

## Measuring the significance of community structure in complex networks

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Many complex systems can be represented as networks, and separating a network into communities could simplify functional analysis considerably. Many approaches have recently been proposed to detect communities, but a method to determine whether the detected communities are significant is still lacking. In this paper, an index to evaluate the significance of communities in networks is proposed based on perturbation of the network. In contrast to previous approaches, the network is disturbed gradually, and the index is defined by integrating all of the similarities between the community structures before and after perturbation. Moreover, by taking the null model into account, the index eliminates scale effects. Thus, it can evaluate and compare the significance of communities in different networks. The method has been tested in many artificial and real-world networks. The results show that the index is in fact independent of the size of the network and the number of communities. With this approach, clear communities are found to always exist in social networks, but significant communities cannot be found in protein interactions and metabolic networks.

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Studies of the community structure of networks have become very important in research on complex networks [1]. Certain properties are likely to be shared among nodes inside a tight-knit community, such as friend subgroups in social networks, thematic clusters on the world wide web (WWW), functional groups in biochemical or neural networks, and so on. Therefore, separating networks into such groups could considerably simplify functional analysis. As a result, two questions related to identification of communities have been the focus of many recent efforts. The first question is how communities can be detected in networks. Plenty of algorithms [2–16] (see [1,6] as reviews) have been proposed in recent studies. The second question is how to evaluate the detected communities. We know that some networks possess clear communities while others do not. However, almost all algorithms could uncover “community structures” in networks in their own ways without considering whether these community structures actually exist. Some algorithms can even find communities in random networks, which are believed to have no community structures. Thus, the second question on community identification regards measuring the “significance of communities.”

Measuring the significance of communities is closely related to evaluating network partitions. The modularity  $Q$  introduced by Newman and Girvan [17] is widely accepted as an index to measure community structures [7–10]. The modularity  $Q$  can be formulated as  $Q = \sum_r (e_{rr} - a_r^2)$ , where  $e_{rr}$  is the fraction of links that connect two nodes inside the community  $r$ , and  $a_r$  is the fraction of links that have one or both vertices inside the community  $r$ . The summation extends to all communities  $r$  in a given network. Generally speaking, a larger value of  $Q$  indicates a clearer community structure. Hence, the value of the modularity can also be used as an index for the significance of communities. Unfor-

tunately, this modularity function presents its own problems. Sometimes, the community structure is unclear in networks that exhibit high modularity [18]. It has also been found that modularity is limited in detecting small communities [19]. Very recently, Good *et al.* proved that the modularity landscape is quite “glassy” [20], which implies that maximizing the modularity  $Q$  is ineffective for treating partition problems in many networks. In this paper, whether  $Q$  is a suitable index to measure the significance of communities is discussed in the results.  $Q$  has been shown to fail for sparse networks. Because the positive and negative aspects of the modularity  $Q$  are well known, maximizing the modularity  $Q$  is still a popular method of dividing networks and has successful applications in real-world networks such as in recent research [21]. In this paper, the spectral algorithm [8] was used to detect the initial community structures, and the extremal optimization algorithm [10] was used to improve the community partitions.

Scientists have also proposed other approaches to measuring the significance of communities. Very recently, Santo Fortunato introduced some related studies in a review article on community detection in graphs [1]. In previous works, Massen and Doye described the significance of communities by analyzing an equilibrium canonical ensemble of partitions with the modularity  $-Q$  playing the role of energy [22]. Furthermore, some scientists think the concept of significance should be related to the robustness of a partition. Intuitively, if a network has clear or significant communities, its community structure should be robust to perturbation. Gfeller *et al.* considered weighted perturbation of networks [23], employing the probabilities of the edges inside each cluster and around a cluster, and designed an entropy-based index. Recently, Karrer, Levina, and Newman presented a degree-conserved disturbance method [24] to analyze the robustness of a community structure. The perturbation consists of removing each edge with a probability  $p$  and putting the removed edge between a pair of loads. Given a probability  $p$ , the communities of the network after perturbation are identified with some method and compared with the community

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structure of the original network. Then the partitions are compared by computing the variation of information  $V$ . As  $p$  is allowed to change,  $V(p)$  becomes a function of  $p$ , which only can give some qualitative information about the significance of the community structure and cannot quantitatively measure the significance of the community structure or compare the significances of two networks with different sizes and average degrees.

