

Consistent Community Identification in Complex Networks

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(Received 28 July 2011, in final form 31 August 2011)

We have found that known community identification algorithms produce inconsistent communities when the node ordering changes at input. We use the pairwise membership probability and consistency to quantify the level of consistency across multiple runs of an algorithm. Based on these two metrics, we address the consistency problem without compromising the modularity. The key insight of the algorithm is to use pairwise membership probabilities as link weights. It offers a new tool in the study of community structures and their evolutions.

PACS numbers: 89.75.-k, 89.75.Hc

Keywords: Complex networks, Community structure, Modularity

DOI: 10.3938/jkps.59.3128

I. INTRODUCTION

Understanding and identifying community structure in a complex network have been major research topics in sociology, physics, biology, and computer science [1]. Various algorithms for discovering communities and modules in networks have been proposed: Some are based on betweenness and similar measures by removing inter-community links [2,3]. Others use cliques [4], information theory [5], random walks on networks [6], and similarity among partitions [7], and the list is not exhausted.

Among these algorithms, greedy modularity maximization is one of the prevalent approaches for community identification. The *modularity*, Q , is a quality measure of partitioned communities. It is defined as

$$Q = \sum_i (e_{ii} - a_i^2), \quad (1)$$

where e_{ii} is the ratio of the number of links between nodes belonging to community i over all links and a_i is

the ratio of all links that cross the boundary of community i over all links. The value of modularity ranges from -1 to 1. The value $Q = 0$ implies that the number of links within a community is no better than random.

Modularity maximization methods (MMMs) are effective in identifying and uncovering community structure in networked systems, but they have some limitations. For example, MMMs fail to identify communities smaller than a certain scale, which is known as the resolution limit [8].

In this work we report another limitation of MMMs, namely, the inconsistency among identified communities in multiple runs of an algorithm. Using empirical network data, we show that all algorithms we have reviewed produce inconsistent communities every time the node names are reordered while the structure of the network remains unchanged.

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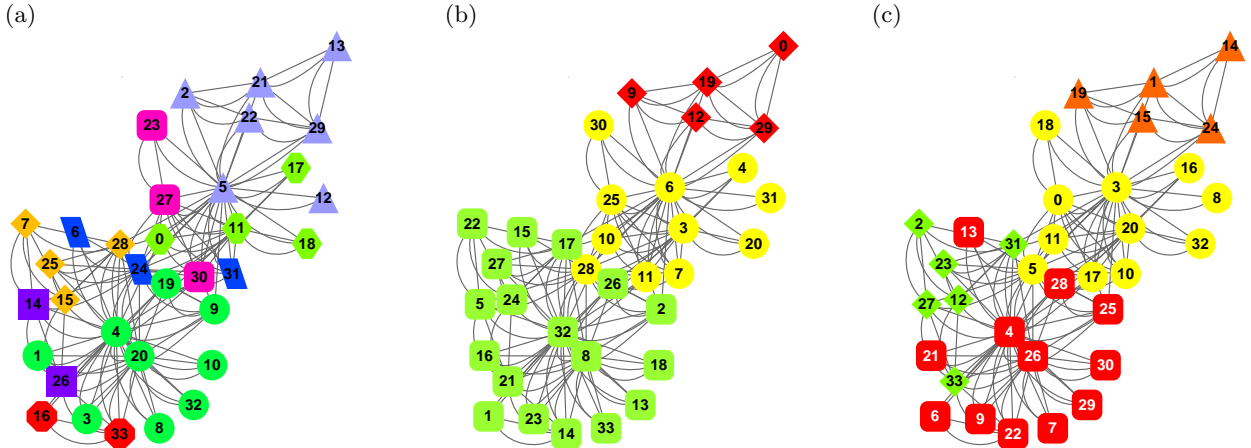


Fig. 1. Visualization of inconsistent community identification in the Karate network [12]. Nodes of a color belong to the same community, and node ordering is depicted as the number in the node. (a) $Q = 0.273176$, (b) $Q = 0.380671$, and (c) $Q = 0.41979$.

