New methods for incorporating network cyclic structures to improve community detection

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Abstract

A distinguishing property of communities in networks is that cycles are more prevalent within communities than across communities. Hence, the detection of these communities may be aided through the use of measures of the local “richness” of cyclic structures. We investigate the use of two methods for quantifying this richness—loop modulus (LM) and renewal non-backtracking random walks (RNBRW)—to improve the performance of existing community detection algorithms. LM solves a quadratic program to find an optimal allocation of edge usage across cycles to minimize cycle overlap, thereby giving a rigorous way to quantify the importance of edges. RNBRW, introduced for the first time in this paper, quantifies edge importance as the likelihood of an edge completing a cycle in a non-backtracking random walk. We argue that RNBRW provides an efficient and scalable alternative to LM. We give simulation results that suggest pre-weighting edges by the proposed methods can improve the performance of popular community detection algorithms substantially. Our methods are especially efficient for the challenging case of detecting communities in sparse graphs.

Keywords: Cyclic topologies; modularity function; loop modulus; retraced non-backtracking random walk
1 Introduction

In many sciences—for example Sociology (Scott, 2017), Biology (Chung et al., 2015), and Computer Science (Hendrickson and Kolda, 2000)—units under study often belong to communities, and units within the same community behave similarly. Hence, understanding the community structure of units is critical in these sciences, and quite a bit of work has been devoted to the development of methods to detect these communities.

Community detection methods often use the framework of mathematical networks: units are nodes (vertices) in the graph, and edges are drawn between two nodes if the corresponding units interact with each other. Under this framework, the problem of community detection becomes a graph partitioning problem where units within each block of the partition are “optimally” connected under some objective. Commonly, communities are identified through edge prevalence; edges are more frequently observed between nodes in the same community than between nodes in different communities.

Optimal detection of communities is often \( \mathcal{NP} \)-hard because of an exponentially increasing number of possible partitions as the number of units \( n \) grows. Numerous efforts and heuristics have been offered that can provide solutions under large \( n \) settings, for example, Blondel et al. (2008) and Clauset et al. (2004)—referred as Louvain and CNM respectively. In this paper, we are particularly interested in methods that can be categorized into one of two general approaches: first, combinatorial optimization of an object, such as maximizing the graph modularity or finding the sparsest graph cut; second, model based approaches that fit a network model, such as the stochastic block model, to the data and discovers communities by maximizing, for example, the likelihood of realizing the observed graph. For an in depth review on community detection algorithms, see Fortunato (2010).

The ability of these algorithms to accurately identify communities may be improved through incorporating additional graph structure—typically integrated into these algorithms through the use of edge weights (De Meo et al., 2013; Sun, 2014; Khadivi et al., 2011). In this paper, we are particularly interested in edge weights derived from the cyclic structure of graphs. Previous works has shown cyclic structure to be useful in detecting communities Newman (2003); Radicchi et al. (2004); Kim and Kim (2005); Vragović and Louis (2006); Zhang et al. (2008). The intuition is that, if edges are more prevalent within a community than across communities, cycles (especially small cycles) may be more prevalent within communities as well. Hence, edge weights that incorporate information about the density of cycles within a graph may be useful in detecting communities within that graph.

Recent work by Shakeri et al. (2017) developed a method for analyzing cyclic structure
in networks called loop modulus (LM). LM finds a probability distribution on all cycles in a graph so that the expected overlap between two cycles sampled from this distribution is minimized; from this distribution, a measure of the overall “richness” or density of cycles can then be obtained. Shakeri et al. (2017) go on to show that weighting edges by its expected usage under the optimal distribution of cycles may be helpful in community detection algorithms. Although this method shows great promise, the amount of computation required for LM prohibits its use in very large networks.

On the other hand, random walks have been proposed as a computationally efficient tool for uncovering the structure of networks. In particular, random walk paths may be helpful for identifying communities. Namely, since the density of edges is higher within communities than across communities, the walks will spend a majority of their time traveling within communities (Hughes 1995; Lai et al. 2010). An important variant of random walk is the non-backtracking random walk (NBRW), in which the random walk is prohibited from returning back to a node in exactly two steps (Alon et al. 2007; Fitzner and van der Hofstad 2013). While work on NBRW currently focuses on its fast convergence rate, we exploit another useful property of NBRW—its ability to identify cyclic structure.

In this paper we extend NBRW to better capture the cyclic structure of networks. We perform an iterative process where, for each iteration, we independently perform an NBRW from a random node until it forms a cycle, record the terminal edge—the edge that completes the cycle, and terminate the NBRW. This amounts to performing a renewal process on NBRWs—hence the name renewal non-backtracking random walk (RNBRW).

We show that, when weighting edges proportionally to the empirical frequency of terminal edges, RNBRW obtains a measure of cyclic density. Moreover, the RNBRW method is very computationally efficient, and can be used for networks on the order of millions of nodes. We give intuition as to why the RNBRW method heuristically approximates loop modulus. We show through simulation that weighting edges through both RNBRW and LM improves the ability of Louvain and CNM methods to detect communities, and community detection using Louvain and CNM using these weightings offers comparable performance in detecting communities to state-of-the-art methods.

