

Sampling properties of random graphs: The degree distribution

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We discuss two sampling schemes for selecting random subnets from a network, random sampling and connectivity dependent sampling, and investigate how the degree distribution of a node in the network is affected by the two types of sampling. Here we derive a necessary and sufficient condition that guarantees that the degree distributions of the subnet and the true network belong to the same family of probability distributions. For completely random sampling of nodes we find that this condition is satisfied by classical random graphs; for the vast majority of networks this condition will, however, not be met. We furthermore discuss the case where the probability of sampling a node depends on the degree of a node and we find that even classical random graphs are no longer closed under this sampling regime. We conclude by relating the results to real *Escherichia coli* protein interaction network data.

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I. INTRODUCTION

Most networks investigated today are parts of much larger networks. These subnets can come in two different forms. First, we can choose a region of a network and consider all nodes that are in this region and only the edges between these nodes (for example a connected component of the larger network would be one such subnet). Looking at networks defined by all servers in a country, or the interaction network of all proteins which are confined to the mitochondria would be real-world examples [1–3]. Such networks may not be representative of the network as a whole but can give valuable insights into communication or biological processes within a defined sphere. More complicated is a second type of subnet where each node of the global network is included in the subnet with a certain probability p and only the connections between pairs of nodes which are both included in the subnet are studied. This type of subnet is radically different from the regional-based subnets. It is, however, a frequent scenario in the analysis of technological and biological networks: most studies of molecular networks, such as protein-protein interaction [4,5], gene-regulation [6], and metabolic networks [7], test for connections between a subset of the known molecular entities (proteins, genes, and enzymes or metabolites, respectively). The process by which these entities (or corresponding probes) are chosen may reflect the bias of the experimenter or merely chance, and this will in turn influence the extent to which the subnet reflects properties of the global network in a meaningful way. In light of the relative straightforwardness of studying the sampling properties of networks, and their obvious importance

for the analysis of current network data sets it is surprising that this problem has not been addressed previously.

Here we will focus on the simplest, and perhaps most parsimonious, process of sampling nodes: the case where each node in the network is included with probability $0 < p < 1$. In the present analysis we will concentrate on the sampling properties of the degree distribution of a network. The degree distribution, henceforth denoted by $\text{Pr}(k)$, specifies the probability for a node to have k connections, $k=0, 1, \dots$, and is probably the most common summary statistic used in the analysis of networks [8]. In particular the potential scale-free nature of real networks is often identified from the empirical degree distribution, which for scale-free networks takes on a power-law form, $\text{Pr}(k) \propto k^{-\gamma}$ [2,9–11]. Frequently a model is considered scale-free if the tail (i.e., for k sufficiently large) of the degree distribution takes such an asymptotic power-law form [1,12]. Here we will consider this case as well as network ensembles with an exact power-law degree distribution. The central question addressed here is whether the degree distribution of randomly sampled subnets has the same properties as the degree distribution of the overall network. Thus far this question has been ignored in the literature, but as we will show, is of great importance in the analysis of real networks, which in their vast majority, are only subnets of larger networks. Unless explicitly stated otherwise we shall consider the thermodynamic limit, $N \rightarrow \infty$.

II. THE DEGREE DISTRIBUTION OF A RANDOM SUBNET

A. Sampling from networks

We use \mathcal{N} to denote a network with N nodes (we allow $N \rightarrow \infty$) drawn from a statistical ensemble of random networks [13,14] defined by some (potentially vector valued) parameter Ω and let $\text{Pr}(k)$ be its degree distribution; the total

