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Chapter 3

Scaling Properties of Complex Networks and Spanning Trees

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We present a relation between three properties of networks: the fractal properties of the percolation cluster at criticality, the optimal path between vertices in the network under strong disorder (i.e., a broad distribution of edge weights) and the minimum spanning tree. Based on properties of the percolation cluster we show that the distance between vertices under strong disorder and on the minimum spanning tree behaves as $N^{1/3}$ for the N vertex complete graph and for Erdős–Rényi random graphs, as well as for scale free networks with exponent $\gamma > 4$. For scale free networks with $3 < \gamma < 4$ the distance behaves as $N^{(\gamma-3)/(\gamma-1)}$. For $2 < \gamma < 3$, our numerical results indicate that the distance scales as $\ln^{\gamma-1} N$. We also discuss a fractal property of some real world networks. These networks present self similarity and a finite fractal dimension when measured using the box covering method.

1. Random Graphs and Complex Networks

About 50 years ago a model for random networks was developed, combining ideas from graph theory with ideas from probability theory. The model was presented and its properties studied in a series of seminal papers by Erdős and Rényi [24, 25, 26] (A somewhat similar model was discussed also by Rapoport [38]). In this model, graphs consist of N vertices and M edges randomly selected between them. That is, in this model all graphs containing N labeled vertices and M edges are equiprobable. This model has come

to be known as the Erdős–Rényi (ER) model. An alternative and closely related model [28] is obtained when considering N labeled vertices selecting edges from the possible $\binom{N}{2}$ edges independently with some probability p. This model has the advantage of avoiding correlations between edges that are present in the original ER model. However, both models behave similarly when the number of edges in not extremely small or extremely large (See, e.g., [7]). We will refer to both models loosely as the "ER model".

The ER model was presented and studied as an abstract mathematical object due to its simplicity and elegance. It was also later applied by researchers in different disciplines to describe various real world network models. In recent years it has become apparent that many of the networks in the real world are not well described by the ER model. Watts and Strogatz [49] observed that in many networks edges are not distributed completely randomly between vertices, but rather, edges tend to cluster, i.e., form more triangles than expected from a completely random distribution. Barabási and Albert [3] observed that in many real world networks the degree distribution is not Poissonian, as obtained in the ER model, but rather a broad, power law, distribution. Faloutsos, Faloutsos and Faloutsos [27] observed the same phenomenon in the Internet router network. For some more recent reviews on the subject see [2, 32, 35, 23]. Several models have been suggested, trying to better describe the nature of real world networks. Most of the models studied today attempting to describe real world networks fall into two main classes. One class of models is based on the Watts–Strogatz small-world model [49], focusing on the small distance versus high clustering occurring in real networks by interpolating between a regular lattice and a random graph. The second class is that of the Barabási–Albert scale free model [3], focusing on the power law degree distribution observed in real world networks, as opposed to the Poisson distribution occurring in ER graphs.

Here we will focus mainly on ER networks and on scale free networks, having degree distribution

$$P(k) = ck^{-\gamma} \,, \tag{1}$$

where k is the degree (number of connections) of a vertex, c is a normalization factor, and γ is some exponent (usually $2 < \gamma < 3$). The BA model and its variants lead to this kind of degree distributions. However, we will focus on the class of equilibrium scale free networks, obtained by the Bollobás configuration model, described below (Sect. 2).

It should be noted that the results supplied here are based on analytical methods providing insight into the problems. They do not constitute rigorous proofs of the presented results, but mostly heuristic arguments. When a rigorous proof exists for a certain result we attempt to supply a reference to the proof. For some of these results no full proof has been obtained, and they may be seen as open challenges for the mathematical community.

2. The Bollobás Configuration Model

The Bollobás configuration model [6] is a model for random graphs with a prescribed degree sequence. Given a degree sequence, all graphs having this degree sequence are equiprobable in this model. In [6] it was shown that an equiprobable distribution on all graphs with a given degree sequence may be obtained by starting with a set of N vertices and assigning to each vertex its degree from the sequence[1]. The vertex is then equipped with this number of "stubs" (i.e., links, currently leading nowhere). Random pairs of stubs are then connected to each other, forming an edge between the respective vertices. This process continues until no stubs are left. It should be noted that this process actually may produce a multi-graph, which is a graph with self loops and multiple links between some pair of vertices, in which case one may discard the graph and restart the process. However, for a sparse graph with no vertices having degrees of order N, the expected number of self loops and multiple edges is of lower order than the node degrees, and thus discarding these leads to a graph with degree sequence very close to the prescribed.

This model leads to a graph having the prescribed degree distribution and no other correlations. That is, it is maximally random for the given degree distribution. Therefore, it can be seen as an "equilibrium" or "maximal entropy" model of random graphs with a prescribed degree distribution. This model can also be seen as an expansion of the ER model, by considering a configuration model network with a Poisson degree distribution,

$$P(k) = \exp(-a)\frac{a^k}{k!}\ , \tag{2}$$

[1]Assuming the degree sequence is also random, the degrees may be assumed to be assigned using the desired degree distribution (such as Eq. (1)). In case the sum of all degrees is odd and a graph can not be constructed, the degrees should be reassigned from the distribution.

where $a = \langle k \rangle$ is the average degree. While this model does not reproduce exactly the ER model probability distribution, it is very close in its properties.

3. Percolation on Random Graphs

One of the simplest and most common models for phase transitions is the percolation model [11, 44, 31]. It is based only on the topological properties of the underlying network and on a single externally tunable parameter. In this model each vertex (for *site percolation*) or edge (for *bond percolation*) is occupied with some probability p and vacant otherwise. Alternatively, it can be thought of as the process of removing vertices or links with probability $q = 1 - p$.

When only a small fraction of the vertices (or links) is occupied the network is, with high probability, composed of a large number of very small components, unreachable from each other through occupied vertices (or links). However, when the occupied fraction becomes large, a *giant component* emerges, connecting a finite fraction of the vertices in the network. This giant component usually appears at some critical concentration, p_c. The percolation transition is usually second order, i.e., the size of the giant component varies continuously from zero below and at p_c to some finite value above p_c.

The subject of percolation in uncorrelated random networks has been studied thoroughly (See, e.g. [16, 12]). Here we present a derivation of the percolation threshold and some properties of the percolating network.