2 Notation and definitions

Let $G = (V, E)$ denote a graph with node set $V$ and edge set $E$. We do not currently make any restrictions on whether $G$ is directed or undirected. Let $n = |V|$ and $m = |E|$. If $G$ is undirected, we will denote the edge between vertices $i$ and $j$ by $ij$, and if $G$ is directed, we
denote the edge from $i$ to $j$ by $\overrightarrow{i j}$. For convenience, we may refer to edges in an undirected graph $G$ using the latter notation; in this case, $\overrightarrow{i j}$ and $\overrightarrow{j i}$ refer to the same edge $ij$. Edges $\overrightarrow{i j} \in E$ may be weighted; let $w_{\overrightarrow{i j}}$ denote the value of this weight. For ease of notation, we assume an unweighted graph has default edge weights $w_{\overrightarrow{i j}} = 1$. An adjacency matrix $A$ for a graph $G$ is an $n \times n$ matrix where element $A_{ij} = 1$ if edge $\overrightarrow{i j} \in E$ and $A_{ij} = 0$ otherwise.

The (possibly weighted) degree of node $i$, denoted $d_i$, is the sum of the edge weights that begin from node $i$.

$$d_i \equiv \sum_{j=1}^{n} w_{\overrightarrow{i j}} \quad (1)$$

We assume edge weights are scaled so that

$$\sum_{i=1}^{n} d_i = 2m. \quad (2)$$

Note that, in the unweighted case, $d_i$ is simply the number of edges beginning from node $i$.

We deviate from conventional literature by defining a walk by the edges it traverses; a walk $c = (\overrightarrow{v_0 v_1}, \overrightarrow{v_1 v_2}, \ldots, \overrightarrow{v_{k-1} v_k})$ is a vector of edges $\overrightarrow{v_{\ell-1} v_{\ell}} \in E, \ell = 1, 2, \ldots, k$ connecting (possibly non-distinct) nodes $v_0, v_1, v_2, \ldots, v_k \in V$. A random walk $c^\ast = (E_1, E_2, \ldots, E_n)$ is a walk such that:

$$P(E_{\ell+1} = \overrightarrow{v_\ell v_{\ell+1}} | E_\ell = \overrightarrow{v_{\ell-1} v_{\ell}}, \ldots, E_1 = \overrightarrow{v_0 v_1})$$

$$= P(E_{\ell+1} = \overrightarrow{v_\ell v_{\ell+1}} | E_\ell = \overrightarrow{v_{\ell-1} v_{\ell}}) = \frac{w_{\overrightarrow{v_\ell v_{\ell+1}}}}{d_\ell} \quad (3)$$

A walk $c$ is a simple cycle if $v_0 = v_k$ and $v_0, v_1, v_2, \ldots, v_{k-1}$ are distinct. Define $C = C_G$ as the set of all simple cycles in $G$.

The nodes $V$ are partitioned into $q$ communities, numbered 1 through $q$. Let $g_v \in \{1, \ldots, q\}$ denote the community to which $v$ belongs. In problems of community detection, we wish to uncover the true label $g_v$ for each node $v \in V$. Let $g = (g_1, g_2, \ldots, g_n)$.

## 2.1 Some community detection methods

One popular approach for the problem of community detection is to choose communities by solving integer programming optimization problem. A common objective function for community detection is the graph modularity \cite{Newman2003}:

$$M(g; A) = \frac{1}{2m} \sum_{i,j} \left( A_{ij} \left( \frac{d_i d_j}{2m} \right) \right) \delta_{g_i g_j}. \quad (4)$$
Intuitively, for a given community label $g$, the modularity function measures how much within-group and across-group edge formation deviates from independence. Better choices of communities $g$ correspond to larger values of $M(g)$. Choosing communities $g$ that maximize the modularity—or almost any other graph partitioning objective—is an $\mathcal{NP}$-hard problem; hence, this approach often focuses on heuristic or approximately optimal solutions (Brandes et al., 2008).

Model-based approaches assume that the network is sampled from a family of possible graphs $\mathcal{G}$; each graph in the family has a computable likelihood of being generated. For example, the degree corrected stochastic block model (DCSBM) family supposes the number of nodes $n$ in the graph is fixed, that the $n$ nodes are partitioned into $q$ communities, where the community assignment is denoted by $g$, and that undirected edges are formed independently (Karrer and Newman, 2011). The probability that an edge is formed between nodes $i$ and $j$ is

$$ P(ij \in E) = d_i^* d_j^* p_{g_i g_j} $$

where $d_i^*$ is a parameter indicating the propensity of edges to include node $i$—the larger $d_i^*$ is, the larger the degree of $i$ is expected to be—and $p_{g_i g_j}$ is a parameter indicating the likelihood of an edge forming between communities $g_i$ and $g_j$. Let $p = \{p_{g_i g_j}\}_{i<j}$ and let $d^* = \{d_i^*\}_{i=1}^n$. Under this model, the likelihood that a graph $G$ is formed is

$$ \mathcal{L}(g, p, d^*|G) = P(G|g, p, k) = \prod_{i<j} (d_i d_j p_{g_i g_j})^{A_{ij}} (1 - d_i d_j p_{g_i g_j})^{1-A_{ij}}. \quad (5) $$

