Network Landscape from a Brownian Particle’s Perspective

Haijun Zhou
Max-Planck-Institute of Colloids and Interfaces, 14424 Potsdam, Germany
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A complex networked system, such as an organism’s metabolic network and genetic interaction network, is composed of a large number of interacting agents. The complexity of such systems originates partly from the heterogeneity in their interaction patterns, aspects of which include the small-world \cite{1} and the scale-free properties \cite{2,3} observed in many social, biological, and technological networks \cite{4,5,6}. Given this high degree of complexity, it is necessary to divide a network into different subgroups to facilitate the understanding of the relationships among different components \cite{7,8}.

A complex network could be represented by a graph. Each component of the network is mapped to a vertex (node), and the interaction between two components is signified by an edge between the two corresponding nodes, whose weight is related to the interaction strength. The challenge is to dissect this graph based on its connection pattern. We know that to partition a graph into two equally sized subgroups such that the number of edges in between reaches the absolute minimum is already a NP-complete problem, a solution is not guaranteed to be found easily; however it is still a well-defined question. On the other hand, the question “How many subgroups should a graph be divided into and how?” is ill-posed, as we do not have an objective function to optimize; and we have to rely on heuristic reasoning to proceed.

If we are interested in identifying just one community that is associated with a specified node, the maximum flow method \cite{9} turns out to be efficient. Recently, it is applied to identifying communities of Internet webpages \cite{10}. An community thus uncovered is usually very small; and for this method to work well one needs a priori knowledge of the network to select the source and sink nodes properly. Another elegant method is based on the concept of edge betweenness \cite{11}. The degree of betweenness of an edge is defined as the total number of shortest paths between pair of nodes which pass through it. By removing recursively the current edge with the highest degree of betweenness, one expects the connectivity of the network to decrease the most efficiently and minimal cutting operations is needed to separate the network into subgroups \cite{7}. This idea of Girvan and Newman \cite{7} could be readily extended to weighted graphs by assigning each edge a length equalling its reciprocal weight. Furthermore, in the sociology literature, there is a relatively long tradition in identifying communities based on the criteria of reachability and shortest distance (see, e.g., \cite{12}).

In this paper, a new method of network community identification is described. It is based on the concept of network Brownian motion: If an intelligent Brownian particle lives in a given network for a long time, what might be its perspective of the network’s landscape? We suggest that, without the need to removing edges from the network, the node-node distances “measured” by this Brownian particle can be used to construct the community structure and to identify the central node of each community. This idea is tested on several social and biological networks and satisfiable results are obtained. Several ways are discussed to extend and improve our method.

Consider a connected network of \( N \) nodes and \( M \) edges. Its node set is denoted by \( V = \{1, \cdots, N\} \) and its connection pattern is specified by the generalized adjacency matrix \( A \). If there is no edge between node \( i \) and node \( j \), \( A_{ij} = 0 \); if there is an edge in between, \( A_{ij} = A_{ji} \geq 0 \) and its value signifies the interaction strength (self-connection is allowed). The set of nearest-neighbors of node \( i \) is denoted by \( E_i \). A Brownian particle keeps moving on the network, and at each time step it jumps from its present position (say \( i \)) to a nearest-neighboring position (\( j \)). When no additional knowledge about the network is known, it is natural to assume the following jumping probability \( P_{ij} = A_{ij} / \sum_{l=1}^{N} A_{il} \) (the corresponding matrix \( P \) is called the transfer matrix). One verifies that at time \( t \ll M \) the probability \( \rho(k) \) for the Brownian particle to be at any node \( k \) is nonvanishing and equals to \( \sum_{j} A_{kj} / \sum_{m,n} A_{mn} \), proportional to the total interaction capacity \( \sum_{j} A_{kj} \) of node \( k \).

