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Robust and Computationally Feasible Community Detection in the Presence of Arbitrary Outlier Nodes

Abstract

Community detection, which aims to cluster NN nodes in a given graph into rr distinct groups based on the observed undirected edges, is an important problem in network data analysis. In this paper, the popular stochastic block model (SBM) is extended to the generalized stochastic block model (GSBM) that allows for adversarial outlier nodes, which are connected with the other nodes in the graph in an arbitrary way. Under this model, we introduce a procedure using convex optimization followed by k -means algorithm with $k=r$. Both theoretical and numerical properties of the method are analyzed. A theoretical guarantee is given for the procedure to accurately detect the communities with small misclassification rate under the setting where the number of clusters can grow with N . This theoretical result admits to the best-known result in the literature of computationally feasible community detection in SBM without outliers. Numerical results show that our method is both computationally fast and robust to different kinds of outliers, while some popular computationally fast community detection algorithms, such as spectral clustering applied to adjacency matrices or graph Laplacians, may fail to retrieve the major clusters due to a small portion of outliers. We apply a slight modification of our method to a political blogs data set, showing that our method is competent in practice and comparable to existing computationally feasible methods in the literature. To the best of the authors' knowledge, our result is the first in the literature in terms of clustering communities with fast growing numbers under the GSBM where a portion of arbitrary outlier nodes exist.

Keywords

Robust community detection, SDP relaxation, dual certificate, k -means clustering

Disciplines

Physical Sciences and Mathematics

ROBUST AND COMPUTATIONALLY FEASIBLE COMMUNITY DETECTION IN THE PRESENCE OF ARBITRARY OUTLIER NODES¹

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Community detection, which aims to cluster N nodes in a given graph into r distinct groups based on the observed undirected edges, is an important problem in network data analysis. In this paper, the popular stochastic block model (SBM) is extended to the generalized stochastic block model (GSBM) that allows for adversarial outlier nodes, which are connected with the other nodes in the graph in an arbitrary way. Under this model, we introduce a procedure using convex optimization followed by k -means algorithm with $k = r$.

Both theoretical and numerical properties of the method are analyzed. A theoretical guarantee is given for the procedure to accurately detect the communities with small misclassification rate under the setting where the number of clusters can grow with N . This theoretical result admits to the best-known result in the literature of computationally feasible community detection in SBM without outliers. Numerical results show that our method is both computationally fast and robust to different kinds of outliers, while some popular computationally fast community detection algorithms, such as spectral clustering applied to adjacency matrices or graph Laplacians, may fail to retrieve the major clusters due to a small portion of outliers. We apply a slight modification of our method to a political blogs data set, showing that our method is competent in practice and comparable to existing computationally feasible methods in the literature. To the best of the authors' knowledge, our result is the first in the literature in terms of clustering communities with fast growing numbers under the GSBM where a portion of arbitrary outlier nodes exist.

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1. Introduction. Driven by applications in a wide range of fields, including engineering, genomics, sociology, psychology and computer science, analysis of graph and network data has drawn significant recent interest. Random graph models have been introduced to characterize the structure of the networks and a large number of algorithmic approaches have been proposed for various applications. See, for example, Fienberg (2010, 2012), Goldenberg et al. (2010), and the references therein for overviews and recent work.

An important problem in the analysis of network data is that of community detection which aims to cluster the nodes in a given graph into distinct groups or communities based on the observed undirected edges. Community detection has proven to be both technically and computationally challenging. It also has deep connections to other fields such as spin-glass theory and signal processing. In terms of statistical modeling, the most well-known model for community detection is perhaps the stochastic block model (SBM) proposed in Holland, Laskey and Leinhardt (1983). Under the SBM, the graph of interest is assumed to be a random one with independent edges, and the within-group edge density is assumed to be greater than the between-group edge density.

To be specific, suppose $G = (V, E)$ is a random graph where V is a fixed set of vertices consisting of n nodes, and E is a random set of edges. Assume that the n nodes are indexed by $[n] := \{1, \dots, n\}$ and each of these nodes belongs to one and only one of the r nonoverlapping groups. This amounts to assigning each node $j \in [n]$ a group label by a labeling function $\phi(j) \in \{1, \dots, r\}$. We denote by $\mathbf{A} = (A_{ij})_{1 \leq i, j \leq n}$ the random adjacency matrix of this random graph. Then for each pair (i, j) , $1 \leq i, j \leq n$, $A_{ij} = 0$ or 1 , indicating whether the nodes i and j are connected or not, respectively. We only consider undirected graph with no self loops, so \mathbf{A} is symmetric, and all its diagonal entries are 0. For pairs (i, j) with $1 \leq i < j \leq n$, A_{ij} 's are assumed to be independent Bernoulli random variables with parameters $B_{\phi(i)\phi(j)}$, where the symmetric matrix $\mathbf{B} \in \mathbb{R}^{r \times r}$ is referred to as the *connectivity* matrix. In a basic model, denote by q^+ and p^- the maximum cross-group density and the minimum within-group density, namely

$$(1.1) \quad q^+ := \max_{1 \leq i < j \leq r} B_{ij}, \quad p^- := \min_{1 \leq i \leq r} B_{ii}.$$

Moreover, the within-group densities are assumed to be greater than the cross-group densities, that is,

$$(1.2) \quad p^- - q^+ := \delta > 0.$$

This is a common assumption in the literature of community detection under the SBM; see, for example, Rohe, Chatterjee and Yu (2011), Chaudhuri, Chung and Tsiatas (2012). Denote the minimum community size by $n_{\min} :=$

$\min_{1 \leq l \leq r} |\phi^{-1}(l)|$, where $|S|$ denotes the cardinality of the set S . Then the difficulty of the community detection problem is determined by the tuple $(n, r, q^+, p^-, n_{\min})$.

Under the SBM, various community detection algorithms have been proposed and studied in the literature, with different emphases on computational complexity and statistical accuracy. These include greedy algorithms, such as hierarchical agglomeration [see, e.g., Clauset, Newman and Moore (2004)]; greedy methods guided by global criterion maximization, such as modularity function maximization [see, e.g., Newman and Girvan (2004)] and profile likelihood function maximization [see, e.g., Bickel and Chen (2009), Zhao, Levina and Zhu (2012)]; stochastic model based methods, such as variational likelihood methods [see, e.g., Bickel et al. (2013), Celisse, Daudin and Pierre (2012)], pseudo-likelihood methods with EM algorithm [see, e.g., Amini et al. (2013)], Bayesian methods with Gibbs sampling, Markov chain Monte Carlo and belief propagation [see, e.g., Snijders and Nowicki (1997), Nowicki and Snijders (2001), Decelle et al. (2011)]; graph distance methods [see, e.g., Bhattacharyya and Bickel (2014)]; spectral clustering, its variations and other spectral methods [see, e.g., McSherry (2001), Giesen and Mitsche (2005), Rohe, Chatterjee and Yu (2011), Chaudhuri, Chung and Tsias (2012), Coja-Oghlan and Lanka (2009/10), Balakrishnan et al. (2011), Sussman et al. (2012), Fishkind et al. (2013), Jin (2015), Joseph and Yu (2013), Sarkar and Bickel (2013), Lei and Rinaldo (2015)]; and convex optimization methods [see, e.g., Mathieu and Schudy (2010), Oymak and Hassibi (2011), Jalali et al. (2014), Ames and Vavasis (2014), Chen, Sanghavi and Xu (2012), Ames (2014)].