Thus, providing an absolute index to characterize the significance of the community structures of complex networks is essential. In this paper, a universal index for measuring the significance of communities based on perturbing the network is proposed. The degree of perturbation of the network is increased by gradually increasing  $p$  from 0 to 1. Then, a similarity value (measured from information shared between the original and the disturbed networks) of the community structures can be obtained for each  $p$ . To provide an absolute meaning to the similarity measure, the null model is also considered, making the measurement unaffected by the network size or number of communities. Finally, the index is computed by integrating all the similarities over  $p$ . With this index, the “significance of communities” can be evaluated for any network. The method is presented in detail in the following sections. In Sec. II, the method is applied to many kinds of networks and provides some interesting conclusions. Social and neural networks have distinct community structures. Protein and metabolic networks also have such structures, though they are not very clear.

## I. METHOD

There are three steps to obtaining the index of a given network. First, the communities in the original network are detected without any perturbation. Second, the network is modified by rewiring a certain number of edges, new communities are detected after this perturbation, and the similarity between the two partitions (the communities of the original network and the disturbed network) is calculated. Third, the proportion of disturbed edges is increased gradually until all edges are modified. At each proportion, the second step is repeated, providing a series of corresponding similarity values as the degree of perturbation increases. Finally, the products of all similarity values with their corresponding degree of perturbation are summed. If the increment in the degree of perturbation is small enough, this summation can be converted to an integration.

*Method of disturbing the network.* There are a number of methods to disturb the edges of a network. In this paper, a relatively simple method known as the absolute random perturbation is adopted. Compared with the method of network perturbation introduced by Karrer *et al.* [24], the number of edges remains unchanged, but the original degree distribution is not sustained. Edges are randomly removed with a probability  $p$ . If a particular edge is removed, it is randomly added between any other two nodes. In this way, if  $p=0$ , no edge is removed, and the disturbed network is the same as the original network. If  $p=1$ , all edges are removed, and a random graph that is uncorrelated with the original network is generated. As  $p$  increases from 0 to 1, a sequence of modi-

fied networks is obtained, ranging from the original network to completely random networks. Moreover, a perturbation method that sustains the original degree distribution has been compared to this method, and it has been found that the resulting index values are almost the same. Thus, in the following discussion, the absolute random perturbation is used for its simplicity and efficiency.

*Measurement of similarity.* After detecting the community structures of the disturbed networks, the similarity between the two partitions must be found. One discriminatory measure is the normalized mutual information index from information theory [6]. A confusion matrix  $N$  is defined, in which the rows correspond to the “real” communities of the original network and the columns correspond to the “found” communities of the disturbed graph.  $N_{ij}$  is the number of nodes in the community  $i$  that appear in the found community  $j$ .  $N_i$  denotes the sum of row  $i$  in matrix  $N_{ij}$  and  $N_j$  denotes the sum over column  $j$ . Therefore, a measure of similarity between the partition  $A$  and  $B$  is

$$I(A,B) = \frac{-2 \sum_{i=1}^{c_A} \sum_{j=1}^{c_B} N_{ij} \log \left( \frac{N_{ij} N}{N_i N_j} \right)}{\sum_{i=1}^{c_A} N_i \log \left( \frac{N_i}{N} \right) + \sum_{j=1}^{c_B} N_j \log \left( \frac{N_j}{N} \right)}. \quad (1)$$

As the discrepancy between the two partitions increases, the value of  $I(A,B)$  decreases from 1. In other words, the “communities without perturbation”  $A$  are compared to the “communities after perturbation”  $A(p)$  to obtain the similarity measure.

