

Properties of highly clustered networks

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We propose and solve exactly a model of a network that has both a tunable degree distribution and a tunable clustering coefficient. Among other things, our results indicate that increased clustering leads to a decrease in the size of the giant component of the network. We also study susceptible/infective/recovered type epidemic processes within the model and find that clustering decreases the size of epidemics, but also decreases the epidemic threshold, making it easier for diseases to spread. In addition, clustering causes epidemics to saturate sooner, meaning that they infect a near-maximal fraction of the network for quite low transmission rates.

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I. INTRODUCTION

In recent years there has been considerable interest within the physics community in the structure and dynamics of networks, with applications to the Internet, the world-wide web, citation networks, and social and biological networks [1–3]. Two significant properties of networks have been particularly highlighted. First, one observes for most networks that the degree distribution is highly non-Poissonian [4–6]. (A network consists of a set of nodes or “vertices” joined by lines or “edges,” and the degree of a vertex is the number of edges attached to that vertex.) Histograms of vertex degree for many networks show a power-law form with an exponent typically between -2 and -3 , while other networks may have exponential or truncated power-law distributions. Second, it is found that most networks have a high degree of transitivity or clustering, i.e., there is a high probability that “the friend of my friend is also my friend” [7]. In topological terms, this means that there is a heightened density of loops of length three in the network, and more generally it is found that networks have a heightened density of short loops of various lengths [8].

It is now well understood how to calculate the properties of networks with arbitrary degree distributions [9–13], but where clustering is concerned our understanding is much poorer. Most of the standard techniques used to solve network models break down when clustering is introduced, obliging researchers to turn to numerical methods [7,14–16].

In this paper, we present a plausible network model that incorporates both non-Poisson degree distributions and non-trivial clustering, and which is exactly solvable for many of its properties, including component sizes, percolation threshold, and clustering coefficient. Our results show that clustering can have a substantial effect on the large-scale structure of networks, and produces behaviors that are both quantitatively and qualitatively different from the simple nonclustered case.

The outline of the paper is as follows. In Sec. II we define our model and in Sec. III we derive exact expressions for a variety of its properties. In Sec. IV we discuss the form of these expressions for some sensible choices of the parameters, and also consider the behavior of epidemic processes within our model. In Sec. V we give our conclusions.

II. THE MODEL

There is empirical evidence that clustering in networks arises because the vertices are divided into groups [17,18] with a high density of edges between members of the same group, and hence a high density of triangles, even though the density of edges in the network as a whole may be low. Our model is perhaps the simplest and most obvious realization of this idea. We describe it here in the anthropomorphic language of social networks, although our arguments could be applied to any network that has an appropriate group structure.

We consider a network of N individuals divided into M groups. A social network, for example, might be divided up according to the location, family ties, occupation, interests, and so forth, of its members. (Many networks are indeed known to be divided into such groups [19].) Individuals can belong to more than one group, the groups they belong to being chosen, in our model, at random. Individuals are not necessarily acquainted with all other members of their groups. If two individuals belong to the same group then there is a probability p that they are acquainted and $q = 1 - p$ that they are not; if they have no groups in common then they are not acquainted. (A more sophisticated model, in which there are many nested levels of groups within groups and a spectrum of acquaintance probabilities depending on these levels, has been proposed and studied by Watts, Dodds, and Newman [20] and independently by Kleinberg [21]. For this paper, however, we confine ourselves to the simpler case.) In addition to the probability p , the model is parameterized by two probability distributions: r_m is the probability that an individual belongs to m groups and s_n is the probability that a group contains n individuals.

Mathematically, the model can be regarded as a bond percolation process on the one-mode projection of a bipartite random graph. The structure of individuals and groups forms the bipartite graph, the network of shared groups is the projection of that graph onto the individuals alone, and the probability p that one of the possible contacts in this projection is actually realized corresponds to a bond percolation process on the projection. See Fig. 1.

III. ANALYTIC DEVELOPMENTS

We can derive a variety of exact results for our model in the limit of large size using generating function methods.

