

Bond percolation on a class of clustered random networks

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(Received 28 April 2009; published 10 September 2009)

Analytical results are derived for the bond percolation threshold and the size of the giant connected component in a class of random networks with nonzero clustering. The network's degree distribution and clustering spectrum may be prescribed and theoretical results match well with numerical simulations on both synthetic and real-world networks.

DOI: [10.1103/PhysRevE.80.036107](https://doi.org/10.1103/PhysRevE.80.036107)

PACS number(s): 89.75.Hc, 64.60.ah, 87.23.Ge

Random network models have been extensively studied with a view to gaining insight into the structure and dynamics of many social, technological, and biological networks [1–3]. However, most analytical approaches rely on treelike approximations of the local network structure and thus neglect the presence of short loops (cycles) in the graphs. The *local clustering coefficient* for a node A is defined as the fraction of pairs of neighbors of node A which are also neighbors of each other [4] and is typically non-negligible in real-world networks. The *degree-dependent clustering* or *clustering spectrum* c_k is the average of the local clustering coefficient over the class of all nodes of degree k [5,6]. The question of how network models with nonzero c_k (taken, for example, from real-world network data) differ from randomly wired (*configuration-model*) networks with the same degree distribution P_k is of considerable interest.

The bond percolation problem for a network may be stated as follows: each edge of the network graph is visited once and *damaged* (deleted) with probability $1-p$. The quantity p is the *bond occupation probability* and the non-damaged edges are termed *occupied*. The size of the *giant connected component* (GCC) of the graph becomes nonzero at some critical value of $p > 0$: this critical value of p is termed the *bond percolation threshold* p_{th} . The bond percolation problem has applications in epidemiology, where p is related to the average transmissibility of a disease and the GCC represents the size of an epidemic outbreak [7,8], and in the analysis of technological networks, where the resilience of a network to the random failure of links is quantified by the size of the GCC [9]. Analytical solutions for percolation on randomly wired networks and on correlated networks are well known [10–13], but these cases have zero clustering in the limit of infinite network size.

In this paper we introduce a class of networks with nonzero clustering and demonstrate analytical solutions for the GCC size and the bond percolation threshold. Most previous studies of clustering effects on percolation rely on numerical simulations using various algorithms to generate clustered networks, e.g., [14–16]. Analytical solutions were found by Newman [17] for a bipartite graph model of highly clustered networks. However, the bipartite graph model (in contrast to the model discussed here) is not amenable to fitting to a prescribed degree distribution P_k . The bipartite graph model of Guillaume and Latapy [18] may be fitted to real-world data but their networks do not permit analytical solution of the percolation problem. Serrano and Boguñá [9,19] also obtained approximate analytical solutions, but only for weak

clustering cases with $c_k < 1/(k-1)$. Trapman [20] introduced a model of clustering in structured graphs based on embedding cliques (complete subgraphs) within a random tree structure. We show below that this model and its generalization [21] are in fact special cases of the model presented here. In a recent paper [22], Newman introduced a triangle-based model of clustered networks which may be seen as complementary to the model presented here: we discuss this model in detail at the end of the paper.

We consider random networks in which each node may be part of a single clique (a fully connected subgraph). Figure 1(a) shows a segment of such a network which contains one 3-clique (triangle), one 4-clique, and a single node which is not a member of a clique (for notational convenience we will refer to such individual nodes as members of a 1-clique). Nodes which are members of a c -clique have $c-1$ edges linking them to neighbors within the same clique. They also have an additional $k-c+1$ neighbors who are not in the same

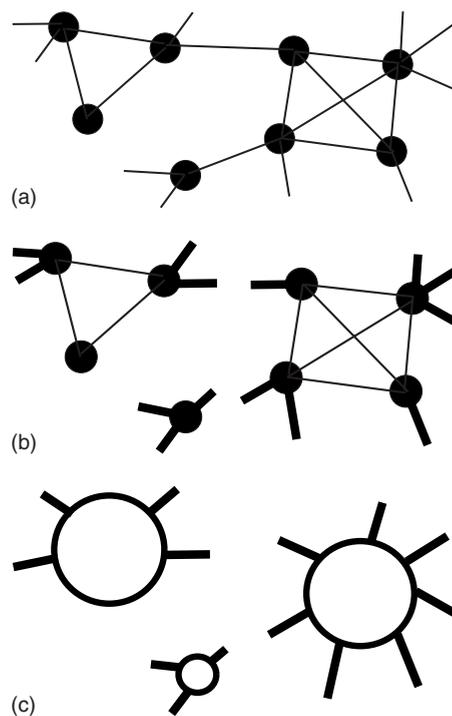
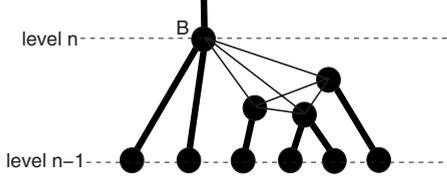


FIG. 1. (a) Segment of a clustered random network; (b) split into disjoint cliques with external links emphasized; (c) corresponding supernodes.