Among these methods, greedy methods are usually computationally feasible, while their statistical accuracy has not been fully established in theory. Modularity or profile likelihood methods are proven to be consistent when the number of groups is fixed. However, they are in principle computationally NP hard. Similarly, stochastic model based methods are usually computationally difficult and not fully justified in theory. Spectral clustering is a popular algorithm for community detection, since it is fast in computation and easy to implement. It has been proven that spectral clustering is consistent even when the number of groups r grows on the order of $O(\sqrt{n})$. Although in practice spectral clustering is believed to work well only for dense graphs, several recent papers, Amini et al. (2013), Sarkar and Bickel (2013), Joseph and Yu (2013), Lei and Rinaldo (2015), have shown that spectral clustering or its variations also work well for sparse graphs.

The SBM is admittedly an oversimplified model for many applications, and different generalizations have been proposed in the literature, which encompass mixture model [see Newman and Leicht (2007)], where the parametric model for the connectivity probabilities is based on the relationship between vertices and groups, instead of between different groups; degree

corrected model [see Coja-Oghlan and Lanka (2009/10), Karrer and Newman (2011), Zhao, Levina and Zhu (2012)]; Latent variable method [see Handcock, Raftery and Tantrum (2007)] and mixed membership model [see Airoldi et al. (2008)]. However, each of these GSBMs focuses on a single latent graph structure, while in practice, due to lack of information, this additional structure is not easy to detect if it only applies to a few nodes of the graph. Different types of outliers may appear in a single graph, and it is difficult to use a complex generalization of the SBM to model multiple types of outlier nodes. The SBM is usually the first model to fit the data because of its simple form, even if it is believed that there is possibly a small portion of nodes which are not modeled well. Robustness in presence of arbitrary outliers is an important property for given community detection algorithms. In this paper we consider robust community detection in the presence of arbitrary outlier nodes, and the main question we wish to answer is the following:

Does there exist a computationally fast community detection method that is robust to a portion of arbitrary outlier nodes with theoretical guarantees?

Our answer is affirmative, and we will introduce our model, methodology, numerical results and theoretical guarantees with rigorous proofs in this paper. We begin by formalizing the GSBM which allows for a small portion of arbitrary nodes.

1.1. *Generalized stochastic block model.* We introduce a flexible model for community detection which covers a range of settings in practice where the usual SBM is not suitable. More specifically, we assume the undirected graph $G = (V, E)$ has $N := n + m$ nodes, among which there are n “inliers” obeying the SBM described above, while the other m nodes are “outliers” which are connected with the other nodes in an arbitrary way. We refer to this model as *generalized stochastic block model (GSBM)*. Denote $V = [N] = I \cup O$, where I is the set of indices of the inliers, while O is the set of indices of outliers. Each inlier node $i \in I$ is assigned a label $\phi(i) \in \{1, \dots, r\}$, while all outliers are simply labeled $\phi(i) = r + 1$. For any two nodes $i, j \in I$, $\mathbb{P}((i, j) \in E) = B_{\phi(i)\phi(j)}$, and moreover we assume the event $\{(i, j) \in E\}$, $i < j \in I$ are independent. The $r \times r$ symmetric connectivity matrix \mathbf{B} only represents the likelihood of connectivity of the inlier nodes. The connectivity between the outliers and the inliers and the connectivity among the outliers themselves are arbitrary. The only restriction of the connectivity of the outliers is that there is no self-loop.

The GSBM can be equivalently expressed in terms of its adjacency matrix \mathbf{A} . To be specific, define

$$(1.3) \quad \mathbf{A} = \mathbf{P} \begin{bmatrix} \mathbf{K} & \mathbf{Z} \\ \mathbf{Z}^\top & \mathbf{W} \end{bmatrix} \mathbf{P}^\top = \mathbf{P} \begin{bmatrix} \mathbf{K}_{11} & \dots & \mathbf{K}_{1r} & \mathbf{Z}_1 \\ \vdots & \ddots & \vdots & \vdots \\ \mathbf{K}_{1r}^\top & \dots & \mathbf{K}_{rr} & \mathbf{Z}_r \\ \mathbf{Z}_1^\top & \dots & \mathbf{Z}_r^\top & \mathbf{W} \end{bmatrix} \mathbf{P}^\top,$$

where $\mathbf{W} \in \mathbb{R}^{m \times m}$ is an arbitrary symmetric 0–1 matrix with all diagonal entries being 0, $\mathbf{Z} \in \mathbb{R}^{n \times m}$ is an arbitrary 0–1 matrix, \mathbf{P} is an unknown $N \times N$ permutation matrix, in which there is only one 1 in each row and column, while all other entries are 0’s, and \mathbf{K} is an $n \times n$ symmetric matrix which captures the connectivity of the inliers, thus corresponding to the usual SBM. The off-diagonal entries of \mathbf{K} are independent Bernoulli variables, with parameter B_{ij} if the entry belongs to the submatrix \mathbf{K}_{ij} . Denote the dimension of \mathbf{K}_{ii} to be l_i for $i = 1, \dots, r$. Then $n = \sum_{i=1}^r l_i$. Similar to SBM, $n_{\min} = \min_{1 \leq i \leq r} l_i$. The parameters p^- and q^+ are defined as in (1.1) and δ in (1.2). Then the difficulty of community detection under the GSBM is parameterized by the tuple $(n, m, r, p^-, q^+, n_{\min})$.

Here we emphasize that \mathbf{Z} and \mathbf{W} are not necessarily fixed with respect to the randomness of \mathbf{K} . Both \mathbf{Z} and \mathbf{W} can depend on \mathbf{K} in arbitrary forms. In other words, the connectivity between the outliers and the inliers is allowed to depend on the connectivity among the inlier nodes. This is also a generalization of standard SBM, where the connectivity between each pair of nodes is stochastically independent of the connectivity between other pairs.

The GSBM is a flexible model and is widely applicable. It covers various types of outliers which are common in practice, and we name a few as follows:

- *Mixed membership.* The SBM assumes that each node belongs to one and only one predetermined cluster. If most nodes obey this property, while there is a small portion of nodes each belonging to more than one clusters, these nodes are referred to as having mixed membership. When only a small portion of nodes have mixed membership, it is natural to treat them as outliers in an ordinary SBM.
- *Hubs.* In social networks and others, it is natural that some nodes have many more connections than most of others. Moreover, it is possible that these nodes belong to several groups without obvious bias to any specific one. These nodes are referred to as hubs, and can be treated as outliers in our GSBM.
- *Small clusters.* The SBMs are usually employed to model big and significant clusters, while small clusters are difficult to detect. Small clusters are often not detectable because they are too small and possibly weak.

The number of small clusters is also difficult to estimate; however, this information is essential for most popular algorithms in the literature, such as spectral clustering and modularity methods. The nodes in the small clusters can be treated as outliers in our GSBM.