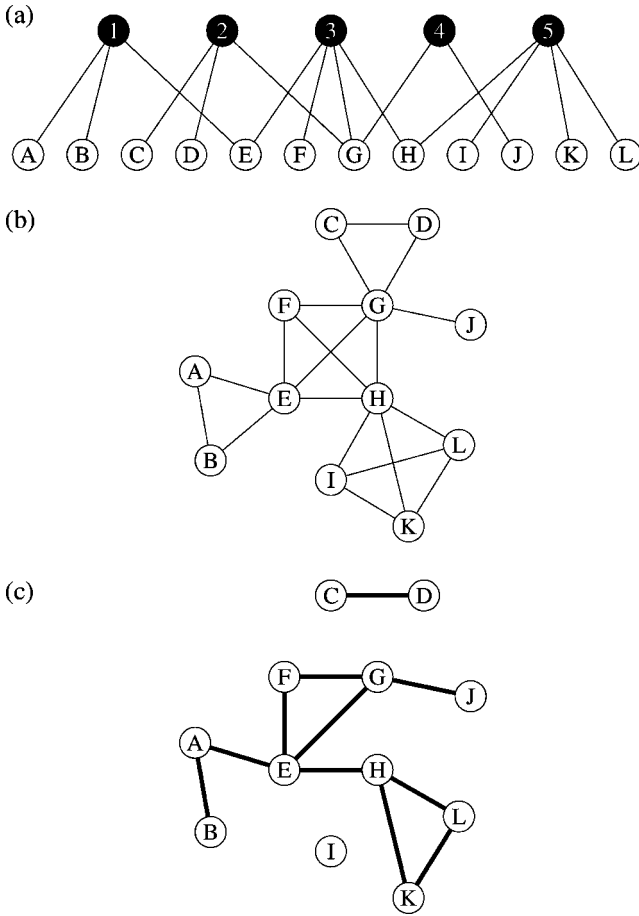


FIG. 1. The structure of the network model described in this paper. (a) We represent individuals (A–L) and the groups (1–5) to which they belong with a bipartite graph structure. (b) The bipartite graph is projected onto the individuals only. (c) The connections between individuals are chosen by bond percolation on this projection with bond occupation probability p . The net result is that individuals have probability p of knowing others with whom they share a group.

There are four fundamental generating functions that we will use:

$$f_0(z) = \sum_{m=0}^{\infty} r_m z^m, \quad f_1(z) = \mu^{-1} \sum_{m=0}^{\infty} m r_m z^{m-1}, \quad (1)$$

$$g_0(z) = \sum_{n=0}^{\infty} s_n z^n, \quad g_1(z) = \nu^{-1} \sum_{n=0}^{\infty} n s_n z^{n-1}, \quad (2)$$

where $\mu = \sum_m m r_m$ and $\nu = \sum_n n s_n$ are the mean numbers of groups per person and people per group, respectively.

A. Degree distribution

Consider a randomly chosen person A , who belongs to some number of groups m . The number j of A 's acquaintances within one particular group of size n is binomially distributed according to $\binom{n-1}{j} p^j q^{n-1-j}$. We represent this distribution by its generating function:

$$\sum_{j=0}^{n-1} \binom{n-1}{j} p^j q^{n-1-j} z^j = [pz + q]^{n-1}. \quad (3)$$

Averaging over group size, the full generating function for the neighbors in a single group is $\nu^{-1} \sum_{n=0}^{\infty} n s_n [pz + q]^{n-1} = g_1(pz + q)$, and for the neighbors of a single person is $f_0(g_1(pz + q))$. This allows us to calculate the degree distribution for any given r_m and s_n , and by judicious choice of these fundamental distributions, we can arrange for the degree distribution to take a wide variety of forms. We give some examples shortly. The mean degree $\langle k \rangle$ of an individual in the network is given by

$$\langle k \rangle = [\partial_z f_0(g_1(pz + q))]_{z=1} = p \mu g_1'(1). \quad (4)$$