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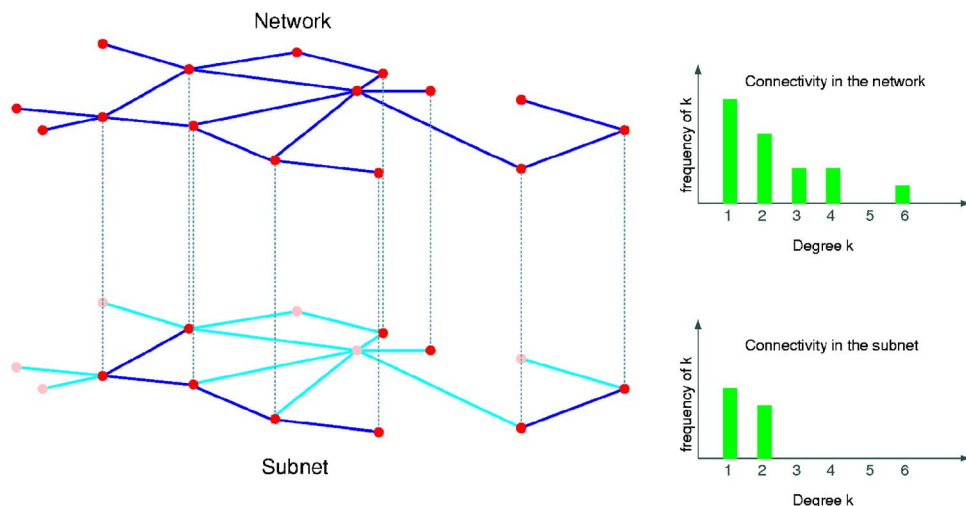


FIG. 1. (Color online) Sampling nodes from the network (top) will give rise to subnets (bottom). If edges are only observed if both nodes incident on an edge are included in the subnet [indicated in bold (dark blue)], then the degree distributions (as well as other characteristics) of the subnet and global network will be different. In the text we show that sometimes, however, degree distributions in both networks can be related under random sampling of nodes.

number of edges is given by M . Here we will be especially concerned with the case of a subnet \mathcal{S} generated from the global network \mathcal{N} by randomly sampling each node $i \in \mathcal{N}$ with a certain probability $0 \leq p_i \leq 1$ (see Fig. 1). Thus if a node of degree k gets picked for inclusion in the subnet, its degree in the subnet will depend on the number of its neighbors that are also included in \mathcal{S} .

1. Random sampling

We start by considering the case where the probability of picking a node is identical for all nodes, $p_i = p$ for all i . Here $p=0$ and 1 are the trivial cases for which $\mathcal{S} = \emptyset$ and \mathcal{N} , respectively. Formally, the probability that a node has connectivity l in \mathcal{S} given it has connectivity k in \mathcal{N} is

$$\Pr(l|k) = \binom{k}{l} p^l (1-p)^{k-l}, \quad (1)$$

where $\Pr(x|y)$ denotes the conditional probability of x given y . The degree distribution in the subnet is thus given by

$$\Pr_{\mathcal{S}}(l) = \sum_{k \geq l}^{\infty} \Pr(l|k) \Pr(k) = \sum_{k \geq l}^{\infty} \binom{k}{l} p^l (1-p)^{k-l} \Pr(k). \quad (2)$$

This is probably the simplest and most parsimonious sampling scheme and may also be a reasonably realistic approximation, e.g., in the study of protein interaction networks where experimenters choose a set of proteins in a more or less haphazard fashion.

From Eq. (2) we can show that

$$\mathbb{E}_{\mathcal{S}}[l] = \mathbb{E}[E[l|k]] = p \mathbb{E}[k] = p\tau, \quad (3)$$

where $\tau := \mathbb{E}[k]$ is the average degree in the network. Similarly we can show that the m th moment of the descending factorial [defined by $x_{[m]} = x(x-1)(x-2) \cdots (x-m+1)$ [15]] for the degree distribution of a network obeys

$$\mathbb{E}_{\mathcal{S}}[l_{[m]}] = p^m \mathbb{E}[k_{[m]}]. \quad (4)$$

Equations (3) and (4) are satisfied for all networks, as long as the moments exist; for scale-free networks with exponent γ , for example, moments of order greater than or equal to $\lfloor \gamma \rfloor$ do not exist.

2. Random sampling dependent on degree

A further sampling scheme will be considered here where the number of connections directly influences the probability $\pi(k)$ of sampling a node of degree k ; in the previous sampling scheme all nodes had the same chance of being sampled, $\pi(k) = p$. We will focus on the particular case of an uncorrelated network.