Define the node-node distance \( d_{i,j} \) from \( i \) to \( j \) as the average number of steps needed for the Brownian particle to move from \( i \) through the the network to \( j \). From some simple linear-algebra calculation \cite{13}, it is easy to see that
\[ d_{i,j} = \sum_{l=1}^{N} \left( \frac{1}{I - B(j)} \right)_{il}, \]

where \( I \) is the \( N \times N \) identity matrix, and matrix \( B(j) \) equals to the transfer matrix \( P \) except that \( B_{ij}(j) = 0 \) for any \( l \in V \). The distances from all the nodes in \( V \) to node \( j \) can thus be obtained by solving the linear algebraic equation \( \{I - B(j)\} \{d_{1,j}, \ldots, d_{N,j}\}^T = \{1, \ldots, 1\}^T \). We are mainly interested in sparse networks with \( M = O(N) \); for such networks there exist very efficient algorithms \([14,15]\) to calculate the root of this equation. If node \( j \) has the property that \( d_{i,j} \leq d_{i,k} \) for any \( k \in V \), then \( j \) is tagged as a *global attractor* of node \( i \) (\( i \) is closest to \( j \) in the sense of average distance). Similarly, if \( j \in E_i \) and \( d_{i,j} \leq d_{i,l} \) for any \( l \in E_i \), then \( j \) is an *local attractor* of \( i \) (\( i \) is closest to \( j \) among all its nearest-neighbors). We notice that, in general the distance from \( i \) to \( j \) \((d_{i,j})\) differs from that from \( j \) to \( i \) \((d_{j,i})\). Consequently, if \( j \) is an attractor of \( i \), node \( i \) is not necessarily also an attractor of \( j \).

If a graph is divided into different subgroups, on the local scale we intuitively expect that each node \( i \) will have a high probability to be in the same subgroup as its local attractor \( j \), since among all the nearest-neighboring nodes in \( E_i \), node \( j \) has the shortest “distance” from node \( i \). For simplicity let us just *assume* this probability to be unity (a possible improvement is discussed later). Thus, we can define a *local-attractor-based community* (or simply a “L-community”) as a set of nodes \( L = \{i_1, \ldots, i_m\} \) such that (1) if node \( i \in L \) and node \( j \) is an local attractor of \( i \), then \( j \in L \), (2) if \( i \in L \) and node \( k \) has \( i \) as its local attractor, then \( k \in L \), and (3) any subset of \( L \) is not a L-community. Clearly, two L-communities \( L_a \) and \( L_b \) are either identical \((L_a \equiv L_b)\) or disjoint \((L_a \cap L_b = \emptyset)\). Based on each node’s local attractor the graph could be decomposed into a set of L-communities.

According to the same intuitive argument, on the global scale we expect that each node will have a high probability to be in the same community as its global attractor, and if assume this probability to be unity we can similarly construct the *global-attractor-based communities* (“G-communities”) based on the global-attractor of each node. For small networks, we expect the L- and G-community structures to be identical; while for large networks, each G-community may contain several L-communities as its subgroups. A community could be characterized by its size \( N_c \) and an instability index \( I_c \). A node \( i \) in community \( C \) is referred to as unstable if its total direct interaction with nodes in any another community \( C' \), \( \sum_{k \in C'} A_{ik} \), is stronger than its total direct interaction with other nodes in its own community, \( \sum_{k \in C \cap i} A_{ik} \). \( I_c \) is the total number of such nodes in each community. We can also identify the *center* of a community (if it exists) as the node that is the global attractor of itself.

Now we test the above-mentioned simple method on some well-documented networks whose community structures are known. The first example is the social network recorded by Zachary \([16]\). This network contains 34 nodes and 77 weighted edges, and it was observed to spontaneously fission into two groups of size 16 and 18, respectively \([16]\) (these two groups are marked by two colors in Fig. 1A). The results of our method is shown in Fig. 1B. Community \( L_1 \) contains 11 elements (node 13 is unstable and has stronger direct interaction with \( L_2 \), \( L_2 \) has 6 elements (node 9 has stronger direct interaction with \( L_3 \)), and \( L_3 \) has 17 elements. Nodes 1 (the manager), 3, and 34 (the officer) are the corresponding centers. We find that for this network the G-communities coincide with the L-communities.

