Bridging Centrality: Identifying Bridging Nodes In Scale-free Networks [*]

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ABSTRACT

Several centrality measures were introduced to identify essential components and compute components' importance in networks. Majority of these centrality measures are dominated by components' degree due to their nature of looking at networks' topology. We propose a novel essential component identification model, bridging centrality, based on information flow and topological locality in scale-free networks. Bridging centrality provides an entirely new way of scrutinizing network structures and measuring components' importance. We apply bridging centrality on real world networks, including one simulated network, two biological networks, two social networks, and one web network, and show that the nodes distinguished by bridging centrality are well located on the connecting positions between highly connected regions through analyzing the clustering coefficient and average path length of those networks. Bridging centrality can discriminate bridging nodes, the nodes with more information flowed through them and locations between highly connected regions, while other centrality measures can not.

Categories and Subject Descriptors

[**Network Analysis**]: Network metrics, Network component importance metrics, Essential component analysis

General Terms

Degree, shortest path, betweenness, clustering coefficient, average path length, singleton

Keywords

Scale-free network, centrality, bridging node, bridging coefficient, bridging centrality, modularity, robusteness, paths protection

1. INTRODUCTION

Many real world systems, e.g., internet, World Wide Web (WWW), social systems, biological systems, etc., can be described as complex networks, which are structured as a set of nodes and a set of edges connecting the nodes. Scale-free network[4] is the most popular and emerging form of network in these real world network systems. Most of these real world networks have been proved to follow some topological statistical features, i.e., features of scale-free network, such as power law degree distribution, small world property, and high modularity [2, 3, 4, 5]. Power law degree distribution depicts the probability of finding a highly connected node decreases exponentially with its own degree, which is the number of edges incident on the node. In other words, there are many low degree nodes, and only a small number of nodes have high degree. The second phenomenon, small world property, describes that the average distance between nodes in a network is relatively shorter than other network types, e.g., random networks of the same size. Namely, any node can be reached within small number of consecutive edges from a node in a network. A module refers to a densely connected, functionally or physically, group of nodes in a network. For the last distinct and the most interesting property, these real world networks have high modularity which indicates that high clustering is one of dominating characteristics of these networks.

Over the past few years, empirical and theoretical studies of networks have been one of the most popular subjects of recent researches in many areas including technological, social, and biological fields. Network theories have been applied with good success to these real world systems, and many centrality indices, measurements of the importance of the components in a network, have been introduced [6, 9, 10, 16, 7, 18]. While these centrality indices have proved that they made outstanding achievements in the analysis and understanding of the roles of nodes in a network, majority of these existing centrality indices focuses only on the extent how much nodes are well located on central positions or play central roles from the stand point of topology and information flow. These existing centrality measures can not help being considerably dominated by nodes' degree due to their nature of computing components' importance. Even

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though these approaches are very good at identifying central components, i.e., central components from any centrality viewpoint, of a network or of a module, they concentrate only on central components and overlook another essential topological aspect in networks.

In this research, we move the focus of the network analysis from the directions of identifying central nodes to another entirely new, fresh, and important direction. From our deeper observation of the high modularity property of scale-free networks, we claim that there should be "bridging" nodes that are located between modules, and we found that there exist "bridging" nodes in real world scale-free networks due to their high modularity phenomenon. So, we also claim that these bridging nodes, which bridge densely connected regions, should be attractive and important essential components in a network. We introduce a novel centrality metric, bridging centrality, that successfully identifies the bridging nodes locating between densely connected regions, i.e. modules, using high modularity or high clustering property which is one of the most important property of scale-free networks. Experiments on several real world network systems are performed to demonstrate the effectiveness of our metric.

Bridging centrality has many potential applications in several areas. First, it can be used to break up modules in a network for clustering purpose. Functional modules or physical modules in biological networks or sub community structures in social and technological networks can be detected using the bridging nodes chosen by bridging centrality. Second, it also can be used to identify the most critical points interrupting the information flow in a network for network protection and robustness improvement purposes for networks. Third, in biological applications, the bridging centrality can be used to locate the key proteins, which are the connecting nodes among functional modules.