Consider a random network with some degree distribution $P(k)$. The degree distribution of a randomly selected vertex is $P(k)$, and its average degree is $\langle k \rangle = \sum kP(k)$. However, when following a link to reach a vertex, the probability of reaching a vertex with degree k is proportional to its number of links, i.e., to its degree. The distribution of degrees of vertices reached by following a random link is therefore $\phi(k) = kP(k)/\langle k \rangle$ and the average degree of a vertex reached this way is $\kappa \equiv \sum k\phi(k) = \langle k^2 \rangle / \langle k \rangle$. Since links are randomly connected, uncorrelated random graphs tend, with high probability, to include almost no small loops, and are locally tree-like. When considering the process of exploring the graph as a branching process, each reached vertex has one link through which it has been arrived at, and $k - 1$ outgoing link leading to new vertices (until most of the graph is

explored and some links may lead back to known vertices). When only a fraction p of the vertices (or links) are occupied, on average only $(k-1)p$ of the "descendants" of the vertex will be reachable, and on average, per an explored vertex, $\tilde{k} = \sum(k-1)p\phi(k) = p(\kappa - 1)$ descendants will be reachable. When $\tilde{k} < 1$ the branching process will die with probability 1 after a finite number of explored vertices, while when $\tilde{k} > 1$ the process may continue indefinitely and a giant component will exist. This leads to the following value for the critical threshold [16],

$$p_c = \frac{1}{\kappa - 1} \,. \tag{3}$$

It should be noted that if the second moment of the degree distribution, $\langle k^2 \rangle$, diverges, $p_c \to 0$, i.e., the network contains a giant component when any finite fraction of the vertices or links are removed [16]. This result has been proven rigorously for the LCD model in [8]. This is the case for scale free degree distributions (Eq. (1) with $\gamma \leq 3$), which is a common distribution for real networks. Therefore, it is expected that these networks will be very resilient to random breakdown of vertices or links. The vanishing percolation threshold also indicates that epidemic diseases and viruses can propagate in the network with no critical threshold. See also [34].

3.1. Generating functions

A different approach for calculating the critical percolation threshold and other important percolation properties is by utilizing the generating functions approach [33, 12].

Denote by $G_0(x)$ the generating function for the vertex degree distribution, $P(k)$, i.e., the formal power series,

$$G_0(x) = \sum_k P(k) x^k. \tag{4}$$

Note that $G_0(1) = 1$ by normalization, and $G_0'(1) = \langle k \rangle$. The generating function for the out degrees of vertices reached by following a link is then

$$G_1(x) = \sum_k \phi(k) x^{k-1} = \sum_k \frac{kP(k)}{\langle k \rangle} x^{k-1} = \frac{G_0'(x)}{G_0'(0)} \,. \tag{5}$$

Note that $G_1(1) = 1$ also by normalization (assuming $\langle k \rangle$ is finite), and that $G_1'(1) = \kappa - 1$, the average outgoing degree of a vertex reached through a link.

Consider the following process in the network: Start exploring the network by picking a link and following it to one of its vertices. Then all other links emanating from this vertex are explored and so on. If no vertex is reached twice during this exploration we may refer to the explored region of the network as a "branch", and view this process as a probabilistic branching process. This process may die out after a finite number of vertices are reached, or it may continue indefinitely.[2] A generating function can be constructed for the sizes of branches defined as above by noticing that this is a branching process where (almost) each link explored leads to a new branch with the same distribution as the original one. The number of branches at each point is distributed according to $\phi(k)$ (or $G_1(x)$). Assuming the concentration of links is p,[3] the generating function for branch sizes is,

$$H_1(x) = (1-p) + pxG_1\big(H_1(x)\big)\,. \tag{6}$$

Note that it is no longer necessarily true that $H_1(1) = 1$. In fact, $H_1(1)$ gives the probability that a branch has a finite size. See Fig. 1 for illustration.

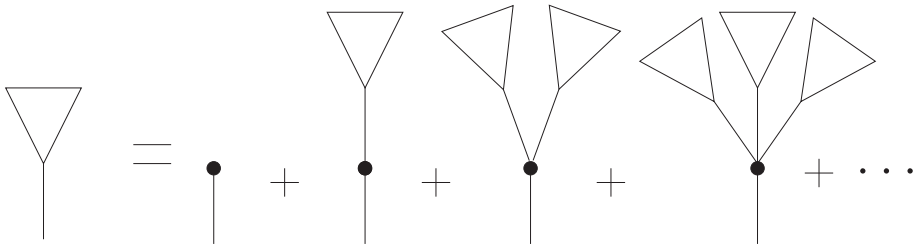

Fig. 1. An illustration of the recursive branch definition

Starting from a random vertex and studying the size distribution of the component to which it belongs, is similar to selecting a degree k, using the distribution $P(k)$, and then summing the sizes of the k branches to which

[2]Naturally, in a finite network the whole network will be explored in a finite time. However, when the size of the network, $N \to \infty$, it can be assumed that as long as the branch size is of $o(N)$, the fraction of edges linking back to explored vertices is of $o(1)$, and therefore the branching process is a good approximation. When $N \to \infty$ the process can continue indefinitely (up to $O(N)$) before loops significantly affect the behavior of the branching process.

[3]From here on we consider link, and not vertex, percolation. Vertex percolation can be handled in a very similar manner. See, e.g, [12] for details.

it leads. Therefore, to find the distribution of component sizes one can construct the following generating function

$$H_0(x) = xG_0\big(H_1(x)\big)\,. \tag{7}$$

Again, $H_0(1)$ does not necessarily equal 1, and gives the probability of a vertex to belong to a finite component. Thus, the probability of a vertex to belong to the infinite component, which is the relative size of the infinite component is,

$$P_\infty = 1 - H_0(1). \tag{8}$$

3.2. Critical exponents

The generating functions presented in Section 3.1 can be used to find the properties of percolating networks near and at the percolation transition point. The behavior near a physical phase transition point is known, both experimentally and using heuristic arguments, to be universal [11, 44], i.e., to depend only on the dimensionality of the physical space in which it occurs, and on the symmetries of the order parameter. It is also known, however, that heterogeneity in space may break the universality and lead to non-universal behavior. Below we present a case in which universality is broken also by heterogeneity in the degrees. We closely follow [15].