II. QUANTIFYING CONSISTENCY

We consider three community identification algorithms: Clauset-Newman-Moore (CNM) [9], Wakita [10], and Louvain [11]. They all take a greedy approach in modularity maximization and are the only known algorithms to work for large networks. However, they all produce different values of modularity for the same network. Even a single algorithm produces different modularities when the input order of nodes changes. We show an example to illustrate the inconsistency even in a small well-studied network. The communities identified in a network by using the Louvain algorithm under three different orderings of nodes are shown in Fig. 1. Although the network has a small number of 34 nodes, identified communities in Figs. 1(a), (b), and (c) are quite different and have different modularities. This example demonstrates that even for a small network, the input order plays a crucial role in determining the community structure in complex networks.

The huge number of ways to partition a graph makes it impossible to optimize modularity exhaustively. From a macroscopic view, this is fine as long as the modularity varies not too much. However, if we are interested in network analysis from a nodal perspective, that is, identifying a community to which a node belongs, it does not make sense for the node to belong to a completely different community every time the input order is perturbed. For example, we have two snapshots of a growing network taken a year apart. How has the community of a node grown in a year? This question is about evolutionary clustering, and inconsistent communities are a problem. What we address in this work is the inconsistency not even over the course of evolution, but within a single snapshot. If the community identification algorithm is so sensitive to the order of the input and produces completely different communities from a node's perspective,

we cannot answer the question raised in the example. Thus, before we identify the community to which a node belongs, we should ask how consistent the community membership is across different input orders.

Over N runs of an algorithm, each with a randomly ordered input set, we quantify the likelihood of a pair of nodes resulting in the same community as

$$p_{ij} = \frac{\sum_{n=1}^N \delta_n(c_i, c_j)}{N}, \quad (2)$$

where

$$\delta_n(c_i, c_j) = \begin{cases} 1, & \text{if } c_i = c_j \text{ in the } n\text{th dataset} \\ 0, & \text{otherwise} \end{cases}$$

and i and j are node indices and c_i and c_j represent communities to which i and j belong, respectively. This metric is the *pairwise membership probability*. The pairwise membership probability p_{ij} represents the empirical probability that two nodes belong to the same community across multiple runs of the same algorithm [18]. We can compute p_{ij} for all possible pairs of nodes. However, for any specific i , p_{ij} is likely to be 0 for most of j due to the sparsity of links in the network, and this tendency grows with the network size. Therefore, we consider p_{ij} only for adjacent nodes; that is, only between neighboring nodes.

A pairwise membership probability of 1 means that the two neighboring nodes always belong to the same community, and 0 means that the two never belong to the same community irrespective of the input order. The larger the number of pairs whose empirical pairwise membership probability is close to either 0 or 1 is, the more consistent the identified communities are. p_{ij} close to 1/2 means that i and j can be in the same community more or less randomly.

Table 1. Summary of the statistics of the network structure for the three empirical networks. \mathbf{N} is the number of nodes, L is the number of links, and C is the global clustering coefficient.

	Karate	Dolphin	Les miserables	Word adjacencies	Football	Political blog	Condensed matter
\mathbf{N}	34	62	77	112	115	1,222	36,458
L	78	159	254	425	613	16,714	171,736
$\langle k \rangle$	4.6	5.1	6.6	7.6	10.7	27.4	9.4
C	0.57	0.26	0.57	0.17	0.40	0.32	0.66

In order to quantify network-wide community membership consistency, we use consistency \mathcal{C} for the entire network

$$\mathcal{C} = \frac{\sum_{(i,j) \in E} (p_{ij} - 1/2)^2}{|E|} \times \frac{1}{(0.5)^2}, \quad (3)$$

where E is the set of links and $|E|$ is the number of links [18]. The consistency \mathcal{C} weighs the pairwise membership probabilities away from $1/2$. The multiplicative term in Eq. (3) normalizes \mathcal{C} from 0 to 1. Our goal is to measure the consistency of the outcomes of the algorithms, independent of the structure of the network. For example, if more community structures are embedded in the entire network, two adjacent nodes are (naturally) likely to fall into different communities. Otherwise, two adjacent nodes are likely to fall into the same community. In this setting, we'd like to consider the consistency as 1 if and only if the algorithm 'consistently' finds the same community partitioning no matter what two nodes are in the same or different communities. Therefore, the pivot value should be 0.5 - the same or not.