2. METHOD

2.1 Terminology and Representation

Real world systems can be represented using graph theoretic methods. The approach presented in this paper focuses on undirected graphs. An undirected graph G = (V, E) consists of a set V of nodes or vertices and a set E of edges, E $\subseteq$ V×V. An edge e(i,j) connects two nodes i and j, e(i,j) $\in$ E.

The neighbors N(i) of node i are defined to be a set of directly connected nodes to node i. The degree d(i) of a node i is the number of the edges connected to node i. A path is defined as a sequence of nodes (n_1,...,n_k) such that from each of its nodes there is an edge to the successor node. The length of a path is the number of edges in its node sequence. A shortest path between two nodes, i and j, is a minimal length path between them. The distance between two nodes, i and j, is the length of its shortest path. The clustering coefficient C_v for a node v is the proportion of links between the nodes within its neighbourhood divided by the number of links that could possibly exist between them, $C_v=\frac{2|\{e(i,j)\}|}{d(v)(d(v)-1)}$: i,j$\in$ N(v), e(i,j)$\in$E [19]. In other words, $|\{e(i,j)\}|$ gives the number of triangles that go through node v, whereas $d(v)(d(v)-1)/2$ is the total number of triangles that could pass through node v. Thus, clustering coefficient of node v indicates how the neighbors of node v are well connected each other. The clustering coefficient of a graph is the average of the clustering coefficients of all nodes in the graph. The average path length of a graph is the average of the shortest paths between all pairs of nodes in the graph.

2.2 Bridging Centrality

A bridging node is a node lying between modules, i.e., a node connecting densely connected components in a graph. The bridging nodes in a graph are identified on the basis of their high value of bridging centrality relative to other nodes on the same graph. The bridging centrality of a node is the product of the betweenness centrality C_B [10] and the bridging coefficient (BC), which measures the global and local features of a node, respectively.

Specifically, the bridging centrality C_R(v) for node v of interest, is defined by:

$$C_R(v) = BC(v) \times C_B(v) \tag{1}$$

The betweenness centrality is a measure of the global importance of a node that assesses the proportion of the shortest paths between all node pairs that pass through the node of interest. The betweenness centrality, C_B(v), for a node v of interest is defined by:

$$C_B(v) = \sum_{\substack{s \neq v \neq t \\ s,v,t \in V}} \frac{\rho_{st}(v)}{\rho_{st}} \tag{2}$$

In the above equation, ρ_{st} is the number of shortest paths from node s to t and ρ_{st}(v) the number of shortest paths from s to t that pass through the node v. The higher C_B(v), more number of shortest paths between all node pairs pass through the node v. So node v is more likely to be located on the shortest paths between all node pairs in the network, i.e., more information travel through the node v.

The bridging coefficient of a node determines the extent how well the node is located between high degree nodes. The bridging coefficient of a node v is defined:

$$BC(v) = \frac{d(v)^{-1}}{\sum_{i \in N(v)} \frac{1}{d(i)}} \tag{3}$$

where d(v) is the degree of node v, and N(v) is the set of neighbors of node v. The bridging coefficient assesses the local bridging characteristics in the neighborhood. The bridging coefficient understands a network as a simple electrical circuit. Intuitively, there should be more congestion on the smaller degree nodes if an unit electrical current arrives on a node since the smaller degree nodes have lesser number of outlets than the bigger degree nodes have. So, if we consider the reciprocal of the degree of a node as the "resistance" of the node, the bridging coefficient can be viewed as the ratio of the resistance of a node to the sum of the resistance of the neighbors. Critical bridging nodes, typically representing rate limiting points in the network and because they connect its densely connected regions, have high "resistance." Thus, higher C_R(v) signifies that more information flows through node v, i.e., higher betweenness centrality(C_B(v)), and more resistance on node v, i.e., higher bridging coefficient(BC(v)), by bridging densely connected regions.

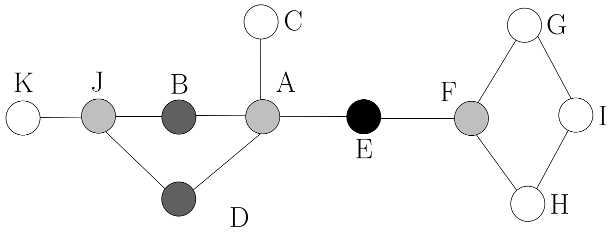


Figure 1: A small synthetic network example. Top six high bridging score nodes are colored.