The connectivity of a node in the subnet thus depends on the degrees of its neighbors. The probability that a node connected to a randomly chosen edge has degree k is given by

$$\Pr^*(k) = \frac{k \Pr(k)}{\tau} \quad (5)$$

where τ is the average degree in the network; the average degree of the neighbors of a randomly chosen node is thus $\mathbb{E}[k^2]/\mathbb{E}[k]$, if the two first moments of the degree distribution exist; below we will limit ourselves to such situations (for finite networks the moments will, of course, exist). Assuming a node is retained in the subnet then the probability of sampling a neighboring node depends also on its connectivity and, in a mean-field approximation, the probability of retaining an edge originating from a node \tilde{p} is thus given by

$$\tilde{p} = \frac{1}{\tau} \sum_k k \Pr(k) \pi(k). \quad (6)$$

The degree distribution of the subnet \mathcal{S} is again given by binomial sampling:

$$\Pr_{\mathcal{S}}(l) = \left[\sum_{k \geq l}^{\infty} \binom{k}{l} \tilde{p}^l (1-\tilde{p})^{k-l} \pi(k) \Pr(k) \right] \Bigg/ \sum_{k=0}^{\infty} \pi(k) \Pr(k). \quad (7)$$

Defining

$$\Pr_0(k) = \pi(k) \Pr(k) \Bigg/ \sum_{k=0}^{\infty} \pi(k) \Pr(k) \quad (8)$$

we can rewrite Eq. (7) in the same form as Eq. (2). With these probabilities the degree distribution in the subnet is given analogously to Eq. (2) as

$$\Pr_S(l) = \sum_{k \geq l} \binom{k}{l} \tilde{p}^l (1 - \tilde{p})^{k-l} \Pr_0(k). \quad (9)$$

Obviously, when setting $\pi(k) = p$ Eq. (9) simplifies to Eq. (2).

We still have to specify the functional form of $\pi(k)$; *a priori* the only constraint is that $\pi(k)$ has to be a probability for all k , i.e., $0 \leq \pi(k) \leq 1, \forall k=0, 1, 2, \dots$. One possible and obvious choice is to let $\pi(k) \propto k$; in order to ensure that $\pi(k) \leq 1$ for large k we set

$$\pi(k) = Ck \quad (10)$$

with C sufficiently small such that $\pi < 1$ for large k (we can always trivially set $C = 2\mathbb{E}[M]$ with $\mathbb{E}[M]$ the expected number of edges in the network). In this case

$$\tilde{p} = \frac{C}{\tau} \sum_k k^2 \Pr(k) = C\mathbb{E}[k^2], \quad (11)$$

i.e., \tilde{p} depends on the degree distribution solely via the first and second moments of $\Pr(k)$. We will refer to this sampling scheme as preferential sampling of nodes.

B. Probability generating functions of random subnets

We represent the degree distribution of a network \mathcal{N} through its probability generating function (PGF) [15,16]

$$G(s) = \sum_{k=0}^{\infty} \Pr(k) s^k. \quad (12)$$

The probability $\Pr(k)$ follows from the PGF via the relationship

$$\Pr(k) = \left. \frac{1}{k!} \frac{d^k G(s)}{ds^k} \right|_{s=0}. \quad (13)$$

With Eqs. (12) and (1) we can straightforwardly derive the PGF for the subnet,

$$\begin{aligned} G_S(s) &= \sum_{l=0}^{\infty} \Pr(l) s^l \\ &= \sum_{l=0}^{\infty} s^l \sum_{k=l}^{\infty} \Pr(l|k) \Pr(k) \\ &= \sum_{k=0}^{\infty} \sum_{l=0}^k \binom{k}{l} p^l (1-p)^{k-l} s^l \Pr(k) \\ &= \sum_{k=0}^{\infty} \Pr(k) (1-p+ps)^k = G(1-p+ps). \end{aligned} \quad (14)$$

If nodes with degree $l=0$ are ignored (as is frequently the case in high throughput protein interaction data) then after deleting all nodes with $l=0$ the PGF in the subnet becomes

$$G_S^*(s) = \frac{G(1-p+ps) - G(1-p)}{1 - G(1-p)}. \quad (15)$$

Equations (14) and (15), respectively, hold generally for the degree distributions of subnets randomly sampled from net-

works, depending on whether orphaned nodes (i.e., those with connectivity $l=0$) are allowed or not [17].

Interestingly, if Eq. (14) holds then also Eq. (15) holds with $G(s)$ replaced by $G^*(s) = [G(s) - \Pr(0)] / [1 - \Pr(0)]$; i.e., networks with orphaned nodes removed are closed under random sampling if the networks with the orphaned nodes retained are.

