Community Detection Using Slow Mixing Markov Models

Ramezan Paravi Torghabeh Member, IEEE, and Narayana Prasad Santhanam Member, IEEE

Abstract

The task of community detection in a graph formalizes the intuitive task of grouping together subsets of vertices such that vertices within clusters are connected tighter than those in disparate clusters. This paper approaches community detection in graphs by constructing Markov random walks on the graphs. The mixing properties of the random walk are then used to identify communities. We use coupling from the past as an algorithmic primitive to translate the mixing properties of the walk into revealing the community structure of the graph. We analyze the performance of our algorithms on specific graph structures, including the stochastic block models (SBM) and LFR random graphs.

Index Terms

Random Walk, Slow Mixing Markov Processes, Graph Partitioning, Community Detection, Correlation Clustering, Coupling From the Past.

I. INTRODUCTION

Applications in biology [1]–[3], social sciences [4] and recommendation systems [5], [6] can be abstracted into community detection problems, where one attempts to find subsets of nodes that share common properties [7]. Typically, one constructs a graph with vertices corresponding to the objects to be organized together, while the graph edges represent connections between them. In the simplest setting for the community detection problem, one would partition the vertices into clusters that are strongly connected within themselves, while the cross-cluster connections are weak. One could consider more nuanced extensions as well, where vertices could belong to multiple clusters, or where edges may be weighted.

To evaluate community detection algorithms, several variants of random graph models play an important role in generating test graphs that capture properties of real networks [8]–[10] in some way. One widely used model is the Stochastic Block Models (SBM). In this case, information theoretic limits for exact and partial recovery has been addressed as well in [11]–[14]. For community detection in SBMs, the approaches that have been widely considered are the maximum likelihood approach, semidefinite programming and belief propagation methods [15]–[17].

Many approaches for community detection implicitly require that the true number of clusters be known a-priori. An alternate approach is taken in Correlation Clustering where an objective function is designed so optimizing the objective function cost will automatically capture the underlying partition [18]. The correlation clustering problem is often formalized as an integer linear program. In [19], a randomized expected 3-approximation algorithm for correlation clustering was provided.

In biological networks, one of the core algorithms used traces back to [2], [20] and is based on what is called centrality indices. The idea is to remove cross-cluster edges–if there are a few tight communities connected sparsely by inter-cluster edges, most cross-community shortest paths will go through the cross-cluster edges. The algorithm formalizes this insight and removes what it thinks are cross-cluster edges, leaving behind the communities.

The authors are with the Department of Electrical Engineering, University of Hawai‘i, Mānoa (Email: {paravi, nsanthan}@hawaii.edu).
The closest other line of work to our approach is spectral clustering [21]–[24]. This method uses a given pairwise similarity between nodes in a network to assign weights to the edges, and uses the eigenvectors of the (symmetric, normalized) graph Laplacian to assign nodes to clusters. For two clusters, the Fiedler eigenvector can be partitioned around the median to yield clusters and for more than two clusters, similar extensions can be used involving \( k \) eigenvectors. While the implementation is simple, a couple of drawbacks need to be addressed—the pairwise similarity is often not automatically given in community detection problems, the Laplacian could be ill conditioned and the number of clusters need to be known in advance, see e.g., [25], [26].

**Markov Processes**

Let \( p \) be an irreducible and aperiodic first-order Markov process \( \{Y_i\}_{i=-\infty}^{\infty} \) taking values in a finite alphabet \( S \) with \( |S| = r \). Let \( Q = [p(s|s')] \) with \( s, s' \in S \) denote the transition probability matrix of the process. Here, \( p(s|s') \triangleq p(Y_1 = s|Y_0 = s') \) denotes the transition probability from \( s' \) to \( s \). Furthermore, let \( \pi \) denote the unique stationary distribution of \( p \), the unique solution of \( \pi Q = \pi \). Namely, \( \pi \) is the unique solution to

\[
\pi(s) = \sum_{s' \in S} \pi(s') p(s|s'),
\]

for all \( s \in S \). Clearly \( p(Y_1 = s) = \pi(s) \).