B. Clustering coefficient

The clustering coefficient C is a measure of the level of clustering in a network [7]. It is defined as the mean probability that two vertices in a network are connected, given that they share a common network neighbor. Mathematically, it can be written as three times the ratio of the number of triangles N_{Δ} in the network to the number of connected triples of vertices N_3 [12]. In the present case, we have

$$N_{\Delta} = \frac{1}{6} N p^3 f_0''(1) g_1''(1),$$

$$N_3 = \frac{1}{2} N p^2 \{f_0''(1)[g_1'(1)]^2 + f_0'(1)g_1''(1)\}, \quad (5)$$

and hence the clustering coefficient is

$$C = \frac{3N_{\Delta}}{N_3} = p \frac{f_0'(1)g_1''(1)}{f_0''(1)[g_1'(1)]^2 + f_0'(1)g_1''(1)} = p C_b, \quad (6)$$

where C_b is the clustering coefficient of the simple one-mode projection of the bipartite graph, Fig. 1(b) [12]. In other words, one can interpolate smoothly and linearly from $C=0$ to the maximum possible value for this type of graph, simply by varying p . (In the limit $C=0$, our model becomes equivalent to the standard unclustered random graphs studied previously [9,12].) The average number of groups to which people belong and the parameter p give us two independent parameters that we can vary to allow us to change C while keeping the mean degree $\langle k \rangle$ constant. (Other parameter choices are also possible, but these are perhaps the simplest to work with.) Alternatively, and perhaps more logically, we can regard C and $\langle k \rangle$ as the defining parameters for the model and calculate the appropriate values of other quantities from these.

The *local* clustering coefficient C_i for a vertex i has also been the subject of recent study. C_i is defined to be the fraction of pairs of neighbors of i that are neighbors also of each other [7]. For a variety of real-world networks C_i is found to fall off with degree k_i of the vertex as $C_i \sim k_i^{-1}$ [17,18]. This behavior is reproduced nicely by our model. Vertices with higher degree belong to more groups in proportion to k_i (provided we keep the mean group size fixed),

while the number of pairs of their neighbors is $\frac{1}{2}k_i(k_i - 1)$, and the combination gives precisely $C_i \sim k_i^{-1}$ as k_i becomes large.

C. Component structure

To solve for the component structure of the model, we focus on acquaintance patterns within a single group. Suppose person A belongs to a group of n people. We would like to know how many individuals A is connected to within that group, either directly (via a single edge) or indirectly (via any path through other members of the group). Let $P(k|n)$ be the probability that vertex A belongs to a connected cluster of k vertices in the group, including itself. We have

$$P(k|n) = \binom{n-1}{k-1} q^{k(n-k)} P(k|k), \quad (7)$$

which follows since we can make an appropriate graph of n labeled vertices by taking a graph of k vertices, all of which A is connected to, and adding $n - k$ others to it, which we can do in $\binom{n-1}{k-1}$ distinct ways, each with probability $q^{k(n-k)}$ (the probability that none of the newly added vertices connects to any of the k old vertices).

Probabilities $P(k|k)$ are polynomials in p of order $s = \frac{1}{2}k(k - 1)$, which can be written in the form

$$P(k|k) = \sum_{l=0}^s M_l^k p^l q^{s-l}, \quad (8)$$

where M_l^k is the number of labeled connected graphs with k vertices and l edges. While some progress can be made in evaluating the M_l^k by analytic methods (see Appendix A), the resulting expressions are poorly suited to mechanical enumeration of $P(k|k)$. For practical purposes, it is simpler to observe that

$$P(k|k) = 1 - \sum_{l=0}^{k-1} P(l|k), \quad (9)$$

which, in combination with Eq. (7), allows us to evaluate $P(k|k)$ iteratively, given the initial condition $P(1|1) = 1$. In Table I we give the first few $P(k|k)$ for k up to 10.