III. CLOSURE UNDER RANDOM SAMPLING FROM NETWORKS

A. Conditions for closure: Generating function

From Eqs. (14) and (15) it is apparent that degree distributions of a subnet \mathcal{S} cannot generally be expected to be of the same type (e.g., a Poisson distribution) as the degree distribution of the global network \mathcal{N} . For some important types of networks, however, it can be shown that random sampling of nodes gives rise to networks with degree distributions of the same type as the global network, but with a different parameter depending on p , i.e., $\Omega' = fn(\Omega, p)$. In this case we say that a network (or its degree distribution) is closed under random sampling of nodes. For a network ensemble to be closed under random sampling the following condition is necessary and sufficient [17]:

$$G_S(s; \Omega) = G(s; \Omega') = G(1-p+ps; \Omega) \quad (16)$$

and

$$G_S^*(s; \Omega) = G(s; \Omega') = \frac{G(1-p+ps; \Omega) - G(1-p; \Omega)}{1 - G(1-p; \Omega)}, \quad (17)$$

when the subnet is not allowed to have orphaned nodes. Necessity and sufficiency follow from Eqs. (14) and (15) and the definition of the properties of a closed subnet.

B. Conditions for closure: Moments

Equations (16) and (17) can be applied to all types of degree distributions. Inspired by Eqs. (3) and (4) we here derive a general condition in terms of moments for a subnet to be of the same type as the global network. We assume the moments determine the degree distribution uniquely (in particular, this implies that all moments exist), which is true under mild regularity conditions. Let an ensemble of random networks be given which is parametrized by Ω . For example, the ensemble of classical or Erdős-Rényi random graphs [13,18] has $\Pr(k) = \exp(-\lambda) \lambda^k / k!$ and $\Omega = \lambda$ is the average connectivity. We seek a condition that, provided nodes are sampled with probability p , ensures that the degree distribution of the subnet remains in the same ensemble of random networks. Without loss of generality we can assume that Ω has the form $\Omega = (\tau, \psi)$, where τ is the average degree in the network and ψ is an additional (potentially vector valued) parameter.

From Eq. (3) we know that the average connectivity in the sampled subnet, τ_p , is given by $\tau_p = p\tau$. We can use Eq. (4) to show that a family of degree distributions is closed under

random sampling of nodes if and only if the descending factorial moments obey the relationship

$$\mathbb{E}[k_{[m]}] = a_m(\psi) \tau^m, \tag{18}$$

where $a_m(\psi)$ is a constant that depends only on m and ψ but not on τ and the sampling probability p , and where $a_1(\psi) = 1$.

To prove that Eq. (18) is necessary we assume that the network is closed under random sampling of nodes and write $\tau = \mathbb{E}(k)$ and $g_m(\tau, \psi) = \mathbb{E}(k_{[m]})$. Because of Eqs. (3) and (4) we can immediately write

$$g_m(p\tau, \psi) = p^m g_m(\tau, \psi) \tag{19}$$

and

$$\frac{g_m(p\tau, \psi)}{(p\tau)^m} = \frac{g_m(\tau, \psi)}{\tau^m}. \tag{20}$$

Thus $g_m(\tau, \psi) / \tau^m = \text{const}$ (for all τ) or

$$g_m(\tau, \psi) = a_m(\psi) \tau^m, \tag{21}$$

with $a_1(\psi) = 1$ as required.

To prove sufficiency assume that the descending moments of $k_{[m]}$ satisfy Eq. (18); using Eq. (4) the descending factorial moments of the nodal degrees in the subnet follow the relationship

$$\mathbb{E}_S[l_{[m]}] = a_m(\psi) (p\tau)^m. \tag{22}$$

Since the descending moments determine the moments $\mathbb{E}(k^m)$ of a degree distribution, which in turn determine the distribution uniquely (by assumption), then the degree distribution of the subnet is given by a distribution that is of the same type as the degree distribution but with a rescaled parameter. Thus Eq. (18) is a necessary and sufficient condition for a network ensemble to be closed under random sampling of nodes. ■

C. Analytical examples

We can use relationships (16) and (18) to determine whether a degree distribution is closed under random sampling. We will discuss this for three commonly observed degree distributions. Note that we only consider a degree distribution to be closed under (random) sampling if the degree distributions of the network and the subnet belong to the same family of probability distributions.