In this work, we have analyzed consistency in community memberships of seven empirical systems from various fields, such as the Karate club [12], dolphin social network [13], the co-appearance network of characters in the novel Les Misérables [14], the adjacency network of common adjectives and nouns in the novel David Copperfield [15], the regular season network of American football games between Division IA colleges during the Fall 2000 [2], a directed network of hyperlinks between weblogs on US politics [16] and the network of coauthorships between scientists posting preprints on the Condensed Matter E-Print Archive [17]. Table 1 shows the basic statistics of the seven networks.

III. CONSISTENT COMMUNITY IDENTIFICATION

In the case of communities detected by using the CNM algorithm in the Karate club, 12.8% of the pairwise membership probabilities are 0, and the rest of the pairs have 1, which means that nodes of a community always belong to the same community over N runs: $\mathcal{C} = 1$. In Fig. 2, we

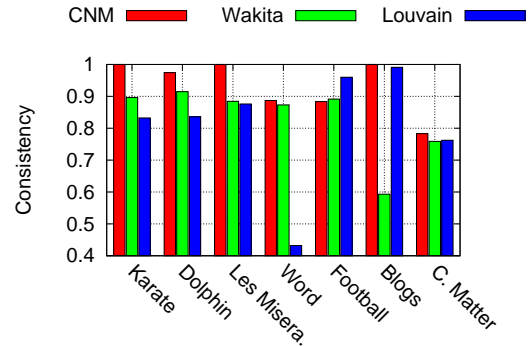


Fig. 2. Consistency of community identification.

show the consistency from the three algorithms. There is no one algorithm that outperforms the other two in all networks, and no consistent correlation between the consistency and the topological characteristics of the network, such as network size, average degree and average clustering coefficient. However, a closer look at pairwise membership probabilities reveals that in all networks far more than 50% of pairs have pairwise membership probabilities either smaller than 0.2 or greater than 0.8 [18], which means that most pairs of nodes are never in the same community or always in the same community, respectively. Based on this observation, we have devised a consistency reinforcing mechanism as follows [18]. After each *cycle* of N runs, we calculate the pairwise membership probabilities and then assign them as link weights. From the second cycle on, we use this weighted network as an input and continue the cycle until \mathcal{C} reaches 0.999 or higher. In a weighted network, an edge of a higher weight is placed within a community while an edge of a lower weight bridges communities. Because we assign the pairwise membership probability as the weight of the corresponding link, an edge of high pairwise membership probability in the prior cycle is more likely to be placed within a community in the next cycle. Therefore, links with higher weights are reinforced through multiple cycles and eventually consistent communities emerge.

Our approach has the effect of removing those links with pairwise membership probabilities of 0 in the next cycle and spreading the unit link weight between 0 and 1, thus reducing ties significantly in calculating ΔQ . When there are ties, can we give preference to nodes based on

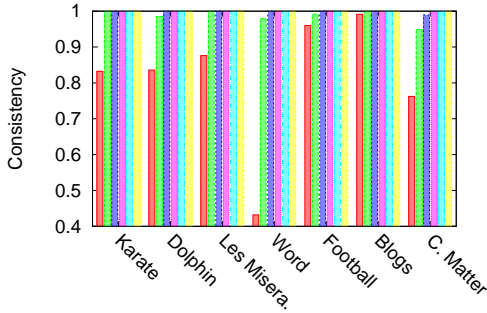


Fig. 3. Convergence of consistency. For each given datum, from left to right, red color bar (first bar), green color bar (second bar), blue color bar (third bar), magenta color bar (fourth bar), and cyan color bar (fifth bar) represent the consistency after first, second, third, fourth, and fifth cycle of applying the algorithm, respectively.

