrary graphs, and rigorous solution for the percolation threshold is confined to some special cases [13,16–18], such as the Barabási-Albert (BA) network [19], two-dimensional lattice, and some other lattices. In most cases (e.g., lattices in three dimensions or above), the percolation threshold is estimated with numerical simulations, which are often time consuming [20]. Thus, finding the threshold exactly is essential to investigating the percolation problem on a particular graph [17].

Perhaps the main reason for studying percolation in complex networks is to understand how the percolation properties are influenced by the underlying topological structure. It has been established that degree distribution has a qualitative impact on the percolation. Recent studies indicated that in uncorrelated scale-free networks the percolation threshold is absent [5,6]. Then a lot of other jobs followed, studying the influences of other properties on the percolation properties in scale-free networks; these include degree correlations [10,21], clustering coefficient [22], and so forth. It was found that degree correlations and clustering coefficient can strongly affect some percolation properties, but they cannot restore a finite percolation threshold in scale-free networks. This raises the question as to whether scale-free degree distribution is the only ingredient responsible for the absence of the percolation threshold; in other words, whether power-law degree distribution suffices to characterize the zero percolation threshold in scale-free networks.

In this paper, we study the effects of power-law degree distribution on the percolation threshold in scale-free networks. To this end, we first construct a class of scale-free networks with identical degree sequence by introducing a control parameter q. We then study analytically or numerically the topological features of the networks and show that this class of networks has unique topologies. Finally, using the renormalization-group theory, we investigate analytically the bond percolation problem in the considered networks and find the existence of nonzero percolation thresholds depending on parameter q. Our findings indicate that the degree distribution by itself is not enough to characterize the percolation thresholds in scale-free networks. On the other hand, since our networks have the same degree sequence and thus the same degree distribution, the model proposed here can serve as a useful tool (substrate model) to check the impact of power-law degree distribution on the dynamical processes taking place on top of scale-free networks.

*zhangzz@fudan.edu.cn
†sgzhou@fudan.edu.cn
‡jhguan@tongji.edu.cn

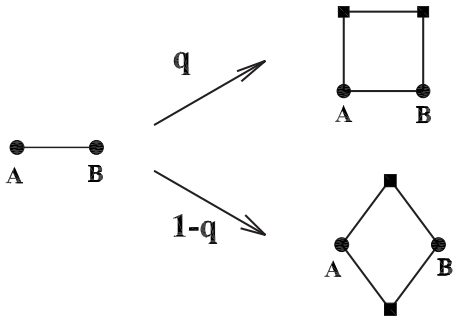

FIG. 1. Iterative construction method of the networks. Each link is replaced by either of the connected clusters on the right-hand side of arrows with a certain probability, where black squares represent new vertices.

II. NETWORK CONSTRUCTION AND STRUCTURAL CHARACTERISTICS

In this section, we study the construction and structural properties of the networks under consideration, with focus on degree distribution, clustering coefficient, and average path length (APL).

A. Construction algorithm

The proposed networks (graphs) are constructed in an iterative way as shown in Fig. 1. Let $H_t\,(t\geq 0)$ denote the networks after t iterations. Then the networks are built in the following way: for $t=0$, the initial network H_0 is two nodes connected by an edge. For $t\geq 1$, H_t is obtained from H_{t-1}. We replace each existing link in H_{t-1} either by a connected cluster of links on the top right of Fig. 1 with probability q, or by the connected cluster on the bottom right with complementary probability $1-q$. The growing process is repeated t times, with the graphs obtained in the limit $t\to\infty$. Figures 2 and 3 show the growth process of two networks for two limiting cases of $q=0$ and $q=1$, respectively.

Now we compute some related quantities such as the number of total nodes and edges in H_t, called network order and size, respectively. Let $L_v(t)$ be the number of nodes generated at step t, and E_t the total number of edges present at step t. Then $L_v(0)=2$ and $E_0=1$. By construction (see Fig. 1), we have $E_t=4E_{t-1}=4^t\ (t\geq 0)$. On the other hand, each existing edge at a given step will yield two new nodes at the next step; this leads to $L_v(t)=2E_{t-1}=2\times 4^{t-1}\ (t\geq 1)$. Then the number of total nodes N_t present at step t is

$$N_t=\sum_{t_i=0}^{t}L_v(t_i)=\frac{2}{3}(4^t+2). \tag{1}$$

The average node degree after t iterations is $\langle k\rangle_t=\frac{2E_t}{N_t}=\frac{3\times 4^t}{4^t+2}$, which approaches 3 for large t.

