

## Epidemic Threshold in Structured Scale-Free Networks

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We analyze the spreading of viruses in scale-free networks with high clustering and degree correlations, as found in the Internet graph. For the susceptible-infected-susceptible model of epidemics the prevalence undergoes a phase transition at a finite threshold of the transmission probability. Comparing with the absence of a finite threshold in networks with purely random wiring, our result suggests that high clustering (*modularity*) and degree correlations protect scale-free networks against the spreading of viruses. We introduce and verify a quantitative description of the epidemic threshold based on the connectivity of the neighborhoods of the hubs.

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The description of the properties of several real networks has manifested that, despite their different natures, they share some common features [1–4]. They typically show a scale-free distribution of degree, high clustering, and a short average path length [5]. Although their topological properties have been studied in detail, a natural question that arises concerns the dynamical properties that result from the different topologies [4]. An example where the interaction network is crucial for the dynamics is the case of disease spreading. The study of complex networks as models of social, technological, and biological interaction has been shown to give valuable insights of how viruses, diseases, and rumors spread [6–9].

Most of these investigations have been performed assuming networks with homogeneous connectivity, where all individuals have approximately the same number (degree) of contacts with others. The network is typically modeled as a regular lattice, a random graph, or a superposition of these two [1]. For such topologies the number of infected individuals undergoes a phase transition: The single-contact transmission probability needs to exceed a critical threshold for a disease to become epidemic [10,11]. Recently, however, it has been discovered that many networks involved in the spread of diseases have a scale-free distribution of degree with a regime of power law decay. In particular, the web of human sexual contacts [12], the web of electronic mail communication [13], and the Internet [14] all contain highly connected individuals or nodes, so-called *hubs*, which had been disregarded by the assumption of homogeneous connectivity in previous works. The first model studies of disease spread in scale-free networks including hubs have revealed the absence of an epidemic threshold. Therefore it has been claimed that in technological and sociological networks even viruses with extremely low transmission probability can spread, and any prophylactic strategies aiming at a reduction of the average infectiveness would never result in a total eradication of a

prevalent virus. However, the alarming predictions have been obtained assuming random mixing. Apart from the scale-free degree distribution, all nontrivial topological properties of real-world sociological and technological networks have been neglected.

This Letter is dedicated to the analysis of virus spreading in networks with local structure. In order to account for the large clustering coefficient and the presence of degree correlations [14], we model the potentially infective contacts by highly clustered scale-free networks [15]. We find that the single-contact transmission probability needs to exceed a finite threshold for a virus to spread and prevail. Thus the behavior of epidemics is qualitatively different in highly clustered scale-free networks as compared with randomly wired scale-free networks. We conjecture that the difference can be explained by the presence or absence of connections between the hubs. Based on this conjecture, we define a new quantity, the secondary reproductive number, which predicts the epidemic threshold for highly clustered and randomly wired scale-free networks, as well as for the Internet graph as an example of a real-world scale-free network [16].

We consider the susceptible-infected-susceptible (SIS) model, as a simple description of epidemic spreading in a population [10]. Each individual in the population is either infected or susceptible at any point in time. The potential infection pathways are described by interpreting the individuals as the nodes of a network. The time-discrete dynamics is defined by synchronously updating the states of all individuals with the following rules: If individual *A* is infected at time  $t - 1$ , it is susceptible at time  $t$ . If, otherwise, individual *A* is susceptible at time  $t - 1$  and is connected to at least one individual infected at the same time, then with probability  $\lambda$  individual *A* is infected at time  $t$ . An important observable is the prevalence  $\rho$ . It is the time average of the fraction of infected individuals reached after a transient from the initial condition. Given

a network, the only parameter of the model is the infection probability  $\lambda$ . The information on the global spreading of a disease is contained in the function  $\rho(\lambda)$ .

The individuals are connected by highly clustered scale-free networks [15]. They are constructed by iteratively adding nodes and links in the following way: Generate a new node and connect it with all active nodes. Set the new node active as well. Set inactive one of the active nodes. The probability for deactivating node  $i$  is inversely proportional to its current number of links  $k_i$ . Close the iteration loop by generating the next new node and so forth, until the network size reaches the desired value  $N$ . Starting from an initial network of  $m$  fully interconnected active nodes, a network with an average degree  $\langle k \rangle = 2m$  links per node is generated. The degree distribution follows a power law  $P(k) = 2m^2 k^{-3}$ , and the clustering coefficient  $C = 5/6$ . Note that the deactivation mechanism mentioned here is only part of the growth mechanism of the network. It is not related to the dynamics of the SIS model which is applied after the network has been constructed.

