

# Reliability of rank order in sampled networks

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**Abstract.** In complex scale-free networks, ranking the individual nodes based upon their importance has useful applications, such as the identification of hubs for epidemic control, or bottlenecks for controlling traffic congestion. However, in most real situations, only limited sub-structures of entire networks are available, and therefore the reliability of the order relationships in sampled networks requires investigation. With a set of randomly sampled nodes from the underlying original networks, we rank individual nodes by three centrality measures: degree, betweenness, and closeness. The higher-ranking nodes from the sampled networks provide a relatively better characterisation of their ranks in the original networks than the lower-ranking nodes. A closeness-based order relationship is more reliable than any other quantity, due to the global nature of the closeness measure. In addition, we show that if access to hubs is limited during the sampling process, an increase in the sampling fraction can in fact decrease the sampling accuracy. Finally, an estimation method for assessing sampling accuracy is suggested.

**PACS.** 89.75.Hc Networks and genealogical trees – 89.75.Fb Structures and organization in complex systems

## 1 Introduction

In recent years, there has been great interest in examining the properties of complex networks such as the World-Wide Web, the Internet, and social and biological networks [1]. Recent research on the networks reveals that many networks have scale-free structures that possess a right-skewed degree distribution. This power-law degree distribution guarantees a noticeable existence of nodes, or hubs, that have a very large number of connections compared with the average node. The essential role of hubs in networks is widely recognised in the contexts of immunisation in epidemic spreading [2], the formation of social trends [3], finding drug targets on biological molecules [4, 5], and optimal path-finding strategies [6]. For example, the study of the spread of viruses on the Internet shows that targeting immunisation on hubs drastically reduces the occurrence of endemic states, even with a very low immunised fraction, whereas uniform immunisation does not lead to a drastic reduction in the infection prevalence [1, 2]. For drug target identification in biological systems, the likelihood that removal of a protein will be lethal correlates strongly with the number of connections to that protein in the protein-protein interaction network [5].

In these examples, accurate identification of the important nodes, i.e. hubs, is an efficient way to resolve the

specified problems. Such identification, however, requires that the ranks of the individual nodes are known, based on their importance and contribution to the entire network. In targeted immunisation on hubs, the more accurate a policy is at identifying the ranks, the smaller the number of necessary cures [7]. In real situations, however, only part of the information on the underlying networks can be exploited, due to severe physical and economical constraints [6, 8–12]. For example, a survey of relationships among participants has to be conducted in order to construct a social network, but the collected network data might be incomplete, since surveys usually target only a limited sample of the whole population. Therefore, the statistical properties of a network must frequently be assessed without complete knowledge of global information on the entire network. Nevertheless, the sampling problem in complex networks has not yet been extensively explored [10, 12, 13], despite the substantial interest in the community of social network analysis [8].

Given that only partial information on a network can be obtained, it is worth investigating how accurately the importance of a node, based on only partial information, reflects the actual importance of the node in the original network. For successful epidemic control, it is important to determine whether or not the hubs identified as critical from the incomplete data remain so even after adding supplementary data [14]. The study of rank reliability in sampled networks can also be applied to many technological

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and biological systems, and avoids possible artifacts depending on a specific numerical scale of data (whereas stretching or compressing the scale does not alter a rank-based result).