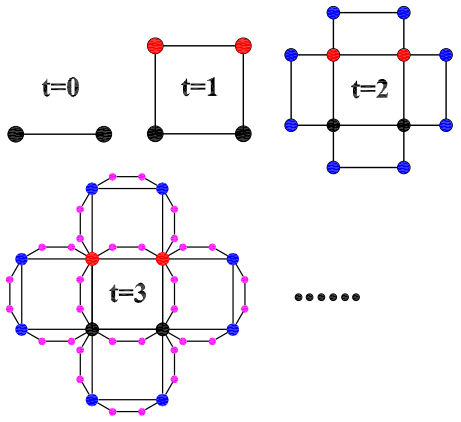

FIG. 2. (Color online) Illustration of the first four evolution steps of the network growth process for the particular case $q=1$.

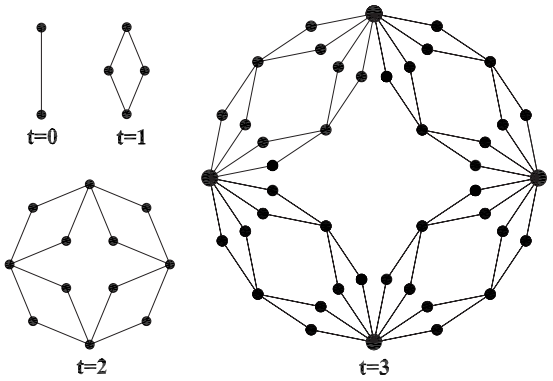

FIG. 3. Sketch of the iteration process of the network for the particular case of $q=0$.

B. Degree distribution

When a new node i is added to the networks at a certain step $t_i\ (t_i\geq 1)$, it has a degree of 2. We denote by $k_i(t)$ the degree of node i at time t. By construction, the degree $k_i(t)$ evolves with time as $k_i(t)=2k_i(t-1)=2^{t+1-t_i}$. That is to say, the degree of node i increases by a factor 2 at each time step. Thus, the degree spectrum of the networks is discrete. In H_t all possible degree of nodes is $2,2^2 2^3,\ldots,2^{t-1},2^t$; and the number of nodes with degree $k=2^{t+1-m}$ is $n_k=L_v(m)=4^{m-1}$. Therefore, all the class of networks H_t have the same degree sequence (thus the same degree distribution) in the full range of q.

Since the degree spectrum of the networks is not continuous, it follows that the cumulative degree distribution [23] is given by $P_{\rm cum}(k)=\frac{N_{t,k}}{N_t}$, where $N_{t,k}=\Sigma_{k'\geq k}n_{k'}$ is the number of nodes whose degree is not less than k. When t is large enough, we find $P_{\rm cum}(k)\sim k^{-2}$. So the degree distribution $P(k)$ of the networks follows a power-law form $P(k)\sim k^{-\gamma}$ with the exponent $\gamma=3$, independent of q. Notice that the same degree exponent has been obtained in the famous BA network [19].

C. Clustering coefficient

By definition, the clustering coefficient [24] of a node i with degree k_i is given by $C_i=2e_i/[k_i(k_i-1)]$, where e_i is the number of existing triangles attached to node i, and $k_i(k_i-1)/2$ is the total number of possible triangles including i. The clustering coefficient of the whole network is the average over all individual $C_i's$. By construction, there are no

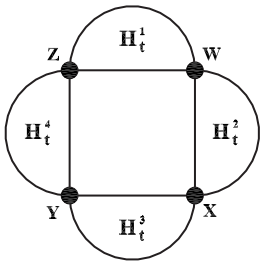

FIG. 4. Second construction method of the network for $q=1$ case that highlights self-similarity: The graph after $t+1$ construction steps, H_{t+1}, is composed of four copies of H_t denoted as H_t^θ ($\theta=1,2,3,4$), which are connected to one another as above.

triangles in H_t, so the clustering coefficient of every node and its average value in H_t are both zero.