Consider percolation in a network. As shown in Section 3, the critical point can be found at $p_c = (\kappa - 1)^{-1}$ (Eq. (3)). P_∞ can by found using Eq. (8) and substituting $H_0(1) = G_0\big(H_1(1)\big)$. $H_1(1)$ is to be found using Eq. (6). This can be done numerically and for some distributions even analytically. However, near the critical point one can find the leading order of the behavior of $H_1(1)$ for a general distribution. At $p = p_c + \delta$, with $\delta \to 0$, the size of the giant component is still very small and the probability of belonging to it is close to zero. Therefore, $u \equiv H_1(1) = 1 - \varepsilon$. Expanding Eq. (6) one obtains

$$1 - \varepsilon = 1 - p_c - \delta + \frac{(p_c + \delta)}{\langle k \rangle} \sum_{k=0}^{\infty} kP(k)(1 - \varepsilon)^{k-1}. \tag{9}$$

The sum in Eq. (9) can be expanded in powers of ε

$$(10) \quad \sum_{k=0}^{\infty} kP(k)u^{k-1} \sim \langle k\rangle - \big\langle k(k-1)\big\rangle\varepsilon + \frac{1}{2}\big\langle k(k-1)(k-2)\big\rangle\varepsilon^2 + \cdots .$$

Using this expansion, Eq. (9) leads to $\varepsilon \sim \delta$, to first order approximation, implying that $P_\infty \sim (p-p_c)$. This is in accordance with the known universal behavior for percolation in high dimension, $d \geq d_c = 6$, where the size of the giant component (or "spanning cluster") grows linearly with $p-p_c$ near the transition point.

For scale free networks, however, the behavior is different. When the degree distribution is given by Eq. (1) with $\gamma < 4$, the term $\big\langle k(k-1)(k-2)\big\rangle$ diverges and Eq. (10) no longer holds. The behavior of the sum near $u = 1$ may be determined using Abelian methods (See, e.g., [50]). In this case

$$(11) \qquad \sum_{k=0}^{\infty} kP(k)u^{k-1} \sim \langle k\rangle - \big\langle k(k-1)\big\rangle\varepsilon + c\Gamma(2-\gamma)\varepsilon^{\gamma-2} + \cdots ,$$

where Γ denotes the Gamma function. Thus, Eq. (6) leads to $\varepsilon^{\gamma-3} \sim \delta$ and therefore,

$$(12) \qquad P_\infty \sim (p-p_c)^\beta, \quad \beta = \frac{1}{\gamma-3} .$$

This result is already non-universal, in the sense that the critical exponent for scale free networks with $\gamma < 4$ is different from that obtained for lattices in high dimensions, for Cayley trees [11], and for ER networks (or scale free networks with $\gamma > 4$).

The distribution of component sizes in the network can also be determined from the coefficients of the expansion of $H_0(x)$ as a power series in x. The coefficient of x^s in this expansion gives $P(s)$, the probability that a vertex belongs to a component of size s. The number of components of size s is denoted by $n_s = NP(s)/s$. In mean-field percolation (i.e., percolation above the critical dimension), it is known (See, e.g., [11, 44, 33]) that near the threshold

$$(13) \qquad n_s \sim s^{-\tau} e^{-s/s^*} ,$$

where $\tau = 2.5$ and s^* diverges exactly at the critical point, leading to a pure power law distribution. To find $P(s)$ one can study Eqs. (7) and (6)

exactly at $p = p_c$. Letting $x = 1 - \varepsilon$ and denoting $\phi(\varepsilon) = 1 - H_1(1 - \varepsilon)$, Eq. (6) leads to

$$-\phi = -p_c + (1-\varepsilon)p_c\left[1 - \frac{\phi}{p_c} + \frac{\left\langle k(k-1)(k-2)\right\rangle}{2\langle k\rangle}\,\phi^2 + \cdots + c\frac{\Gamma(2-\gamma)}{\langle k\rangle}\,\phi^{\gamma-2}\right]. \tag{14}$$

Again, the analytical terms dominate for ER networks and scale free networks with $\gamma > 4$ and the non analytical term dominates for scale free networks with $\gamma < 4$. Using Tauberian theorems, linking between the analytical properties of a function and its power series expansion, one obtains that $P(s) \sim s^{-\tau+1}$ with $\tau = 2.5$ for ER networks and scale free networks with $\gamma > 4$ and $\tau = \frac{2\gamma-3}{\gamma-2}$ for $\gamma < 4$.

To find the size of the largest component in the network at criticality, one may consider the number of components of size s, n_s. The extreme value statistics on the largest component size, S may be estimated by taking the integral over the tail of the distribution to equal $1/N$, as this signifies that approximately one component will have this size. Thus,

$$\frac{1}{N} = \int_S^\infty n_s ds = c_1 \int_S^\infty s^{-\tau} ds = c_2 s^{-\tau+1}. \tag{15}$$

It follows that the size of the largest component scales as

$$S \sim N^{1/(\tau-1)}\,, \tag{16}$$

where, as above, $\tau = 2.5$ for ER networks and $\tau = \frac{2\gamma-3}{\gamma-2}$ for scale free networks with $\gamma < 4$. For ER networks and for scale free networks with $\gamma > 4$ at the transition point this leads to the well known result $S \sim N^{2/3}$ [7].

3.3. Fractal dimensions

Several, not necessarily equivalent, definitions exist to the concept of a dimension. One of the common definitions of the dimension of a graph (as well as of continuous objects) is based on the dependence of the number of vertices (or "mass") as a function of the distance from some initial vertex, i.e., the size of the l-neighorhood of a random vertex. If the number of

vertices, M_l, up to some large distance, l, from some initial vertex, scales as $M_l \sim l^d$, then the dimension of the graph is considered to be d. This is true for regular lattices in all dimensions, as well as for many other graphs embedded in finite dimensional space. In Configuration Model random graphs, the number of vertices at a distance l from a vertex usually (for high enough average degree) grows as $M_l \sim b^l$ with some b.[4] This exponential growth is faster than any power law, and therefore random graphs are usually considered to be infinite dimensional.