In the present work, we analyse the Barabási-Albert (BA) model as the prototype example of a scale-free network [1]<sup>1</sup>, which allows us to clearly discriminate the contribution of the power-law degree distribution to the sampling effect from the contribution of additional specific biases that appear in other networks. Furthermore, to consider realistic effects that are disregarded in the BA model, we also analyse several real networks, such as the Los Alamos e-Print Archive coauthorship network [15], the Internet AS [16], and protein-protein interaction networks [5,17]. We concentrate only on cases where the accessible information on the networks is limited to the connectivity between randomly sampled nodes, although in reality, there are other kinds of allowable information, including the connectivity from snowball sampling, and that from randomly sampled links [13]. Snowball samples consist of identified nodes to which all linked nodes are then used to refer to other nodes, and are usually employed by Web search engines. Randomly sampled links describe the randomly gathered connectivity between nodes, e.g. in the case of poorly gathered contact information between patients. It is expected that snowball sampling provides rare sampling biases with literally conserved topologies during the sampling, while the possible nontrivial results from randomly sampled links can be sufficiently analogous to those from randomly sampled nodes with some correspondence between them [13]. Thus, the focus on randomly sampled nodes could be considered a reasonable step towards investigating the network-sampling problems, although the study of only randomly sampled nodes here has limitations for understanding more specific problems in real situations. In this regard, the possible deviations between our results and reality could be further reduced by additional investigation of different sampling schemes.

## 2 Measured quantities

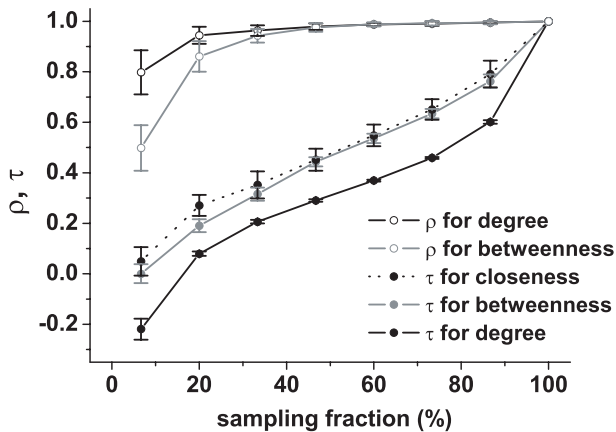
In sampled or entire networks, individual nodes can be properly ranked according to their importance or *prestige* [18], like degree. With the set of sampled nodes, we first define a measure for the rank correlation between the sampled nodes and the nodes in the original network, denoted by  $\tau$ , which is a variant of *Kendall's Tau* [19], representing how faithfully the rank order is preserved in the sampled network. For an arbitrary pair of sampled nodes  $\{i, j\}$ , the nodes have assigned importance, like degrees, such as  $\{k_i, k_j\}$  in the sampled network and as  $\{k_i^o, k_j^o\}$  in the original network. If  $k_i < k_j$  ( $k_i > k_j$ ) and  $k_i^o < k_j^o$  ( $k_i^o > k_j^o$ ), or  $k_i = k_j$  and  $k_i^o = k_j^o$ , we consider that the pair is then ordered similarly in the sampled and original networks. Otherwise, it is regarded as ordered dissimilarly. To quantify the preservability of rank order, the

dominance of pairs ordered similarly in both the sampled and original networks is normalised by the total number of pairs that are considered in the calculation, through  $\tau = (N_+ - N_-)/(N_+ + N_-)$ , where  $N_+$  is the number of pairs ordered similarly for sampled and original networks, and  $N_-$  is the number of pairs that are ordered dissimilarly.  $\tau$  can have a value from  $-1$  to  $1$ , indicating complete disagreement and full agreement, respectively. Without any tied ranks, if the ranks are more preserved in sampling than expected by random shuffling,  $\tau$  is positive. For the probability  $p$  that an arbitrary pair is ordered similarly, we can obtain the relationship  $p = (\tau + 1)/2$ .