Moreover, the similarity index is improved by accounting for the null model. The similarity index  $I(A,A(p))$  is not only determined by discrepancies between the communities but is also influenced by the size of the network and the number of communities in  $A$  and  $A(p)$ . The null model is included to eliminate the random background and effects of scale, and the measurement becomes

$$S(p) = I(A,A(p)) - I(A_r,A_r(p)), \quad (2)$$

where  $A_r$  contains the same number of communities with the same number of nodes as  $A$ , and  $A_r(p)$  contains the same number of communities with the same number of nodes in each community as  $A(p)$ . In contrast to  $A$  and  $A(p)$ , which are correlated with the original network, the nodes in  $A_r$  and  $A_r(p)$  are randomly selected from the entire set of nodes. Thus,  $I(A_r,A_r(p))$  only depends on the partitions. Figure 1 shows the expected values of  $I(A_r,A_r(p))$  when a set of nodes is divided into two partitions in  $A_r$  and  $A_r(p)$ . The values are dependent on the total number of nodes and the partitions.

*Index from integrating the similarities.* Using the method above, a series of  $S(p)$  can be obtained by incrementally increasing the probability  $p$  (indicating the degree of perturbation) from 0 to 1; an increment of 0.02 was chosen. Generally, a higher degree of perturbation corresponds to a lower value of  $S(p)$ . The process should be performed several times in numerical simulations to obtain the expected average value of  $E[S(p)]$ . Naturally, the area of the region bounded by the curve  $E[S(p)]$  is used to calculate the index. Thus, the

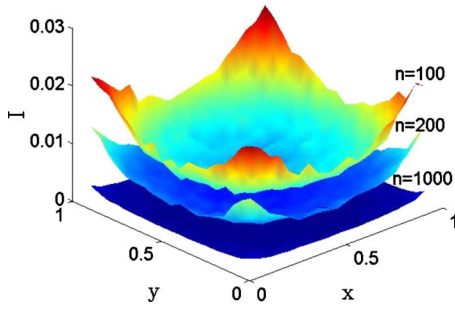


FIG. 1. (Color online) The expected values of the mutual information  $I(A_x, A_y)$  of two partitions  $A_x$  and  $A_y$ . Each partition divides the  $n$  nodes into two groups.  $x$  and  $y$  represent the fractions of nodes in the first group for the partitions  $A_x$  and  $A_y$ , respectively. The nodes in each group are randomly selected from the entire set of nodes. From the bottom to the top,  $n$  is 1000, 200, and 100, respectively.

index can be found by integrating all of the expected values of  $E[S(p)]$  as follows:

$$R = \int_0^1 E[S(p)] dp, \tag{3}$$

where  $p$  refers to the degree of perturbation and  $E[S(p)]$  is the corresponding expected similarity value between the original communities and the communities in the disturbed network. The value of the similarity is a function of the parameter  $p$ . The similarity value of a given network starts at about 1 when  $p=0$ , which can be regarded as an unperturbed network. Then the similarity value falls and approaches a minimum when  $p=1$ . The index  $R$  is the integral of the similarity function  $E[S(p)]$ . If a network has distinct community structures, the value of the significance  $R$  is high. On the contrary, a network with fuzzy community structures presents a lower value of  $R$ . Because of the fluctuations in  $I(A, A(p))$  and  $I(A_r, A_r(p))$ ,  $S(p)$  will sometimes be negative for networks with clear community structures when  $p$  is very close to 1. However, at this time,  $I(A, A(p))$  and  $I(A_r, A_r(p))$  have little correlation, and  $S(p)$  will tend to 0. Thus, although  $S(p)$  can sometimes be negative, the result is not affected at all. The correlation between  $A$  and  $A(p)$  is weak in a random network. Thus, for each  $p$ ,  $S(p)$  should be very close to 0, although fluctuations can make  $S(p)$  negative in a random network. For random networks, the expected value of  $R$  is positive and close to 0. From the numerical experiments, large networks containing two completely unconnected subnetworks of equal size can have  $R$  values over 0.9. Additionally, the value of  $R$  is lower than 0.03 for large random networks with proper average degrees. The analysis above implies that  $R \in (0, 1)$ .