**Core idea**

Empirical properties of finite sized samples from Markov processes need not reflect stationary properties—e.g., the number of occurrences of a string \( w \) in a finite sized sample from a Markov process \( p \) need to yield a good estimate of \( p(w) \). Roughly speaking, when the empirics of the sample eventually reflect the stationary properties, we say that the process has mixed. The core idea in this paper revolves around interpretation of the random walk before mixing has occurred. Naturally then, to build clustering and community detection algorithms on graphs, we build Markov random walks such that the restriction of the random walk to within any one cluster mixes much faster than the overall walk itself. Once we obtain a walk like that, a careful interpretation of samples from the random walk along the lines of the theorems we obtain in [27] should reveal the community structure of the graph.

**II. Community Detection Using Slow Mixing Markov Processes**

In order to identify communities in the graph, we define random walk on the graph, such that the mixing properties of the walk reveal the clusters. To do so, we use Coupling From The Past (CFTP) [28] to sample appropriately from the constructed random walk. CFTP was devised by Prop and Wilson and allows to obtain samples distributed according to the exact stationary distribution of a Markov process. In CFTP, the idea is to simulate different copies of a given Markov chain, each starting from a different initial state, but in a way that is often described as “backwards” in time—details will be outlined in Section II-B. While each chain is marginally faithful to the same Markov law, different copies are not independent from each other. Rather, the joint evolution is set up so that chains coalesce—once chains hit the same state at the same time, their future evolution is identical. When all copies of the chain coalesce at time 0, the obtained sample is distributed perfectly according to stationary distribution.

Rather than sampling from the stationary distribution, we adapt the CFTP approach to identify clusters before the chains coalesce. To achieve this, we will identify subsets of state space which coalesce together faster. In following section, we introduce the notion of restriction of a Markov process to a subset \( G \subseteq S \) which will be translated into algorithmic rules for community detection in graphs.
A. Restriction of a Markov Process to G

Let \(G\) be an arbitrary nonempty subset of the state space \(S\) of the Markov process \(p\) with \(|G| = r'\). Let \(\{\tilde{Y}_j\} = \{\cdots, \tilde{Y}_{-1}, \tilde{Y}_0, \tilde{Y}_1, \cdots\}\) be the restriction of \(p\) to \(G\). Note that \(\tilde{Y}_j \in G\), for all \(j\). We will refer to restricted process \(\tilde{p}\). By the strong Markov property, \(\tilde{p}\) is also a Markov process over \(G\). Furthermore, if \(\tilde{p}\) is aperiodic, then it has a stationary distribution which will be denoted by \(\tilde{\pi}\). Let \(\pi(G)\) denote the stationary distribution of \(G\), i.e.

\[
\pi(G) = \sum_{w \in G} \pi(w).
\]

The transition probability matrix of the process, \(Q\), can be written as

\[
Q = \begin{pmatrix} Q_{GG} & Q_{GB} \\ Q_{BG} & Q_{BB} \end{pmatrix},
\]

(2)

where \(B = S \setminus G\). Note that \(Q_{GG}\) and \(Q_{BB}\) are square matrices of size \(r' \times r'\) and \((r - r') \times (r - r')\), respectively.

Before proceeding further, we prove following useful lemma.

**Lemma 1.** Let \(A\) be an \(m \times m\) matrix with \(\max_{1 \leq i \leq m} |\lambda_i| < 1\) where \(\lambda_i\)'s are the eigenvalues of \(A\). Then,

\[
(I - A)^{-1} = I + A + A^2 + A^3 + \cdots
\]

**Proof** The condition \(\max_{1 \leq i \leq m} |\lambda_i| < 1\) insures that the infinite series \(I + A + A^2 + A^3 + \cdots\) is convergent. The equality follows by direct multiplication. \(\square\)

**Theorem 2.** The transition probability matrix of the Markov process \(\tilde{p}\) is given by

\[
\tilde{Q} = Q_{GG} + Q_{GB}(I - Q_{BB})^{-1}Q_{BG},
\]

(3)

where \(I\) is the identity matrix with size \(r - r'\). Furthermore, \(\tilde{p}\) has a unique stationary distribution \(\tilde{\pi}\) given by

\[
\tilde{\pi}(w) = \frac{\pi(w)}{\pi(G)},
\]

(4)

for all \(w \in G\). \(\square\)

B. Partial CFTP

In this section, we first briefly review CFTP algorithm and then introduce the notion of partial coupling which is the core idea to identify clusters in our proposed community detection algorithm. Recall that \(S\) is the state space of the Markov process \(p\) with \(|S| = r\). In CFTP algorithm, we run coupled copies of \(p\), a different copy from every state in \(S\). We use Dobrushin coupling [29] to couple the different chains.