Because the statistical properties of many real networks follow a universal characteristic like a power-law distribution, their preservability in sampled networks has been of basic interest in previous studies [10,13]. These statistical properties, however, are rarely affected by interchanging the prestiges of nodes. Hence, it is worth comparing the preservability of these individual-prestige-insensitive properties in sampled networks to that of the individual-prestige-sensitive properties such as  $\tau$ . Therefore, we introduce another complementary measure,  $\rho$ , which represents the similarity between two probability distributions of centrality — one from sampled nodes and the other from the original network — where the latter one obeys a power law. First, we obtain the cumulative distribution of variable  $k$ ,  $\mathcal{P}_S(k)$  from the sampled nodes, and  $\mathcal{P}_O(k)$  from the original network. Using  $k_i$  of the  $i$ th sampled node, we find  $k_i^o$ , satisfying  $\mathcal{P}_S(k_i) = \mathcal{P}_O(k_i^o)$ , and calculate the Pearson correlation  $\rho$  between  $k_i$  and  $k_i^o$  for  $i = 1, 2, \dots, N$ , where  $N$  is the number of sampled nodes.  $\rho$  can achieve its maximum value of 1 if  $k_i$  is proportional to  $k_i^o$ . This means that when  $\mathcal{P}_S(k) \propto k^{-\alpha}$  and  $\mathcal{P}_O(k) \propto k^{-\beta}$ ,  $\rho$  can achieve its maximum value of 1 if  $\alpha = \beta$ , i.e. in the case of identical power-law distributions. By applying proper normalisation, we transform the measure  $\rho$  so as to take a value from 0 to 1 in its significant range<sup>2</sup>.  $\rho$  gives the preservability of probability distributions rather than that of the node rank, thus  $\rho$  can have a large value under the similar probability distributions, even if the ranks themselves are severely altered. In a practical sense, it is possible to directly evaluate the exponent difference of the power-law distribution between sampled and original networks, and the detail of the results exhibits some notable properties, including a slight overestimation of the exponents during the random sampling [13]. For the degree distribution of the BA model, a sampling overestimation of the exponent by a factor of 1.2 corresponds to  $\rho = 0.8$ . It should be noted that an isolated node, which had no links to the other connected sampled nodes, was excluded in the calculation of  $\tau$  and  $\rho$ . We can easily apply these measures to other quantities, such as betweenness centrality, as will be shown below.

<sup>1</sup> Performing the analysis on the configuration model [23] instead of the BA model does not alter the current results.

<sup>2</sup> To this end, we calculate the Pearson correlation  $\rho_{th}$  between  $k_i$  and  $k_i^o$  as if  $\mathcal{P}_S(k)$  is a simple linear function of  $k$ . We finally obtain the value of  $\rho$  as  $\rho \rightarrow (\rho - \rho_{th})/(1 - \rho_{th})$ . Therefore,  $\rho$  becomes positive if the probability distribution from the sampled nodes resembles that from the original network more than a simple linear curve does.



**Fig. 1.** The horizontal axis represents the sampling fraction (the number of sampled nodes divided by the number of total nodes), while the vertical axis represents the calculated  $\tau$  and  $\rho$  at each sampling fraction. We use the BA model with 30 000 nodes and average degree of 8.