Classical random graphs have a Poisson degree distribution $\text{Po}(\lambda)$. It is straightforward to show that the descending moments of the Poisson distributed random variables are given by

$$\mathbb{E}[k_{[m]}] = \tau^m = \lambda^m. \tag{23}$$

Thus $a_m = 1$ for all $m \geq 1$ and the degree distribution of classical random graphs is closed under random sampling of nodes. If we therefore have a subnet \mathcal{S} of size M drawn from a larger network \mathcal{N} of known size N we can determine λ from λ_S as $\lambda = \lambda_S N / M$. The subnet is therefore informative about the global network.

Networks that grow by random attachment of new nodes give rise to exponential degree distributions such that asymptotically (large N) $\text{Pr}(k) = (1 - e^{-\alpha}) e^{-k\alpha}$. For such a distribution it is easily shown that

$$\mathbb{E}[k_{[m]}] = \frac{m! e^{-m\alpha}}{(1 - e^{-\alpha})^m} = m! \tau^m, \tag{24}$$

since $\mathbb{E}[k] = e^{-\alpha} / (1 - e^{-\alpha})$. This means that $\mathbb{E}[k_{[m]}]$ can be written in the form specified by Eq. (18) and therefore exponential degree distributions are closed under random sampling. Binomial (as for classical finite-sized random graphs) and negative binomial distributions are also closed under random sampling as is easily verified. An explicit construction of probability distributions which are closed is discussed in the Appendix.

If the probability of attaching to a node is proportional to its degree the resulting network will asymptotically have a power-law degree distribution with exponent 3 [12]. For models where an existing node is duplicated and each of its connections is kept with certain probability degree distributions will also be power-law-like but with exponents $2 < \gamma < 3$ [19].

We first consider the sampling properties of network ensembles with degree distribution given by an exact power law $\text{Pr}(k) = k^{-\gamma} / \zeta(\gamma)$. In the asymptotic limit $N \rightarrow \infty$, all moments greater than $\lceil \gamma \rceil$ diverge and we therefore have to use the PGF formalism. The PGF for the global network is given by

$$G(s; \gamma) = \frac{1}{\zeta(\gamma)} \sum_{k=1}^{\infty} s^k k^{-\gamma} \tag{25}$$

and since $k=0$ is explicitly forbidden in a scale-free network, we use Eq. (17) to construct the PGF in the subnet, whence

$$G_S^*(s; \gamma) = \frac{\sum_{k=1}^{\infty} [(1-p+ps)^k - (1-p)^k] k^{-\gamma}}{\zeta(\gamma) - \sum_{k=1}^{\infty} (1-p)^k k^{-\gamma}}. \tag{26}$$

Clearly for $p \rightarrow 1$ we obtain the original PGF $G(s; \gamma)$. For $0 < p < 1$, however, it is impossible to determine an exponent γ' such that G_S could be written in terms of the PGF of a power law. Therefore random subnets drawn from exact scale-free networks are not themselves scale-free. This can also be shown explicitly using a series expansion [17]. We note, however, that the tail of the degree distribution of the subnet still takes on a power-law form for k sufficiently large. The same analysis applied to other fat-tailed probability distributions also shows that other fat-tailed degree distributions such as the log-normal and the stretched exponential families [20] are not closed under random sampling.

D. Numerical examples

The effect of random sampling on the degree distribution is most straightforwardly illustrated using numerical solutions of Eqs. (2) and (6)–(9). Here we do this for networks of