To run the CFTP for 1 step, we start all coupled copies from time \(-1\), and run them for one step. To run it for the second step, we start coupled copies of the Markov process from every state in \(S\) at time \(-2\), and run the chains for one step. Now we reuse the evolution from step \(-1\) to 0. See [28] for why we choose this peculiar way of running the chains backward in time.

We represent the samples of \(p\) starting from time \(-n\) with state \(s\) by \(\{Y_{-i}^{(s,-n)}\}\) where superscript \(s\) denotes the initial state. Note \(Y_{-n}^{(s,-n)} = s\).

**Definition 1.** We say that the CFTP algorithm has coalesced in the regular sense in \(n\) steps if \(n\) is the smallest number such that for all \(s, s' \in S\)

\[
Y_0^{(s,-n)} = Y_0^{(s',-n)}.
\]
Let $Y_0$ denote the element that all chains have coalesced to, namely $Y_0 = Y_0^{(s-n)}$, $s \in S$. Note also that the definition does not imply that time 0 is the point at which the chains $Y_0^{(s-n)}$ first coalesce.

We will refer to $Y_0$ in Definition 1 as the output of CFTP algorithm.

**Theorem 3.** [From [28]] Let $Y_0$ be the output of the CFTP algorithm. Then, for all $s \in S$
\[
\mathbb{P}(Y_0 = s) = \pi(s),
\]
where $\mathbb{P}$ and $\pi$ denote the coupling distribution and the stationary distribution of $p$, respectively.

**Definition 2.** We say that the CFTP algorithm at time $-n$ is partially coalesced with respect to $G$ if $-n$ is the smallest time index such that for all $w, w' \in G$
\[
Y_0^{(w, -n)} = Y_0^{(w', -n)}, \text{ and } N_n^w = N_n^{w'}.
\]

Let $\tilde{Y}_0 = Y_0^{(w, -n)}$ for all $w \in G$. We refer to $\tilde{Y}_0$ as the output of the algorithm.

**Theorem 4.** Let $p$ be a Markov process over state space $S$ and let $G$ be an arbitrary nonempty subset of $S$. Assume that the CFTP algorithm at time $-n$ has partially coalesced w.r.t. $G$ with $\tilde{Y}_0 \in S$ as the output of the CFTP algorithm per Definition 2. Suppose we further continue the simulation of the chain (starting from cont), and let $j$ be the first time $Y_j \in G$ for some $j \geq 1$. Let $Y = Y_j$. Then, for all $w \in G$, we have
\[
\mathbb{P}(\tilde{Y} = w) = \frac{\pi(w)}{\pi(G)},
\]
where $\pi$ denotes the stationary distribution of $p$, respectively.

### C. Algorithm for Community Detection

The mixing properties of the process can be used to identify communities in the set of states of the process. To this end, we need to consider finding a partition $C = \{C_1, \cdots, C_m\}$ of the state space $S$ such that $C_i \subseteq S$, $C_i \neq \emptyset$ for all $i$ and $C_i \cap C_j = \emptyset$ for $i \neq j$ with $\bigcup_{i=1}^m C_i = S$. We will refer to individual $C_i$ as a cluster.

Note that we can associate to every partition $C$, a cost function $J(C)$ depending on the application. For instance, in the context of random walks on graphs, one convenient choice can be cluster editing cost as we will discuss in section III-A. The other parameter is the number of clusters $m$. In our approach, in contrast to traditional methods such as $k$-means, $m$ need not to be known a-priori. In the Algorithm 1, the number of clusters will automatically be determined by the algorithm and its value depend on the cost function $J$ we consider. The algorithm is based on Theorem 4 which essentially describes how to identify a subset of states which have been partially coalesced. In essence, the algorithm identifies communities which have coalesced together during one sample run of CFTP algorithm.