By extensive simulations we have obtained the prevalence  $\rho(\lambda)$  for populations of  $N = 10^5$  individuals connected by highly clustered scale-free networks. In Fig. 1 we plot the fraction of infected individuals in the stationary state,  $\rho$ , for different values of the average connectivity. Only when  $\lambda$  is increased above a value  $\lambda_c$  is a significant prevalence observed. The effect of the topological properties of the highly clustered scale-free networks becomes clear when comparing the shape of the prevalence curves with those obtained for randomly wired scale-free net-

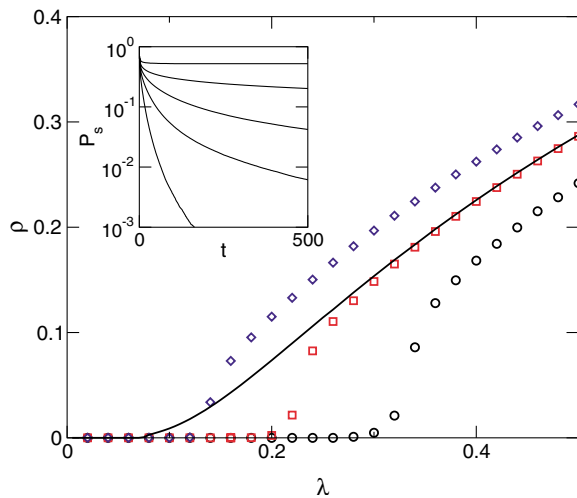


FIG. 1 (color online). Prevalence  $\rho$  (fraction of infected individuals in the stationary state) as a function of the spreading rate  $\lambda$  for highly clustered scale-free networks, with  $\langle k \rangle = 4$  (circles), 6 (squares), and 10 (diamonds), and for random scale-free networks with  $\langle k \rangle = 6$  (solid curve). The simulations have been run in networks containing  $10^5$  nodes and averaging over 100 different realizations. Inset: Survival probability,  $P_s$ , for a localized infection after  $t$  time steps. Parameter values (from bottom to top)  $\lambda = 0.15, 0.18, 0.2, 0.22, 0.25$ ; and  $\langle k \rangle = 6$ .

works. In the latter case no change of behavior is apparent as the prevalence and its slope vary smoothly when  $\lambda$  is increased.

Further insight into the behavior of epidemics in highly clustered scale-free networks is gained from the time evolution of the survival probability  $P_s$  shown in the inset of Fig. 1. Taking initial conditions with exactly one randomly chosen site infected,  $P_s(t)$  is the fraction of realizations that contain at least one infected site after  $t$  time steps. For values of  $\lambda$  well below the threshold  $\lambda_c$  the disease dies out exponentially, whereas for  $\lambda$  above  $\lambda_c$  the survival probability  $P_s$  approaches a nonzero plateau value. The change of behavior from rapid eradication to nonzero prevalence is observed at a finite value of the transmission probability, independent of the system size. Thus the prevalence of the SIS model in highly clustered scale-free networks undergoes a phase transition at a finite critical value  $\lambda_c$  of the transmission probability. In other words, viruses with a low transmission probability do not prevail in these networks.

In order to understand the role played by the topology we consider the average connectivity of the neighbors of a node  $i$

$$k_i^{nn} = \frac{1}{k_i} \sum_{j \in \mathcal{V}} k_j \tag{1}$$

where  $k_j$  is the degree of node  $j$  and the neighborhood of node  $i$  (i.e., the set of nodes directly connected to node  $i$ ) is called  $\mathcal{V}$ .

The structure of the highly clustered scale-free networks gives rise to correlations between the degree of a node and the degrees of its neighbors (see Fig. 2). For weakly connected nodes,  $\langle k^{nn} \rangle$  decays. For the hubs,  $k \gg \langle k \rangle$ , it reaches a constant value [17]