II. RESULTS

A measurement of  $R$  must be developed that can describe the significance of communities. A series of important questions also present themselves. Is  $R$  independent of the network size? What will happen if the number of communities and the linkage density change? Moreover, can the measure-

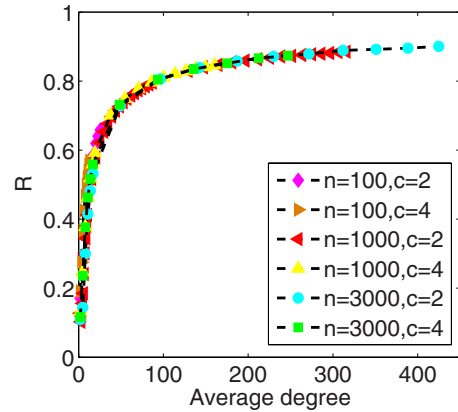


FIG. 2. (Color online) The dependence of  $R$  on the network size, average degree and number of communities. In the plot,  $n$  denotes the number of nodes and  $c$  the number of predetermined communities of the same size. Every predetermined community (subnetwork) is an ER random network and is detached from the others. According to the plot, the value of  $R$  increases as the average degrees of the subgraphs increase, and  $R$  is almost independent of the network size and the number of communities.

ment  $R$  work well in networks in which the index  $Q$  is invalid [18]?

*About the scale effect.* To answer the questions above, the measure  $R$  was tested in networks with different sizes, numbers of communities, and linkage densities. The networks for testing the performance of the index  $R$  were constructed as follows. The network consists of several subgraphs. Each subgraph is an Erdős-Rényi (ER) random network, and no edge exists between any of the subnetworks. Thus, the network has distinct communities. Then the networks are disturbed, and the index  $R$  is found for each one.  $R$  is the average value of 50 realizations of each kind of network. Obviously, when the average degree in each subgraph increases, the communities become more distinct, and the value of  $R$  increases correspondingly (as shown in Fig. 2). The numerical experiments also showed that the value of the index  $R$  is roughly independent of the size of the network and the number of communities. A spectral algorithm [8] is used to detect the initial community structure. The time complexity is at least  $O(n^3)$ , so it is not easy to deal with large networks. In Fig. 2, the maximum network size is 3000.

*Comparison with other indexes.* The index  $Q$  is compared with  $R$  in both ER random and Barabási-Albert (BA) scale-free networks. It is known that the index  $Q$  cannot measure ER and BA networks, especially sparse ones [18]. The modularity  $Q$  of BA and ER networks with small average degrees could be very high. The index  $R$  was tested in such networks, and the numerical results show that the index  $R$  works better than  $Q$  (as shown in Fig. 3).

Previous works have attempted to improve the performance of  $Q$ . For example, the modularity  $Q$  has been normalized by the corresponding value of the modularity  $Q_{rand}$  in a null model [25]. Other measurements, such as the  $Z$  score, which is used to measure by how many standard deviations the real modularity exceeds the mean value of the random graph, have also been employed [26,27]. The  $Q/Q_{rand}$  and  $Z$  score were investigated in the same bench-