**Description of the Algorithm:** We consider one run of the CFTP algorithm and our setup is the same as original CFTP. We emphasize that the chains are simulated backward in time and the the random variables used during execution are reused. Recall that $|S| = r$. Initially, we have a partition of state space which consists of all singletons, i.e., $C_0 = \{C_1, \cdots, C_r\}$ such that $C_i = \{s\}$ for some $s \in S$. As we proceed backward in time to obtain a sample
from stationary distribution, we will identify a set of critical times denoted by $T$, which are the times which some clusters have been coalesced.

**Definition 3.** During execution of CFTP algorithm, we say that a time index $n$ is a critical time if there exist at least two clusters $C_1$ and $C_2$ such that for all $w, w' \in C_1 \cup C_2$

$$Y_0^{(w,-n)} = Y_0^{(w',-n)} \text{ and } N_n^w = N_n^{w'},$$

where

$$N_n^w = \sum_{i=0}^{n-1} \mathbb{1}(Y_i^{(w,-n)} \in C_1 \cup C_2).$$

Note that above definition can naturally be extended to more than two clusters. As a consequence, we can identify clusters which have been merged in critical times. Observe that when all the chains coalesce, we have a single partition consisting of all states. In other terms, we start off with all-singleton partition up to the point where we have a single partition. However, during this process, at critical times, we can identify clusters which merge together to yield a coarser partition. We can compute the cost associated to the particular partition that the sampling process yields and find the optimal partition $C^*$ with respect to the cost function $J$.

In following pseudo-code, we represent all-singleton partition by $C_0$ and $CFlag$ denotes the coalescence flag. Here, we assume that we are minimizing a cost function $J$. A container $T$ is used to store the critical times.

**Algorithm 1** Detecting Communities in a Markov Process

**Input:** A Markov process $p$ over $S$.

**Output:** A partition $C^*$ of $S$.

**Initialize:** $k \leftarrow 1$, $C = C_0$, $C^* = C_0$, $T = [0]$, $CFlag = False$.

**while** $CFlag = False$ **do**

- Simulate $r$ copies of the chain starting at time $-k$.

- if $k$ is a critical time then

  - Update $C$ by merging clusters which are coalesced;
  - $T = T.Append\{k\}$;
  - if $J(C) \leq J(C^*)$ then

    - $C^* = C$;

  - end

- if All $r$ chains reach to some common state at time 0 then

  - $CFlag = True$;

- else

  - $k \leftarrow k + 1$

- end

**return** $C^*$

**Remark** We need to carefully define the Markov process depending on the application on hand to exploit mixing properties of the process for revealing the underlying community structure. Furthermore, the choice of cost function depends on how the Markov process is defined.

**Remark** Note that in general, the algorithm can stop at any critical time and still yields a partition (though perhaps not optimal). A criteria which empirically seems to be effective is to record the difference $\Delta T_i \triangleq T_i - T_{i-1}$
between consecutive critical times. If the difference exceeds a prescribed threshold, the algorithm will stop. As we discuss simulation results in next chapter, we will see that if the process is slow mixing, then the resulted clusters usually coincide with ground truth communities.

### III. Simulation Results

Our algorithm creates a random walk on the nodes of the graph. We start different, coupled random walks from different nodes. We then adapt the coupling from the past approach to to identify clusters before the chain mixes (rather than sample from the stationary distribution).

**Construction of Random Walk:** In order to use Algorithm 1 for graph partitioning problem, first we define a *non-uniform* random walk on the graph as follows:

Given an undirected graph $G = (V, E)$ and $v \in V$, let $\mathcal{N}(v)$ be the set of neighbors of $v$ in $G$. We assign a weight to every edge $e = (v, w) \in E(G)$ given by

$$w(e) \triangleq w(v, u) = f\left(|\mathcal{N}(v) \cap \mathcal{N}(u)|\right),$$

where $f(x) = x^r$ for some $r \in \mathbb{Z}^+$. Then, for all $u \in \mathcal{N}(v)$, the transition probability of the walk is given by

$$\mathbb{P}(u|v) = \frac{w(v, u)}{\sum_{u' \in \mathcal{N}(v)} w(v, u')}.$$  

The above scaling can be interpreted how different similar neighbor nodes vote on transition probabilities. A similar scaling method (with exponential function) was used in [23] for image segmentation applications. This reflects the fact that cross-cluster edges have smaller weight compare to in-cluster edges.