D. Average path length

Let d_{ij} represent the shortest path length from node i to j, then the average path length d_t of H_t is defined as the mean of d_{ij} over all couples of nodes in the network:

$$d_t = \frac{D_t}{N_t(N_t-1)/2}, \tag{2}$$

where

$$D_t = \sum_{\substack{i\in H_t, j\in H_t \\ i\neq j}} d_{ij} \tag{3}$$

denotes the sum of the shortest path length between two nodes over all pairs.

For general q, it is difficult to derive a closed formula for the APL d_t of H_t. But for two limiting cases of $q=1$ and $q=0$, both the networks are deterministic, so we can obtain the analytic solutions for APL.

1. Case of $q=1$

In the special case (see Fig. 2), the networks are reduced to the (1,3)-flower proposed in [25]. This limiting case of the network has a self-similar structure that allows one to calculate d_t analytically. The self-similar structure is obvious from an equivalent network construction method: to obtain H_{t+1}, one can make four copies of H_t and join them in the hub nodes. As shown in Fig. 4, network H_{t+1} may be obtained by the juxtaposition of four copies of H_t, which are consecutively labeled as H_t^1, H_t^2, H_t^3, and H_t^4. Then we can write the sum D_{t+1} as

$$D_{t+1} = 4D_t + \Delta_t, \tag{4}$$

where Δ_t is the sum of length over all shortest paths whose end points are not in the same H_t branch.

The paths that contribute to Δ_t must all go through at least one of the four *connecting nodes* (i.e., W, X, Y, and Z in Fig. 4) at which the different H_t branches are connected. The analytical expression for Δ_t, called the length of crossing paths, is found below.

Denote $\Delta_t^{\alpha,\beta}$ as the sum of length for all shortest paths with end points in H_t^α and H_t^β, respectively. If H_t^α and H_t^β meet at a connecting node, $\Delta_t^{\alpha,\beta}$ rules out the paths where either end point is that shared connecting node. For example, each path contributed to $\Delta_t^{1,2}$ should not end at node W. If H_t^α and H_t^β do not meet, $\Delta_t^{\alpha,\beta}$ excludes the paths where either end point is any connecting node. For instance, each path contributed to $\Delta_t^{1,3}$ should not end at nodes W, X, Y or Z. Then the total sum Δ_t is

$$\Delta_t = \Delta_t^{1,2} + \Delta_t^{1,3} + \Delta_t^{1,4} + \Delta_t^{2,3} + \Delta_t^{2,4} + \Delta_t^{3,4} - 4. \tag{5}$$

The last term at the end compensates for the overcounting of certain paths: the shortest path between W and Y, with length 2, is included in $\Delta_t^{1,4}$ and $\Delta_t^{2,3}$; the shortest path between X and Z, also with length 2, is included in both $\Delta_t^{1,2}$ and $\Delta_t^{3,4}$.

By symmetry, $\Delta_t^{1,2}=\Delta_t^{1,4}=\Delta_t^{2,3}=\Delta_t^{3,4}$ and $\Delta_t^{1,3}=\Delta_t^{2,4}$, so that

$$\Delta_t = 4\Delta_t^{1,2} + 2\Delta_t^{1,3} - 4. \tag{6}$$

In order to find $\Delta_t^{1,2}$ and $\Delta_t^{1,3}$, we define quantity s_t as

$$s_t = \sum_{\substack{i\in H_t \\ i\neq W}} d_{iW}. \tag{7}$$

Considering the self-similar network structure, we can easily know that at time $t+1$, the quantity s_{t+1} evolves recursively as

$$\begin{aligned} s_{t+1} &= 2s_t + [s_t + (N_t-1)] + [s_t + (N_t-1) - 2] \\ &= 4s_t + \frac{4}{3}(4^t - 1). \end{aligned} \tag{8}$$

Using $s_1=4$, we have

$$s_t = \frac{1}{9}(4 + 5\times 4^t + 3t\times 4^t). \tag{9}$$

On the other hand, by definition given above, we have

$$\begin{aligned} \Delta_t^{1,2} &= \sum_{\substack{i\in H_t^1, j\in H_t^2 \\ i,j\neq W}} d_{ij} \\ &= \sum_{\substack{i\in H_t^1, j\in H_t^2 \\ i,j\neq W}} (d_{iW} + d_{jW}) \\ &= (N_t-1)\sum_{\substack{i\in H_t^1 \\ i\neq W}} d_{iW} + (N_t-1)\sum_{\substack{j\in H_t^2 \\ j\neq W}} d_{jW} \\ &= 2(N_t-1)\sum_{\substack{i\in H_t^1 \\ i\neq W}} d_{iW} \\ &= 2(N_t-1)s_t. \end{aligned} \tag{10}$$