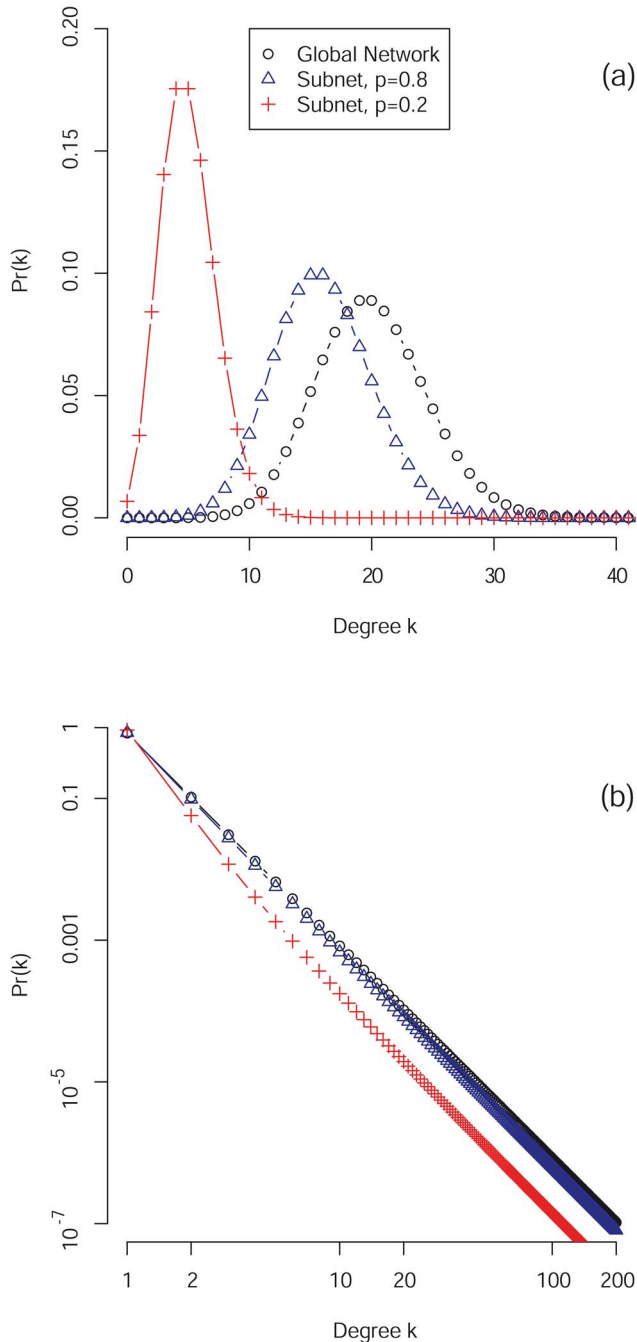


FIG. 2. (Color online) Degree distributions of full network and subnets obtained by sampling each node with probability $p=0.8$ and 0.2 , respectively, for classical random graphs (a) and scale-free networks (b).

infinite size and for simplicity focus on the canonical models of the classical random graph and the exact scale-free network, respectively.

In Fig. 2(a) we show the Poisson distribution with $\lambda=5$ and the distributions of random subnets with $p=0.8$ and 0.2 , respectively. The subnet distributions are identical with the Poisson distributions with parameters $\lambda=4$ and 2 . This also means that as $p\lambda$ becomes smaller than 1 the subnet will move through the phase transition where the giant connected

component dissolves and the size distribution of connected parts of the subnet becomes exponential.

In Fig. 2(b) we show the power-law distribution with $\gamma=3$ and again the corresponding subnet degree distributions [renormalized such that $\Pr_S(0)=0$ in the subnet]. We find that the subnet degree distributions are no longer straight lines but that as k becomes large they run parallel to the original distributions. That is, as already described above, the tails of degree distributions of subnets sampled randomly from scale-free networks also fall off in the same power-law fashion as the original network. But at low connectivities the departure from the scale-free network is quite pronounced: probability mass moves from the tail toward the low-connected nodes with $k=1$, which become more abundant than would be expected for a true scale-free network. This will have quite considerable effects for finite-size networks. The deviation of the subnet degree distribution from a pure power law at small to intermediate connectivities increases with γ (as well as, naturally, with decreasing sampling probability p). We note, however, that the tail of the degree distribution will retain a power-law form; thus for an alternative definition of scale-free behavior which only requires $\Pr_N(k) \propto k^{-\gamma}$ for $k \rightarrow \infty$ random subnets will retain scale-free behavior in the sense that the tail is still described by a power law $\Pr_S(k) \propto k^{-\gamma'}$ for $k \rightarrow \infty$. In general, however, when the whole degree distribution is considered scale-free networks are not closed under random sampling.

IV. CONNECTIVITY DEPENDENT SAMPLING

There is no unique and obvious way in which the probability of sampling a node may depend on the connectivity. Here we briefly outline the behavior of the degree distribution under the simple schemes outlined above where the probability of sampling a node is no longer uniform but linearly proportional to its connectivity, i.e., if $\pi(k) \propto k$; we assume that $\tilde{p}(k)$ is given by Eq. (11).