 FIG. 2. Tree diagram for updating the state of node B .

clique as themselves, where k is the node degree (with $k \geq c-1$). Edges which are not internal to a clique are termed *external links*. In Fig. 1(b) the external links are highlighted with thick lines, but for the purposes of the bond percolation problem they are indistinguishable from clique edges. In networks of this type each node is a member of at most one clique, and so the network can be decomposed into disjoint cliques which are linked together by the set of external links; see Fig. 1(b) [27]. If each clique is regarded as a *supernode* [Fig. 1(c)] then realizations of the random network may be generated by connecting together randomly chosen pairs of the external link stubs as in the configuration model for standard random networks [12].

The fundamental quantity describing networks of this type is the joint probability distribution $\gamma(k,c)$ giving the probability that a randomly chosen node in the network has degree k and is a member of a c -clique. Note $\gamma(k,c)=0$ for $k < c-1$, i.e., k -degree nodes can only be members of c -cliques if their degree is high enough to provide links to all $c-1$ clique neighbors. The degree distribution P_k of the network (probability that a random node has k neighbors) is obtained from γ by averaging over all cliques:

$$P_k = \sum_{c=1}^{k+1} \gamma(k,c) = \sum_c \gamma(k,c). \quad (1)$$

A node chosen at random from the set of all k -degree nodes is a member of a c -clique with probability $\gamma(k,c)/P_k$. As a member of a c -clique, it is part of $\binom{c-1}{2}$ triangles and so its local clustering coefficient is $\binom{c-1}{2}/\binom{k}{2}$. Therefore, the degree-dependent clustering coefficient c_k is given in terms of γ by

$$c_k = \sum_c \frac{\gamma(k,c)}{P_k} \frac{(c-1)(c-2)}{k(k-1)}. \quad (2)$$

The class of networks described by the joint pdf $\gamma(k,c)$ includes the well-studied configuration model [12] for which $\gamma(k,c) = \delta_{c1} P_k$. This limit contains no cliques and hence the clustering (in the infinite network size limit) vanishes. Also contained within the class of networks is the Trapman model [20,21] in which a fraction f_k of k -degree nodes form cliques of precisely k nodes giving $\gamma(k,c) = \delta_{c1}(1-f_k)P_k + \delta_{ck}f_k P_k$.

To determine the expected size of the GCC in the damaged network we choose a random node A of the network and approximate the network as a tree structure, with the node A at the top (root) of the tree. Each level of the tree structure (see Fig. 2) is accessed from the level above by traversing one external link. If a node is part of a c -clique, the remaining $c-1$ clique neighbors are shown at an inter-

mediate level. Because the graph of supernodes [Fig. 1(c)] is connected using the configuration model, this tree structure is a locally accurate approximation to the original network in the limit of infinite system size.

To calculate the probability that node A is part of the GCC, we apply a tree-based approach which is generalizable to a variety of cascade dynamics on networks [23] and is related to work on the random field Ising model [24]. We label nodes which are part of a connected component as *active* with the remaining nodes termed *inactive*. All nodes of the tree are initially considered inactive and we examine the propagation of the active state upward through the tree (from leaves to root) as an infection process beginning from an infinitesimally small fraction of active nodes infinitely deep in the tree. Consider a node at level n , e.g., node B in Fig. 2. Initially B (and its parent at level $n+1$) is inactive, but suppose nodes at level $n-1$ are active with probability q . If B has degree k and is a member of a c -clique (e.g., $k=6$ and $c=4$ in Fig. 2), it has $k-c+1$ external links, one of which necessarily leads to its parent at level $n+1$. The node B will become active if any one of its $k-c$ externally linked children at level $n-1$ is active provided that an occupied edge joins that child to B ; thus, the probability that B is *not* activated in this fashion is $(1-pq)^{k-c}$. The other mechanism whereby B may be activated is via its neighbors in the c -clique; writing Q_c for the probability that the top node (such as B) of a c -clique is activated by its clique neighbors, we have the total probability of activation for B of $1 - (1-pq)^{k-c}(1-Q_c)$. The probability Q_c is calculated using the $P(m|k)$ functions introduced and tabulated in [17], which are polynomials in p giving the probability that a randomly chosen node in a damaged (i.e., taking into account bond percolation) c -clique belongs to a connected cluster of m nodes (including itself) within the clique. Since node B is activated if any one of its $m-1$ connected neighbors is active, we have