At the percolation critical point, however, the network becomes very diluted, and the growth of M becomes slower. To find the behavior of M_l we use the following consideration (See [18]). Consider N_l, the generating function for the distribution of the number of vertices at a distance l along some branch, i.e., l hops from a random vertex arrived by following some link. At the end of a followed link there is always one vertex. Therefore $N_0(x) = x$. The distribution of the number of this vertex's neighbors (excluding the link through which this vertex was reached to) is $G_1(x)$. In general, each such branch consists of a vertex whose degree distribution is represented by the generating function G_1, and each of whose links leads to a new branch. The total number of neighbors at distance l from the vertex consists of the total number of $l-1$-distance neighbors of this vertex's neighbors. Thus, the generating function of this distribution can be found using the recursive equation

$$N_l(x) = G_1\big(N_{l-1}(x)\big)\,. \tag{17}$$

Since at criticality the branching factor, $p_c(\kappa - 1)$ is exactly 1, the average number of vertices at distance $l+1$ is exactly the average number at distance l. However, we are only interested in branches that survive at least l layers. That is, branches in which at least one vertex is at a distance l from the origin. Since $N_l(x)$ is the generating function for the number of vertices at distance l, the coefficient of x^0 gives the probability of dying before or at the lth layer. Therefore, the probability to die before the lth layer is given by $N_l(0)$. The average number of vertices at the lth layer for surviving branches, A_l is thus given by the average for all branches divided by the survival probability

$$A_l = \frac{1}{1 - N_l(0)}\ . \tag{18}$$

[4]For equilibrium random graphs with finite κ, $b = \kappa - 1$, and when κ diverges, M grows even faster. See, e.g., [7, 33, 17, 48].

To find the behavior of $N_l(0)$ for large l, one should expand Eq. (17) at the critical point. Assuming $\kappa - 1 = 1$,[5] one obtains

(19)
$$G_1(1-\varepsilon) = 1 - \frac{1}{\langle k\rangle}\left[\langle k\rangle - \big\langle k(k-1)\big\rangle\varepsilon + \frac{\big\langle k(k-1)(k-2)\big\rangle}{2}\,\varepsilon^2 + \cdots\right].$$

Letting $N_l(1-\varepsilon) = 1 - \varepsilon_l$, Eq. (17) leads to

$$1-\varepsilon_{l+1} = 1-\frac{1}{\langle k\rangle}\left[\langle k\rangle - \big\langle k(k-1)\big\rangle\varepsilon_l + \frac{\big\langle k(k-1)(k-2)\big\rangle}{2}\,\varepsilon_l^2 + \cdots\right]. \tag{20}$$

Guessing a solution of the form $\varepsilon_l \approx Bl^{-h}$ leads to

(21)
$$B(l+1)^{-h} = B(l^{-h} - hl^{-h-1}) + \cdots = Bl^{-h} - \frac{\big\langle k(k-1)(k-2)\big\rangle}{2\langle k\rangle}\,Bl^{-2h}\,,$$

and thus, $h = 1$. From Eq. (18) follows $A_l \sim l$. Therefore,[6]

$$M_l \approx \sum_{\ell=1}^{l} A_l \sim l^{h+1} \sim l^2\,, \tag{22}$$

and the fractal dimension is $d_l = 2$.[7] For scale free networks with $3 < \gamma < 4$ similar considerations lead to $d_l = (\gamma-2)/(\gamma-3)$ [18].

[5]For simplicity of notation we assume here that the original graph is at criticality, rather than arriving at criticality through a dilution of the links or vertices. See [29] for a more complete treatment.

[6]Note that A_l is the average number of vertices in the lth layer provided the branch survived at least up to the lth layer. This is not the same as the average number of vertices in the lth layer provided the branch survived $l + l'$ layers. However, A_l gives a lower bound for this quantity and $A_{l+l'}$ gives the upper bound.

[7]Notice that there is no real embedding space here, and the dimension is based on the shortest distance metric on the graph itself. This is actually known in physics as the "chemical dimension", whereas the fractal dimension depends on the embedding space and for random embedding it is twice the chemical dimension [11].

4. Weighted Networks

In the following we consider a network in which every link is associated with a weight – a positive number representing some property of the link. This property can be the cost, time or capacity of the link. In physical systems this weight is usually associated with the energy of the bond. We assume that the weights are randomly selected from some distribution. We will mainly concentrate on the behavior of the "optimal path" between vertices, i.e., the path with minimal total weight connecting the two vertices. We begin by considering distances between vertices in networks with no disorder.

4.1. Shortest paths in networks

Since networks are usually not considered to be embedded in real space, no a-priori notion of the distance between vertices exists. Therefore, distances should be defined based only on the topology of the network. The most natural definition of a distance between vertices is the "hop distance", i.e., the minimal number of links that need to be transversed to reach one vertex from the other. This is analogous to assigning a weight of 1 to each link and considering the minimal weight path between vertices.

Considering a two dimensional lattice, the distance between vertices using the above definition is the "Manhattan distance", i.e., the sum of the absolute difference between the x and y coordinates. Considering an $L \times L$ lattice, with $N = L^2$ vertices, the average distance between two randomly chosen vertices is $L/3$ in the x coordinate ad $L/3$ in the y coordinate. Therefore, the average total distance is $l = 2L/3$, which scales as $l \sim L \sim \sqrt{N}$. This behavior, $N \sim l^d$ or $l \sim N^{1/d}$ implies that the network has dimension d. In this case $d = 2$. This shows that the dimension of a lattice can be defined even if no a-priori assumptions about an embedding space is made.

For a configuration model random graph, the scaling of the distance is quite different. As stated above, the random graph has no small loops and therefore is locally tree-like. Thus, it behaves locally as a branching process with average branching factor $\kappa - 1$. The average number of vertices at a distance l scales as $(\kappa - 1)^l$. As this is an exponential growth process (for $\kappa > 2$), the number of vertices up to distance l is proportional to that of

the lth layer. This implies that the average distance between vertices scales logarithmically with the size of the network $\langle l \rangle \sim \log N / \log(\kappa - 1)$ (See, e.g., [7, 46] for a more detailed account). For scale free networks with $\gamma < 3$, κ diverges, and therefore the distances are even shorter than logarithmic. For $2 < \gamma < 3$ the distances behave as [19, 17, 22, 48]

$$\langle l \rangle \sim \ln \ln N / \left| \ln(\gamma - 2) \right| . \tag{23}$$

4.2. Strong and Weak Disorder

Assume now that random weights are associated to the links. The weights are drawn from some distribution $P(w)$. The total weight of a path is the sum of the weights of the links along the path. The "optimal path" between vertices is the path of minimal total weight between these vertices. Two classes of behavior are possible, with a crossover regime between them [13, 14]. If the weights are drawn from a relatively narrow distribution, the weight of a path will be closely related to its hop number, as every link will contribute a similar weight. Thus, the length of the optimal path is expected to be proportional to the length of the shortest path. This case is known as "weak disorder". If the distribution of weights is broad enough, such that, e.g., each weight is at least twice as large as the next highest weight, the total weight of a path is determined by the highest weight along the path, and is almost independent of all other weights. In this case, paths can be compared by the highest weight on them. If they share the highest weight links, the lower weight path is determined by comparing the highest weight between the non-shared links. This is termed "strong disorder".