The parameters $d^*$ are assumed to satisfy a constraint to make likelihood maximization over $g$, $d^*$, and $p$ identifiable. Much like with modularity maximization, maximizing this likelihood is an $\mathcal{NP}$-hard problem that can be difficult to solve even for small $n$. Hence, typically, model-based methods use approximations and heuristics for the likelihood (e.g. substituting the Bernoulli random variables for Poisson random variables with expectation $d_i^* d_j^* p_{g_i g_j}$) to simplify the maximization problem. Model-based approaches then estimate the labels $g$ and probabilities $p$ to obtain an approximate maximum of the likelihood.

Under some models, modularity maximization and maximum likelihood are equivalent problems. For example, Newman (2016) shows equivalence of these approaches under the DCSBM.

### 2.2 Heuristics for modularity maximization

Since maximizing the modularity function is an $\mathcal{NP}$-hard problem, heuristics are offered to provide approximate, scalable solutions to find the node memberships $g$. In this paper,
we briefly discuss two popular heuristic algorithms for modularity maximization, the CNM method ([Clauset et al., 2004]) and the Louvain method ([Blondel et al., 2008]).

2.2.1 CNM method

The CNM method is a greedy algorithm in which communities are iteratively merged so that each merger maximizes the change in modularity. More specifically, each node begins in its own singleton community. The change of modularity obtained from merging communities $i$ and $j$ into a single community, denoted by $\Delta Q_{ij}$, is initialized for all possible pairs of nodes:

$$\Delta Q_{ij} = \begin{cases} 1/m - 2d_id_j/(2m)^2 & \text{if } A_{ij} \neq 0 \\ 0 & \text{otherwise} \end{cases} \quad (6)$$

Once the initializations are complete, the algorithm repeatedly selects the best merger, then updates the $\Delta Q$ values, until no further mergers are possible. CNM then selects communities according to the largest found modularity. The computational complexity of CNM algorithm is $O(n^2 \log n)$.

2.2.2 Louvain method

The Louvain method is divided into two phases. The first phase initializes each node into its own community and considers increasing modularity locally by changing a node’s community label to that of a neighboring community. For example, the modularity change obtained by moving singular node $i$ from its community to a neighboring community is calculated by:

$$\Delta Q = \left[ \frac{\Sigma_{in} + d_{i,in}}{2m} - \left( \frac{\Sigma_{tot} + d_i}{2m} \right)^2 \right] - \left[ \frac{\Sigma_{in}}{2m} - \left( \frac{\Sigma_{tot}}{2m} \right)^2 \right] - \left( \frac{d_i}{2m} \right)^2 \quad (7)$$

where $\Sigma_{in}$ is sum of internal edge weights within the neighboring community, $\Sigma_{tot}$ is the sum of all edge weights incident to nodes in the neighboring community, and $d_{i,in}$ is the sum of the weights of edges between node $i$ and nodes in the neighboring community, and $m$ is the sum of the edge weights of the entire network. For each node $i$, this change in modularity is computed for each community neighboring $i$, and $i$ is then assigned the community label that corresponds with the largest change. If no positive change in modularity is possible, then $i$ does not change its community label.

In the next phase, the algorithm generates a new network. Each community is condensed into a single node, and edges between two (possibly non-distinct) communities are
condensed into a single edge with weight equal to the sum of the corresponding between-community edge weights. In particular, self-loops in the new network may be formed if the corresponding community in the previous network has more than one node.

These two phases are repeated iteratively until no local improvement in the modularity is possible. The Louvain algorithm examines fewer mergers (only adjacent ones) compared to CNM, and hence, the time complexity is reduced—it appears to run in approximately $O(n \log n)$.

2.3 Preprocessing the graph by analyzing cyclic topologies

The quality of community detection may be improved by adding a pre-process step to weight the graph. We briefly go over some proposed weighting schemes in the literature.

Inspired by message propagation, [De Meo et al. (2013)] introduce a method called weighted edge random walk-K path (WERW-Kpath) that runs a $k$-hop random walk and weights edges on the walk based on their ability in passing a message. WERW-Kpath works as follows: Given a graph $G = (V, E)$, WERW-Kpath initially assigns to each edge $e \in E$ a weight $w_e = 1$. runs many random walks from a randomly chosen source node based on the node degree. They suggested $n \log n$ number of iteration for the algorithm. WERW-Kpath runs many biased random walks from a randomly chosen source node based on the node degree. The walk length is $\leq k$ and algorithm weights the edges based on their appearance on the walks, which are biased toward edges that already have been seen in the previous walks. We will discuss this method more in Results section. Moreover, [Lai et al. (2010)] suggest using random walk to explore local structures of communities. An edge $\{u, v\}$ gets a higher weight if the nodes $u$ and $v$ are more cosine similar. They suggested Random walk of $\log(n)$.