The generating function for the number of vertices to which A is connected, by virtue of belonging to this group of size n , is

$$h_n(z) = \sum_{k=1}^n P(k|n) z^{k-1} = \sum_{k=1}^n \binom{n-1}{k-1} q^{k(n-k)} P(k|k) z^{k-1}. \quad (10)$$

Notice the appearance of z^{k-1} . This is a generating function for the number of vertices A is connected to excluding itself. Averaging over the size distribution of groups then gives $h(z) = \nu^{-1} \sum_n n s_n h_n(z)$, and the total number of others to whom A is connected via all the groups they belong to is generated by $G_0(z) = f_0(h(z))$, where $f_0(z)$ is defined in Eq. (1). If we reach an individual by following a randomly chosen edge, then we are more likely to arrive at individuals who belong to a large number of groups. This means that the

TABLE I. Polynomials $P(k|k)$ for values of k up to 10.

k	$P(k k)$
1	1
2	p
3	$3 p^2 q + p^3$
4	$16 p^3 q^3 + 15 p^4 q^2 + 6 p^5 q + p^6$
5	$125 p^4 q^6 + 222 p^5 q^5 + 205 p^6 q^4 + 120 p^7 q^3 + 45 p^8 q^2 + 10 p^9 q + p^{10}$
6	$1296 p^5 q^{10} + 3660 p^6 q^9 + 5700 p^7 q^8 + 6165 p^8 q^7 + 4945 p^9 q^6 + 2997 p^{10} q^5 + 1365 p^{11} q^4 + 455 p^{12} q^3 + 105 p^{13} q^2 + 15 p^{14} q + p^{15}$
7	$16807 p^6 q^{15} + 68295 p^7 q^{14} + 156555 p^8 q^{13} + 258125 p^9 q^{12} + 331506 p^{10} q^{11} + 343140 p^{11} q^{10} + 290745 p^{12} q^9 + 202755 p^{13} q^8 + 116175 p^{14} q^7 + 54257 p^{15} q^6 + 20349 p^{16} q^5 + 5985 p^{17} q^4 + 1330 p^{18} q^3 + 210 p^{19} q^2 + 21 p^{20} q + p^{21}$
8	$262144 p^7 q^{21} + 1436568 p^8 q^{20} + 4483360 p^9 q^{19} + 10230360 p^{10} q^{18} + 18602136 p^{11} q^{17} + 28044072 p^{12} q^{16} + 35804384 p^{13} q^{15} + 39183840 p^{14} q^{14} + 37007656 p^{15} q^{13} + 30258935 p^{16} q^{12} + 21426300 p^{17} q^{11} + 13112470 p^{18} q^{10} + 6905220 p^{19} q^9 + 3107937 p^{20} q^8 + 1184032 p^{21} q^7 + 376740 p^{22} q^6 + 98280 p^{23} q^5 + 20475 p^{24} q^4 + 3276 p^{25} q^3 + 378 p^{26} q^2 + 28 p^{27} q + p^{28}$
9	$4782969 p^8 q^{28} + 33779340 p^9 q^{27} + 136368414 p^{10} q^{26} + 405918324 p^{11} q^{25} + 974679363 p^{12} q^{24} + 1969994376 p^{13} q^{23} + 3431889000 p^{14} q^{22} + 5228627544 p^{15} q^{21} + 7032842901 p^{16} q^{20} + 8403710364 p^{17} q^{19} + 8956859646 p^{18} q^{18} + 8535294180 p^{19} q^{17} + 7279892361 p^{20} q^{16} + 5557245480 p^{21} q^{15} + 3792906504 p^{22} q^{14} + 2309905080 p^{23} q^{13} + 1251493425 p^{24} q^{12} + 600775812 p^{25} q^{11} + 254183454 p^{26} q^{10} + 94143028 p^{27} q^9 + 30260331 p^{28} q^8 + 8347680 p^{29} q^7 + 1947792 p^{30} q^6 + 376992 p^{31} q^5 + 58905 p^{32} q^4 + 7140 p^{33} q^3 + 630 p^{34} q^2 + 36 p^{35} q + p^{36}$
10	$100000000 p^9 q^{36} + 880107840 p^{10} q^{35} + 4432075200 p^{11} q^{34} + 16530124800 p^{12} q^{33} + 50088981600 p^{13} q^{32} + 128916045720 p^{14} q^{31} + 288982989000 p^{15} q^{30} + 573177986865 p^{16} q^{29} + 1016662746825 p^{17} q^{28} + 1624745199910 p^{18} q^{27} + 2352103292070 p^{19} q^{26} + 3096620034795 p^{20} q^{25} + 3717889913655 p^{21} q^{24} + 4078716030900 p^{22} q^{23} + 4093594934220 p^{23} q^{22} + 3761135471805 p^{24} q^{21} + 3163862003211 p^{25} q^{20} + 2435820178050 p^{26} q^{19} + 1714943046390 p^{27} q^{18} + 1102765999275 p^{28} q^{17} + 646542946125 p^{29} q^{16} + 344847947664 p^{30} q^{15} + 166867565040 p^{31} q^{14} + 73005619995 p^{32} q^{13} + 28759950345 p^{33} q^{12} + 10150589610 p^{34} q^{11} + 3190186926 p^{35} q^{10} + 886163125 p^{36} q^9 + 215553195 p^{37} q^8 + 45379620 p^{38} q^7 + 8145060 p^{39} q^6 + 1221759 p^{40} q^5 + 148995 p^{41} q^4 + 14190 p^{42} q^3 + 990 p^{43} q^2 + 45 p^{44} q + p^{45}$