While in weak disorder the behavior of the optimal path length is very similar to that of shortest paths, in the strong disorder regime the behavior is quite different. In strong disorder the optimal paths attempts to avoid high weight links whenever possible. This implies that the optimal path may follow a very long distance to avoid passing through nearby high weight links. In lattices it is well-known [13, 14, 37] that optimal paths in strong disorder are fractal, i.e., have dimension higher than 1.[8] On the other hand, in weak disorder the optimal paths are only self-affine, meaning they still

[8]This implies that if the shortest hop distance between two vertices is l, the optimal path length will scale as $l_{\rm opt} \sim l^{d_{\rm opt}}$ with some $d_{\rm opt} > 1$.

scale similarly to the shortest paths, but allow some small deviations to find a lower weight path.[9]

Strong disorder also appears in cases where a path is determined by the highest weight link without summation. An example of such a case is circuit allocation in a communication network, where the bandwidth of a path is determined by the minimum bandwidth of a link along the paths. In this case only one link determines the bandwidth of the path. However, it may happen that one wishes to optimize also the bandwidth of the next lowest bandwidth links to prevent congestion. In this case the optimal between two paths will be determined by comparing the minimal bandwidth between their non-shared links. An illustration is presented in Fig. 2.

4.3. Minimum Spanning Trees

Spanning trees are trees that span the network. That is, trees containing a subset of the links in the network, while still connecting all vertices in the network. Minimum spanning trees (MSTs) are the spanning trees that have the lowest total weight of all spanning trees. When all weights are equal, all trees are minimal, as they all have the same weight (since all trees on N vertices have $N-1$ links). This model, where all spanning trees are equiprobable, is called uniform spanning tree (UST). When weights are drawn from a continuous distribution, ties between the weights of different links become statistically insignificant, as their probability approaches zero, and the MST becomes unique.

An interesting feature of the minimum spanning tree is that it induces global, rather than local, optimization. The tree is selected to minimize the total weight of links under the constraint that all vertices must be connected. This implies that paths between vertices on the MST are not chosen to minimize the distance between vertices, but rather are the result of the global optimization of the tree weight. Therefore, these paths may be very long compared to the shortest distance between vertices in the original network. Furthermore, paths between vertices in the tree are unique, so for the paths between three vertices, A, B and C, it must hold that one of these paths is the sum of the other two. This structure is, in some sense, "super-critical", as it represents a backbone that has been diluted to the maximum

[9]Formally, self-affinity implies that the width of the path (i.e., the deviations from the shortest path) scales as $W \sim l^{\alpha}$ with some $\alpha < 1$. Therefore, the optimal path length is still proportional to l with some higher order corrections [4, 10].

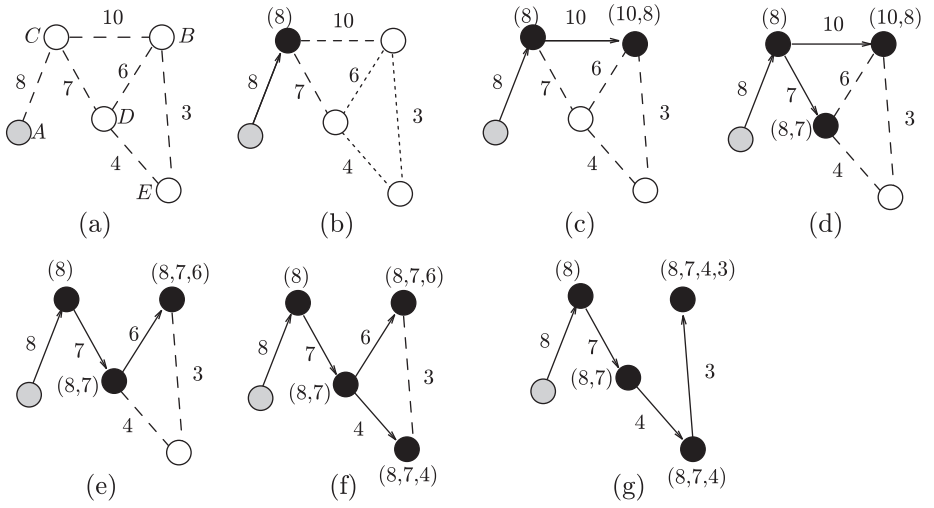

Fig. 2. Searching for the optimal path between vertices A and B in a network with strong disorder. The length of a path is calculated using lexicographic comparison rather than the sum of weights. The first (shortest) path found is $(8, 10)$. However, the subsequent paths found $(8, 7, 6)$ and $(8, 7, 4, 3)$ have lower weight, although they are longer. After [9]

possible level while maintaining connectivity. The structure of the minimum spanning tree in a network is thus very similar to the optimal paths in strong disorder. However, due to their globally optimized nature, MSTs maintain this behavior for every distribution of weights, even a narrow one.

Two widespread algorithms exist to find the MST: The Prim algorithm and the Kruskal algorithm (See, e.g., [20]). The Kruskal algorithm operates by starting from a forest of N vertices and no edges and adding each time the minimal weight edge that does not close a loop. The Prim algorithm starts from a vertex, and at each step adds to the tree the lowest weight adjacent link that does not close a loop. The order at which the edges are added is random, since the weights were chosen randomly and independently. Hence, the Kruskal algorithm resembles percolation and the Prim algorithm resembles invasion percolation [36]. The main difference is that both are "guarded" percolation, i.e., percolation with the modification that only the removal of links that do not disconnect the network is allowed. The percolation process ends when no loops are left and the remaining network is a tree [21].