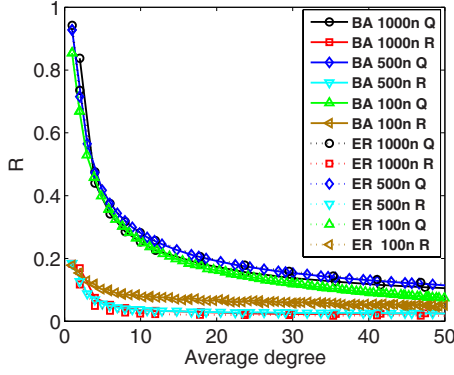


FIG. 3. (Color online) Comparison of the modularity  $Q$  with the index  $R$  on BA and ER networks with no distinct community structures. According to the plot,  $Q$  is very large when the average degree is about 1, while  $R$  is near 0.2. Thus, when the average degree is near 1, the  $Q$  index indicates a very strong community structure, while  $R$  shows fuzzy community structures [fuzzy community structure exists when  $R=0.2$  according to the numerical results in artificial networks (see Fig. 5)]. However,  $Q$  falls more slowly than  $R$  as the average degree increases. When the average degree is larger than or equal to 2,  $R$  is very low and reaches a stable state, which shows that the  $R$  index performs well in both BA and ER networks.

mark tests shown in Fig. 2, and the results are shown in Fig. 4. These two indexes are sensitive to the network size and the number of communities and cannot describe the significance of communities in different networks. However, the index  $R$  performs better in all of the aspects mentioned above.

When the average degree is larger than or equal to 2, the index  $R$  is approximately 0.1. When the average degree is 1,

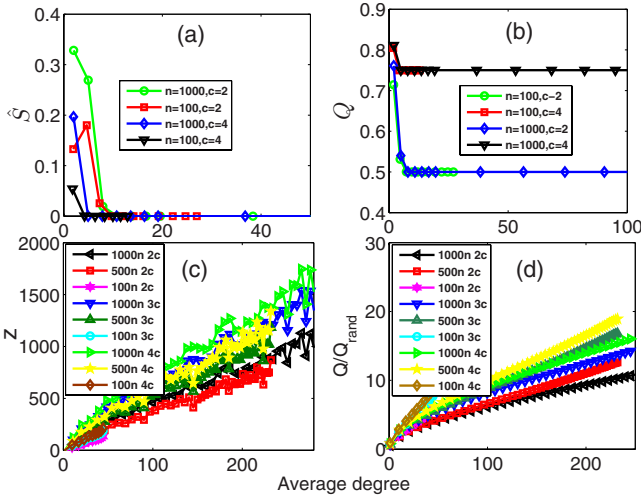


FIG. 4. (Color online) Numerical results of testing (a)  $\hat{S}$  [23], (b)  $Q$ , (c)  $Z$  score, and (d)  $Q/Q_{rand}$  with the benchmark employed in Fig. 2. The  $\hat{S}$ ,  $Z$  score, and  $Q/Q_{rand}$  are all sensitive to the size of the network and the number of communities.  $Q$  is sensitive to the network size. Moreover,  $\hat{S}$  falls to 0 very rapidly, which implies that it cannot measure the significance when the community structure is clear.

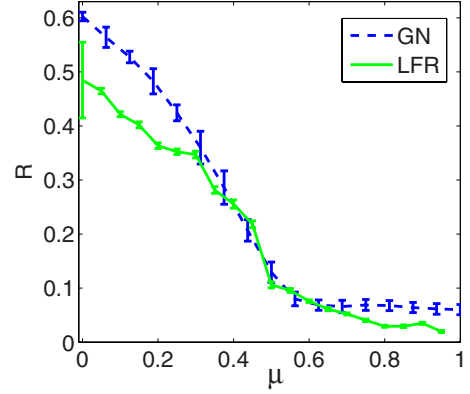


FIG. 5. (Color online) The performance of index  $R$  in both the GN-benchmark and LFR-benchmark tests. In the GN-benchmark test,  $k_{out}$  is the average number of connections between communities and  $\mu = \frac{k_{out}}{16}$ . In the LFR-benchmark test,  $\mu$  is the mixing parameter, meaning that each node shares a fraction  $1 - \mu$  of its links with the nodes of its community and a fraction  $\mu$  with the nodes outside of its community. Each  $R$  corresponding to a given  $\mu$  is the average value of more than 20 numerical experiments, and a new independent network is generated each time.

the  $R$  is slightly less than 0.2. According to the following applications on artificial networks (as shown in Fig. 5),  $R < 0.1$  indicates the absence of distinct communities in the network. However, a value of  $R=0.2$  wrongly indicates the existence of fuzzy communities in the network. Hence, this index performs well except in some sparse networks with average degrees less than 1. Fortunately, such networks seldom exist.