$$\langle k_h^{nn} \rangle = \langle k \rangle - 1. \tag{2}$$

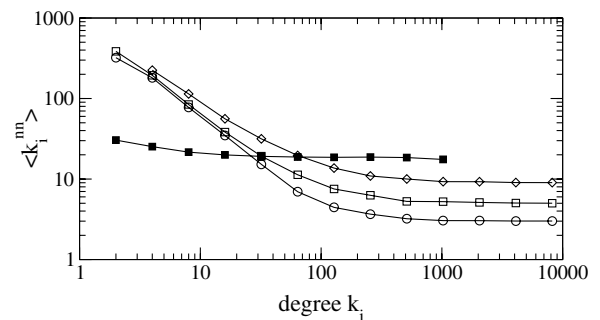


FIG. 2. Average degree of the neighbors of a node with connectivity  $k$  in the structured networks with  $\langle k \rangle = 4$  (circles), 6 (open squares), and 10 (diamonds). The asymptotic values for large  $k$  are  $3.0 \pm 0.1$ ,  $5.1 \pm 0.3$ , and  $9 \pm 1$  to be compared with the theoretical prediction  $\langle k_h^{nn} \rangle = \langle k \rangle - 1 = 3, 5$ , and  $9$ , respectively [cf. Eq. (3)]. The filled squares are the average degrees of the neighbors in random scale-free networks with  $\langle k \rangle = 6$ .

For comparison we also calculate  $\langle k^{nn} \rangle$  for random scale-free networks. If  $P_c(k'|k)$  is the conditional probability that a link belonging to a node with connectivity  $k$  points to a node with connectivity  $k'$ , then

$$\langle k^{nn} \rangle = \sum_{k'} k' P_c(k'|k) = \sum_{k'} \frac{(k')^2}{\langle k \rangle} P(k') = \frac{\langle k^2 \rangle}{\langle k \rangle}, \quad (3)$$

where we have used  $P_c(k'|k) \propto k' P(k')$  for random networks. Now we specifically consider randomly wired scale-free networks with the degree distribution  $P(k) = 2m^2 k^{-3}$ , the same distribution as in the highly clustered scale-free networks considered before. The networks are generated using the algorithm introduced in Ref. [2]. We identify a node by its rank  $i$  according to decreasing degree. Then node  $i$  has degree

$$k_i(N) = \frac{\langle k \rangle}{2} \left( \frac{N}{i} \right)^{0.5}. \quad (4)$$

Inserting  $\langle k^2 \rangle = \sum_{i=1}^N k_i^2(N) = \langle k \rangle^2 / 4 \ln N + \mathcal{O}(N^{-1})$  into Eq. (3) we obtain

$$\langle k^{nn} \rangle = \frac{\langle k \rangle}{4} \ln N, \quad (5)$$

independent, on average, of the node under consideration. This independence is confirmed numerically; see Fig. 2. It reflects the absence of correlations in the connectivity. Figure 3 shows the logarithmic dependence of  $\langle k^{nn} \rangle$  on system size, in contrast with the constant value obtained for the hubs in the structured (highly clustered scale-free) networks.

Now the different connectivity of the hubs in the highly clustered and random scale-free networks (both having the

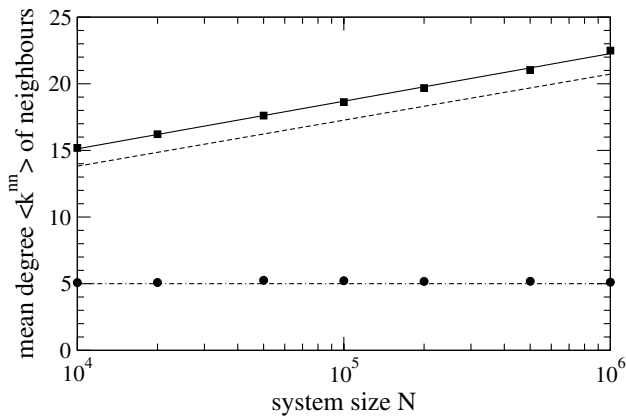


FIG. 3. Dependence of the average degree of the neighbors of a node with system size  $N$ . For the case of highly clustered scale-free networks, the value has been obtained averaging for nodes with  $k > 1000$ . The theoretical predictions  $\langle k \rangle - 1$  are also plotted (dash-dotted line). For the case of the randomly wired networks, the values are the average over the full range of available connectivities. The theoretical prediction  $\langle k \rangle / 4 \ln N$  is also plotted (dashed line).

same degree distribution) is clear: Whereas in the random case a hub is connected to other highly connected nodes, in the highly clustered networks the hubs are almost exclusively connected to low degree nodes. This difference is essential for the dynamics.

But how is this topological property related to the transmission threshold found of the SIS model? Let us define the *secondary reproductive number* as

$$R_2 = \lambda \langle k_h^{nn} \rangle. \quad (6)$$

We show below that the condition  $R_2 = 1$  recovers a previous prediction for the epidemic threshold in randomly wired networks, and gives a good estimate for the highly clustered scale-free networks and the Internet graph.