The idea of using cyclic structure to identify communities relays on the known fact that flows tend to stay intra-communities. For example, [Klymko et al. (2014)] focused on using the smallest cycles–triangles–to improve community detection in directed networks by weighting the edges based on 3-cycle cut ratio. Furthermore, [Radicchi et al. (2004)] incorporate the importance of triangles using edge clustering coefficient. This method is similar to [Newman and Girvan (2004)] in which at each iteration the edge with the smallest clustering coefficient is removed. The complexity of this algorithm is in $O(m^4/n^2)$ and $O(n^2)$ on a sparse graph. This algorithm performs poorly in graphs with few short cycles. [Castellano et al. (2004)] modified the edge clustering coefficient for the weighted networks, in which number of cycles is multiplied by the edge weight. Also, [Zhang et al. (2008)] extended this to bipartite graphs with even number of cycles. Moreover, [Vragovic]
and Louis (2006) introduced node loop centrality measure such that communities are build around nodes with high centrality in graph cycles. This algorithm has time complexity of $O(nm)$. Therefore, we want to take into account the cycles as a measure for group quality and thus find communities by maximizing their richness of cycles. In next sections, we explain a notion called modulus that enables us to analytically quantify richness of loops and edge participation in them. Then motivated by these concepts, we introduce a stochastic approach that is able to handle large graphs efficiently.

The weighting step is readily applied before the community detection, for example the update step of CNM in (6) is changed as following for weighted adjacency matrix $A^\rho$

$$
\Delta Q^\rho = \begin{cases} 
\frac{1}{\rho^T \mathbf{1}} - \frac{2d_i^\rho d_j^\rho}{(2\rho^T \mathbf{1})^2} & \text{if } A_{ij}^\rho \neq 0 \\
0 & \text{otherwise}
\end{cases} 
$$

where $k_i^\rho = \sum_j \rho_{ij}$ is the new weighted degree.

### 3 Loop Modulus

As discussed previously, cycles are more prevalent within communities than across communities. Hence, community detection algorithms may be improved by finding edge weights that quantify the local “richness” of the cyclic structure. Shakeri et al. (2017) provide a novel method for finding these weights called loop modulus (LM). Here, we briefly recall the basic concepts.

Let $\mathcal{P}(C_G)$ denote the family of all probability mass functions (pmfs) on $C_G$. Loop modulus minimizes the expected overlap of two random cycles over the set of all possible pmf’s $\mu \in \mathcal{P}(C_G)$.

More precisely, we construct a $(|C_G| \times m)$ matrix $\mathcal{N}$ where entry $N(c, e)$ indicates whether cycle $c \in C_G$ contains $e \in E$:

$$
\mathcal{N}(c, e) := \begin{cases} 
1, & e \in c, \\
0, & \text{otherwise}.
\end{cases} 
$$

Given two cycles $c_1$ and $c_2$, the overlap is the number of shared edges between them. We write this in matrix notation using the $(|C_G| \times |C_G|)$ overlap matrix $\mathcal{C}$ with entries:

$$
\mathcal{C}(c_1, c_2) := \sum_{e \in E} \mathcal{N}(c_1, e)\mathcal{N}(c_2, e) = |c_1 \cap c_2|.
$$
With this notation, given a pmf $\mu \in \mathcal{P}(C)$, the expected overlap of two independent random cycles with distribution $\mu$ is given by

$$E_{\mu}|c_1 \cap c_2| = \sum_{e \in E} \sum_{c_1, c_2 \in C} \mu(c_1) \mu(c_2) N(c_1, e) N(c_2, e) = \mu^T N N^T \mu = \mu^T C \mu,$$

where the underlined $\underline{c}$ denotes a random variable.

The minimum expected cycle overlap (MECO) problem is the following optimization:

$$\begin{align*}
\text{minimize} & \quad E_{\mu}|c_1 \cap c_2| \\
\text{subject to} & \quad \mu \in \mathcal{P}(C).
\end{align*}$$

Although an optimal pmf $\mu^*$ for (11) is always guaranteed, it is in general not unique and computationally not easy to obtain precisely. However, [Albin and Poggi-Corradini 2016] have shown that (11) can be reformulated as a modulus problem and thus approximately optimal pmfs can be generated using a simple algorithm that we will describe below.