4.4. Fractal properties of optimal paths

To study the behavior of optimal paths and MSTs we use the following algorithm (which may be seen as the inverse of the Kruskal algorithm for MSTs): We begin with the full network, and then start removing the highest weight links. Whenever the removal of a link will break a component into two smaller components, the link will be "guarded" and will not be removed. Since the weights are randomly and independently chosen, the order of link removal is random, and there is no need to actually draw the weights, as their numerical value plays no role in the model. This algorithm is naturally justified for the MST, as discussed above. For strong disorder, it is known that the weight of the highest weight link is larger than the sum of all weights below it, so, as long as an alternative path with lower weights exists, it will always be preferable over the higher weight link.

In configuration model random graphs, the analogy between optimal paths and percolation becomes more exact [9]. Unlike finite dimensional percolating lattices, in random graphs the components at criticality are tree like and contain almost no loops. Thus, the percolation components at and below criticality are subgraphs of the MST. We expect the properties of the MST or optimal path tree in strong disorder to be similar to that of the percolation components at criticality.

As discussed in Section 3.2, at p_c the size of the largest component at the percolation threshold scales as $S \sim N^{1/(\tau-1)}$. The distances between vertices in this component scale as $l_{\text{opt}} \sim S^{1/d_l}$, where d_l is the fractal dimension. Most of the path is along the largest percolation components [30, 1]. It follows that the distances scale as

$$l_{\text{opt}} \sim N^{1/\left(d_l(\tau-1)\right)} \,. \tag{24}$$

This leads to the conclusion that in ER networks optimal paths scale as [9]

$$l_{\text{opt}} \sim N^{1/3} \,. \tag{25}$$

This scaling also holds when starting from the complete graph, K_N, as ER graphs are obtained by randomly removing links from the complete graph. On the other hand, distances in uniform spanning trees of the complete graph and ER graphs are known to scale as $l \sim N^{1/2}$ [45]. It therefore follows that MSTs are more compact than USTs, due to the global constraint on MSTs, forcing them to be drawn from a different distribution than the uniform one.

In scale free networks with $\gamma > 4$ the behavior, as for the other critical exponents, is similar to that of ER networks. When $3 < \gamma < 4$ the behavior is [9], according to Eq. (24),

$$l_{\text{opt}} \sim N^{(\gamma-3)/(\gamma-1)} \,. \tag{26}$$

When $\gamma < 3$ the analogy to percolation gives only little insight, as percolation is only achieved in the limit of zero concentration. However, simulation results indicate that the optimal path lengths are polylogarithmic. Thus, the dimension of the MST is still infinite. However, these distances are exponentially larger than the hop distances, which scale as $\log \log N$, see Eq. (23).

To complete the investigation of the length of the optimal path, one should establish that the percolation components connect between them in a compact way through the guarded links. This would establish the above estimation of l_{opt} also as an upper bound and therefore establish that the scaling is correct. An investigation of the properties of optimal paths and their partition to percolation components and guarded links is presented in [51].

A recent paper [1] finally establishes a tight bound on the optimal path length for MSTs on the complete graph and ER networks. To establish the compactness of the connections between components of the network, the links are divided to three regimes. Up to the critical concentration all links that do not form loops are added, leading to a critical network with $O(N^{1/3})$ path length as presented above, Eq. (25). Then, a series of a few steps in which the size of the largest component grows from $O(N^{2/3})$ to $O(N/\ln N)$. In every such step the length of the optimal path does not increase too much. Eventually, after reaching a component of size $O(N/\ln N)$, all other components are considerably smaller and then connect to the largest component through a short sequence of small components. For full details see [1].

It is well known that in most physical models weak disorder does not affect the scaling of the optimal path (See, e.g, [11]. See also [47] for a rigorous result.). Therefore, when disorder is weak, the optimal path lengths are expected to scale similarly to the shortest paths. Simulations confirm this expectation. Simulation results [9] indicate that the distances in both ER and scale free networks with $\gamma > 3$ behave logarithmically with the network size, similarly to shortest paths. For scale free networks with $2 < \gamma < 3$ simulation results lead to the conjecture that the optimal path

length also scales as powers of $\log N$, which is different than the $\log \log N$ scaling of the shortest path length. We have no explanation or analytical confirmation for these results.

5. Fractal Networks

As discussed earlier, the dimension of scale free networks and mean field random graph models, such as ER graphs, can be considered to be infinite, as the growth of the number of vertices at a distance l from an arbitrary node grows exponentially with l. This seems to stand in contradiction with the notion that the "scale free" nature of a network implies some fractal properties of this network. However, as shown below, a recent study [42] indicates that actually these notions can be reconciled. To explain how, we first present two methods of finding the fractal dimension.[10]

5.1. The cluster growing method

In the cluster growing method one begins with an arbitrary vertex of the network, the distance l neighborhood of the vertex (i.e., all vertices at a distance at most l from it) is explored, and the number of vertices at a distance at most l, M_l, is plotted. Results obtained by starting from many initial vertices are then averaged, and the growth of M_l determines the fractal dimension. That is, if $M_l \sim l^d$ for some d then d is the fractal dimension.

5.2. The box covering method

In the box covering method, the fractal is covered by a minimal number of boxes of some (Euclidean) linear size l. Since the fractal does not cover the full space, the smaller the boxes, the more holes can be left uncovered. The dependence of the number of boxes on l determines the fractal dimension of the network. That is, if the number of boxes of linear size l needed to cover the fractal is $N_B(l) \sim Nl^{-d_B}$, d_B being the fractal dimension of the

[10]It should be noted that several models have been presented to scale free networks with fractal structure. See, e.g., [39].

network. Since the networks discussed here are not embedded in Euclidean space a analogous algorithm is covering the network with "boxes", each of which contains the nodes within a hop distance L from some starting node.

5.3. The fractal nature of scale free networks

In a recent paper [42, 43], Song et al investigated the fractal properties of several real world networks. As discussed above it was widely believed that due to the exponential growth of the number of vertices at a distance l there can be no fractal properties to scale free networks. Song et al introduce the following idea: While the cluster growing method always leads to exponential behavior, the box covering method may lead to a different behavior. To uncover this behavior one should notice the following point: A box with linear dimension l covers several vertices within a distance l of some initial node. More boxes are added to cover the rest of the network, where a covered vertex is not to be covered again. This last requirement stems from the fact that high degree nodes have a large number of nodes in their neighborhood. Allowing their repeated use would lead to a large boxes containing the same nodes with their sizes growing exponentially with l.