For a Poisson degree distribution with parameter λ we have $E[k^2]=\tau^2+\tau=\lambda^2+\lambda$ and $E[M]=N\lambda/2$ (assuming the network is large and finite) whence $\tilde{p}=(\lambda+1)/(N\lambda)$ and

$$\Pr_0(k) = \frac{e^{-\lambda}\lambda^{k-1}}{(k-1)!}, \quad (27)$$

if we set $C=2E[M]$ in Eq. (10). In this case Eq. (9) becomes

$$\Pr_S(l) = \sum_{k \geq l} \binom{k}{l} \tilde{p}^l (1-\tilde{p})^{k-l} \Pr_0(k) = \frac{(\lambda\tilde{p})^l}{l!} e^{-\lambda\tilde{p}} \left(1 - \tilde{p} + \frac{l}{\lambda}\right) \quad (28)$$

for $l=0, 1, \dots$. The distribution in the subnet is thus not a pure Poisson distribution but one multiplied by a factor $1 - \tilde{p} + l/\lambda$. Under this connectivity dependent sampling classical random graphs are therefore not closed and subnets S are qualitatively (if perhaps only rather slightly) different from the overall network N .

For scale-free networks with $\gamma \leq 3$ the second moment diverges, $E[k^2] \rightarrow \infty$, and we therefore focus on finite (though potentially very large) networks. Networks with a power-law

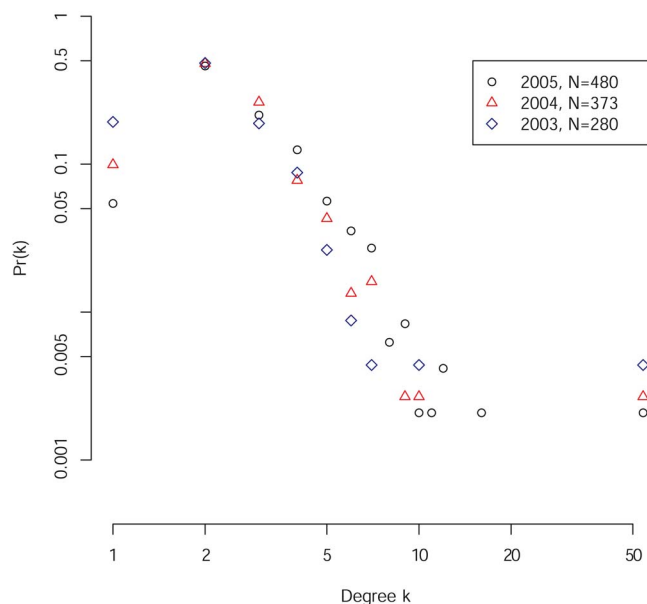


FIG. 3. (Color online) Degree distributions of protein interaction network data available for *E. coli* in April of the years 2003, 2004, and 2005, respectively. As the fraction of sampled proteins decreases, statistical weight is shifted from the tail toward lower degrees.

degree distribution can, for example, be constructed using standard methods [21–23]. For such a scale-free graph with N nodes we have to numerically evaluate the expected number of edges $\mathbb{E}[M] = \frac{1}{2} \sum_{k=1}^N k^{-\gamma+1} / \zeta(\gamma)$ and \tilde{p} , given by Eq. (11). For $\text{Pr}_0(k)$ we obtain for scale-free networks

$$\text{Pr}_0(k) = \frac{k^{1-\gamma}}{\zeta(\gamma-1)}. \quad (29)$$

Proportional sampling from a scale-free network defined by a power-law exponent γ is thus identical to sampling from a network with power-law exponent $\gamma-1$ and sampling probability \tilde{p} . Therefore we can use the results obtained above and conclude that the scale-free network (in the strict sense outlined above) is not closed under proportional sampling of nodes; for sufficiently large degrees, however, the tail of the degree distribution will still have a power-law form.