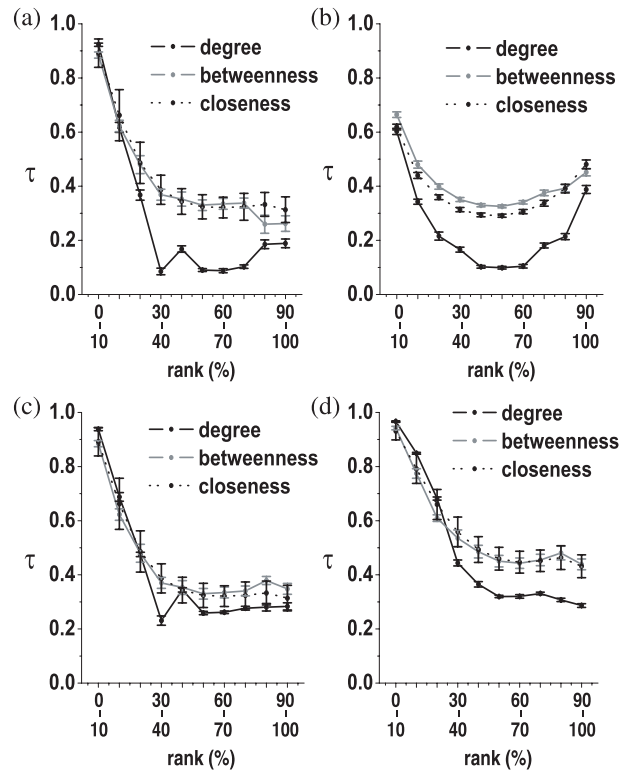
### 3 Simulation and results

In this paper, we rank-order individual nodes using the three centrality measures of complex networks: degree, betweenness, and closeness, in order to calculate  $\tau$  [15, 20]<sup>3</sup>. We also calculate  $\rho$  for degree and betweenness, based on their power-law statistics [1, 21]. Using randomly sampled nodes, Figure 1 displays the result for the BA model, which reflects results typical for other real networks with regard to the qualitative distinction between  $\tau$  and  $\rho$ . In Figure 1, as the sampling fraction increases,  $\tau$  grows gradually while  $\rho$  grows quickly and saturates at 1<sup>4</sup>. It has been verified that the early saturation of  $\rho$  is due to the overall proportional relationship between the centrality measure obtained from the randomly sampled nodes and that from the original networks [13]. On the other hand, the continuous and rather slow growth of  $\tau$  indicates the sensitivity of individual-level prestige to the sampling, especially for the low rank nodes, as will be presented below.

Interestingly, the contribution of an individual node to the value of  $\tau$  is not uniform over all nodes, and strongly depends on the rank of the node. To examine this property in detail, we divide the sampled nodes into subgroups according to their individual ranks in the sampled nodes. For example, in the case of degree-based ranks, each node would belong to one of 10 groups — the highest 0 ~ 10%, 10 ~ 20%, ..., 90 ~ 100% ranks — in descending order of degree. To obtain the contribution to  $\tau$  made by each group, we calculate  $\tau$  over pairs of nodes  $\{i, j\}$  where the  $i$ th node is a member of the given group, and the  $j$ th node is a member of any group. Figure 2a illustrates the result for the BA model; the groups of higher-ranking

<sup>3</sup> The closeness of the  $i$ th node is defined as the average of the reciprocal distances from the  $i$ th node to all other nodes.

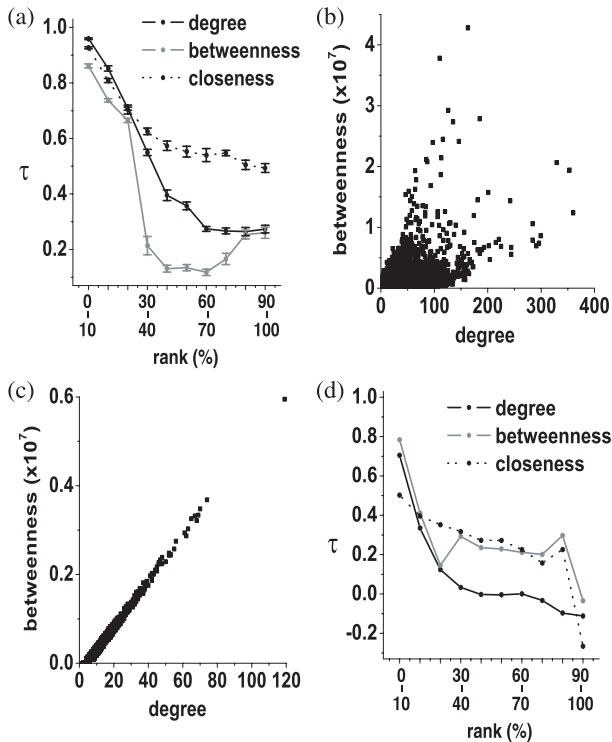
<sup>4</sup> Randomly sampled nodes are inevitably composed of several disconnected clusters. Nonetheless, the main difference between  $\tau$  and  $\rho$  is still valid even if we consider only the largest component from these clusters.