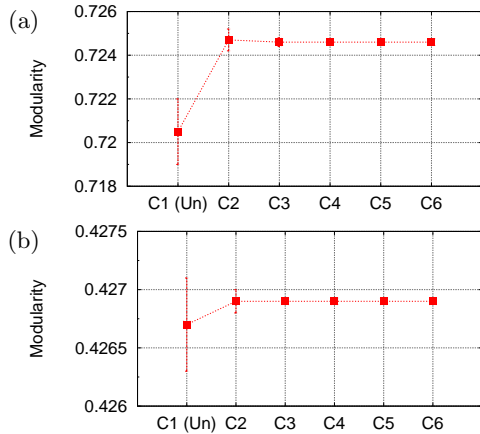


Fig. 4. Convergence of modularity ('Un' indicates modularity of unweighted network). C1 represents the modularity of the original data. C2, C3, C4, C5, and C6 represent the modularity after first, second, third, fourth and fifth cycle of applying the algorithm, respectively. (a) Condensed matter and (b) Political blogs.

other metrics, such as degrees or betweenness centrality [2]? To assess the benefit of other metrics, if any, we order nodes by the degree, clustering coefficient, degree correlation, and betweenness centrality and compute modularity.

Even if we employ all the metrics in tie breaking, we cannot eliminate ties completely [18]. In other words, no single topological characteristic consistently stands out to work better than others in all networks. We have looked at edge betweenness as well, and found no correlation between edge betweenness and pairwise membership probability.

Our approach of reinforcing consistency in multiple cycles is applicable to any of the three algorithms. We include only the results from the Louvain algorithm in this paper, for it is the fastest and only one that scales up to billions of links. We report that the other two algorithms have similar results.

The convergence of consistency after 5 cycles is shown in Fig. 3. All networks consistency reaches 1 in 5 cycles. In Fig. 4, we show how the modularity converges over 5 cycles. The modularity converges almost to a single point after 2 cycles. Furthermore, the modularity after convergence is higher. Figure 4 demonstrates that our approach has no negative impact on modularity and even improves it in certain networks.

So far, we have shown that our solution of using pairwise membership probabilities as link weights has improved consistency greatly. Now, we check if communities from different trials come out identically. We turn our focus to individual communities in two independent trials. A cycle is N runs for a given network. A trial is M cycles of a given ordering of the network. We use $M = 6$ and $N = 100$. In order to check if the communities are identical across trials, we calculate the maximum Jaccard coefficient (the ratio of the intersection to the union of two communities) of a community against all communities of another trial. A Jaccard coefficient of 1 means that the same communities are produced in both trials. We compare the Jaccard coefficients for all pairs of trials, and most Jaccard coefficients are found to be greater than 0.95.

IV. CONCLUSION

In summary, we have investigated the inconsistencies among communities when existing community identification algorithms (CNM [9], Wakita [10], and Louvain [11]) are applied. Using empirical network data, we have shown that all three algorithms produce inconsistent communities every time the node ordering changes even when the size of networks are small. Similar results based on very large online social networks are also reported [18]. To quantify the consistency of identified communities, we introduced pairwise membership probability and consistency. The former quantifies the likelihood of two nodes resulting in the same community, and the latter represent the global level of consistency derived from pairwise membership probabilities of a network. We analyze seven empirical networks in terms of the above two metrics and show that no one algorithm outperforms the other two in all networks. However, most pairwise membership probabilities are close to either 0 or 1 (that is, never in the same community or always in the same community, respectively). Based on this observation, we use a consistency reinforcing mechanism that improves the consistency without compromising the modularity. The key idea is to set the pairwise membership probability as the link weight and to find communities in the weighted network iteratively. We have demonstrated the convergence of consistency within 6 or fewer cycles. Resulting communities exhibit consistent grouping through multiple trials.

ACKNOWLEDGMENTS

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MEST) (No. 2011-0028908).

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