$$Q_c = \sum_{m=1}^c P(m|c) [1 - (1-\bar{q}_c)^{m-1}], \quad (3)$$

where \bar{q}_c is the probability of a c -clique member at the intermediate level being activated by his level- $(n-1)$ children:

$$\bar{q}_c = \sum_{k'} \frac{\gamma(k',c)}{\sum_{k''} \gamma(k'',c)} [1 - (1-pq)^{k'-c+1}]. \quad (4)$$

Here $\gamma(k',c)/\sum_{k''} \gamma(k'',c)$ is the degree distribution of nodes which are members of cliques of size c and the remaining term is the probability that a k' -degree node in a c -clique is activated by one of its $k'-c+1$ children at level $n-1$.

Given q , we can therefore calculate, using Eqs. (3) and (4), the probability of B becoming active. To close the system of equations, we consider the parent of B at level $n+1$, for whom q is the probability that one of its children is active. Since node B has $k-c+1$ external links in total, the probability of it being a child of a random level- $(n+1)$ node is $\Pi_{kc} = (k-c+1)\gamma(k,c)/z_e$, where $z_e = \sum_{k',c'} (k'-c'+1)\gamma(k',c')$ is the average number of external links per node. Combining the equations above gives the closure relation

$$q = \sum_{k,c} \Pi_{kc} [1 - (1-pq)^{k-c} (1-Q_c)] \equiv G(q). \quad (5)$$

Equations (3)–(5) are solved by iterating from an infinitesimally small value of q to a steady-state solution: this determines the probability (in an infinite network) that a node is active, conditional on its parent being inactive. The final calculation of the GCC size considers the node A at the top (root) of the tree: with probability $\gamma(k,c)$ this has $k-c+1$ direct links to the level below. By similar arguments to before, node A is active with probability

$$S = \sum_{k,c} \gamma(k,c) [1 - (1-pq)^{k-c+1} (1-Q_c)], \quad (6)$$

where q is the solution of Eqs. (3)–(5) and S is the expected fractional size of the GCC.

Note that if we set $\gamma(k,c) = \delta_{c1} P_k$, Eqs. (5) and (6) reduce to their well-studied configuration model versions (using $Q_1=0$). The bond percolation results of [20,21] for the generalized Trapman model are also a special case of Eqs. (3)–(6). Also of interest is the GCC size in an undamaged network—this is obtained from our equations by setting $p=1$ [for which $P(m|c) = \delta_{mc}$].

The bond percolation threshold is the value of p at which the GCC size first becomes nonzero. This may be determined from the cascade condition [21,23] $G'(0)=1$, where $G(q)$ is defined in Eq. (5). The resulting polynomial equation for p may be written in the form

$$\frac{1}{z_c} \sum_{k,c} (k-c+1) \gamma(k,c) [p(k-c) + (z_c - c + 1) D_c(p)] = 1, \quad (7)$$

where $D_c(p) = p \sum_{m=1}^c (m-1) P(m|c)$ (see [21]) and z_c is the average degree of nodes in cliques of size c : $z_c = \sum_k k \gamma(k,c) / \sum_k \gamma(k',c)$.

We now describe an algorithm for generating realizations of random networks with a prescribed distribution $\gamma(k,c)$. For a large number \tilde{N} (which is related to the number N of nodes in the final network, see below), we choose \tilde{N} random numbers c_i ($i=1$ to \tilde{N}) with pdf $[\sum_k \gamma(k,c)/c] / [\sum_{k,c'} \gamma(k,c')/c']$ to be the clique sizes in the network realization. For each c_i , we create c_i nodes in a complete subgraph and assign their degrees k_j ($j=1$ to c_i) by drawing random numbers from a distribution with density $\gamma(k,c_i) / \sum_{k'} \gamma(k',c_i)$. Node j in clique i then has $k_j - c_i + 1$ external link stubs associated with it. Having created all \tilde{N} cliques in this fashion, we randomly choose pairs of external link stubs and connect them together to create the random network (cf. Fig. 1). The expected number of nodes in a network generated using this algorithm is $N = \tilde{N} / [\sum_{k,c} \gamma(k,c)/c]$, which allows us to estimate the value of \tilde{N} needed to produce a final network of size N . For finite-sized networks, the presence of cliques means this algorithm is not guaranteed to give exactly N nodes in the final network, but in practice we find the variation in the network size is negligibly small for sufficiently large N .