**Fig. 2.** The horizontal axis represents the groups according to their constituting ranks in sampled nodes, while the vertical axis represents  $\tau$  for each group. (a) 40% sampled from the BA model with 30 000 nodes and an average degree of 8; (b) the same condition as (a) in the Erdős-Rényi model; (c)  $\tau$  calculated without counting the pairs in tied prestiges from (a); (d) increased sampling fraction with 60% from (c).

nodes have large  $\tau$ 's, indicating that the higher-ranking nodes of the sampled nodes provide better characterisation of their ranks in the original networks [11]. This point will be universally carried in scale-free networks, because the nodes of large degree hardly face the shuffling of their ranks in sampling due to their relatively small population. In the Erdős-Rényi model, the intermediate ranks comprise a greater proportion of the population than either the high or low ranks. It is expected that  $\tau$  would reach the minimum value with intermediate ranks, as observed in Figure 2b.

From observations in the BA model, we have found that  $\tau$ 's for betweenness and closeness have larger values than  $\tau$  for degree, except in a few of the highest rank groups. Even in these highest rank groups,  $\tau$  for degree is comparable to the other  $\tau$ 's, and does not dominate them. In an attempt to explain the smallness of  $\tau$  for degree in most groups, one might consider the discreteness effect of degree, e.g. the majority of the nodes would possess a degree of 1 in a small sampling fraction. This severe discreteness could hide the original ordinal information between the nodes, thus leading to a smaller value of  $\tau$ . Nevertheless, the discreteness effect does not sufficiently explain our observation. To clarify this point, we calculate  $\tau$  while excluding the pairs of sampled nodes in tied prestiges, which



**Fig. 3.** (a) Rank vs.  $\tau$  in the 30% sampled nodes from the Archive coauthorship. (b) Individual degree vs. betweenness in the Archive coauthorship. (c) Individual degree vs. betweenness in the highest 30% of highly correlated degree and betweenness. (d) Rank vs.  $\tau$  of the nodes from (c).

reduces the discreteness effect. Figures 2c and 2d show the results of sampling fractions of 40% and 60%, respectively, but well represent the generic consequence along all sampling fractions. Although  $\tau$  for degree becomes large in a small sampling fraction (see Fig. 2c), the similar feature in Figure 2a eventually recovers as the sampling fraction increases (see Fig. 2d). This result implies that the small value of  $\tau$  for degree can be attributed to the intrinsic property of the local centrality, by which individual prestige is sensitive to the random sampling due to the local fluctuation of the network topology.

For comparison with the BA model, we consider real networks, and observe some different results. In real networks,  $\tau$  for betweenness becomes suppressed and is no longer comparable to  $\tau$  for closeness (see Fig. 3a). Here, we present the case of the Los Alamos e-Print Archive coauthorship network, although similar results are observed in other real networks, including the Internet AS and protein-protein interaction networks.

The suppressed  $\tau$  for betweenness reflects the sensitivity of the betweenness measure to the network modularity. Unlike random networks including the BA model, many real networks have structural sub-units, namely modular structures, that significantly affect the centrality measures in unexpected ways in random networks. For example, the presence of nodes with small degree and large betweenness shown in Figure 3b indicates the existence of loose connections between tightly-knit modules [22], such

that the nodes on the loose connections that bear a considerable number of inter-modular communication paths exhibit large betweenness centrality despite their small degree. In this sense, during the random sampling, violating modularity in the networks can significantly alter the betweenness-based node prestige, thereby lowering  $\tau$  for betweenness. One way to confirm this effect is to observe what happens if the modularity effect is reduced. To discard the modularity effect, we sample only the nodes with highly correlated degree and betweenness rather than do random sampling, and calculate the corresponding  $\tau$ <sup>5</sup>. Under the reduced-modularity effect, we can identify the range of the sampling fraction (in the Archive coauthorship,  $\lesssim 50\%$ ) in which  $\tau$  for betweenness becomes comparable to  $\tau$  for closeness as in the BA model (see Figs. 3c and 3d). This shows that the modularity effect is indeed essential to the suppression of  $\tau$  for betweenness.