To evaluate the performance of the algorithm we considered random graph generative models including the (i) Stochastic Block Models (SBM), (ii) LFR models (random graphs with power law degree distribution having well defined community structure [30]), and (iii) real world networks with known community structure are used to test the algorithm. The number of communities is not known to our algorithm in advance, nor is any generative model we may have used. Where relevant, we used cluster edit distance (number of addition and deletion of edges needed to turn a graph into disjoint cliques) and compared the results with the state-of-the-art Correlation Clustering (CC-PIVOT) [19] algorithm.

#### A. Stochastic Block Model

Let $G(n, p, q, k)$ be the random graph model which will has following properties. Let $V = \{1, \cdots, n\} \triangleq [n]$ be the set of the nodes in $G$. Assume that there exists an underlying true partition $V = \bigcup_{i=1}^{k} V_i$ of the nodes such that $\sum_{i=1}^{k} |V_i| = n$. In this generative model, for all $w, v \in V$, if $v \in V_i$ and $w \in V_j$ for some $i \neq j$, then $w$ is connected to $v$ with probability $q$. If $v, w \in V_i$ for some $i$, then $w$ is connected to $v$ with probability $p$. All choices of edges are independent from each other and $E(G)$ denote the set of edges in the $G$.

For SBM random graphs $G(n, p, q, k)$, we tested the performance of algorithm by varying model parameters $n$, $p$ and $q$ and number of communities in the graph. Note that given a partition of graph a $G$, we can associate a cost to that partition. One convenient choice is the number of edge addition and deletion in order to turn the graph into disjoint clusters. This measure is known as *cluster editing cost* [31]. This is in the spirit of *correlation clustering* setting in which one tries to transform a given graph into disjoint cliques by using minimum number of edge deletion or edge addition [18].

In order to evaluate the quality of the recovered communities in the SBM, we first consider the average cluster editing cost. For random graphs with roughly equal size ground truth communities, we computed and compared
TABLE I: Comparison of average cost of our algorithm and CC-PIVOT on 10 samples taken uniformly at random from \(G(n, p, q)\). All cluster have the same size while the number of clusters in the graph varies.

| Cluster-Size | Num-Cluster | p    | q    | Our-Cost | CCPivot-Cost |
|--------------|-------------|------|------|----------|--------------|
| 5            | 60          | 0.95 | 0.05 | 3020.3   | 3572.3       |
| 5            | 60          | 0.95 | 0.2  | 9803.4   | 11992.4      |
| 5            | 60          | 0.8  | 0.1  | 5249.1   | 6518.6       |
| 10           | 30          | 0.95 | 0.05 | 3382.5   | 4243.4       |
| 10           | 30          | 0.95 | 0.2  | 10425.2  | 12725.3      |
| 10           | 30          | 0.8  | 0.1  | 5748.9   | 7023.4       |
| 20           | 15          | 0.85 | 0.05 | 4059.8   | 5030.6       |
| 20           | 15          | 0.8  | 0.1  | 6646     | 8119.2       |
| 20           | 30          | 0.9  | 0.05 | 13977.6  | 17569.8      |
| 20           | 30          | 0.9  | 0.2  | 41432    | 51590.5      |
| 20           | 30          | 0.8  | 0.2  | 41042.9  | 51225.3      |
| 20           | 30          | 0.7  | 0.2  | 40594    | 50628.8      |
| 30           | 20          | 0.8  | 0.1  | 24626.5  | 31612.9      |
| 30           | 10          | 0.9  | 0.05 | 22302.9  | 22466.3      |
| 60           | 10          | 0.9  | 0.1  | 29711.2  | 36251.1      |
| 60           | 10          | 0.8  | 0.2  | 47510.2  | 57262.2      |
| 60           | 10          | 0.7  | 0.1  | 28827.9  | 35849.5      |
| 60           | 10          | 0.7  | 0.2  | 47028    | 55923.3      |
| 75           | 8           | 0.9  | 0.1  | 33773.6  | 37830.4      |
| 75           | 8           | 0.9  | 0.2  | 51431.9  | 59086        |
| 75           | 8           | 0.8  | 0.1  | 32683.4  | 38469.7      |
| 75           | 8           | 0.8  | 0.2  | 49895.8  | 58606        |
| 75           | 8           | 0.7  | 0.1  | 31452.8  | 38101.2      |
| 75           | 8           | 0.7  | 0.2  | 48284.7  | 57460.1      |
| 100          | 6           | 0.9  | 0.1  | 38898.6  | 39732.2      |
| 100          | 6           | 0.9  | 0.2  | 55986.7  | 61159.9      |
| 100          | 6           | 0.8  | 0.1  | 37517.8  | 40637.8      |
| 100          | 6           | 0.8  | 0.2  | 53975.2  | 61695.5      |
| 100          | 6           | 0.7  | 0.1  | 35612.8  | 41015        |
| 100          | 6           | 0.7  | 0.2  | 51948.8  | 60161        |