*Testing the index in computer-generated networks.* Another way to test the validity of the index is to apply it to computer-generated random networks with a well-known predetermined community structure. The index was first tested with the Girvan-Newman (GN)-benchmark. In the GN-benchmark test, each network has  $n=128$  nodes, which are divided into four communities of 32 nodes each. Edges are generated between pairs of nodes with varying probability depending on whether the two nodes belong to the same community or not: every node has  $\langle k_{in} \rangle$  links on average to its fellows in the same community and  $\langle k_{out} \rangle$  links to nodes in other communities, where  $\langle k_{in} \rangle + \langle k_{out} \rangle = 16$ . As  $k_{out}$  increases, the communities become fuzzy. Thus, the significance of the communities tends to weaken, and the index  $R$  decreases. To validate the expectation that  $R$  falls as  $k_{out}$  decreases, the value of  $R$  was calculated while  $k_{out}$  was varied from 0 to 12. The index was also tested on the more challenging LFR benchmark presented by Lancichinetti, Fortunato, and Radicchi [28]. In the LFR benchmark, each node is given a degree whose distribution obeys a power law distribution with an exponent  $\gamma$ , and the sizes of the communities are taken from a power law distribution with an exponent  $\beta$ . Moreover, each node has a fraction  $1 - \mu$  of its links connecting it to other nodes in its community and a fraction  $\mu$  connecting it to other nodes in the network.  $\mu$  is referred to as the mixing parameter. The significance of the community structure can be adjusted through the mixing parameter  $\mu$ . In the LFR-benchmark, the parameters chosen were  $n$

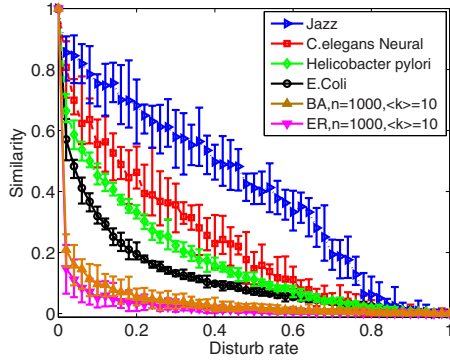


FIG. 6. (Color online) The  $x$  axis represents the perturbation probability, while the  $y$  axis is the corresponding similarity value  $S(p)$ . In each network, we highlight the maximum, minimum, and mean values of 20 realizations. The networks are social network (Jazz), neural network (*C. elegans*), metabolic network (*Helicobacter pylori*), protein interaction network (*E. coli*), BA scale-free network and ER random network up-down.

= 1000,  $\gamma = 1.5$ ,  $\beta = 2.5$ , maximum community size = 100, and minimum community size = 10.

The results are shown in Fig. 5. As expected, the value of  $R$  varies from 0.58 to 0.05 as the  $k_{out}$  varies from 0 to 12 in the GN-benchmark, indicating that the index is able to measure the significance of communities in artificial networks. The index  $R$  decreases as a function of  $k_{out}$ , indicating that the community structures discovered by the algorithm are relatively significant when  $k_{out}$  is relatively low. In the LFR-benchmark, Fig. 5 illustrates behavior similar to that demonstrated in the GN-benchmark. As  $\mu$  increases from 0 to 1,  $R$  decreases from 0.48 to 0.03. A different community detecting algorithm [29] was also used to calculate  $R$ . The results were similar in behavior, but the values of  $R$  were not the same, implying that the index  $R$  is not independent of the algorithm. When this method is used to measure the significance of community structure, it is necessary to declare which algorithm is employed.