The large number of vertices in the l-distance neighborhood of high degree vertices leads to the covering of high degree vertices quickly in the process. This effectively lowers the number of high degree vertices for the rest of the network; thus reducing the expansion of the network. This allows the growth to become slower than exponential despite the fast growth of the cluster growing method.

Empirical results show that the application of the optimal box covering method to networks such as the WWW and protein interaction networks results in a power law

$$N(l) \sim l^{-d_B} \ , \tag{27}$$

where d_B is the fractal dimension obtained by the box covering method. For the WWW, $d_B \approx 4.1$ and for protein interaction networks, $d_B \approx 2.3$. For the Internet network, as well as for different models for network formation no fractality is found, and no power law can be fitted to $N_B(l)$.

The fractal nature of networks is also seen by applying the renormalization technique. In the renormalization process each box is replaced by a "super-vertex" and two such super-vertices are connected if there is a link

between vertices in the respective boxes. The process of renormalization produces a new degree distribution of the super-vertices $P(k')$ whose tail is invariant under the renormalization, $P(k') \sim P(k) \sim (k')^{-\gamma}$.

From empirical results, the number of links in each box is proportional to the number of links in the highest degree vertex in the box, with some proportionality factor depending on the box size l. This implies

$$k \to k' = s(l)k \; . \tag{28}$$

The proportionality factor also behaves as a power law in l satisfying $s(l) \sim l^{-d_k}$ for some d_k. For the WWW $d_k \approx 2.5$. Consider now the transformation $k \to k'$. Since $n(k)dk = n'(k')dk'$, where $n(k) = NP(k)$ and $n'(k') = N'P'(k')$ are the respective number of vertices of degree k (before the renormalization transformation) and k' (after the renormalization transformation) respectively. Using $P(k) \sim k^{-\gamma}$, $P(k') \sim (k')^{-\gamma}$ and Eq. (28), it follows that $N' = Ns^{\gamma-1}$. Since $N' = N_B(l)$, the number of boxes of size l needed to cover the network, it follows that $N_B(l) \sim Ns^{\gamma-1} = Nl^{-d_k(\gamma-1)}$. By definition $N_B(l) \sim Nl^{-d_B}$. Therefore, there exists a relation between the fractal dimensions and the degree distribution exponents,

$$\gamma = 1 + d_B/d_k \; . \tag{29}$$

The box covering and renormalization methods are illustrated in Fig. 3.

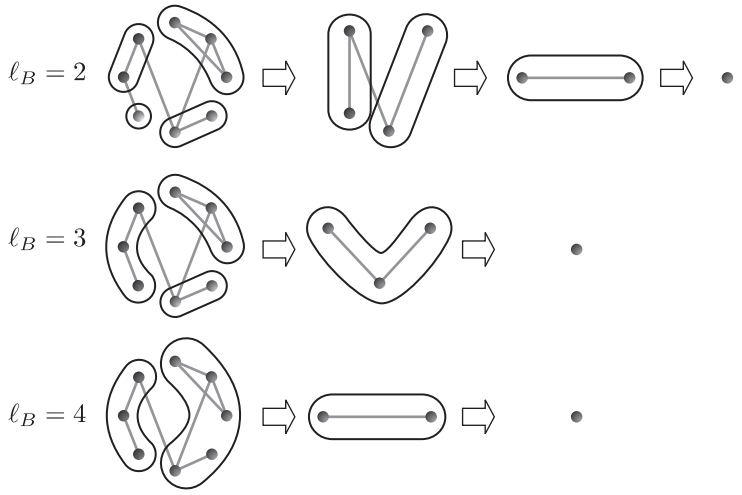

Fig. 3. The box covering method and the renormalization of the network for different box sizes. After [42]

6. Fractal Properties of Network Boundaries

Most work on distances in networks focused on the average, or typical distance between vertices. In a recent work [40, 41], however, the properties of the vertices far from a given vertex were investigated. It was found that the number of vertices at a large distance from an arbitrary vertex follows a power law distribution.

Consider an N-vertex network with some degree distribution $P(k)$. Start from some arbitrary vertex and observe the vertices at distance l from this vertex. For ER networks and small l, the growth with l is approximately exponential. The average hop distance between vertices is approximately $\langle l \rangle \sim \log N / \log(\kappa - 1)$ when κ is finite. In the following, we study the structure of layers with $l > \langle l \rangle$. That is, we study the properties of the vertices at a distance l from an arbitrary vertex, where l is larger than the average distance in the network.

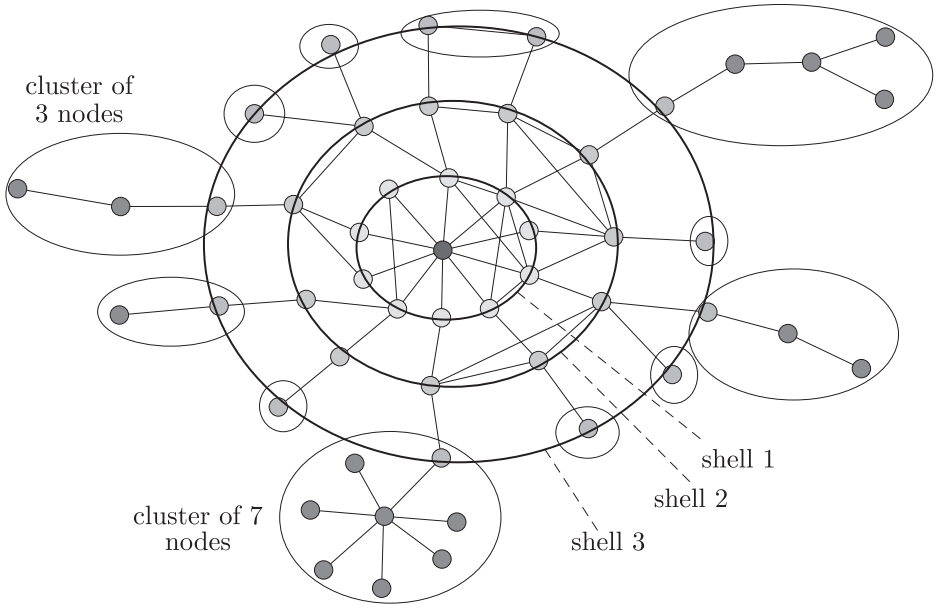

Fig. 4. Shell and cluster (component) structure of the boundary of a network. After [41]

6.1. Distribution of outer shells population

We now follow [41] to prove that the distribution of the number of vertices in the nth shell for large n follows $p(y_n) \sim y_n^{-2}$. When exploring the network, the probability of reaching a vertex with k outgoing links through a link is $\tilde{p}(k) = (k+1)P(k+1)/\langle k\rangle$. Define $g(k) = \sum \tilde{p}(k)x^k$, and $\langle\tilde{k}\rangle = \sum k\tilde{p}(k)$. The generating function for the number of vertices at the nth shell of a branch is therefore $G_n(x) = G_{n-1}\big(g(x)\big)$. We denote by $\tilde{p}_n(K_n)$ the probability of finding K_n vertices at the nth shell. $\tilde{p}_n(K_n)$ are the coefficients of the Taylor expansion of $G_n(x)$.