As another example, the scientific collaboration network of Santa Fe Institute \([17]\) is considered. The giant connected component contains 118 nodes and 200 weighted edges, the weights are assigned according to the measure in \([17]\). The present method divides the network into six L-communities, see Fig. 1B. All the nodes in community \( L_1 \) (size 14), \( L_2 \) (41), \( L_3 \) (8), \( L_4 \) (26), and \( L_6 \) (17) are locally stable, and one node in \( L_4 \) has stronger direct interaction with community \( L_6 \). Same as the above example, the G-community structure is also identical to the L-community structure. Girvan and Newman divided this network into four major groups by recursively removing edges of highest degree of betweenness \([17]\); the largest of which was further divided into three subgroups and the second largest was divided into two subgroups. There are still some minor differences between the six subgroups obtained by the present method and those obtained in \([17]\), which may be attributed to the fact that, in the treatment of \([17]\) the network was regarded as unweighted.

The method is further tested on a relatively more complicated case, the foot-ball match network compiled by Girvan and Newman \([17]\). It contains 115 nodes and 613 unweighted edges. These 115 teams were distributed into 12 conferences by the game organizers. Based on the connection pattern, the present method divides them into 15 L-communities, of which 11 are locally stable: \( L_2 \) (size 9), \( L_3 \) (13), \( L_4 \) (14), \( L_5 \) (10), \( L_6 \) (8), \( L_7 \) (6), \( L_8 \) (7), \( L_9 \) (6), \( L_{10} \) (4), \( L_{11} \) (6), and \( L_{13} \) (size 9). One element of \( L_1 \) (size 9) has stronger interaction with \( L_{10} \), and one element of \( L_{12} \) (size 10) has stronger interaction with \( L_3 \), and all the elements of \( L_{14} \) (size 2) and \( L_{15} \) (size 2) are locally unstable. The G-communities of this network are also identical to the L-communities. In Fig. 1C the community structure of this network is shown, where nodes belonging to each identified community are located together, and the different colors encode the actual 12 conferences \([17]\). Figure 1C indicates that the predicted communities coincide very well with the actual communities. The community structure obtained by the present method is also in very good correspondence with that obtained by Girvan and Newman \([17]\) based on edge betweenness.

The above-studied networks all have relatively small network sizes and the identified G-communities coincide
with the L-communities. Now we apply our method to
the protein interaction network (yeast core [16, 14]) of
baker's yeast. The giant connected component of this
network contains 1471 proteins and 2770 edges (assumed
to be unweighted, since the interaction strengths be-
tween the proteins are generally undetermined). The
present method dissect this giant component into 14 G-
communities (Table I) and into 69 L-communities (11
of them contain one locally unstable node, 15 of them
have 2-7 locally unstable nodes, all the others are stable).
The relationship between the G- and L-communities is
demonstrated in Fig 1D, where proteins are grouped into
L-communities and those of the same G-community have
the same color. We see from Fig 1D that if two nodes
are in the same L-community, they are very probable to
be in the same G-community. The largest G-community
(G1) contains more than half of the proteins and is cen-
tered around nucleoporin YMR047C, which, according to
SWISS-PROT description [20], is "an essential com-
ponent of nuclear pore complex" and "may be involved in
both binding and translocation of the proteins during
nucleocytoplasmic transport". YMR047C interact directly
only with 39 other proteins (it is even not the most con-
nected node in the system), but associated with it is a
group of 935 proteins as suggested by the present method.
The protein interaction network may be evolved to facil-
itate efficient protein transportation by protein-mediated
indirect interactions.

What will happen if the protein YMR047C is removed
from the network? The resulting perturbed system has
1463 nodes and 2729 edges, and we find that its L-
community structure does not change much. Altogether
72 L-communities are identified, and most of them con-
tain more or less the same set of elements as in the un-
perturbed network. However, there is a dramatic change
in the G-community structure. There are now 21 G-
communities (the largest of which has 574 proteins),
while G1 of the original system breaks up into eight
smaller G-communities. It was revealed that the most
highly connected proteins in the cell are the most im-
portant for its survival, and mutations in these proteins
are usually lethal [21]. Our work suggests that, these
highly connected proteins are especially important be-
cause they help integrating many small functional mod-
ules (L-communities) into a larger unit (G-community),
allowing the cell to perform concerted reactions in re-
sponse to environment stimuli.