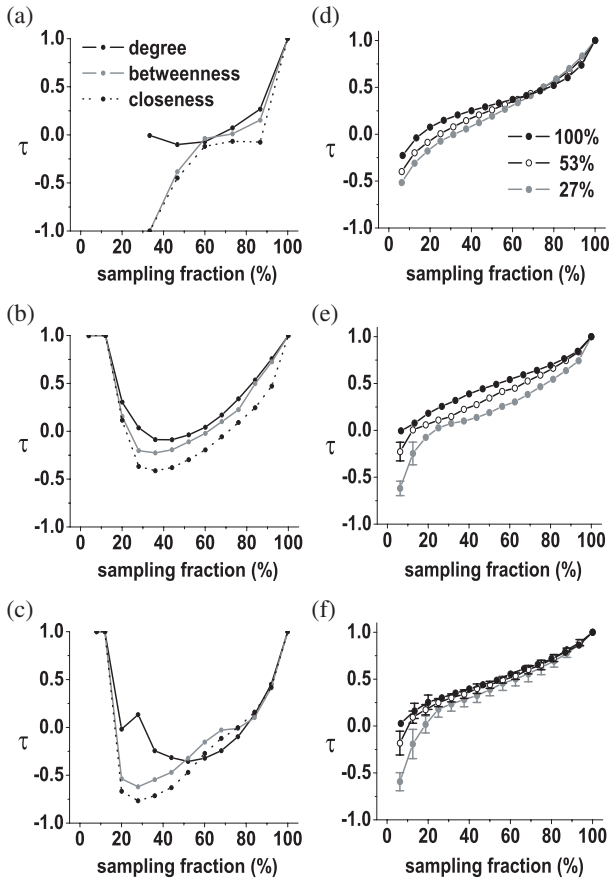
Consequently, the  $\tau$  for each centrality measure relies on the sensitivity of the centrality measure to the sampling. Indeed, a small  $\tau$  for degree comes from the fact that the ranks of degree suffer from their shuffling due to the local fluctuation of topology during the sampling process. Although it is based upon global information on the networks, betweenness concerns the number of *shortest* paths across a node itself, thus the rank can be sensitive to the topological variation in the proximity of the node, and especially to modular-level fluctuations. On the other hand, closeness is relatively tolerant to such topological fluctuations, and contributed to by the robust global information of the network, averaged path lengths outward from a node. Therefore, the closeness-based rank order possesses a larger  $\tau$  than any other quantity, due to the unique globality of the closeness being insensitive to the sampling.

Because such a global characteristic of closeness is responsible for the large  $\tau$  for closeness, the value of  $\tau$  for closeness can be suppressed if access to the hubs that bind the network together globally is restricted in the sampling process. To simplify this situation, we sample the nodes in ascending order of their centrality measures, rather than randomly as presented before. Figures 4a–4c display the results gathered when nodes are selected in ascending order of degree, and similar results are produced for betweenness and closeness in the other cases. As discussed above, the value of  $\tau$  for closeness is no longer superior to any other quantity. Surprisingly, we further identify that in real networks,  $\tau$  obtains its minimum value in an intermediate range of the sampling fraction, and thus has a convex shape (see Fig. 4b). This directly indicates that with small sampling fractions, if access to hubs is limited, an increase in the sampling fraction (i.e. more nodes are sampled) can in fact decrease the sampling accuracy

<sup>5</sup> We choose the nodes in ascending order of

$$\left| \frac{x_i - \langle x_i \rangle}{\sqrt{\langle x_i^2 \rangle - \langle x_i \rangle^2}} - \frac{y_i - \langle y_i \rangle}{\sqrt{\langle y_i^2 \rangle - \langle y_i \rangle^2}} \right|,$$

where  $x_i$ ,  $y_i$  stand for the degree and betweenness of the  $i$ th node, and  $\langle \dots \rangle$  is the average over all nodes.