- *Independent neutral nodes.* In a given graph, in addition to the well-classified nodes, there might be some nodes which do not belong to any significant groups, and also have fewer connections than most other nodes. We refer to these objects as independent neutral nodes. For example, in the political blogs data set introduced later, a small portion of blogs have very few connections. Such blogs may have strong preference in politics; however, this cannot be seen from only the graph representation. Therefore, these nodes are regarded as independent neutral nodes, which are naturally taken as outliers.

In practice, it is difficult or even impossible to modify the usual SBM to model precisely the possible combinations of mixed membership, hubs, small clusters, independent neutral nodes and other types of settings. Moreover, complex statistical models may also result in overfitting and high computational complexity in clustering. Therefore, the SBM is usually set up based on the basic properties of the graph. For example, in the political blogs network application discussed in Section 4.2, an SBM with 2 clusters is preferred, since it is known that there are mainly two significant clusters: liberals and conservatives. However, it is also known that there are many independent groups advocating various causes that lie outside of the two main clusters.

The GSBM can also be taken as a criterion to evaluate the robustness of community detection algorithms. When an SBM is adopted based on the properties of most nodes of a given graph, or equivalently, most nodes can be well modeled by an SBM in use, the robustness of a given community detection algorithm depends on whether a small portion of outliers will completely change the clustering result, or most nodes can be still well clustered. Therefore, a graph clustering algorithm is robust if it is guaranteed to have good performance under the GSBM.

1.2. *Organization of the paper.* The rest of the paper is organized as follows. In Section 2 the method of convexified likelihood method is introduced, followed by a detailed alternating directional augmented Lagrangian algorithm. Section 3 is focused on the theoretical consistency of the convex optimization method in the inference of the underlying groups specified by the GSBM. Numerical results on the analyses of the simulated data and a real data set about political blogs are presented in Section 4. A discussion is given in Section 5, and the proofs of the main theoretical results are contained in Section 6. Additional technical proofs are given in the Supplementary Material.

2. Methodology. In this section we propose a community detection algorithm which is robust and computationally feasible with theoretical guarantee of consistency. In the literature, greedy algorithms such as hierarchical clustering are not fully justified in theory, while modularity and profile maximum likelihood methods are computationally NP hard. Stochastic model based methods, such as maximum likelihood or variational likelihood method, have been proven to have certain consistency when the number of blocks is fixed as the number of nodes going to infinity. However, they are also computationally difficult. EM algorithm is naturally proposed for solving relevant maximum likelihood formulation, but there is no theoretical guarantee of convergence with reasonable rate. Bayesian methods such as Gibbs sampling and belief propagation have also been proposed in the literature without rigorous theoretical justifications.

Unlike the aforementioned methods, the spectral clustering methods have the advantage of fast algorithms. Spectral clustering algorithms are easy to implement because there is no tuning parameter. Moreover, strong theoretical results have been established under various conditions; see the references mentioned in the previous section. However, as indicated in Joseph and Yu (2013), ordinary spectral clustering applied to the graph Laplacian may not work due to the existence of small and weak clusters. We use a simulated data set to illustrate that ordinary spectral clustering applied to the graph Laplacian or the adjacency matrix is not consistent under the GSBM. Other types of numerical examples can be found in Joseph and Yu (2013).

First, we create a data set of $n = 1000$ nodes obeying the ordinary SBM with $r = 2$ clusters. We also assume that the two clusters are perfectly balanced; that is, there are 500 nodes in each cluster. The within-group probability is $p = 0.17$, while the cross-group probability is $q = 0.11$. Under this set-up, the adjacency matrix is shown as in Figure 1.

Spectral clustering applied directly to either the graph Laplacian or the adjacency matrix of this graph data has good performance of clustering. To illustrate this, we plot the eigenvectors corresponding to the top two eigenvalues (in absolute value) of the graph Laplacian and the adjacency matrix, respectively, in Figure 1. In each case, the two eigenvectors combined are capable of discriminating between the two clusters. Therefore, spectral clustering methods work for our data set when there are no outliers.

Now we consider the GSBM by adding only $m = 30$ outliers into the above model with $r = 2$ clusters. To specify this GSBM, it suffices to explain \mathbf{Z} and \mathbf{W} in (1.3). We assume \mathbf{W} is the adjacency matrix of a random graph with 30 nodes and independent edges. Moreover, we assume the probability of connectivity is 0.7. We define \mathbf{Z} as a 1000×30 with independent Bernoulli entries. We also let $\mathbb{E}\mathbf{Z} = \boldsymbol{\beta}\mathbf{1}^\top = [\boldsymbol{\beta}, \boldsymbol{\beta}, \dots, \boldsymbol{\beta}]$. The components of $\boldsymbol{\beta}$ are 1000 i.i.d. copies of U^2 , and U is a uniform random variable on $[0, 1]$. The unordered and ordered adjacency matrices are given in Figure 2.

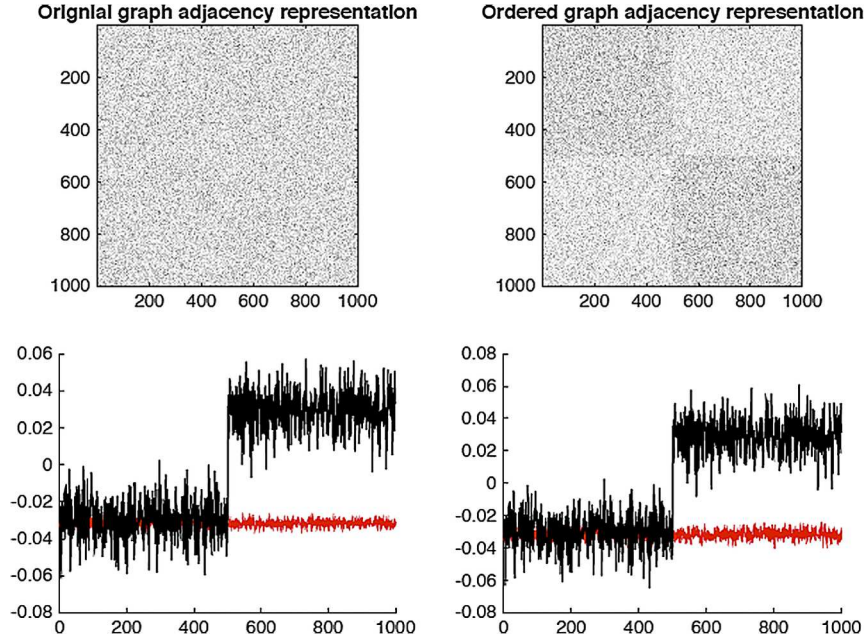


FIG. 1. The upper left panel illustrates the adjacency matrix of 1000 nodes satisfying the ordinary SBM. The upper right panel is the adjacency matrix obtained by permuting the adjacency matrix such that nodes 1 to 500 belong to the same cluster while the remaining ones constitute another cluster. The lower left panel plots the eigenvectors of the graph Laplacian corresponding to the top 2 eigenvalues in absolute value (red for the first and black for the second), while those for the adjacency matrix are plotted in the lower right panel. In both cases, these two eigenvectors are capable of discriminating between the two communities.