distribution of other groups to which such an individual belongs is generated by the function $f_1(z)$ in Eq. (1), and the number of other individuals to which they are connected is generated by $G_1(z) = f_1(h(z))$.

Armed with these results, we can now calculate a variety of quantities for our model. We focus on two in particular, the position of the percolation threshold and the size of the giant component. The distribution of the number of individuals one step away from person A is generated by the function $G_0(z)$, while the number of individuals two steps away is generated by $G_0(G_1(z))$. (In this case, a “step” includes all people who can be reached by any path via the individuals in a single group. This definition is necessary to make the independence assumptions of the generating function formalism correct.) There is a giant component in the network if and only if the average number of individuals two steps away exceeds the average number of individuals one step away [12]. (This is a natural criterion: it implies that the number of people reachable is increasing with distance.) Thus, there is a giant component if $[\partial_z(G_0(G_1(z)) - G_0(z))]_{z=1} > 0$. Substituting for G_0 and G_1 , this result can be written

$$f'_1(1)h'(1) > 1. \tag{11}$$

When this condition is satisfied and there is a giant component, we define u to be the probability that one of the individuals to whom A is connected is *not* a member of this giant component. A is also not a member provided all of its neighbors are not so that u satisfies the self-consistency condition $u = G_1(u)$. Then the size of the giant component is given by $S = 1 - G_0(u)$.

IV. RESULTS

As an example of the application of these results, consider the simple version of our model in which all groups have the same size $n = \nu$. Then $h(z) = h_\nu(z)$ and the degree distribution is dictated solely by the distribution r_m of the number of groups to which individuals belong. We consider two examples of this distribution, a Poisson distribution and a power-law distribution.

Let us look first at the Poisson case $r_m = \mu^m e^{-\mu}/m!$, for which the calculations are particularly simple. The Poisson distribution corresponds to choosing the members of each group independently and uniformly at random. From Eqs. (4) and (6) we have

$$\langle k \rangle = p\mu(\nu - 1), \quad C = \frac{p}{1 + \mu(\nu - 1)/(\nu - 2)}. \tag{12}$$

In the right-hand panel of Fig. 2 we show results for the size of the giant component as a function of clustering for the case of groups of size $\nu = 10$ with $\langle k \rangle = 5$. As the figure shows, the giant component size decreases sharply as clustering is increased. The physical insight behind this result is that high clustering means more edges in all components, including the giant component, than are strictly necessary to hold the component together—there are many redundant paths between vertices formed by the many short loops of edges. Since fixing $\langle k \rangle$ also fixes the total number of edges, this means that the components must get smaller; the redun-