Node	Degree	C_B	BC	C_R
E	2	0.53333	0.85714	0.45713
B	2	0.15555	0.85714	0.13333
D	2	0.15555	0.85714	0.13333
F	3	0.47777	0.22222	0.10617
A	4	0.65555	0.10000	0.06555
J	3	0.21111	0.16666	0.03518

Table 1: Top six centrality values of Figure 1, including Betweenness(C_B), bridging coefficient(BC), and bridging centrality(C_R).

Figure 1 and Table 1 clearly illustrates the essence of bridging centrality. Although node A has the highest degree and betweenness value, nodes E, B, and D have much higher bridging centrality values since node A is located on the center of a module not on a bridge which results in the lowest bridging coefficient value. In other words, far more number of shortest paths goes through node A than other three nodes, but nodes E, B, and D position on bridges much better. So, nodes E, B, and D have higher bridging centrality values since they are on the bridges between modules which leads much higher bridging coefficient values than node A. Betweenness centrality decides only the extent how much important the node of interest is from information flow standpoint, and it does not consider the topological locations of the node. On the other hand, nodes B and D have the same bridging coefficient value with node E, but nodes B and D have much less betweenness centrality values since far more number of shortest paths passes through node E than through nodes B and D. Even though nodes E, B, and D are located on similar local topological positions, i.e., similar local topological surroundings, node E is taking a much more important location than nodes B and D in the information flow viewpoint. Bridging coefficient measures only the extent how well the node is located between highly connected regions, and it does not deliberate the node's importance from information flow standpoint. Without a doubt, we can figure out that node E is taking a better bridging position than nodes B and D are in Figure 1. Bridging nodes should be positioned between modules and also located on important positions in information flow standpoint. So, bridging centrality combines these two measurements, betweenness centrality and bridging coefficient, since none of these two indices can differentiate the bridging nodes alone, as we saw in the above. So bridging centrality combines global and local features, betweenness centrality and bridging coefficient respectively, of the node not focusing only on one topological factor like other centrality indices do, and discriminates the bridging nodes which are located on the critical positions for information flow viewpoint and also are positioned on the bridges.

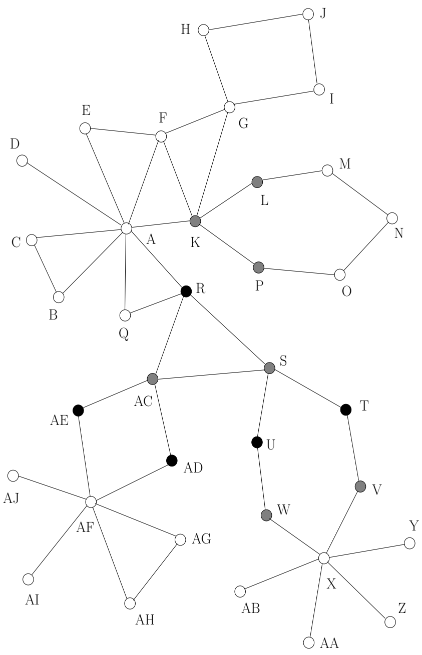


Figure 2: A synthetic network with 36 nodes and 46 edges. The nodes with the highest 0-10th percentile of values for the bridging centrality are highlighted in black circles, the nodes with the 10th-25th percentiles of bridging centrality are highlighted in gray circles. The letters are node labels.

3. RESULTS

The focus of this research and performance analysis is mainly on the top 25% high bridging centrality score components in all examples, since the significance and the interest are rapidly reduced below top 25 percentile. Furthermore, bridging centrality values and the range of the bridging nodes can be arbitrary according to the network topology dealt with. Empirical studies on several real world network systems made us define "bridging nodes" as the top 25 percentile.