Suppose the data set is still modeled approximately by the SBM with $r = 2$. For this new data set, the two eigenvectors corresponding to the top two eigenvalues (in absolute value) of the graph Laplacian or the adjacency matrix cannot discriminate between the two major clusters. Even if we treat the 30 outliers as a single group due to their homogeneous behavior in the graph and thereby use $r = 3$, the third eigenvector of the adjacency matrix is still unable to distinguish the two major clusters. The third eigenvector of the graph Laplacian can only discriminate a part of nodes in the two major clusters. Actually, our numerical simulation shows that after applying spectral clustering on the graph Laplacian with $r = 3$, the misclassification rate among the inliers is above 30 percent. These three eigenvectors are plotted in Figure 2 for both cases. The figures indicate that standard spectral clustering is not a robust community detection method in the presence of very few adversarial outliers.

It was shown in Joseph and Yu (2013) that under certain conditions, penalized spectral clustering may reduce the effects of the small weak clus-

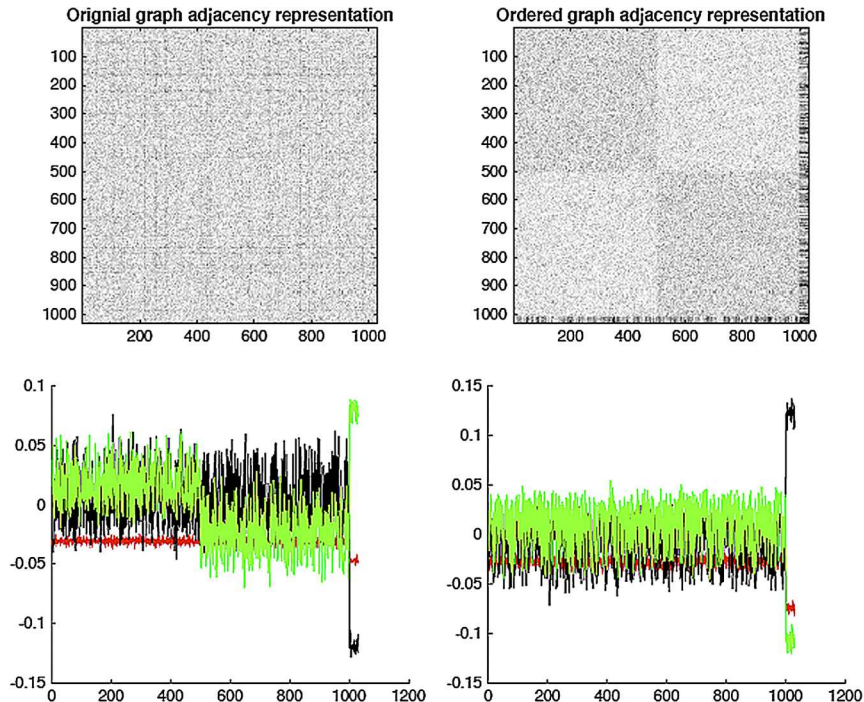


FIG. 2. The upper left panel illustrates the adjacency matrix of 1030 nodes satisfying the GSBM with two major clusters and 30 outliers. The upper right panel is obtained by permuting the nodes such that nodes belonging to the same group are consecutive. The lower left panel plots the eigenvectors of the graph Laplacian corresponding the top 3 eigenvalues in absolute value (red for the first, black for the second and green for the third), while those for the adjacency matrix are plotted in the lower right panel. Ordinary spectral clustering with $r = 2$ or $r = 3$ is ineffective or even powerless on this data set since the top three eigenvectors cannot clearly discriminate between the two main communities.

ters, but it is not clear whether penalized spectral clustering applied to the graph Laplacian can diminish the influence of other types of outliers. Another method to improve standard spectral clustering methods is to detect outlier nodes based on the first several eigenvectors. However, it is not clear whether there exists an approach which can uniformly detect all kinds of outliers with a theoretical guarantee.

In order to find in one shot the major clusters among the inlier nodes, we introduce in Section 2.1 a convex optimization method as well as a detailed algorithm which is implementable. It will be shown in Section 3 that the proposed procedure is robust against a small portion of arbitrary outliers with theoretical guarantees.

2.1. *Convex optimization.* In this section, we will choose the method of semidefinite programming (SDP) to fit the GSBM, followed by a k -means

clustering. Numerically, SDP is well known to be computationally feasible, and various efficient algorithms were proposed for solving different types of SDP. Theoretically, under the ordinary SBM, SDP methods are shown to be capable in detecting communities; see Mathieu and Schudy (2010), Oymak and Hassibi (2011), Jalali et al. (2014), Ames and Vavasis (2014), Chen, Sanghavi and Xu (2012). We propose a new convex optimization method inspired by existing SDP methods in the literature. The significantly novel part is that we will prove that this SDP method can consistently cluster the nodes when there is a portion of arbitrary type of outliers. The formal statement is given in Section 3, and all the proofs are deferred to Section 6 and the supplemental article Cai and Li (2015).

First, we derive the convex optimization from the viewpoint of fitting a parametric model. This viewpoint was originally proposed in Chen, Sanghavi and Xu (2012), but we are going to derive a different convex optimization. For now we only consider the ordinary SBM, which implies that $m = 0$ and $N = n$. By the definition of SBM, for all $1 \leq i < j \leq n$, the events $\{A_{ij} = 1\}$ are independent. Recall that here \mathbf{A} is the observed adjacency matrix. Moreover, we define a symmetric matrix \mathbf{X} with all diagonal entries equal to 1. For any $1 \leq i < j \leq n$, we let $X_{ij} = 0$ if the labeling functions $\phi(i) \neq \phi(j)$, while $X_{ij} = 1$ if $\phi(i) = \phi(j)$. Obviously, this matrix \mathbf{X} is of rank r since there are r groups.

Moreover, we consider a special case of the ordinary SBM. Suppose $1 > p > q > 0$. For any $1 \leq i < j \leq N$, when $X_{ij} = 0$ let $\mathbb{P}(A_{ij} = 1) = q$; otherwise let $\mathbb{P}(A_{ij} = 1) = p$. This gives

$$\log \mathbb{P}(A_{ij} = 1 | X_{ij}) = X_{ij} \log p + (1 - X_{ij}) \log q$$

and

$$\log \mathbb{P}(A_{ij} = 0 | X_{ij}) = X_{ij} \log(1 - p) + (1 - X_{ij}) \log(1 - q).$$

Since $\{A_{ij} = 1\}$ are independent events, we have the log-likelihood function

$$\begin{aligned} \ell(\mathbf{A} | \mathbf{X}) = & \sum_{1 \leq i < j \leq n} [A_{ij}(X_{ij} \log p + (1 - X_{ij}) \log q) \\ & + (1 - A_{ij})(X_{ij} \log(1 - p) + (1 - X_{ij}) \log(1 - q))]. \end{aligned}$$