Continuing analogously,

$$\Delta_t^{1,3} = \sum_{\substack{i\in H_t^1, i\neq W,Z \\ j\in H_t^3, j\neq X,Y}} d_{ij}$$

$$= \sum_{\substack{i\in H_t^1, i\neq W,Z \\ d_{iW}<d_{iZ} \\ j\in H_t^3, j\neq X,Y}} (d_{iW} + d_{WX} + d_{jX})$$

$$+ \sum_{\substack{i\in H_t^1, i\neq W,Z \\ d_{iZ}<d_{iW} \\ j\in H_t^3, j\neq X,Y}} (d_{iZ} + d_{ZY} + d_{jY})$$

$$= 2 \sum_{\substack{i\in H_t^1, i\neq W,Z \\ d_{iW}<d_{iZ} \\ j\in H_t^3, j\neq X,Y}} (d_{iW} + d_{WX} + d_{jX}), \tag{11}$$

where the symmetry property has been used. After simple calculations, we obtain

$$\Delta_t^{1,3} = 2(N_t - 1)s_t + (N_t - 1)^2 - 2\left(\frac{N_t}{2}\right)^2 - 2(s_t + N_t - 3) - 1. \tag{12}$$

Substituting Eqs. (10) and (12) into Eq. (6), we obtain after simplification

$$\Delta_t = \frac{4}{9}(-2 + 11 \times 16^t + 6t \times 16^t). \tag{13}$$

Thus

$$D_{t+1} = 4D_t + \frac{4}{9}(-2 + 11 \times 16^t + 6t \times 16^t). \tag{14}$$

Using $D_1 = 8$, Eq. (14) is solved inductively,

$$D_t = \frac{1}{27}(8 + 16 \times 4^t + 3 \times 16^t + 6t \times 16^t). \tag{15}$$

Inserting Eq. (15) into Eq. (2), one can obtain the analytical expression for d_t:

$$d_t = \frac{2}{3} \times \frac{8 + 16 \times 4^t + 3 \times 16^t + 6t \times 16^t}{4 \times 16^t + 10 \times 4^t + 4}, \tag{16}$$

which approximates t in the infinite t, implying that the APL shows a logarithmic scaling with network order. Therefore, in the case of $q=1$, the network exhibits a small-world behavior. We have checked our analytic result against numerical calculations for different network order up to $t=10$ which corresponds to $N_{10}=1\,048\,577$. In all the cases we obtain a complete agreement between our theoretical formula and the results of numerical investigation.

2. Case of $q=0$

For this particular case, our networks turn out to be the hierarchical lattice introduced in [26], which is also self-similar. Using a method similar to but a little different from that applied in the preceding subsection, we can compute analytically the average path length d_t. We omit the calculation process and give only the exact expression as below:

$$d_t = \frac{22 \times 2^t \times 16^t + 8^t(21t + 42) + 27 \times 4^t + 98 \times 2^t}{42 \times 16^t + 105 \times 4^t + 42}. \tag{17}$$

Equation (17) recovers the previously obtained result in [27] and has been confirmed by extensive numerical simulations. In the large t limit, $d_t \sim \frac{11}{21}2^t$. On the other hand, for large t limit, $N_t \sim 4^t$, so d_t grows as a square root of the number of network nodes. Thus, in the case of $q=0$, the network exhibits a "large-world" behavior of typical node-node distances.