3.1 Application on Simulated Data

To obtain a preliminary assessment of the underlying network characteristics identified by the bridging centrality, we applied the metric to a synthetic network consisting of 36 nodes and 46 edges shown in Figure 2. The synthetic network investigated contains key elements such as hub nodes, peripheral nodes, cycles and bridging nodes that are commonly found in biological networks. The overall degree distribution followed a power law distribution but the overall size was kept small so that any patterns present could be easily detected by visual inspection.

In Figure 2, we have highlighted the nodes in the highest 0-10th percentiles of bridging centrality values with black-filled circles whereas nodes in the highest 10th-25th percentiles of bridging centrality values are shown in gray-filled circles. Visual inspection of the synthetic network reveals

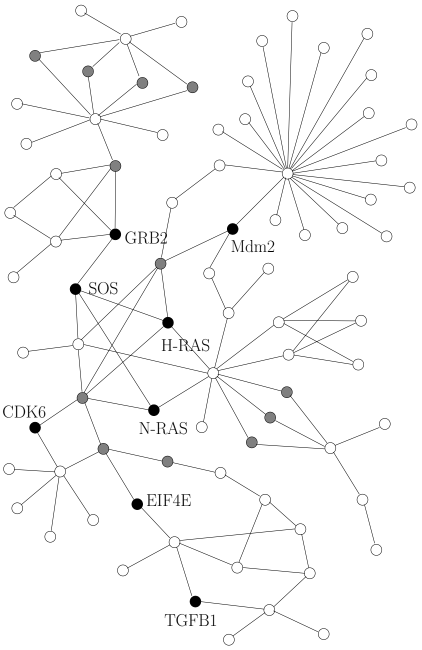


Figure 3: The schematic of undirected graph network model for the p53 protein with 82 nodes and 106 edges. The nodes with the highest 0-10th percentile of values for the bridging centrality are highlighted in black circles; the nodes with the 10th-25th percentiles of bridging centrality are highlighted in gray circles. The labels are abbreviations of gene names.

that the bridging centrality values of peripheral nodes (e.g., D, Y, Z, AA, AB, AI, AJ), hub nodes (e.g., A, AF, X) and nodes in simple cycles (e.g., A, B, C; M, N, O) do not occur in the highest percentiles of bridging centrality. The highest values of bridging centrality occur in the nodes that connect the modules and highly connected regions of the network.

3.2 Application on the p53 Network

Based on the encouraging performance of the bridging centrality metric on the synthetic network, we evaluated its performance on a simple undirected graph network model for the p53 related regulatory network[13]. The p53 protein is a critical tumor suppressor molecule and because it is often mutated in many human tumors, its interactions could potentially provide targets for anti-cancer drugs.

Figure 3 is the schematic of the undirected graph model for the p53 regulatory network. Similar to Figure 2, the nodes with the highest top 10 percentile bridging centrality values are shown with the black circles, whereas top 25 percentile with the grey circles. We can easily validate that the distinguished bridging nodes (e.g. Mdm2, GRB2, SOS, CDK6, EIF4E, TGFB1, H-RAS, N-RAS) are clearly standing on the boundary between modules.

3.3 Application on the Yeast Metabolic Network

In the next step, we extended the promising results obtained with the simple p53 regulatory network model to the undirected yeast metabolic network[17]. The yeast metabolic network is relatively well modularized and clustered according to their cellular functions. Figure 4 shows that bridging centrality successfully identifies the bridging nodes and the nodes lying on the borders of modules. Importantly, the majority of its key bridging nodes can be readily identified by visual inspection.