For any fixed p and q , given \mathbf{A} , we would like to choose an appropriate \mathbf{X} to maximize $\ell(\mathbf{A} | \mathbf{X})$. If we let

$$(2.1) \quad \lambda = \frac{\log(1 - q) - \log p}{\log p - \log q + \log(1 - q) - \log(1 - p)},$$

since the diagonal entries of \mathbf{A} are all equal to 1, the maximization is equivalent to

$$\max_{\mathbf{X}} \langle \mathbf{X}, (1 - \lambda)\mathbf{A} - \lambda(\mathbf{J}_N - \mathbf{I}_N - \mathbf{A}) \rangle,$$

where \mathbf{J}_N is the $N \times N$ matrix with all entries 1. Now let us figure out the constraint of \mathbf{X} . By the SBM, it is easy to check that \mathbf{X} must have the following form:

$$(2.2) \quad \mathbf{X} = \mathbf{P} \begin{bmatrix} \mathbf{J}_{l_1} & & \\ & \ddots & \\ & & \mathbf{J}_{l_r} \end{bmatrix} \mathbf{P}^\top,$$

where \mathbf{P} is some unknown permutation matrix, while \mathbf{J}_s is an $s \times s$ matrix with all entries 1's. Solving optimization (2.2) under such constraint is computationally infeasible, so we seek for some relaxed form. Here we notice there are three major features of \mathbf{X} . First, it is positive semidefinite; second, all its entries are between 0 and 1; third, it is of rank- r , which is relatively low. If we convexify the second integer constraint and neglect the third requirement, the relaxed maximum likelihood method becomes

$$\begin{aligned} \max \quad & \langle \tilde{\mathbf{X}}, (1 - \lambda)\mathbf{A} - \lambda(\mathbf{J}_N - \mathbf{I}_N - \mathbf{A}) \rangle \\ \text{subject to} \quad & \tilde{\mathbf{X}} \succeq \mathbf{0}, \\ & 0 \leq \tilde{X}_{ij} \leq 1 \quad \text{for } 1 \leq i, j \leq N. \end{aligned}$$

The above optimization method is different from that in Chen, Sanghavi and Xu (2012), where the relaxation is based on the observation that \mathbf{X} is of low rank and hence a nuclear norm penalization is added up to the original objective function. On the contrary, our convex relaxation is derived from the observation that \mathbf{X} is both low-rank and positive semidefinite, and consequently we impose constraint of the positive semidefinite cone.

Now let us come back to the robust community detection under the GSBM. To control the possible outliers as formalized in the GSBM model, for the convenience of theoretical analysis, we add an additional term in the objective function to penalize the trace

$$\begin{aligned} \min \quad & \langle \tilde{\mathbf{X}}, \alpha\mathbf{I}_N - (1 - \lambda)\mathbf{A} + \lambda(\mathbf{J}_N - \mathbf{I}_N - \mathbf{A}) \rangle \\ \text{subject to} \quad & \tilde{\mathbf{X}} \succeq \mathbf{0}, \\ & 0 \leq \tilde{X}_{ij} \leq 1 \quad \text{for } 1 \leq i, j \leq N, \end{aligned}$$

which is equivalent to

$$(2.3) \quad \begin{aligned} \min \quad & \langle \tilde{\mathbf{X}}, \mathbf{E} \rangle \\ \text{subject to} \quad & \tilde{\mathbf{X}} \succeq \mathbf{0}, \\ & 0 \leq \tilde{X}_{ij} \leq 1 \quad \text{for } 1 \leq i, j \leq N, \end{aligned}$$

where

$$(2.4) \quad \mathbf{E} := \alpha\mathbf{I}_N - (1 - \lambda)\mathbf{A} + \lambda(\mathbf{J}_N - \mathbf{I}_N - \mathbf{A}).$$

REMARK 2.1. At first glance, there are seemingly two tuning parameters: α and λ . In our theoretical result as shown later in Section 3, the parameter α is required to be much greater than the number of outlier nodes m . The introduction of α amounts to the trace penalization of $\tilde{\mathbf{X}}$, which is usually adopted in the literature of SDP relaxation in order to recover a low-rank structure; see, for example, Candès, Strohmer and Voroninski (2013), Li and Voroninski (2013). In our problem, we intend to use (2.3) to solve for a low-rank matrix to reveal the clustering structure of the GSBM, so this trace penalization is possibly a natural heuristic. However, in our numerical simulations in Section 4, the clustering effectiveness of the convex optimization method (2.3) is not significantly improved by choosing a positive α . Instead, (2.3) works even by letting α be a small constant or zero. On the contrary, there is a risk for choosing a large α , which may result in a positive definite \mathbf{E} . If so, the solution to (2.3) must be $\mathbf{0}$, which is useless in analyzing the networking data.

Therefore, we only need to tune the parameter λ in practice, and it has a clear statistical meaning as indicated in (2.1) in a special case of the ordinary SBM. In Section 3, it is shown that if λ lies in an interval determined by p^- and q^+ as defined in (1.1), under mild technical conditions, any solution $\tilde{\mathbf{X}}$ to (2.3) is capable of detecting the underlying group structure among the inliers. A simple and heuristic data dependent choice of λ is given in Section 4, where we also show numerically that the performance of our method for clustering is robust to the choice of λ .

When $\hat{\mathbf{X}}$ is obtained, in the pursuit of an explicit clustering solution, a further step of k -means clustering is conducted to the normalized column vectors of $\hat{\mathbf{X}}$ with $k = r$, provided the number of major clusters r is assumed known. Furthermore, in Section 3 it is shown that the misclassification rate after the k -means clustering can be tightly controlled.

In summary, our proposed community detection procedure consists of the following two steps:

Step 1. Choose an appropriate tuning parameter λ , and then solve (2.3). The solution is denoted as $\hat{\mathbf{X}}$.

Step 2. Conduct k -means clustering algorithm to the normalized column vectors of $\hat{\mathbf{X}}$ with $k = r$, so that we can solve for the assigning function $\hat{\phi}$ that maps from $\{1 \leq i \leq N\}$ to $\{1, \dots, r\}$.

Finally, we introduce the augmented Lagrange multiplier algorithm to solve (2.3). Augmented Lagrange multiplier algorithms have been employed in a variety of SDP optimizations in order to recover the underlying low-rank matrix structure; see, for example, Lin, Liu and Su (2011), Candès et al. (2011), Jalali et al. (2014), Chen, Sanghavi and Xu (2012) and a nice

review paper on alternating direction method of multipliers (ADMM) Boyd et al. (2010). Notice that (2.3) can be rewritten as

$$\begin{aligned} \min_{\mathbf{Y}, \mathbf{Z}} \quad & \iota(\mathbf{Y} \succeq \mathbf{0}) + \iota(\mathbf{0} \leq \mathbf{Z} \leq \mathbf{J}_N) + \langle \mathbf{Y}, \mathbf{E} \rangle, \\ \text{subject to} \quad & \mathbf{Y} = \mathbf{Z}, \end{aligned}$$

where the indicator function $\iota(a \in A)$ is defined as

$$\iota(a \in A) = \begin{cases} 0, & a \in A, \\ +\infty, & a \notin A. \end{cases}$$

By this definition, we can easily conclude that $\iota(a \in A)$ is a convex function if and only if A is a convex set. Define the augmented Lagrangian of this optimization problem as

$$L_\rho(\mathbf{Y}, \mathbf{Z}; \mathbf{\Lambda}) := \iota(\mathbf{Y} \succeq \mathbf{0}) + \iota(\mathbf{0} \leq \mathbf{Z} \leq \mathbf{J}_N) + \langle \mathbf{Y}, \mathbf{E} \rangle + \frac{\rho}{2} \|\mathbf{Y} - \mathbf{Z} + \mathbf{\Lambda}\|_F^2.$$