First, note that given a pmf $\mu \in \mathcal{P}(C)$, every edge $e \in E$ acquires an edge-usage probability

$$\eta(e) := \mathbb{P}_\mu(e \in \underline{c}) = \sum_{c \in C} \mu(c) N(c, e) = (N^T \mu)(e),$$

namely, the probability that an edge $e$ belongs to a random cycle with law $\mu$. In particular, the expected overlap given $\mu$ can be rewritten as an energy (2-norm) of the vector $\eta$:

$$E_{\mu}|c_1 \cap c_2| = \mu^T N N^T \mu = \eta^T \eta = \|\eta\|_2^2.$$

Then (11) can be rewritten as

$$\begin{align*}
\text{minimize} & \quad \eta^T \eta \\
\text{subject to} & \quad \eta = N^T \mu, \quad \mu \in \mathcal{P}(C),
\end{align*}$$

and this is shown in [Albin and Poggi-Corradini 2016] to be related to the dual problem of the following convex optimization problem known as Loop Modulus.

$$\begin{align*}
\text{minimize} & \quad \rho^T \rho \\
\text{subject to} & \quad \rho \geq 0, \quad N \rho \geq 1.
\end{align*}$$
Here, \( \rho \in \mathbb{R}^E \) is thought as a cost function for using an edge and \( \mathcal{N}\rho \geq 1 \) means that every cycle \( c \in C \) gives rise to a constraint on \( \rho \), namely, the total cost paid by \( c \)

\[
\ell_\rho(c) := \sum_{e \in E} \mathcal{N}(c,e) \rho(e)
\]

should be at least 1 dollar.

We write \( \text{Mod}_2(C) \) to denote the optimal value in (13) and recall that, since this is a quadratic minimization, there always is a unique optimal density \( \rho^* \). The theory of convex duality gives rise to a relation between \( \rho^* \) for (13) and the unique optimal vector of edge-probabilities \( \eta^* \) for (12). Namely,

\[
\eta^*(e) = \frac{\rho^*(e)}{\text{Mod}_2(C)} = \mathbb{P}_{\mu^*}(e \in \xi),
\]

for any optimal pmf \( \mu^* \) for (11).

In the pre-processing step using loop modulus, see Figure 1(b), We use \( \eta^* \) to weight the edges in the graph. The idea is that \( \eta(e) \) is larger if edge \( e \) is likely to belong to many cycles in the support of optimal measures.

**Remark 3.1.** The optimal measures \( \mu^* \) are normalized optimal Lagrange multipliers for (13). In particular, by complementary slackness, if a loop \( \gamma \) is in the support of some optimal measure \( \mu^* \), then the \( \rho^* \)-length, \( \ell_{\rho^*}(\gamma) \), is 1.

We now describe a simple modulus algorithm. Modulus has nice monotonicity properties. In particular, given two families of loops \( C_1, C_2 \),

\[
C_1 \subset C_2 \implies \text{Mod}_2(C_1) \leq \text{Mod}_2(C_2).
\]

With this in mind, one way to compute modulus is to start with an empty family of loops \( C' \) and a density \( \rho' \equiv 0 \). At every pass, we then find a loop \( c \in C \) that violates the constraint \( \ell_{\rho'}(c) \geq 1 \) and add it to the growing family \( C' \). Finally, we compute optimal \( \rho^* \), \( \eta^* \), and \( \mu^* \) for problems (13), (12), and (11) (respectively), for the smaller family \( C' \). This algorithm was shown to converge in [Albin et al., 2017] and in practice when the algorithm stops the family \( C' \) is of size \( O(|E|) \). Algorithm 1 provides a version of this basic algorithm where at each iteration one looks for the most violated constraint, i.e., one looks for the lightest cycle given the edge-weights \( \rho' \). See [Shakeri et al., 2017] for details.

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### Algorithm 1
Basic algorithm for approximating densities for $\text{Mod}_2(C)$ with tolerance $0 < \epsilon_{\text{tol}} < 1$.

1: \( \rho' \leftarrow 0; \rho_0 \leftarrow 1 \)
2: \( C' \leftarrow \text{ShortestLoop}(\rho_0) \)
3: while \( \exists c \in C \) such that \( \ell_{\rho'}(c) \leq 1 - \epsilon_{\text{tol}} \) do
4: \( C'' \leftarrow C' \cup \{c\} \)
5: \( \rho' \leftarrow \text{argmin}\{\rho^T \rho : N \rho \geq 1\} \)
6: end while

### 4 Renewal non-backtracking random walk (RNBRW)

We can obtain the expected usage of each edge in important loops by minimizing the overlap in \[11\]. However, available methods for finding this usage are not yet able to be scaled up to moderate size networks. Therefore, we propose a different approach that can be scaled for large networks using a variant of random walk called non-backtracking random walk that closely follows a similar concept as modulus.