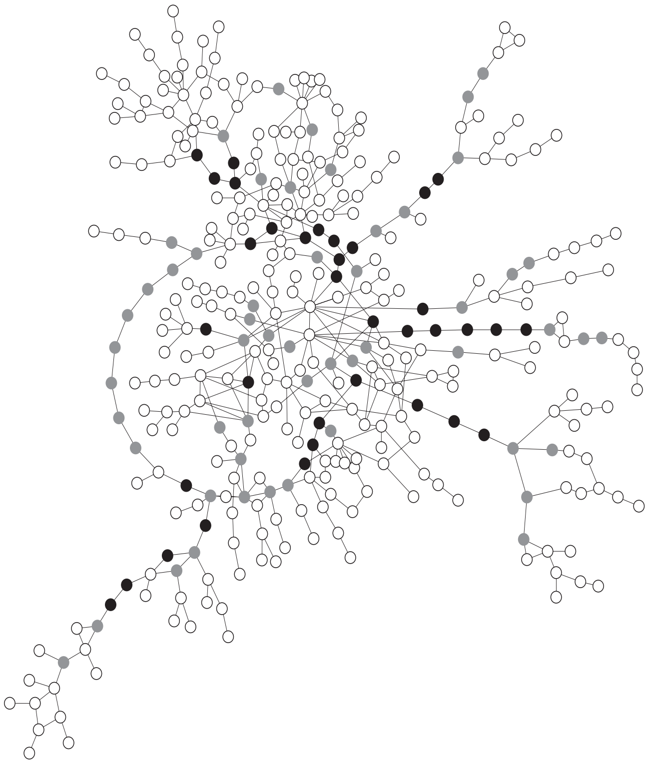


Figure 4: The yeast metabolic network with 359 nodes and 435 edges. The nodes with the highest 0-10th percentile of values for the bridging centrality are highlighted in black circles; the nodes with the 10th-25th percentiles of bridging centrality are highlighted in gray circles.

3.4 Application on Social Networks

Encouraged by the outstanding performance of bridging centrality metric on the biological networks, we shift gear to social networks, an academic collaboration network[15] and a character relationship network in a novel, Les miserable[15]. Figures 5 and 6 exhibits the bridging centrality results on the academic collaboration network in physics research and the character network of Les Miserable, respectively. As can be seen in Figures 5 and 6, the bridging nodes are well positioned on the road between modules, even though the networks are much more complex and highly cross connected in the core area than the previous examples. Furthermore, it is obviously shown that network information should pass through the highlighted bridging nodes if it tries to move from a module to a module.

3.5 Application on a Web Network

One of the most emerging real world networks is a web network, i.e., networks that connect web pages in World Wide Web. Figure 7 visualizes a small section web network[1][15]. This network is simple but highly modular with many pe-

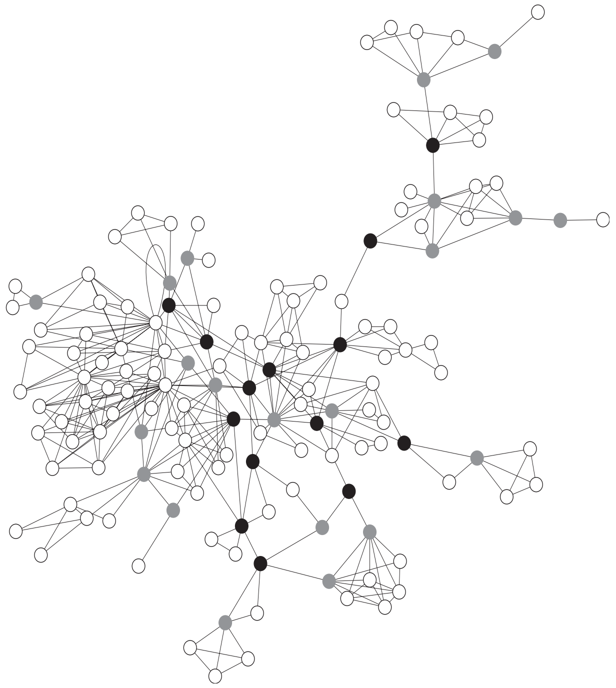


Figure 5: The academic collaboration network in physics research with 142 nodes and 340 edges. The nodes with the highest 0-10th percentile of values for the bridging centrality are highlighted in black circles; the nodes with the 10th-25th percentiles of bridging centrality are highlighted in gray circles.