If both $\mathbf{\Lambda}$ and \mathbf{Z} are fixed, and we aim to minimize $L_\rho(\mathbf{Y}, \mathbf{Z}; \mathbf{\Lambda})$ with respect to \mathbf{Y} , it is equivalent to minimizing

$$\iota(\mathbf{Y} \succeq \mathbf{0}) + \frac{\rho}{2} \left\| \mathbf{Y} - \mathbf{Z} + \mathbf{\Lambda} + \frac{\mathbf{E}}{\rho} \right\|_F^2.$$

For any symmetric matrix \mathbf{X} whose eigenvalue decomposition is $\mathbf{V}\mathbf{\Sigma}\mathbf{V}^\top$, define $\mathbf{X}_+ := \mathbf{V}\mathbf{\Sigma}_+\mathbf{V}^\top$. Then the solution to the above minimization has an explicit form

$$\operatorname{argmin}_{\mathbf{Y}} L_\rho(\mathbf{Y}, \mathbf{Z}; \mathbf{\Lambda}) = \left(\mathbf{Z} - \mathbf{\Lambda} - \frac{\mathbf{E}}{\rho} \right)_+.$$

REMARK 2.2. This step has dominating computational complexity in each iteration of ADMM. In fact, an exact implementation of this subproblem of optimization requires a full SVD of $\mathbf{Z} - \mathbf{\Lambda} - \frac{\mathbf{E}}{\rho}$, whose computational complexity is $O(N^3)$. When N is as large as hundreds of thousands, the full SVD has scalability issue. An open question is how to facilitate the implementation, or whether there exists a surrogate that is computationally inexpensive. A possible remedy is applying the low-rank iterative method, which means in each iteration of ADMM, the full SVD is replaced by a partial SVD where only the leading eigenvalues and eigenvectors are computed. Although this type of method may be stuck in local minimizers, given the fact that SDP implementation can be viewed as a preprocessing before k -means clustering, such a low-rank iterative method might be helpful. We leave this large-scale computing problem as a future research project.

On the other hand, if both $\mathbf{\Lambda}$ and \mathbf{Y} are fixed, to minimize $L_\rho(\mathbf{Y}, \mathbf{Z}; \mathbf{\Lambda})$ with respect to \mathbf{Z} is equivalent to minimizing

$$\iota(\mathbf{0} \leq \mathbf{Z} \leq \mathbf{J}_N) + \frac{\rho}{2} \|\mathbf{Z} - \mathbf{Y} - \mathbf{\Lambda}\|_F^2.$$

Again, we have a closed-form solution

$$\operatorname{argmin}_{\mathbf{Z}} L_\rho(\mathbf{Y}, \mathbf{Z}; \mathbf{\Lambda}) := \min(\max(\mathbf{Y} + \mathbf{\Lambda}, \mathbf{0}), \mathbf{J}_N),$$

which changes the negative entries of $\mathbf{Y} + \mathbf{\Lambda}$ into zeros and those greater than one into one.

As to the Lagrange multiplier, as the convention in the literature of augmented Lagrange multiplier algorithms, $\mathbf{\Lambda}$ is updated to $\mathbf{\Lambda} + (\mathbf{Y} - \mathbf{Z})$.

The above augmented Lagrange multiplier method derives an iterative algorithm for solving the convex optimization (2.3), which is summarized in Algorithm 1. In numerical simulations, we let $\mathbf{Z}_0 = \mathbf{0}$ and $\mathbf{\Lambda}_0 = \mathbf{0}$ for initialization, and simply choose $\rho = 1$ and run the algorithm for $iter = 100$ iterations. Numerical analyses of the algorithm applied to simulated data and a real data set of political blogs are deferred to Section 4, where its efficiency and effectiveness are clearly demonstrated. Moreover, for the purpose of comparison, we also implement ordinary spectral clustering methods on the synthetic data sets. The numerical simulations clearly show that our method outperforms spectral clustering methods in terms of robustness against outliers.

3. Theoretical guarantees. In this section, we will introduce our main theoretical results that guarantee that the clustering procedure derived in the previous section can detect the underlying communities under the GSBM.

Algorithm 1 Robust community detection via alternating direction method

Initialization: $\mathbf{Z}_0 = \mathbf{0}$, $\mathbf{\Lambda}_0 = \mathbf{0}$, $\rho = 1$ and $iter = 100$.

while $k < iter$

1. $\mathbf{Y}_{k+1} := (\mathbf{Z}_k - \mathbf{\Lambda}_k - \frac{\mathbf{E}}{\rho})_+$;
2. $\mathbf{Z}_{k+1} := \min(\max(\mathbf{Y}_{k+1} + \mathbf{\Lambda}_k, \mathbf{0}), \mathbf{J}_N)$;
3. $\mathbf{\Lambda}_{k+1} := \mathbf{\Lambda}_k + (\mathbf{Y}_{k+1} - \mathbf{Z}_{k+1})$;

end while.

Output the final \mathbf{Y}_{iter} .

The following theorem provides an explicit condition of the parameters n , m , p^- , q^+ and n_{\min} , as well as the tuning parameters (α, λ) , under which the solution to (2.3) is capable of unveiling the underlying group structures among the inliers in presence of a portion of outlier confounders.

THEOREM 3.1. *Let \mathbf{A} be the adjacency matrix of the semi-random graph under the GSBM, as defined in (1.3). Let $\widehat{\mathbf{X}}$ be a solution to the semidefinite program (2.3) and the density gap δ be defined as in (1.2), and the minimum within-group density p^- and the maximum cross-group density q^+ be defined as in (1.1). As defined in Section 1, the integer n denotes the number of inlier nodes, m denotes the number of outlier nodes and n_{\min} denotes the minimum community size among the inliers. Suppose that $p^- \geq C \frac{\log n}{n_{\min}}$, $\alpha \geq 3m$ and*

$$(3.1) \quad \delta > C \left(\sqrt{\frac{p^- \log n}{n_{\min}}} + \frac{\alpha}{n_{\min}} + \frac{\sqrt{nq^+}}{n_{\min}} + \frac{m\sqrt{r}}{n_{\min}} + \frac{nmp^-}{(\alpha - 2m)n_{\min}} \right)$$

for some sufficiently large numerical constant C , and the tuning parameter λ satisfies

$$(3.2) \quad q^+ + \frac{\delta}{4} < \lambda < p^- - \frac{\delta}{4}.$$

Then with probability at least $1 - \frac{1}{n} - \frac{2r}{n^2} - \frac{cr}{n_{\min}^4}$ for some numerical constant c , $\widehat{\mathbf{X}}$ must be of the form

$$(3.3) \quad \widehat{\mathbf{X}} = \mathbf{P} \begin{bmatrix} \mathbf{J}_{l_1} & & \widehat{\mathbf{Z}}_1 \\ & \ddots & \vdots \\ & & \mathbf{J}_{l_r} & \widehat{\mathbf{Z}}_r \\ \widehat{\mathbf{Z}}_1^\top & \cdots & \widehat{\mathbf{Z}}_r^\top & \widehat{\mathbf{W}} \end{bmatrix} \mathbf{P}^\top,$$

where \mathbf{P} is defined as in (1.3).