A non-backtracking random walk (NBRW) starting from node \( v_0 \) with length \( k \) is a sequence of vertices that uniformly drawn from the following set

\[
W = \{(v_0, v_1, \cdots, v_k) : v_i \in V, v_i, v_{i+1} \in E, v_{i-1} \neq v_{i+1}\}
\]  

There are numerous advantages for NBRW; Alon et al. (2007) showed that NBRW explores the graph more efficiently and also mixes faster, reaches the stationary distribution faster, than simple random walk with the cost of losing Markov property on the steps. However, by replacing each edge \( uv \) in \( E \) with two directed edges \( \vec{uv} \) and \( \vec{vu} \), we can translate NBRW on nodes to directed edges while having Markov chain properties—we denote the set of directed edges with \( \vec{E} \). Therefore, we can derive the transition probability (Kempton, 2016)

\[
\text{Pr}(\vec{u}v, \vec{i}j) = \begin{cases} 
\frac{1}{d_i - 1} & \text{if } v = i \text{ and } j \neq u \\
0 & \text{otherwise} 
\end{cases} \tag{16}
\]

where \( d_i - 1 \) is the out-degree of node \( i \).

In previous works such as De Meo et al. (2013), the notion of simple random walk has been used to quantify the idea of information passing and to identify nodes or edges that are more capable of passing information. Both random walk and NBRW behave similarly in the long run and their stationary distribution depends only on the degree of nodes.
To reduce this dependability, we rather keep the walk length $k$ small by stopping the NBRW.

**Definition 4.1 (Retracing edge).** When a NBRW meets one of the previously visited node $v_k$, the last hopped edge $v_{k-1}v_k$ is the retracing edge.

Therefore, we stop the walk once it meets the previously traversed nodes; this leads to produce a simple loop. For example, in Figure 1(a), we illustrate a NBRW that retraced itself and the *retraced edge* (shown by dotted edge) is particularly important for our subsequent analysis. Note that, if the NBRW reaches a node with degree 1, we discard the walk.

**Definition 4.2 (Renewal non-backtracking random walk (RNBRW)).** A renewal non-backtracking random walk (RNBRW) is a NBRW that terminates and renew the walk by visiting a retracing edge.

Retracing edges should be part of loops that overlap with lots of other loops. In other words they are more important in the community structures in the graph. Therefore, to quantify the importance of edges in this regard, we look at the number of appearances of each edge as a retracing edge for a NBRW. For undirected graphs, each ordering of the edge will be counted.

### 4.1 Example

For the house graph presented in Figure 1(b), given an edge, we first compute the probability of its participation in important loops using the modulus algorithm and (14). Subsequently, we also compute the proportion of appearances of the same edge as a retracing edge in the NBRW process. As we can see, the values are closely related but not identical. The differences arise from the fact that modulus only considers loops that are active constraints in (13). In fact, both $[c,d,e,c]$ and $[a,b,c,d,a]$ in this example have $\rho$-length equal to 1 (for the optimal $\rho$), while the longer loop $[a,b,c,e,d,a]$ has $\rho$-length strictly greater than 1, hence is never included in the support of optimal measures $\mu$ for (11) (see Remark 3.1). However, a fairly large number of NBRW’s may traverse any given loop. Furthermore, different edge retracing values of $\{b,c\}$, $\{a,d\}$ with $\{a,b\}$ are because more NBRW, e.g., one starting from either $(a,d)$ or $(e,c)$, can be retraced in $(a,d)$ and $(b,c)$.

Therefore, modulus and RNBRW are conceptually close with the difference that modulus is trying to minimize the variance of the edge probabilities arising from families of random cycles, while the RNBRW values arise from a specific family of random cycles.
Figure 1: (a) A schematic of a non-backtracking random walk. Dotted edge represents the retraced ordered edge. (b) House graph with weights $w_1$, $w_2$, where $w_1 = P_{\gamma \sim \mu^*}$ (edge $\in \gamma$) and $w_2$ is normalized retracing values on the edges.

4.2 Algorithm for RNBRW

We use Monte carlo method that builds on repeated random sampling to find the probability of retracing of edges. Each run of the algorithm runs a NBRW and returns the retracing edge (if any) as the sample of retracing edge. The number of times each edge has been retraced by a NBRW corresponds to its probability of retracing with some constant coefficient. The algorithm only requires the graph data and each run is independent of the other. Therefore, we can collect samples in parallel leading to fast convergence. Each run of the algorithm constitutes the following steps:

1. Choosing a random edge $v_0v_1$ in $\tilde{E}$.

2. Form the walk $w = [v_0, v_1]$.

3. (For $k = \{1, \cdots \}$) The walker continues her walk from $v_k$ to a neighboring node $v_{k+1} \neq v_{k-1}$.

4. If $v_{k+1}$ is already in $w$, return $v_kv_{k+1}$ as the retracing edge. Otherwise add $v_{k+1}$ to $w$ and go to Step 3 with incrementing $k = k + 1$. 

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Algorithm 2 Algorithm for RNBRW from a random directed edge $\vec{uv}$.

1: $walk \leftarrow \text{empty set}$
2: add $u,v$ to $walk$
3: while True do
4: $nexts \leftarrow \text{neighbors of } v$
5: remove $u$ from $nexts$
6: if $nexts$ is empty break
7: $next \leftarrow \text{choose a node from } nexts$ randomly
8: if $next \in walk$ then
9: return $(v,next)$ as the retracing edge
10: end if
11: add $next$ to $walk$
12: $u \leftarrow v$
13: $v \leftarrow next$
14: end while

In the Algorithm 2, we present the pseudo-code for NBRW and the retracing edge (if any). By employing a swarm of walkers and picking up their obtained retracing edges, we count the number edge appearances as its retracing value.