V. PROTEIN INTERACTION NETWORK DATA

In Fig. 3 we show three degree distributions corresponding to the protein interaction network (PIN) data from *Escherichia coli* which was available in April 2003, 2004, and 2005 in the database of interaction proteins (DIP; dip.doe-mbi.ucla.edu); the resulting networks are made up of the interactions among 228, 373, and 480 proteins and have 293, 515, and 760 interactions, respectively. Figure 3 confirms the results of the theoretical analysis presented above: as the fraction of sampled network nodes decreases statistical weight shifts from the tail toward lower degrees; the degree of the single highly connected node, $k=54$, was already known in the 2003 data set (no further interactions have been added to this node since). The statistical weight of sparsely

connected nodes, $k=1$, increases as the fraction of sampled nodes decreases. We note that the present data sample only a small subnet of the *E. coli* PIN which consists of interactions among approximately 4000 proteins. Moreover (i) it is well established that PIN data are highly unreliable and very noisy, and (ii) the true sampling scheme underlying the sampling scheme will generally be more complicated than the first order model employed here. The behavior appears, however, to be qualitatively similar to our theoretical analysis.

VI. CONCLUSION

Both sampling schemes discussed here are necessarily simpler than is the case in many real situations, such as the analysis of protein interaction networks (see, e.g., [24,25]). We believe, however, that between them they retain some vestiges of reality. Crucially, however, we wish to stress the incomplete nature of many network data sets. For many of these data sets in fact, including protein interaction network data, it appears that some form of random sampling is more realistic than a process in which the neighborhood of a node is explored and neighboring sites are recruited iteratively into the experimental setup. No matter what the sampling process is, it has to be included into the analysis from the outset: making inferences from incomplete (in the sense that not all nodes have been sampled) network data may give misleading results. If a network is closed under random (or connectivity dependent) sampling then it is straightforward to infer properties of the overall network from the subnet. For some, notably Erdős-Rényi, random graphs, this is indeed the case. In general, however, the degree distributions of the network and sampled subnets will be qualitatively different (as illustrated in Fig. 1). For example, while power-law tails will also give rise to power-law tails in the subnet, a network which has an exact power-law degree distribution is not closed under random sampling. The same is true for other broad-tailed degree distributions such as log-normal or stretched exponential distributions.

Sampling properties will also affect other network statistics, including network diameter and average path length, clustering coefficient, and network motifs. These will be studied in a companion paper. We believe that sampling properties ought to be included explicitly and from the outset into any network analysis, unless there is good evidence that the whole (or the majority) of the network's nodes have been included in the data. Quite apart from the relevance of this work in the analysis of real data we believe that a detailed analysis of sampling properties of graphs is a rich field which, surprisingly, appears to have been neglected thus far.

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APPENDIX: CONSTRUCTION OF CLOSED DEGREE DISTRIBUTIONS

We have shown that Eq. (18) is both a necessary and sufficient condition for a degree distribution to be closed under binomial random sampling. We can also use Eq. (18) to construct closed distributions *de novo* as any series of positive numbers a_k , $k=1,2,\dots$, where $a_1=1$ defines a family of random variables closed under binomial sampling via the condition

$$\mathbb{E}[k_{[m]}] = a_m \tau^m \quad (\text{A1})$$

for some $\tau \in T = [0, t]$ and $t \geq 0$.

First, the degenerate distribution $\Pr(k=0)=1$ is defined by $\mathbb{E}[k_{[m]}]=0$ for all $m > 0$. Therefore 0 must be in the interval T and T is nonempty as the degenerate distribution is trivially closed under binomial sampling. Now assume that $\tau \geq 0$ de-

finer the distribution of k through Eq. (A1). Any τ^* with $0 \leq \tau^* \leq \tau$ defines the degree distribution after binomial sampling of nodes from k with probability $p = \tau^*/\tau$ which, by construction, has degree distribution given by $\mathbb{E}[l_{[m]}] = a_m (\tau^*)^m$. The distributions defined by Eq. (A1) are therefore closed under random sampling of nodes.

Equation (A1) can be used to to construct arbitrary degree distributions that are closed under binomial sampling. Non-trivial examples are possible; for example,

$$a_k = (k+1)2^{-k} \quad \text{for } k = 1, 2, \dots \quad (\text{A2})$$

defines a distribution closed under random sampling,

$$\Pr(k) = \frac{(2\tau)^k}{k!} (k+1-2\tau)e^{-2\tau} \quad (\text{A3})$$

where $\tau = \mathbb{E}[k] \in [0, 0.5]$ [note that for $\tau=0.5$, $\Pr(k-1)$ defined by Eq. (A3) is Poisson distributed].

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