For high shell numbers, by the law of large numbers, we expect the number of vertices to increase by a factor of $\langle\tilde{k}\rangle \equiv \kappa - 1$ at every consecutive shell. (For ER networks $\langle\tilde{k}\rangle = \langle k\rangle$.) Hence, we can conclude that $G_n(x)$ converges to a function of the form $\tilde{f}\big((1-x)\langle\tilde{k}\rangle^n\big)$ for large n.

The solution of $g(f_\infty) = f_\infty$ gives the probability of a vertex not to connect to infinity, i.e., not to belong to the giant component. Near criticality we can guess a solution of the form $f(y) = f_\infty + ay^{-\alpha}$. Expanding g we obtain,

$$g(f_\infty + ay^{-\alpha}) = g(f_\infty) + g'(f_\infty)ay^{-\alpha} + o(y^{-\alpha}). \tag{30}$$

Solving $g\big(f(y)\big) = \langle\tilde{k}\rangle f(y)$ we obtain $\alpha = -\ln g'(f_\infty)/\ln\langle\tilde{k}\rangle$. In [5], the behavior of supercritical branching processes was studied. It was proved that the tail of the distribution of layer sizes follows a power law, $p_n(K_n) \sim K_n^{\mu}$, with $\mu = \alpha - 1$.

Let y_n be the fraction of vertices not connected after the nth shell. Then $y_n = \sum \tilde{p}(k)y_{n-1}^k$, and thus $y_n = g(y_{n-1})$. Accordingly, the relation between any two shells, m and n, is given by

$$y_n = f\big((1-y_m)\langle\tilde{k}\rangle^{n-m}\big) = f_\infty + a(1-y_m)^{-\gamma}\,. \tag{31}$$

Using the same reasoning as above we obtain $\gamma = \ln g'/f_\infty \ln\langle\tilde{k}\rangle$.

For a large m, $y_m = 1 - \sum_{l=1}^{m} K_l$, where K_l is the fraction of vertices in the lth shell. For large enough l, by the law of large numbers $K_{l+1} = \langle\tilde{k}\rangle K_l$. Thus, the sum is a geometric series equal to $\langle\tilde{k}\rangle K_m/(\langle\tilde{k}\rangle - 1)$. Therefore, $y_n \sim \big(\langle\tilde{k}\rangle K_m/\big(\langle\tilde{k}\rangle - 1\big)\big)^{-\gamma}$.

As shown above $P(K_m) \sim K_m^{\mu}$. Using $p(y_n)dy_n = p(K_m)dK_m$, we obtain $p(y_n) \sim y_n^{-\beta}$, where $\beta = 1 + (\mu+1)/\gamma$. For ER networks $\mu + 1 = \gamma$, and thus $\beta = 2$, leading to $p(y_n) \sim y_n^{-2}$.

6.2. Component size distribution

We now turn to study the distribution of the component sizes left when vertices up to distance l from a given vertex are removed from the network [41]. The component size distribution in percolation at some concentration p is determined using the formula

$$P_p(s > S) \sim S^{-\tau+1} \exp\big(- S|p - p_c|^{-1/\sigma}\big). \tag{32}$$

This distribution can be approximated by considering the exponent to introduce a sharp cutoff,

$$P_p(s > S) \sim \begin{cases} S^{-\tau+1}, & S < |p - p_c|^{-1/\sigma}, \\ 0, & S > |p - p_c|^{-1/\sigma}. \end{cases} \tag{33}$$

When links are uncovered one by one as the percolation threshold is approached in a uniform way, so for any a, $P(p - p_c < a) \sim a$. Therefore, it follows that

$$P(s > S) = P_p(s > S)P\big(S < |p - p_c|^{-1/\sigma}\big) = S^{-\tau+1}S^{-\sigma}. \tag{34}$$

Therefore, the component size distribution follows $n_s \sim s^{-(\tau+\sigma)}$. For ER networks $\sigma = 1/2$ and $\tau = 5/2$ and thus $n_s \sim s^{-3}$.

7. Summary

Complex networks present several different types of scaling behavior. A well-studied property is the scale free nature of the degree distribution of numerous real networks. The Internet, both at the AS and router levels, and the WWW present a power law degree distribution for several orders of magnitude. Several other natural, technological and social networks are also believed to posses a power law degree distribution.

In physics, it is well known that systems at a critical point exhibit fractal, scale invariant, properties. We discussed the critical exponents associated with the percolation phase transition in general random networks and in particular in ER and scale free networks. We surveyed the behavior in different power law regimes and showed that scale free networks have

anomalous percolation properties even when the critical concentration is finite. We have shown that the structure of the percolation components at the phase transition point is fractal, and discussed how to calculate the fractal dimension. We also calculated the size and typical length of the largest components at the critical point and showed that it is a fractional power of the network size.

We have also shown that despite an apparent contradiction between the infinite dimensional nature of random networks and the notion of fractality, many naturally occurring scale free networks have fractal properties even far from criticality. This property is not present in most equilibrium and growth models of scale free networks. However, it is observed in many biological and socio-technological networks in the real world. This seems to hint some scale free properties of the underlying mechanism for the network formation.

Finally, it was shown that the distribution of the number of vertices at a large distance from an arbitrary vertex follows a power law. The sizes of components left after the removal of the l closest layers of a certain vertex for large l also follow a power law distribution. Thus, even equilibrium random networks far from criticality exhibit scaling properties in some of their features.

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