We can utilize Algorithm 4.2 by sending a swarm of walkers independently from each other and starting from a randomly chosen edge and collect the returned retraced edges at the end. Therefore, one can execute this process as array jobs on cluster of computers efficiently.

5 Results

We primarily investigate the performance of two community detection methods Louvain and CNM with and without the proposed weighting methods. Moreover, we compare the performance of Louvain and CNM community detection algorithms, both preprocessed and unweighted, with other popular techniques that follow different paradigms such as Info map [Rosvall and Bergstrom, 2007], Label propagation [Raghavan et al., 2007], Edge betweenness [Girvan and Newman, 2002], Spin glass [Reichardt and Bornholdt, 2006], and Walk trap [Pons and Latapy, 2005].

To show the effectiveness of the algorithms, we apply them on LFR benchmarks [Lanci-
Figure 2: Performance analysis on LFR benchmark networks with $n = 500$, average degree 7, and community sizes ranging from 30 to 70. The mixing rate $\mu$ adjusts the ratio of within-communities links over all links. (a) The plot depicts the normalized mutual information for community memberships found by Clauset Newman Moore with the improved performances by weighting by Loop modulus and RNBRW. (b) The plot depicts the normalized mutual information for community memberships found by Louvain method with the improved performances by weighting by Loop modulus and RNBRW.

[2008] and measure their similarity to the ground truth data using normalized mutual information (NMI) [2005].

5.1 Comparison of Loop modulus and RNBRW

Both modulus and RNBRW are following similar principles and the resultant edge weights are based on their participation in cyclic topologies in the network. Therefore, we expect similar improvement on community detection methods using both methods. We illustrate this in Figure 2 where we show the improvements on community detection for standard LFR benchmark networks. We plot the mutual information for both the derived membership from the algorithm on each network and the weighted version, compared to the ground truth from LFR. One of our surprising result is that weighted CNM is as good as weighted Louvain.
Figure 3: Performance of Louvain equipped by RNBRW weighting is compared with Infomap \cite{Rosvall2007}, Label propagation \cite{Raghavan2007}, Edge betweenness \cite{Girvan2002}, Spinglass \cite{Reichardt2006}, and Walktrap \cite{Pons2005} algorithms. The LFR benchmark networks have 500 nodes with average degree 7, and community sizes ranging from 30 to 70. The mixing rate $\mu$, for adjusting ratio of intra-communities links over all links are 0.1, 0.2, and 0.3.

5.2 Performance of weighted algorithm compared to the other algorithms

For the rest of the paper, we focus on weighting by RNBRW, because it scales better with graph size compared to modulus and they show similar performance behavior. For example, we compare five popular algorithms with the Louvain method \cite{Blondel2008} equipped with the pre-processing RNBRW step. These algorithms are introduced in Section 5 and listed as Infomap, Label propagation, Edge betweenness, Spinglass, and Walktrap. In Figure 3(b)-(f), the same benchmarks are used as in Figure 2. As shown, the weighted Louvain method performs better community detection compared to other algorithm.
Figure 4: (a) Performance of community detection with increasing the number of walkers in both CNM and Louvain using RNBRW weighting for LFR networks with \( n = 10,000 \) and average degrees 9 and 27. (b) Weighting of Erdős-Rényi graphs with \( n \) and \( p = 2 \log n/n \) using WERW-Kpath (cannot be paralleled) and RNBRW (with 2 and 5 cores).

5.3 Sufficient number of walkers

Since each iteration of RNBRW is independent of others, this facilitates efficient parallel implementations. For instance, an advantage of RNBRW is that its computation is significantly less expensive than WEW-Kpath (see Section 2.3). Since we can use Algorithm 2 in a simple parallel fashion mapping each random walk to cores in a computer cluster, we can easily scale the algorithm for large networks.

In Figure 4b, we illustrate the time spent to weight Erdős-Rényi random networks with \( n \) and \( p = 2 \log n/n \) with WERW-Kpath and RNBRW. We first employ two cores for RNBRW and then 5 cores to show the improvements of performance with the increase of resources.

Furthermore, Figure 4a illustrates another interesting aspect about the efficiency of our algorithm. Namely, we obtain a satisfactory detection quality after only a number \( m \) (size of the edge-set) of walkers.\(^1\)

\(^1\)Our implementation is in Python 2.7 running on Linux Redhat with AMD processors each with 2799.9 MHz cpu and 2Mb cash.
5.4 Challenges with average degree and community size

Zhao et al. (2012) showed consistent detection of communities if the average degree grows at least logarithmically with network size. We test the performance of CNM and Louvain algorithms with and without preprocessing and evaluate how they perform for networks with low average degree.