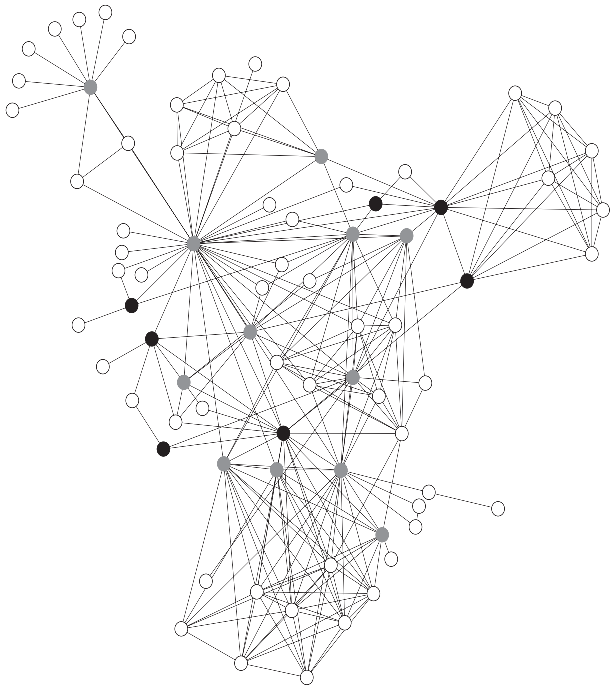


Figure 6: The character network of Les Miserable with 77 nodes and 254 edges. The nodes with the highest 0-10th percentile of values for the bridging centrality are highlighted in black circles; the nodes with the 10th-25th percentiles of bridging centrality are highlighted in gray circles.

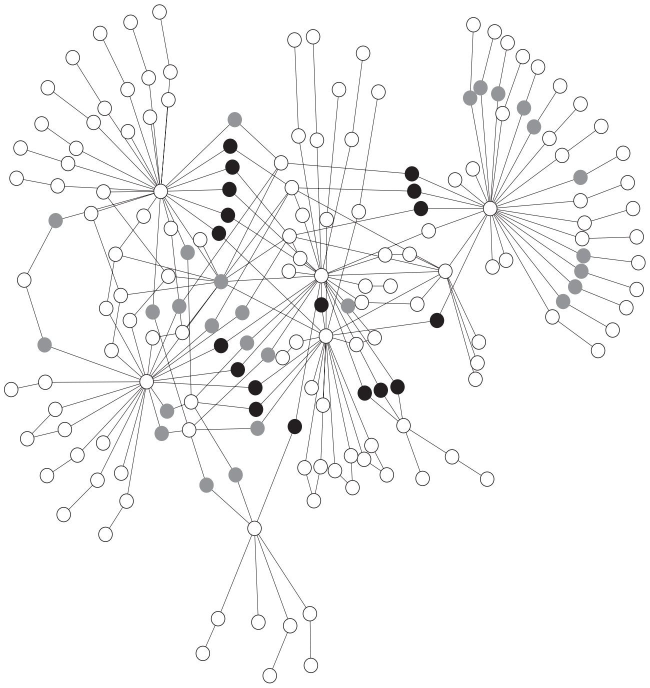


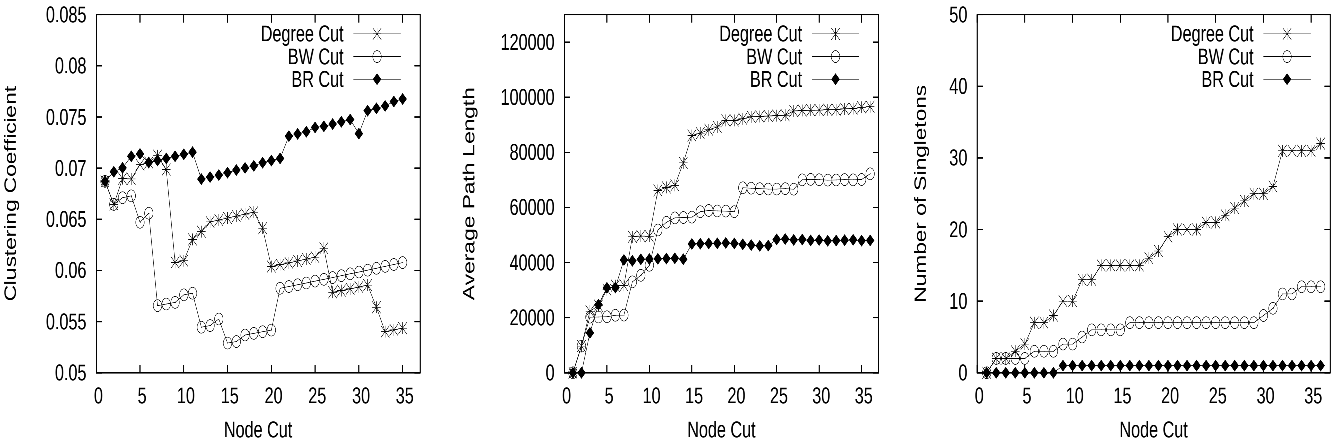
Figure 7: The web network with 180 nodes and 228 edges. The nodes with the highest 0-10th percentile of values for the bridging centrality are highlighted in black circles; the nodes with the 10th-25th percentiles of bridging centrality are highlighted in gray circles.