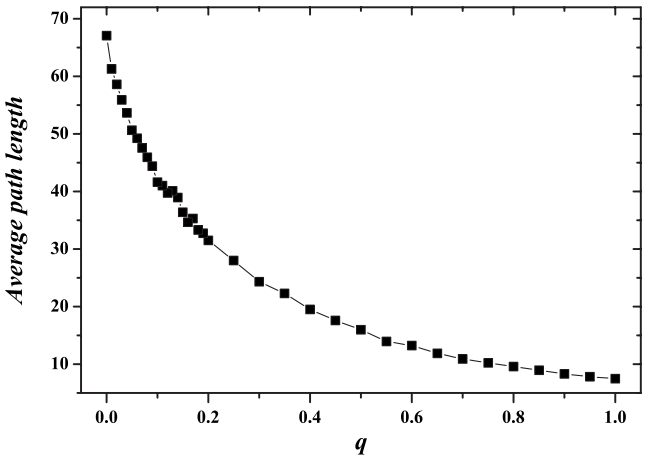

FIG. 5. Graph of the dependence of the average path length on the tunable parameter q.

3. Case of $0<q<1$

For $0<q<1$, in order to obtain the variation of the average path length with the parameter q, we have performed extensive numerical simulations for different q between 0 and 1. Simulations were performed for network N_7 with order 10 924, averaging over 20 network samples for each value of q. In Fig. 5, we plot the average path length as a function of q. We observe that, when q increases from 0 to 1, the average path length drops drastically from a very high value to a small one, which shows that there is a crossover between small-world and large-world. This behavior is similar to that in the Watts-Strogatz (WS) model [24].

III. THRESHOLD OF BOND PERCOLATION

As discussed in Sec. II, the networks exhibit many interesting properties, i.e., they have the same degree sequence independent of parameter q; they are scale-free and nonclustered; and they display a crossover between large-world and small-world. All these features are not shared simultaneously by any previously reported networks. Hence, it is worthwhile to investigate the processes taking place upon the model to find the different impact on dynamic processes compared with other networks such as the BA network. In what follows

we will study bond percolation, which is one of the most important issues in statistical physics [1].

In bond percolation every bond (link or edge) on a specified graph is independently either "occupied" with probability λ, or not with the complementary probability $1-\lambda$. In our case the percolation problem can be solved using the real-space renormalization-group technique [28–32], giving exact solution for the interesting quantity of percolation threshold. Let us describe the procedure in application to the network considered. Assuming that the network growth stops at a time step $t\to\infty$, when the network is spoiled in the following way: for a link present in the undamaged network, with the probability λ we retain it in the damaged network. Then we invert the transformation in Fig. 1 and define $n=t-\tau$ for this inverted transformation, which is actually a decimation procedure [31]. Further, we introduce the probability λ_n that if two nodes are connected in the undamaged network at $\tau=t-n$, then at the nth step of the decimation for the damaged network, there exists a path between these vertices. Here, $\lambda_0=\lambda$. We can easily obtain the following recursion relation for λ_n:

$$\lambda_{n+1} = q(\lambda_n + \lambda_n^3 - \lambda_n^4) + (1-q)(2\lambda_n^2 - \lambda_n^4). \tag{18}$$

Equation (18) has four roots (i.e., fixed points), among which the root $\lambda=-\frac{1-q}{2}-\frac{1}{2}\sqrt{5-6q+q^2}$ is invalid, because it is less than 0. The other three fixed points are as follows: two stable fixed points at $\lambda=0$ and $\lambda=1$, and an unstable fixed point at λ_c that is the percolation threshold. The reason for the unstable fixed point corresponding to the threshold is as follows: at any $0<\lambda_0<\lambda_c$, λ_n approaches 0 as $n\to\infty$, which means there is no percolation; while at any $\lambda_c<\lambda_0<1$, λ_n approach 1, indicating an existence of the percolating cluster.

The exact expression of λ_c as a function of q is

$$\lambda_c = -\frac{1-q}{2} + \frac{1}{2}\sqrt{5-6q+q^2}. \tag{19}$$

Interestingly, for the case of $q=0$, λ_c is equal to $\frac{\sqrt{5}-1}{2}$, which is the inverse of the golden ratio ϕ ($\phi=\frac{\sqrt{5}+1}{2}$) and is the same value as the site percolation threshold for the "B" lattice discussed in [16,17]. We present the dependence of λ_c on q in Fig. 6, which indicates that the threshold λ_c decreases as q increases. When q grows from 0 to 1, λ_c decreases from $\frac{\sqrt{5}-1}{2}\approx 0.618$ to 0.

Thus, in a large range of parameter q (i.e., $q<1$), there exists a critical nonzero percolation threshold λ_c such that for $\lambda>\lambda_c$ a giant component appears spanning the entire network, and for $\lambda<\lambda_c$ there are only isolated small clusters. The existence of percolation thresholds in our networks is in sharp contrast with the null threshold found in a wide range of previously studied scale-free networks [5,6,10,21,22].