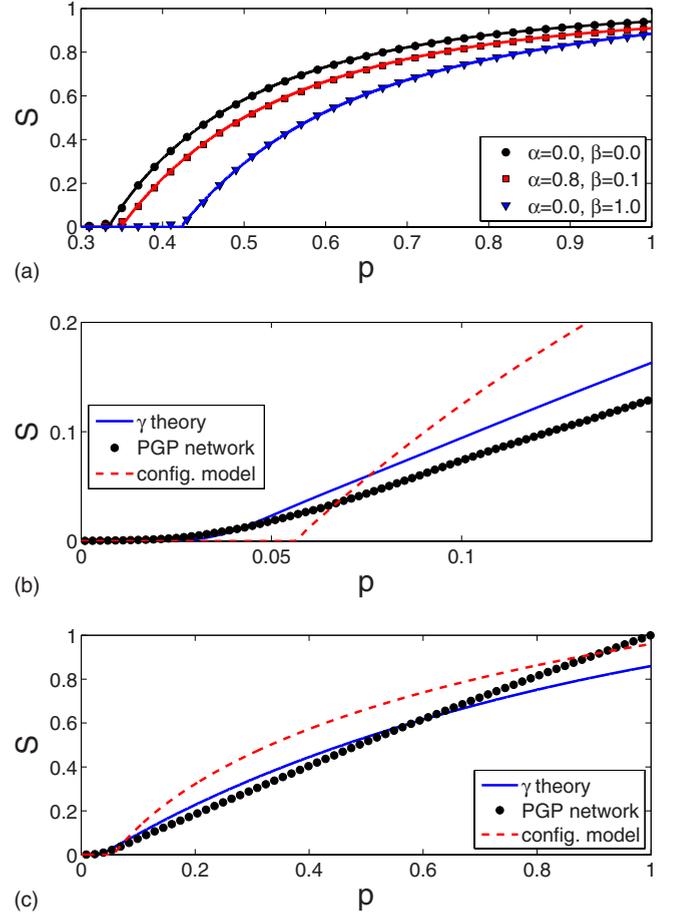


FIG. 3. (Color online) Size of giant connected component as a function of bond occupation probability for (a) synthetic networks with Poisson degree distribution; (b) pretty-good-privacy network, for p near p_{th} ; (c) as (b), but for all p values.

Figure 3(a) shows a comparison between GCC sizes from theory [from Eqs. (3)–(6)] and numerical simulations on networks with the Poisson degree distribution $P_k = z^k e^{-z} / k!$ and mean degree $z=3$. We create nonzero clustering in the networks by inserting 3-cliques (triangles) and 4-cliques; specifically, we set $\gamma(k,c) = [(1-\alpha-\beta)\delta_{c1} + \alpha\delta_{c3} + \beta\delta_{c4}]P_k$ for $k \geq 3$. This embeds a fraction α and β of k -degree nodes in 3-cliques and 4-cliques, respectively, with the remainder as individuals (i.e., 1-cliques). Since nodes of degree k cannot be part of c -cliques when c exceeds $k+1$, we deal with nodes of degree $k < 3$ as follows: $\gamma(2,c) = [(1-\alpha)\delta_{c1} + \alpha\delta_{c3}]P_2$, and $\gamma(k,c) = P_k \delta_{c1}$ for $k=0$ or 1 . The case $\alpha=\beta=0$ gives the standard configuration model network with zero clustering. We also show results for $\alpha=0.8, \beta=0.1$ and for $\alpha=0, \beta=1$. Using Eq. (2), the first of these corresponds to a global clustering coefficient $C = \sum_k P_k c_k$ of 0.31, while the second case, which contains only 4-cliques, has $C=0.35$. The corresponding bond percolation thresholds may be calculated from the polynomial Eq. (7) using (see [21]) $D_3(p) = 2p^2(1+p-p^2)$ and $D_4(p) = 3p^2(1+2p-7p^3+7p^4-2p^5)$. The resulting values are $p_{th}=0.349$ and $p_{th}=0.422$, both exceeding the configuration model value of $p_{th}=1/z=1/3$ [10,11]. Numerical simulation results on networks of size $N=10^5$ are shown by the symbols, while the curves are the theoretical predictions of

Eqs. (3)–(6). The agreement between theory and numerics is excellent.