**Fig. 4.** (a)–(c) Sampling under limited hub-accessibility. The horizontal axis represents the sampling fraction in ascending order of degree, while the vertical axis represents  $\tau$  at each sampling fraction, for (a) the BA model with 30 000 nodes and average degree of 8; (b) the Archive coauthorship; and (c) a random network given the same degree distribution as that of the Archive coauthorship. Results similar to those shown in (b) and (c) are also shown for other real networks. (d)–(f) Sampling from randomly sampled networks. The horizontal axis for a sampling fraction out of 100%, 53%, and 27%-sampled nodes from the BA model with 30 000 nodes and average degree of 8, and the vertical axis for  $\tau$  at each sampling fraction. (d)  $\tau$  for degree. (e)  $\tau$  for betweenness. (f)  $\tau$  for closeness.

(small  $\tau$ ) without a gain in valuable information. To avoid this type of error in the analysis of social networks, a sufficient sampling size of social individuals must be assured when access to the central leadership is restricted. Also, for the study of small data sets in bioinformatics, the presence of hubs should be of concern, because if they are not available, the ordinal information extracted from the small data set is not reliable. This exotic behaviour from real networks is essentially solely caused by the properties of the degree distribution of real networks, rather than by other structural properties embedded in real networks, e.g. the modularity. Figure 4c exhibits the results for the random networks given the same degree distribution as that of the real networks [23], which produce a feature similar to that shown in Figure 4b.

For predictive purposes, is it possible to presume the value of  $\tau$  for nodes sampled randomly from entire networks? In real situations, since the information available to us is that of sampled networks rather than that of entire networks, we can only evaluate the  $\tau$  of the nodes against *a priori* sampled networks, but not against the entire networks, which are rarely achievable. Despite such limitations, we can exploit the  $\tau$  of the nodes sampled from these sampled networks to approximate that from the entire networks. In random sampling, since decreasing the sampling fraction makes the network more homogeneous, with small degrees [13], it is expected that the  $\tau$  of the subset in randomly sampled nodes underestimates that of the subset in the entire network with the same sampling fraction. For the BA model, Figures 4d–4f establish the corresponding tendency, manifested especially in low sampling fractions, which is consistently revealed in the cases of other real networks only except for the betweenness of the Internet AS<sup>6</sup>. In this regard, we can use this underestimation to approximate the actual  $\tau$  of an arbitrary sampling fraction for the entire network by providing its lower bound. For example, in the case of the protein-protein interaction network,  $\tau$  for the degree of 30% sampled nodes in our data is equal to 0.35, which means that the  $\tau$  for 30% sampled nodes in a complete data set would be greater than 0.35 if the sampling method is close to random node sampling. Likewise, for 30% sampled nodes in the Archive coauthorship,  $\tau$  for degree is equal to 0.45, thereby indicating that  $\tau$  would be larger than 0.45 for the 30% sampled nodes in the complete data set.

## 4 Conclusions

In summary, we have investigated the accuracy of order relationships in sampled networks, and found that the properties of complex networks, such as degree heterogeneity and structural modularity, are responsible for the various results. The higher-ranking nodes in sampled networks preserve their positions in the original networks more robustly than the lower-ranking nodes, and the closeness-based order relationship gives the best measure for faithful ordinal information in sampled networks. Interestingly, we discovered that limiting the access to hubs during the sampling can in fact decrease the accuracy of the sampling as the sampling fraction increases. We emphasise the role of hubs in characterising a sampled network, and the effect of the perturbed scale of the network, to which each centrality measure responds sensitively. Beyond these analyses, a methodology providing the lower bound for sampling accuracy is suggested. Our results can be helpful for understanding the properties of sampled networks, especially for social and criminal networks, for which analysis suffers from various types of sampling error and other

<sup>6</sup> For the betweenness of the Internet AS, the tendency becomes reversed such that  $\tau$  of the subset in randomly sampled nodes overestimates that of the subset in the entire network with the same sampling fraction.

limitations [8,12,24]. The sampling problems in complex networks, including the detection of errors in power-law statistics and the suggestion of useful sampling protocols, are currently being explored [10,12,13].

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