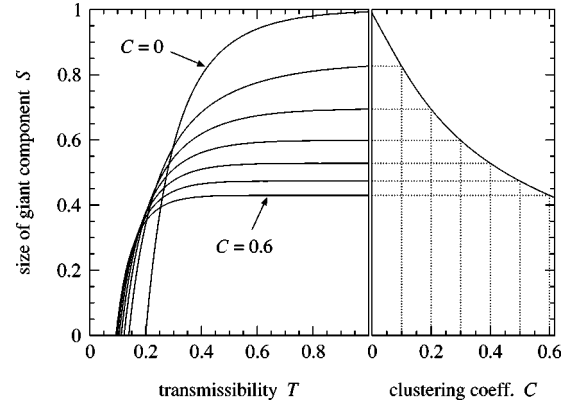


FIG. 2. Right panel: the size of the giant component of the graph as a function of clustering coefficient for the Poisson case with group size $\nu = 10$ and mean degree $\langle k \rangle = 5$. Left panel: the size of an epidemic outbreak for a susceptible/infective/recovered model on our network as a function of transmissibility T , for values of C from 0 to 0.6 in steps of 0.1.

dant edges are in a sense wasted, and the percolation properties of the network are similar to those for a network with fewer edges.

A. Epidemics

A topic of particular interest in the recent literature has been the spread of disease over networks. The classic susceptible/infective/recovered or SIR model of epidemic disease [22] can be generalized to an arbitrary contact network and mapped onto a bond percolation model on that network with bond occupation probability equal to the transmissibility T of the disease [23,24]. (The transmissibility is the mean probability that an infective individual will transmit the disease to a susceptible network neighbor, integrated over the entire time for which they are susceptible.) Since we have already solved the bond percolation problem for our networks, we can also immediately solve the SIR model, by making the substitution $p \rightarrow pT$. We show some results in the left-hand panel of Fig. 2 for the same choice of degree distributions as before. In general, we see a percolation transition at some value of T , which corresponds to the epidemic threshold for the model (denoted by $R_0 = 1$ in traditional mathematical epidemiology). Above this threshold there is a giant component whose size measures the number of people infected in an epidemic outbreak of the disease.

The size of the epidemic tends to the size of the giant component for the network as a whole as $T \rightarrow 1$, as represented by the dotted lines in the figure, and is therefore typically smaller the higher the value of the clustering coefficient. However, it is interesting to note also that as C becomes large the epidemic size saturates, becoming virtually independent of T , long before we reach $T = 1$, suggesting that in clustered networks epidemics will reach most of the people who are reachable even for transmissibilities that are only slightly above the epidemic threshold. This behavior stands in sharp contrast to the behavior of ordinary fully mixed epidemic models, or models on random graphs without clustering, for which epidemic size shows no such satu-

ration [22,25]. It arises precisely because of the many redundant paths between individuals introduced by the clustering in the network, which provide many routes for transmission of the disease, making it likely that most of the individuals who can catch the disease will encounter it by one route or another, even for quite moderate values of T .

As we can also see from Fig. 2, the position of the epidemic threshold *decreases* with increasing clustering. At first this result appears counterintuitive. The smaller giant component for higher values of C seems to indicate that the model finds it harder to percolate, and we might therefore expect the percolation threshold to be higher. In fact, however, the many redundant paths between vertices when clustering is high make it easier for the disease to spread, not harder, and so lower the position of the threshold. Thus, clustering has both bad and good sides where the spread of disease is concerned. On the one hand clustering lowers the epidemic threshold for a disease and also allows the disease to saturate the population at quite low values of the transmissibility, but on the other hand the total number of people infected is decreased.