Theorem 3.1 guarantees that any solution to (2.3) $\widehat{\mathbf{X}}$ satisfies $\widehat{X}_{jk} = 1$ for $\phi(j) = \phi(k) \leq r$, and $\widehat{X}_{jk} = 0$ for $\phi(j) \neq \phi(k)$ and $\phi(j) \leq r, \phi(k) \leq r$. In other words, for each pair of inlier nodes j and k , whether they belong to the same group or not solely depends on whether \widehat{X}_{jk} equals 1 or 0. It is noteworthy that condition (3.2) is similar to the tuning parameter condition imposed in Chen, Sanghavi and Xu (2012).

To interpret condition (3.1), it is helpful to consider two examples. First, let us consider the very sparse case where $p^- \simeq q^+ \simeq \delta \simeq O(\frac{\log n}{n})$, $n_{\min} \simeq O(n)$ and hence $r \simeq O(1)$. This condition implies that our procedure works even for a graph whose average degree of inlier nodes is on the order of

$O(\log n)$. This is consistent with the best-known result in the literature of community detection without outliers by spectral clustering based on the adjacency matrices or graph Laplacians [see Lei and Rinaldo (2015)], although the $\log n$ barrier could be resolved by more sophisticated nonbacktracking matrix methods; see Krzakala et al. (2013). In this case, condition (3.1) becomes

$$\delta > C \left(\frac{\log n}{n} + \frac{\alpha}{n} + \frac{m}{n} + \frac{m}{\alpha - m} \frac{\log n}{n} \right).$$

Then by letting $\alpha = \log N$, $m = \log n$ outliers are allowed.

In the second example, we assume $\delta \simeq p^- \simeq q^+ \simeq O(1)$, and the number of clusters r grows with n . As a specific example, we let $r \simeq n^{1/4}$. Moreover, we assume $n_{\min} \simeq n^{3/4}$. Then condition (3.1) becomes

$$1 \gtrsim \sqrt{\log nn}^{-3/8} + \alpha n^{-3/4} + \sqrt{\log nn}^{-1/4} + mn^{-5/8} + n^{1/4} \frac{m}{\alpha - 2m}.$$

Then by letting $\alpha = N^{3/4}$, $m = O(n^{1/2-\varepsilon})$ outliers are allowed for any $\varepsilon > 0$.

A prominent feature of Theorem 3.1 is its consistency with the state-of-the-art community detection under the ordinary SBM in the literature. Assume there is no outlier node, that is, $m = 0$, and we simply let $\alpha = O(1)$ or just $\alpha = 0$. Then condition (3.1) becomes

$$\delta > C \left(\sqrt{\frac{p^- \log n}{n_{\min}}} + \frac{\sqrt{nq^+ \log n}}{n_{\min}} \right).$$

If the number of clusters is fixed, that is, $r = O(1)$, we also assume the size of the smallest community $n_{\min} = O(n)$. As mentioned above, this condition is guaranteed by letting the minimum within-group density p^- to be as low as $O(\frac{\log n}{n})$ and the density gap $\delta = O(\frac{\log n}{n})$. In another example where $p^- = O(1)$, $q^+ = O(1)$ and $\delta = O(1)$, condition (3.1) is equivalent to $n_{\min} \geq O(\sqrt{n \log n})$. By modifying Lemma 6.7 as discussed in Section 6, this condition can be relaxed to $n_{\min} \geq O(\sqrt{n})$. This is consistent with the state-of-the-art result in the community detection literature by spectral clustering [see, e.g., Chaudhuri, Chung and Tsias (2012)], and planted partition [see, e.g., Giesen and Mitsche (2005), Shamir and Tsur (2007), Oymak and Hassibi (2011), Ames (2014), Chen, Sanghavi and Xu (2012)] where the within-group densities are usually assumed to be the same, so do the cross-group densities. The $O(\sqrt{n})$ barrier of the small cluster size is well known in the literature of planted clique problems; see Deshpande and Montanari (2015) and the references therein.

REMARK 3.1. The proof of Theorem 3.1 is involved, and the details are given in Section 6. It is helpful to understand the intuition behind the proof.

The optimization (2.3) consists of two parts: a linear objective function and a constraint set which is the intersection of a polytope and the semidefinite cone. In order to show that the solution of (2.3) has the form of (3.3), we find a point on the boundary of the constraint set such that this point has the form of (3.3). Moreover, we prove that a level set of the linear objective function is tangent to the tangent cone of the constraint set at the selected point. This shows that the selected point is the solution of (2.3). It is noteworthy that the level set of the linear objective function is in fact a hyperplane with co-dimension 1, so the selected point is a sharp vertex of the constraint set. For more details, see the remark before the proof Lemma 6.10 in the supplemental article Cai and Li (2015).

Theorem 3.1 shows that the semidefinite programming (2.3) can discriminate the different groups among the inlier nodes. However, the clustering result is not clear by only the observation of $\widehat{\mathbf{X}}$, and it is not clear how the outliers could affect the final clustering result. Given the extra knowledge of the number of clusters, we propose to cluster the normalized column vectors of $\widehat{\mathbf{X}}$ by k -means with parameter r . To be specific, without loss of generality, let us assume $\mathbf{P} = \mathbf{I}$, and define

$$\widehat{\mathbf{X}} = \begin{bmatrix} \mathbf{J}_{l_1} & & & \widehat{\mathbf{Z}}_1 \\ & \ddots & & \vdots \\ & & \mathbf{J}_{l_r} & \widehat{\mathbf{Z}}_r \\ \widehat{\mathbf{Z}}_1^\top & \dots & \widehat{\mathbf{Z}}_r^\top & \widehat{\mathbf{W}} \end{bmatrix} = [\mathbf{x}_1, \dots, \mathbf{x}_N].$$

Moreover, define $\mathbf{y}_i = \mathbf{x}_i / \|\mathbf{x}_i\|_2$. Then all \mathbf{y}_i 's belong to the set of N -dimensional vectors with two-norm 1 and all coordinates being nonnegative. Notice that if $\mathbf{x}_i = \mathbf{0}$, we then define \mathbf{y}_i as an arbitrary nonnegative vector with norm 1. Then, for any inlier indices $i, j \in I$ and $\phi(i) \neq \phi(j)$, we have

$$\|\mathbf{y}_i - \mathbf{y}_j\|_2^2 = 2 - 2\mathbf{y}_i^\top \mathbf{y}_j \geq 2 - \frac{2m}{n_{\min}},$$

and for any $i, j \in I$ and $\phi(i) = \phi(j) = k$, we have

$$\|\mathbf{y}_i - \mathbf{y}_j\|_2^2 = 2 - 2\mathbf{y}_i^\top \mathbf{y}_j \leq 2 - \frac{2l_k}{l_k + m} = \frac{2m}{l_k + m} \leq \frac{2m}{l_k}.$$

Moreover, for any \mathbf{y}_i and \mathbf{y}_j , since both of them are nonnegative, we have

$$\|\mathbf{y}_i - \mathbf{y}_j\|_2^2 = 2 - 2\mathbf{y}_i^\top \mathbf{y}_j \leq 2.$$