One of the motivations for the introduction of the γ networks is the ability to obtain analytical results for networks with given degree distribution P_k and clustering spectrum c_k . Equations (1) and (2) constrain the distribution $\gamma(k, c)$ to fit a desired P_k and c_k , which may be measured, for example, in a real-world network. However, these constraints still permit significant freedom in choosing $\gamma(k, c)$. It is convenient therefore to consider a parametrization of $\gamma(k, c)$ which allows straightforward fitting to given network data. We suppose that the distribution of clique sizes c occupied by nodes of degree k is given by a binomial distribution, defining

$$\gamma(k, c) = P_k \binom{k}{c-1} g_k^{c-1} (1-g_k)^{k-c+1}, \quad (8)$$

for $c=1$ to $k+1$. This distribution clearly satisfies Eq. (1) and it distributes the probability mass corresponding to the k -degree nodes over the c -clique sizes via the single parameter g_k . The relationship between the parameters g_k and the clustering spectrum c_k is remarkably simple; substituting parametrization (8) into Eq. (2) yields $c_k = g_k^2$. Thus, form (8) for γ may immediately be fitted to the P_k and c_k of a real-world data set by setting $g_k = \sqrt{c_k}$.

Figures 3(b) and 3(c) show the results of applying parametrization (8) to match the degree distribution and clustering spectrum of the connected component of the pretty-good-privacy (PGP) network [25]. The PGP network is highly clustered, with $c_k > 1/(k-1)$ for most k [9]. Numerical calculations of the GCC size in this network are shown by the symbols on Figs. 3(b) and 3(c); also shown are the theoretical predictions for the zero-clustering (configuration model) case and the results of Eqs. (3)–(6) with parametrization (8). The effects of clustering on the percolation threshold are well captured by the γ theory; see Fig. 3(b). Note that here, in contrast to the example in Fig. 3(a), clustering acts to decrease the percolation threshold: Eq. (7) gives $p_{th} = 0.0236$, which is less than half the configuration model value of 0.0559. The γ theory gives quite a good approximation to the actual GCC size for bond occupation probabilities

of p up to about 0.5 [Fig. 3(c)]; however, the behavior at larger p values is less accurate, with the predicted GCC in the undamaged ($p=1$) network being substantially smaller than its true value. This inaccuracy may be attributable to excessive clustering being induced by parametrization (8) for the large p case.

In summary, we have introduced a class of clustered random networks with arbitrary degree distribution and clustering spectrum and analytically determined the size of the GCC and the bond percolation threshold. Numerically generated networks show excellent agreement with the theoretical results and we have demonstrated the applicability of the theory by fitting to the pretty-good-privacy network to produce accurate predictions of the GCC size for small p . We have used a cascade-based approach here in preference to a generating function method, because (as we show in a subsequent paper) this approach generalizes to give analytical results for k -core sizes, Watts' threshold decision model, and other cascading dynamics on clustered networks [23].

It is instructive to compare our γ -theory networks with the clustered network model recently introduced by Newman [22]. In his model, a k -degree node may be a member of up to $k/2$ disjoint triangles (3-cliques) and thus have a local clustering coefficient of up to $1/(k-1)$. In contrast, nodes in the γ -theory networks can be members of only a single clique, but using large cliques can give arbitrarily high clustering. The restriction $c_k \leq 1/(k-1)$ imposed on Newman's model networks inhibits a direct fit to most real-world networks in contrast to our results in Fig. 3. It would be interesting to explore the possibility of modeling networks with multiple cliques per node (as in [22]) while allowing the cliques to be larger than triangles (as here). Indeed, a general model of this type is proposed in [26] but it seems unlikely that easily computable analytical solutions, as found here and in [22], can be obtained in this more general setting.

Discussions with Sergey Melnik, Adam Hackett, and Mason Porter are gratefully acknowledged. This work was funded by Science Foundation Ireland under Programme No. 06/IN.1/I366 and MACSI Programme No. 06/MI/005.

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