In the above examples, the network studied are all from
real-world. We have also tested the performance of our
method to some artificial networks generated by com-
puter. To compare with the result of Ref. [7], we gen-
erated an ensemble of random graphs with 128 vertices.
These vertices are divided into four groups of 32 vertices
each. Each vertex has on average 16 edges, zout of which
are to vertices of other groups, and the remaining are to
vertices within its group; all these edges are drawn ran-
domly and independently in all the other means. Using
the method of Girvan and Newman, it was reported [7]
that when zout < 6 all the vertices could be classified
with high probability. Our present method in its sim-
plest form could work perfectly only when zout < 2.5.
In the artificial network, the vertices are identical with
each other in the statistical sense and there is no correla-
tion between the degrees of two neighboring edges. Our
method seems not to be the best for such kind of random
networks.

In summary, we have suggested a simple way of group-
ing a graph of nodes and edges into different subgraphs
based on the node-node distance measured by a Brown-
ian particle. The basic idea was applied to several real
networked systems and very encouraging results were ob-
tained. The concept of random walking was also used in
some recent efforts to facilitate searching on networks
(see, e.g., [22, 23]), the present work may be the first at-
tempt in applying it on identifying network community
structure. Some possible extensions of our method are
immediately conceivable: First, in the present work we
have assumed that a node will be in the same commu-
nity as its attractor with probability 1. Naturally, we can
introduce a "inverse temperature" β and suppose that
node i be in the same community as node j with prob-
ability proportional to exp(−βdij). The present work
discusses just the zero temperature limit. We believe
that the communities identified at zero temperature will
persist until the temperature is high enough. Second,
we can construct a gross-grained network by regarding
each L-community as a single node, and defining the dis-
tance from one L-community to another as the average
node-node distance between nodes in these two commu-
nities. The present method can then be applied, and the
relationship between different L-communities can be bet-
ter understood. Third, for very large networks, it is im-
pRACTICAL to consider the whole network when calculating
node-node distance. Actually this is not necessary, since
the length of the shortest path between a given node and
its attractor should be small. We can therefore focus on
a localized region of the network to identify the attractor
of a given node.

Furthermore, based on the distance measure of the
present paper, we can define a quantity called the dis-
similarity index for any two nearest-neighboring nodes.
Nearest-neighboring vertices of the same community tend
to have small dissimilarity index, while those belonging
to different communities tend to have high dissimilarity
index. Extensions of the present work will be reported
in a forthcoming paper [24].

An interesting task is to use extended versions of the
present method to explore the landscape of the Internet's
autonomous system [8] and that of the metabolic network
of E. coli [9, 25].

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TABLE I: G-communities of yeast’s protein interaction network [18, 19]. $N_c$ is the community size, $I_c$ is the number of locally unstable nodes.

| Index | $N_c$ | $I_c$ | Center |
|-------|-------|-------|--------|
| $G_1$ | 935   | 7     | YMR047C |
| $G_2$ | 90    | 3     | YNL189W |
| $G_3$ | 17    | 4     | YER148W |
| $G_4$ | 57    | 5     | YFL039C |
| $G_5$ | 97    | 3     | YDR388W |
| $G_6$ | 59    | 0     | YJR022W |
| $G_7$ | 22    | 0     | YDR448W |
| $G_8$ | 52    | 1     | YBR109C |
| $G_9$ | 37    | 1     | YGR218W |
| $G_{10}$ | 19   | 2     | YML109W |
| $G_{11}$ | 26   | 0     | YDR167W |
| $G_{12}$ | 24   | 0     | YDL140C |
| $G_{13}$ | 13   | 0     | YGL051W |
| $G_{14}$ | 23   | 0     | YJR091C |
FIG. 1: (Color) Community structure of some model networks (the nodes of the same L-community are spatially grouped together). (a) The karate club network compiled by Zachary [16] (here nodes are colored according to their actual groupings); (b) the scientific collaboration network compiled by Girvan and Newman [7]; (c) the foot-ball match network compiled by Girvan and Newman [7] (nodes are colored according to their actual groupings); and (d) the yeast protein interaction network [18, 19], here nodes of the same G-community are encoded with the same color (open circles denote nodes in $G_1$).