ripheral nodes, and importantly, the majority of its key bridging nodes can be readily identified by visual inspection. Most of the top 10 percentile scored nodes resides on the bridging positions and other relatively low scored nodes, which are between 10% and 25% and colored in grey, also well positioned on the boundary of modules. We can clearly differentiate modules by inspecting the bridging nodes as frontier of modules.

3.6 Theoretical Analysis on Yeast Metabolic Network

The main objective of this study is to analyze the potential of bridging centrality score to select the nodes that position on true bridging locations. We use the yeast metabolic network for further analyses since it has better scale-free network properties, e.g., power law distribution, high modularity, than other examples in the above and also has moderate size that enables us to observe the performances precisely. In order to investigate the topological locality of the bridging nodes picked up by bridging centrality in networks, we analyzed and compared the behaviors of the clustering coefficient, the average path length, and the number of singletons occurrence with other two famous centrality measures.

Figure 8(a) compares the behaviors of the clustering coefficient of the network in the consequence of consecutive removals of top 10 percentile high centrality score nodes for three centrality measures, degree centrality(or node degree), betweenness centrality (BW), and bridging centrality (BR). The clustering coefficient behaviors for these three centrali-



(a) (b) (c)

Figure 8: Analysis on the Yeast Metabolic Network. (a)Average Path Length Changes, (b)Clustering Coefficient changes, (c) Singleton Changes. Changes of the clustering coefficient, average path length, number of singletons followed by the consecutive top 10 percentile high score node removals for three centrality measures(degree, betweenness(BW), bridging(BR)) .

ties explain some interesting and important features of the nodes picked by these three different centrality measures. For more clear understanding of the clustering coefficient behaviors, one needs to observe the behaviors together with the changes of number of singletons simultaneously. Figure 8(c) shows the changes of the number of singletons produced by the same node removals. The removals by the other two centrality indices, degree centrality and betweenness centrality, did not show monotonic behaviors of the clustering coefficients, and they rather considerably decreased the clustering coefficient about 20%. Furthermore, they produced many more singletons than bridging centrality did in the same intervals. Needless to say, the nodes caught by the other two centrality indices are located on the center of modules and the removals of those nodes damaged the modularity of the network and mass-produced singletons. However, as we removed the highest bridging centrality score nodes one by one, the clustering coefficient of the network was increased about 10% constantly for almost all intervals while only one singleton was produced in the same interval. In other words, cutting the high bridging centrality nodes enhanced the modularity of the network without producing many singletons, i.e., the nodes picked up by bridging centrality are located between modules neither on the center of modules nor on the peripheral of the network.

As the second evidence of the bridging centrality's superiority on targeting the bridging nodes, we observed the topological properties of the bridging nodes discriminated by bridging centrality from the alternative paths availability and average path length point of view. Figure 8(b) describes the changes of the average path length followed by the removals of top 10 percentile high centrality score nodes. Increment of the average path length by a node removal means that there are some node isolations from the other part of the network or there are some alternative paths but longer than the removed path. The changes of the average path lengths should be also scrutinized along with the changes of the number of singletons, Figure 8(c), to comprehend more precisely. The changes of the average path length for the other two centrality indices, degree centrality and betweenness centrality, were increased more than the case of bridging centrality. But it is clear that their increment behaviors are caused by the mass-production of singletons in the same interval as can be seen in Figure 8(c) since the nodes distinguished by these two centrality indices mostly are located on the center of modules that have many peripheral nodes with one degree. Therefore, interrupting the nodes caught by these two centrality measures caused many single node isolations and turned out to be the larger increment of the average path length. On the other hand, the average path length of the interruptions on the bridging nodes discriminated by bridging centrality were also increased significantly with generating only one singleton in the same intervals. This behavior insists that interruptions on the bridging nodes resulted in much longer alternative paths or isolations of larger modules not singletons.