B. Power-law degree distributions

Now consider the case of a power-law degree distribution. Networks with power-law degree distributions occur in many different settings and have attracted much recent attention [2,6,26,27]. Percolation processes on random graphs with power-law degree distributions notably always have a giant component, no matter how small the percolation probability [28]. This means, for example, that a disease will always spread on such a network, regardless of its transmissibility. This result can be modified by more complex network structure, such as correlations between the degrees of adjacent vertices [29,30], but, as we now argue, it is not affected by clustering. To see why this is so, note that according to the findings reported here, we would have to reduce clustering to increase the threshold above zero, but this is not possible starting from a random graph, which has $C=0$ to begin with in the limit of large size. (C is fundamentally a probability and hence cannot take a negative value.) Mathematically, we can demonstrate that our network always percolates using Eq. (11). We can create a power-law degree distribution by making the distribution of number of groups an individual belongs to follow a power law $r_m \sim m^{-\alpha}$. (If we wish, we can also make the distribution of group sizes follow a power law—it doesn't change the qualitative form of our results.) The bond occupation probability, and hence the transmissibility, enters Eq. (11) through the function $h(z)$, but does not affect $f_1(z)$. We have $f_1'(1) = \sum_m m(m-1)r_m = \langle m^2 \rangle - \langle m \rangle$. For $\alpha < 3$, this diverges and hence Eq. (11) is always satisfied as long as p and T are both nonzero.

V. CONCLUSIONS

We have introduced a solvable model of a network with nontrivial clustering and used it to demonstrate, for instance, that increasing the clustering of a network while keeping the mean degree constant decreases the size of the giant compo-

nent. Increasing the clustering also decreases the size of an epidemic for an epidemic process on the network. On the other hand, it also allows the epidemic to saturate the network even for quite low infection rates, and it decreases the epidemic threshold. Among other things, this means that no amount of clustering will provide us with a nonzero epidemic threshold in networks with power-law degree distributions.

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APPENDIX: PROBABILITIES FOR CONNECTED GRAPHS

Equation (8) implies that we can find a general expression for $P(k|k)$ if we can calculate the number M_l^k of connected graphs with a given number of vertices k and number of edges l . The standard method for counting such graphs is to write down the exponential generating function for possibly disconnected graphs and perform an inverse exponential transform to give the so-called Riddell formula [31]:

$$\sum_{kl} M_l^k \frac{x^k}{k!} y^l = \log \left(1 + \sum_{n=1}^{\infty} (1+y)^{n(n-1)/2} \frac{x^n}{n!} \right). \quad (A1)$$

Putting $y \rightarrow p/q$, $x \rightarrow x\sqrt{q}$, and making use of Eq. (8), we then derive the following generating function for $P(k|k)$:

$$\sum_{k=1}^{\infty} q^{-k^2/2} P(k|k) \frac{x^k}{k!} = \log \left(\sum_{n=0}^{\infty} q^{-n^2/2} \frac{x^n}{n!} \right). \quad (A2)$$

The sum on the right-hand side is strongly divergent for $|q| < 1$, but progress can be made by allowing q to take a non-physical value greater than 1 and then analytically continuing to the physical regime. Using the fact that the Gaussian is its own Fourier transform:

$$e^{-t^2/2} = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-z^2/2} e^{izt} dz, \quad (A3)$$

the sum can be written [32] as

$$\begin{aligned} & \sum_{n=1}^{\infty} \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-z^2/2} e^{izn\sqrt{\log q}} dz \frac{x^n}{n!} \\ & = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} \exp \left(-\frac{1}{2} z^2 + x e^{iz\sqrt{\log q}} \right) dz, \end{aligned} \quad (A4)$$

where we have interchanged the order of sum and integral. Unfortunately, the integral cannot be carried out in closed form, and although some asymptotic results can be derived using saddle-point expansions, it does not appear at present that a closed-form solution for the generating function $h_n(z)$, Eq. (10), can be simply derived.