Another problem that arises with modularity maximization methods is their resolution limit in detecting small communities. This is a critical shortcoming since small size communities are common in large social networks and their size are not necessarily growing with graph size. Fortunato and Barthélemy (2007) addresses this issue and explain that communities with number of internal edges less than $\sqrt{2|E|}$ are most likely mis-detected. This leads to, a resolution limit that holds back heuristics for maximizing the likelihood for stochastic block models and also modularity maximizations Fortunato and Barthélemy (2007). Analyzing the network with the proposed stopped random walk allows to reduce the effect of this problem significantly.

In the following, we test the methods and see how they withstand the challenges of low average degree and existence of small communities for LFR benchmarks, with power law distribution of community size distributions and degree. The community sizes are varying between an upper and a lower bound that falls below the resolution limit and the average degree is changing for different size graphs.

We compare the improvements of CNM algorithm with both preprocessing methods: RNBRW and WERW-Kpath in Figure 5. We observe that with varying average degree of the network, WERW-Kpath fails to improve the detection consistently. Also, with increasing $\mu$ to a high mixing ratio of 0.4, WERW-Kpath is unable to improve CNM anymore while RNBRW consistently improves the performance of CNM in all range of $\mu$ and average degrees.

We repeat our experiments for larger benchmarks and test the same question for a constant mixing rate $\mu = 0.3$ and different average degree in terms of log $n$ with network sizes 500, 10,000, 100,000 and 1,000,000 nodes and the same improvements in Figure 6 confirm the efficacy of our method.

We summarize the simulations for sparse LFR benchmarks in Table 1 with different sizes and illustrate the utility of our proposed preprocessing methods compared to other algorithms (Edge betweenness algorithm is not included due to its cubic time complexity which is prohibitive for large networks in our Python implementations).

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1 We use Beocat for the large networks. Beocat is a computer cluster located in Kansas State University https://support.beocat.ksu.edu/BeocatDocs/index.php/Main_Page

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Figure 5: Performance analysis of weighting methods on LFR benchmark networks with varying average degree. Comparing the performance of weighting RNBRW with the raw algorithm (no weighting) and weighting WERW-Kpath with the raw algorithm (no weighting).

Table 1: Performance of algorithms for sparse LFR networks with $\mu = 0.3$ and average degree $\approx \log n$.

| network size | average degree | Infomap  | LP  | WT   | CNM   | Louvain | RNBRW+CNM | RNBRW+Louvain |
|--------------|----------------|----------|-----|------|-------|---------|-----------|---------------|
| 10,000       | $\log n$       | 0.912    | 0.992| 0.763| 0.263 | 0.740   | 0.974     | 0.970         |
|              | $2\log n$      | 1        | 0.995| 1    | 0.276 | 0.757   | 1         | 1             |
|              | $3\log n$      | 1        | 1    | 1    | 0.232 | 0.882   | 1         | 1             |
| 100,000      | $\log n$       | 0.73     | **0.988** | 0.644 | 0.154 | 0.524   | 0.975     | 0.960         |
|              | $2\log n$      | 1        | 1    | 1    | 0.159 | 0.649   | 1         | 1             |
|              | $3\log n$      | 1        | 1    | 1    | 0.118 | 0.713   | 1         | 1             |
| 1,000,000    | $\log n$       | 0.994    | 0.998| —    | 0.050 | 0.192   | **0.989** | **0.969**     |
Figure 6: Substantial performance boosting in both CNM and Louvain using RNBRW weighting with increasing graph size simultaneously with sparsity. (left) LFR networks with $n = 10,000$ nodes with average degree in x-axis. (right) LFR networks with $n = 100,000$ nodes with average degree in x-axis.
The time complexity of LP, WT, and CNM algorithms compared to Louvain is larger by a \( \geq n \) factor—Infomap \( O(n^2) \), Label propagation \( O(n^2) \), Spinglass \( O(n^{3.2}) \) for sparse networks, and walktrap \( O(n^2 \log n) \). Therefore adding a very fast preprocessing step by RNBRW to Louvain seems very reasonable while the performance is often as good as best algorithms out there.

6 Conclusion

Communities can be identified by the “richness” of cycles; more short cycles occur within a community than across communities. Hence, existing community detection algorithms may be enhanced by incorporating information about the cyclic structure of the graph. We investigate how two quantitative measures for the cyclic structure—loop modulus (LM) and renewal non-backtracking random walks (RNBRW)—can improve popular community detection algorithms. LM minimizes the overlap of all cycles using the optimal allocation of edge usage across them. These usages represent the role of edges in the cyclic structures. RNBRW quantifies edge importance as the likelihood of an edge completing a cycle in a non-backtracking random walk, providing a scalable alternative to LM. We show that weighting the graph with LM and RNBRW can substantially improve the detection of ground-truth communities even in the sparse networks. Furthermore, these preprocessing steps can overcome the problem of resolution limit in modularity maximization methods. Finally, in the case of large, sparse, networks, RNBRW has been shown to be quite effective; RNBRW can improve the efficacy of available community detection algorithms without sacrificing their computational efficiency.

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