*Results of empirical analysis.* Following the benchmark simulations, the measurement technique was applied to many real networks. The data were sourced from the following references and websites [10,30–37]. Scientists usually classify real networks into three categories: social networks (such as scientists’ collaboration and friendship networks), biological networks (such as proteins’ interaction and metabolic networks), and technological networks (such as the Internet). Distinct communities have been observed in different kinds of networks, especially in social networks. This method and the index  $R$  were applied to the largest connected component of many real networks. More details are given in Fig. 6 and Table I. Figure 6 shows the curves of the similarity  $S(p)$  of four networks. The results are the average value of 20 realizations. The maximum, minimum, and mean values of the simulations are also shown in the figure. The similarity measure of the Jazz network decreases more slowly than that of the other three networks, implying that the communities in the Jazz network are more robust than the communities in the other three. In addition, Table I shows all of the networks to which the index was applied. The

TABLE I. The values of the index  $R$  for some real networks. The column denotes the number of nodes and edges of the network.  $\hat{S}$  denotes the entropy based on similarity from Ref. [23]. The community structure is more significant for smaller values of  $\hat{S}$ . Except for the *C. elegans* neural network, the  $\hat{S}$  and  $R$  indexes do not exhibit considerable qualitative differences.

Network	Size	$\hat{S}$	$R$	Type
E.coli	1442, 5873	0.19	0.11	
Yeast	1458, 1971	0.57	0.12	Protein
H.Sapiens	693, 982	0.13	0.18	
C. elegans metabolic	453, 2032	0.29	0.17	
Aquifex aeolicus	1473, 3354	0.26	0.17	
<i>Helicobacter pylori</i>	1341, 3087	0.31	0.17	Metabolic
Yersinia pestis	1922, 4389	0.29	0.15	
43 metabolic networks	1472, 3395	0.28	0.17	
C. elegans neural	297, 2148	0.19	0.22	Neural
Santa Fe scientists	118, 200	0.10	0.27	
Zachary karate	34, 78	0.15	0.25	
Dolphin	62, 159	0.01	0.24	
College football	115, 613	0.11	0.34	Social
Jazz	198, 2742	0.08	0.40	
Political blogs	1222, 19090	0	0.27	
Political books	105, 441	0.04	0.31	

results measured by the similarity  $\hat{S}$  presented by Gfeller *et al.* [23] are also shown in the table. They give results similar to the index  $R$ . According to the table, different networks have different  $R$  values. Several social networks were analyzed first, including the Zachary karate club network [30], the dolphin network [31], the college football network [16], the Jazz network [34], the scientific collaboration network [35] and so on. A relatively high  $R$  was found in these networks, demonstrating the existence of strong community structures in these networks.

In addition, some biological networks such as protein interaction networks of *E.coli* [36], *Yeast* [37] and *H. sapiens* [36], metabolic networks [37], and a *C. elegans* neural network were analyzed. The  $R$  values of protein interaction networks are low except in the case of *H. sapiens* (the average degree of this network was less than 2). 43 metabolic networks were calculated, all of which had  $R$  indexes around 0.17. Therefore, community structures are fuzzy in some protein interaction networks (such as *E.coli* and yeast) and metabolic networks, as listed in Table I. Meanwhile, the *C. elegans* neural network presented significant communities.

### III. CONCLUSION AND DISCUSSION

This paper presents the index  $R$ , which can measure the significance of communities for different networks. The in-

dex is computed by integrating similarity values that compare the community structures before and after perturbation. This index was applied to many artificial and real world networks including social, neural, metabolic, and protein interaction networks. The results show that this index is roughly independent of the network size and group number. Moreover, social networks usually have significant communities, while communities are relatively fuzzy in biological networks, especially in some protein interaction networks and metabolic networks.

The index  $R$  introduced in this paper is actually based on the robustness of the communities. One problem with this approach is that the community structure must first be found. Thus, the value of the index is related to the algorithm to detect communities. In contrast, the significance of commu-

nities is a basic property of the network. It should be evaluated before the division of networks and should thus be unrelated to the identification algorithm. Developing an index to measure the significance of communities based directly on the adjacent matrix is an interesting problem for further research.

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