Note that since the susceptible-infected-removed (SIR) model can be mapped to the bond percolation problem [8–10], for the SIR model on our networks the epidemic prevalence undergoes a phase transition at a finite threshold λ_c of the transmission probability. If infection rate is above λ_c, the disease spreads and infects a finite fraction of the population. On the contrary, when infection rate is below λ_c, the total number of infected individuals is infinitesimally small in the limit of very large populations. The existence of epidemic thresholds in the present networks is compared to the result for some other scale-free networks, where arbitrarily small infection rate shows finite prevalence [33].

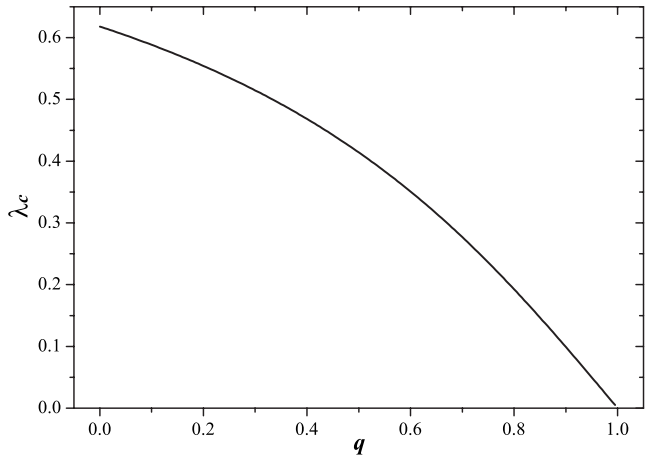

FIG. 6. The dependence relation of percolation threshold λ_c on the parameter q.

From Eq. (19), one can see that for different q, the networks have distinct percolation thresholds. As known from Sec. II, the whole class of the networks exhibits identical degree sequence (power-law degree distribution) and (zero) clustering coefficient, which shows that degree distribution and clustering coefficient are not sufficient to characterize the threshold of bond percolation in scale-free networks. One may ask why the considered networks have disparate percolation thresholds. We speculate that the diverse thresholds in our networks lie with the average path length, which needs further confirmation in the future.

IV. CONCLUSIONS

We have demonstrated that power-law degree distribution alone does not suffice to characterize the percolation threshold on scale-free networks under bond percolation. To this end, by introducing a parameter q, we have presented a family of scale-free networks with the same degree sequence and (zero) clustering coefficient. We provided a detailed analysis of the topological features and showed that the model exhibits a rich structural behavior. In particular, using a renormalization method, we have derived an exact analytic expression for the thresholds of bond percolation in our networks. We found that finite thresholds are recovered for our networks in the case of $q<1$, which is in contrast to the conventional wisdom that null percolation threshold is an intrinsic nature of scale-free networks. Therefore, care should be needed when making general statements about the percolation problem in scale-free networks.

It should be mentioned that the model generation of scale-free networks with the same degree sequence is a very common problem in complex network research. Actually, in the study of the impacts of other characteristics (besides degree distribution) of scale-free networks on the dynamical processes defined on the networks, the interference of power-

law degree distribution should be avoided. In this case, such a model is necessitated. Traditionally, the interchanging algorithm (through rewiring two links between four end points) is frequently used to achieve this goal [34]. But this algorithm may lead to disconnection of the whole network. We have shown that the scale-free networks proposed here have identical degree sequence and are always connected. So our networks can overcome above deficiency. They may be helpful for investigating how other features (say, average path length), other than power-law degree distribution, are relevant to the performance of scale-free networks.

Finally, we stress that since we were only concerned with the percolation phase transition point, we merely gave the exact position of the percolation thresholds, omitting some other properties of bond percolation, such as the value of the critical exponents governing behavior close to the transition, the complete distribution of the cluster sizes, and closed-form expressions for the mean and variance of the distribution. All these are worth studying further in the future, which is beyond the scope of this paper.

Note added. A relevant publication [35] about bond percolation has come to our attention, where the authors showed that different percolation thresholds exist for different networks having the same degree distribution (not degree sequence as addressed in this present paper).

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