- [1] S.H. Strogatz, *Nature (London)* **410**, 268 (2001).
- [2] R. Albert and A.-L. Barabási, *Rev. Mod. Phys.* **74**, 47 (2002).
- [3] M.E.J. Newman, *SIAM Rev.* **45**, 167 (2003).
- [4] R. Albert, H. Jeong, and A.-L. Barabási, *Nature (London)* **401**, 130 (1999).
- [5] M. Faloutsos, P. Faloutsos, and C. Faloutsos, *Comput. Commun. Rev.* **29**, 251 (1999).
- [6] L.A.N. Amaral, A. Scala, M. Barthélémy, and H.E. Stanley, *Proc. Natl. Acad. Sci. U.S.A.* **97**, 11 149 (2000).
- [7] D.J. Watts and S.H. Strogatz, *Nature (London)* **393**, 440 (1998).
- [8] G. Caldarelli, R. Pastor-Satorras, and A. Vespignani, e-print cond-mat/0212026.
- [9] M. Molloy and B. Reed, *Random Struct. Algorithms* **6**, 161 (1995).
- [10] M. Molloy and B. Reed, *Combinatorics, Probab. Comput.* **7**, 295 (1998).
- [11] W. Aiello, F. Chung, and L. Lu, in *Proceedings of the 32nd Annual ACM Symposium on Theory of Computing* (Association of Computing Machinery, New York, 2000), pp. 171–180.
- [12] M.E.J. Newman, S.H. Strogatz, and D.J. Watts, *Phys. Rev. E* **64**, 026118 (2001).
- [13] F. Chung and L. Lu, *Annals of Combinatorics* **6**, 125 (2002).
- [14] K. Klemm and V.M. Eguiluz, *Phys. Rev. E* **65**, 036123 (2002).
- [15] P. Holme and B.J. Kim, *Phys. Rev. E* **65**, 026107 (2002).
- [16] Y. Moreno and A. Vázquez, *Eur. Phys. J. B* **31**, 265 (2003).
- [17] S.N. Dorogovtsev, A.V. Goltsev, and J.F.F. Mendes, *Phys. Rev. E* **65**, 066122 (2002).
- [18] E. Ravasz and A.-L. Barabási, *Phys. Rev. E* **67**, 026112 (2003).
- [19] M. Girvan and M.E.J. Newman, *Proc. Natl. Acad. Sci. U.S.A.* **99**, 8271 (2002).
- [20] D.J. Watts, P.S. Dodds, and M.E.J. Newman, *Science* **296**, 1302 (2002).
- [21] J.M. Kleinberg, in *Proceedings of the 2001 Neural Information Processing Systems Conference*, edited by T.G. Dietterich, S. Becker, and Z. Ghahramani (MIT Press, Cambridge, MA, 2002).
- [22] H.W. Hethcote, *SIAM Rev.* **42**, 599 (2000).
- [23] P. Grassberger, *Math. Biosci.* **63**, 157 (1983).
- [24] L.M. Sander, C.P. Warren, I. Sokolov, C. Simon, and J. Koopman, *Math. Biosci.* **180**, 293 (2002).
- [25] M.E.J. Newman, *Phys. Rev. E* **66**, 016128 (2002).
- [26] S.N. Dorogovtsev and J.F.F. Mendes, *Adv. Phys.* **51**, 1079 (2002).
- [27] A.-L. Barabási and R. Albert, *Science* **286**, 509 (1999).
- [28] R. Cohen, K. Erez, D. ben-Avraham, and S. Havlin, *Phys. Rev. Lett.* **85**, 4626 (2000).
- [29] M.E.J. Newman, *Phys. Rev. Lett.* **89**, 208701 (2002).
- [30] A. Vázquez and Y. Moreno, *Phys. Rev. E* **67**, 015101 (2003).
- [31] R.J. Riddell, Jr. and G.E. Uhlenbeck, *J. Chem. Phys.* **21**, 2056 (1953).
- [32] P. Flajolet, B. Salvy, and G. Schaeffer, INRIA Research Report No. 4581, 2002 (unpublished).