The average cost of partitions obtained by our algorithm and CC-PIVOT. The simulation results are summarized in TABLE I. The result show that the partitions found by our method are usually have smaller cluster editing cost.

Remark The values of \(p\) and \(q\) are designed such that the resulting random graphs have well-knit clusters. Here, the emphasize is to only compare cluster editing cost obtained by our method with those obtained by CC-PIVOT.

The actual performance for recovering communities is depicted in Fig. 1 where matrix representation of the adjacency matrix of a realization of a SBM is used to visualize community structure. As it can be seen from the figure, almost all identities are recovered correctly.

B. LFR Random Graphs

Stochastic block models are not realistic in the sense that they usually have communities with approximately the same size and furthermore, all vertices have the same degree. In realistic networks, the degree distributions are usually skewed and size of communities varies. We consider another class of random graphs introduced in [30] which is known as LFR benchmark graphs. In these models, the distributions of both node degrees and number of communities admit power laws.

The construction is as follows: Let \(n\) be the number of nodes. First a sequence of community sizes distributed by power law with exponent \(\tau_1\) is generated. The degree of each node is distributed by power law with exponent \(\tau_2\). Each node within a community of size \(k\), shares a fraction \(1 - \mu\) of his corresponding edges with the members of his community and a fraction \(\mu\) of his edges with other communities. The connection of edges is done similar to Configuration Model in such a way that the degree sequence is maintained.
Fig. 1: (a) Matrix representation of a realization of an SBM with $n = 300$, $k = 5$, $p = 0.55$, $q = 0.07$. (b) Same graph with random relabeling of nodes which serves as is the input to the algorithm. (c) Communities recovered by our algorithm. (d) Communities recovered by CC-PIVOT algorithm.

Fig. 2 shows a realization of LFR graph with $n = 200$ nodes and 6 communities and parameters $\tau_1 = 2$, $\tau_2 = 3$ and $\mu = 0.25$ with average degree equals 30. The communities are showed with different colors in circular layout for convenience. As it can be seen, the CC-PIVOT tends to create lots of singletons compared to ours. Observe that in our algorithm if we wait and track the clusters up before coalescence happens, we actually can recover communities as depicted in Fig. 2 (d).

C. Real World Network

We tested the performance of the algorithm on a real world benchmark network of American football games between Division IA colleges during regular season Fall 2000 [2]. There are in total 115 teams and 615 edges in the graph. Every edge represents a game between corresponding end nodes. As depicted in Fig. 3, almost all nodes in the graph are assigned to their corresponding community correctly. The nodes with same color belong to the same cluster (note that the identity of nodes is not revealed to the algorithm).
Fig. 2: (a) An LFR random graph with 200 nodes and 6 communities. (b) Communities recovered by our algorithm. (c) Communities recovered by CC-PIVOT algorithm. (d) Communities recovered by our algorithm with fine tuning of algorithm parameters.
Fig. 3: (a) American Football College benchmark network with 115 nodes. (b) Communities recovered by our algorithm. (c) Communities recovered by CC-PIVOT algorithm.
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