Previously, the behavior of the epidemics has been described in terms of the *basic reproductive number*,  $R_0$  [19]. It is defined as the average number of secondary infections produced by an infectious individual in a totally susceptible population and indicates whether a disease can ever invade a population. For random networks with broad degree distribution, the basic reproductive number is given by

$$R_0 = \lambda \frac{\langle k^2 \rangle}{\langle k \rangle}. \quad (7)$$

Only if  $R_0$  is larger than unity does the infection prevail. Employing Eq. (3) we find  $R_0 = R_2$ , such that in randomly wired networks the basic and secondary reproductive numbers coincide. Therefore, the condition  $R_2 = 1$  recovers the standard prediction of the epidemic threshold used in epidemiology, assuming random mixing of the population.

For the highly clustered scale-free networks, applying the condition  $R_2 = 1$  and using Eq. (2) predicts a threshold

$$\lambda_c = \frac{1}{\langle k \rangle - 1}. \quad (8)$$

The onset of nonzero prevalence found numerically (Fig. 1) is in good agreement with the prediction. Note that for the highly clustered scale-free networks in general  $R_2 \neq R_0$ . In particular,  $R_0$  diverges with system size  $N$  as  $\ln N$  leading to a false prediction of  $\lambda_c = 0$  in the limit of large highly clustered scale-free networks.

In order to check the applicability of the secondary reproductive number to empirical networks we investigate the Internet graph. We simulate the SIS model in the network of the autonomous systems at three different time stages of its evolution [20]. Figure 4 shows the prevalence of the SIS model as a function of the transmission probability. The threshold values predicted by the condition  $1 = \lambda_c \langle k_h^{nn} \rangle$  give a good estimate of the minimum transmission rate above which the disease spreads. However, using the basic reproductive number instead [Eq. (7)] gives threshold values 0.012, 0.009, and 0.007 for years 1997, 1998, and 2000, respectively. This underestimates the threshold

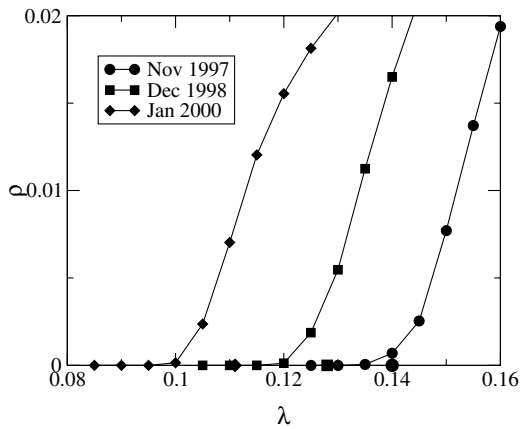


FIG. 4. Prevalence  $\rho$  as a function of the spreading rate  $\lambda$  for the Internet graph at three different times. The large filled symbols indicate the transmission threshold calculated according to the secondary reproductive number [Eq. (6)]. The value of  $\langle k_h^{nn} \rangle$  has been obtained as an average over the two largest hubs.

found in the simulations by at least 1 order of magnitude. Similar to the highly clustered scale-free networks, the Internet graph displays considerable degree correlations [14]. The mean connectivity in the neighborhoods of the hubs is much lower than expected for random wiring. This explains the failure of the description by the basic reproductive number which neglects the strong correlations. The secondary reproductive number, however, gives a satisfactory prediction.

We have shown the existence of a finite epidemic threshold in highly clustered scale-free networks in the limit of infinite system size. Our study has considered for the first time scale-free networks with realistic topological properties as a model for the potentially infective contacts between individuals or nodes. We have conjectured that the value of the threshold is related to the degree correlations in the network, such that the product of the transmission probability  $\lambda$  and the mean connectivity  $\langle k_h^{nn} \rangle$  of the neighbors of the hubs needs to exceed unity for the epidemic to prevail. This criterion holds precisely for highly clustered scale-free networks. For randomly wired scale-free networks it coincides with the standard prediction in epidemiology given by the basic reproductive number. The transmission probability required for spreading on the real Internet graph is approximated well by our criterion, whereas the basic reproductive number drastically underestimates the value.

The existence of an epidemic threshold in highly clustered scale-free networks contrasts with the result for randomly wired networks, where arbitrarily weak viruses show finite prevalence. This suggests that the spreading of viruses in networks with scale-free degree distribution may be suppressed by nonrandom wiring. In particular, degree correlations including the absence of direct connections

between highly connected nodes [21] may provide protection against epidemics.

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