4. DISCUSSION AND CONCLUSION

Jeong's group has espoused the degree of a node as a key basis for essential components identification[14]. These high degree nodes are called hubs, and hubs have been found to be important determinants of survival in network perturbation. Power-law networks are very robust to random attacks but very vulnerable to targeted attack in this model[2]. Hahn's group looked for differences in degree, betweenness, and closeness centrality between essential and nonessential genes in three eukaryotic protein interaction networks: yeast, worm, and fly[12]. These three interaction networks are found to have remarkable similar structure and the proteins that have a more central position in networks, regardless of the number of direct interactors, evolve more slowly and are more likely to be essential for survival. Estrada's group introduces a new centrality measure, which is called subgraph centrality that characterizes the participation of each node in all subgraphs in a network[8][9]. The subgraph centrality is better able to discriminate the lethal nodes of a network than any other measures in protein interaction networks. Palumbo's group tried to find lethal nodes by arc deletion, which could lead to sub components isolation. They showed that lethality corresponds to the lack of alternative paths in the perturbed network linking the nodes affected by the enzyme deletion on yeast metabolic network which is a directed network[17]. Existing approaches are focusing only on finding central and lethal nodes, and it has been proven that these existing approaches can discriminate lethal nodes very well. We argue that identifying network's essential components with these existing methods is likely to prove suboptimal because of their limited view of looking at the problem. Guimera's group devised a clustering method to identify functional modules in metabolic pathways and categorized the role of each component in the pathway according to their topological location relative to detected functional modules[11]. Annotating locality of components in network's topology based on a certain clustering method is totally biased by the used clustering method. So identifying components' topological location, e.g., hubs, peripheral nodes, or bridging nodes, independent from any other methods is more preferable.

While other existing approaches are focusing on targeting high degree, high central, and high lethal components in network topology, our bridging centrality discriminates the bridging nodes with more information flowed through them, i.e., more central from the information flow aspect, and also positioned between highly connected regions. We have shown that bridging centrality successfully distinguishes the bridging nodes in several real world scale-free networks including social, biological, and technical networks. Theoretical analysis of the yeast metabolic network, observing the clustering coefficient changes and the average path length behaviors, were performed and showed that the nodes picked up by bridging centrality are well positioned on the connecting spots between modules.

Throughout the experiments we performed in this paper, bridging centrality did a great job on identifying the bridging nodes in real world networks. Bridging centrality have many possible applications on many research areas. The recognition of the bridging nodes and information about the bridging nodes should be very valuable knowledge for further fruitful achievements in biological researches and in other fields too. For example, identifying functional or physical modules or identifying the key components in biological networks using the bridging centrality will provide a very effective and totally new way of looking biological network structures. This promising outcome should also be applicable to social networks for detecting sub community structures or discovering the key elements in them. As we observed in the previous section, while the perturbations on hubs or the nodes selected by other centrality indices caused a few local singleton isolations and might have many alternative paths due to their high clustering property, which is one of the main properties of the scale-frre networks, among neighbors inside the module, the failures on the bridging nodes, unsurprisingly, caused whole module isolations from the rest of the network and might have longer alternative paths or no alternative path at all. So the interruptions on the bridging nodes could be much more lethal, and the cost of network failure by interrupting the bridging nodes would be much higher than the failure on the other nodes. Therefore, we claim that the bridging nodes picked up by bridging centrality also reside on the critical positions and also are worth getting attentions for the network robustness improvement and paths protection standpoint.

5. FUTURE WORK

It was clearly shown that the bridging nodes discriminated by bridging centrality are well positioned between highly connected modules in scale-free networks. Using this bridging centrality superiority, clustering analysis on scale-free networks can be accomplished through differentiating modules by considering the bridging nodes as the boundary of clusters.

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