By definition, the solution to the k -means applied to $\{\mathbf{y}_1, \dots, \mathbf{y}_N\}$ is

$$(3.4) \quad \operatorname{argmin}_{S, \boldsymbol{\mu}_1, \dots, \boldsymbol{\mu}_r} \sum_{k=1}^r \sum_{\mathbf{y}_j \in S_k} \|\mathbf{y}_j - \boldsymbol{\mu}_k\|^2,$$

where $\mathcal{S} = \{S_1, \dots, S_r\}$ is all r nonoverlapping partitions of $[N]$. It is obvious that $\boldsymbol{\mu}_k = \frac{1}{|S_k|} \sum_{\mathbf{y}_j \in S_k} \mathbf{y}_j$. We define $D_i = \phi^{-1}(k)$ for all $k = 1, \dots, r+1$, and choose $\tilde{\boldsymbol{\mu}}_k$ as any vector \mathbf{y}_i belonging to the k th community, that is, $\phi(i) = k$. Then there holds

$$\begin{aligned}
(3.5) \quad \min_{\mathcal{S}, \boldsymbol{\mu}_1, \dots, \boldsymbol{\mu}_r} \sum_{k=1}^r \sum_{\mathbf{y}_j \in S_k} \|\mathbf{y}_j - \boldsymbol{\mu}_k\|^2 &\leq \sum_{k=1}^{r-1} \sum_{\mathbf{y}_j \in D_k} \|\mathbf{y}_j - \tilde{\boldsymbol{\mu}}_k\|^2 + \sum_{\mathbf{y}_j \in D_r \cup D_{r+1}} \|\mathbf{y}_j - \tilde{\boldsymbol{\mu}}_r\|^2 \\
&\leq \sum_{k=1}^r \sum_{\mathbf{y}_j \in D_k} \|\mathbf{y}_j - \tilde{\boldsymbol{\mu}}_k\|^2 + \sum_{\mathbf{y}_j \in D_{r+1}} \|\mathbf{y}_j - \tilde{\boldsymbol{\mu}}_r\|^2 \\
&\leq \left(\sum_{k=1}^r l_k \frac{2m}{l_k} \right) + 2m = 2mr + 2m.
\end{aligned}$$

Suppose the solution to the k -means clustering is $\widehat{S}_1, \dots, \widehat{S}_r$ and $\widehat{\boldsymbol{\mu}}_k = \frac{1}{|\widehat{S}_k|} \sum_{\mathbf{y}_j \in \widehat{S}_k} \mathbf{y}_j$. For each $j \in \widehat{S}_k$, define $\widehat{\phi}(j) := k$. Now we show that if $m < \frac{n_{\min}}{2r+4}$, each D_i , $i = 1, \dots, r$ must account for more than 50 percent in some cluster \widehat{S}_k . Assume this is not true. Then there is a D_i being minority in each \widehat{S}_k , and hence for each $\mathbf{y}_{a_j} \in D_i$, there exists a $\mathbf{y}_{b_j} \notin D_i$, but $\widehat{\phi}(\mathbf{y}_{a_j}) = \widehat{\phi}(\mathbf{y}_{b_j})$. Moreover, all these $2l_i$ indices are distinct. This implies

$$\sum_{k=1}^r \sum_{\mathbf{y}_j \in \widehat{S}_k} \|\mathbf{y}_j - \widehat{\boldsymbol{\mu}}_k\|^2 \geq \sum_{j=1}^{l_i} \frac{1}{2} \|\mathbf{y}_{a_j} - \mathbf{y}_{b_j}\|_2^2 \geq (l_i - m) \left(1 - \frac{m}{n_{\min}} \right).$$

We then have $(n_{\min} - m)(1 - \frac{m}{n_{\min}}) \leq 2m(r+1)$, which is contradictory to the assumption $m < \frac{n_{\min}}{2r+4}$.

Since each D_i is the majority of some estimated community \widehat{S}_k , we can give the definition of misclassification rate among the inliers: suppose there are p pairs $(\mathbf{y}_{a_1}, \mathbf{y}_{b_1}), \dots, (\mathbf{y}_{a_p}, \mathbf{y}_{b_p})$ such that all $2p$ indices are distinct, $1 \leq \phi(\mathbf{y}_{a_j}) < \phi(\mathbf{y}_{b_j}) \leq r$ for all $j = 1, \dots, p$ but $\widehat{\phi}(\mathbf{y}_{a_j}) = \widehat{\phi}(\mathbf{y}_{b_j})$. The misclassification rate among the inliers is defined as $\max \frac{p}{n}$ for all possible p satisfying the above property. Now we give an example showing why this definition of misclassification rate is appropriate. Suppose n balls have r colors as well as m uncolored balls, and we assign them into r boxes. In the i th box, we assume there are s_i balls having color i , while there are t_i balls which are colored other than i . Moreover, we also assume the assignment is acceptable in the sense that $s_i > t_i$. In the i th box, there are at most t_i distinct pairs of colored balls such that in each pair the colors are different. By our definition, the misclassification rate is $\frac{t_1 + \dots + t_r}{n}$, which is the natural definition.

Back to our robust community detection problem, if we assume the misclassification rate among the inliers is $\frac{p}{n}$, we have

$$\sum_{k=1}^r \sum_{\mathbf{y}_j \in \hat{S}_k} \|\mathbf{y}_j - \hat{\boldsymbol{\mu}}_k\|^2 \geq \frac{1}{2} \sum_{j=1}^p \|\mathbf{y}_{a_j} - \mathbf{y}_{b_j}\|_2^2 \geq p \left(1 - \frac{m}{n_{\min}}\right).$$

Therefore, we have

$$\frac{p}{n} \leq \frac{2mr + 2m}{(1 - (m/n_{\min}))n} \leq \frac{(2r + 3)m}{n}$$

provided $m < \frac{n_{\min}}{2r+4}$. In summary, we have proven the following theorem, which guarantees that the misclassification rate among the inliers can be well controlled:

THEOREM 3.2. *Suppose the assumptions in Theorem 3.1 hold as well as $m < \frac{n_{\min}}{2r+4}$. Then, with high probability, the misclassification rate among the inlier nodes $i \in I$ is less than or equal to $\frac{(2r+3)m}{n}$.*

Rigorously speaking, k -means minimization is computationally NP-hard, although in practice it is often easy and fast to implement with a number of repetitions. However, as shown in Kumar, Sabharwal and Sen [(2011), Theorem 4.9], there is a $(1 + \varepsilon)$ approximate k -means clustering for (3.4) with computational time $O(2^{(r/\varepsilon)^{O(1)}} N^2)$, which is polynomial time when r is a constant. Suppose $\{\check{S}_1, \dots, \check{S}_r\}$ is a polynomial time approximate k -means solution, such that

$$\begin{aligned} \sum_{k=1}^r \sum_{\mathbf{y}_j \in \check{S}_k} \|\mathbf{y}_j - \check{\boldsymbol{\mu}}_k\|^2 &\leq (1 + \varepsilon) \min_{S, \boldsymbol{\mu}_1, \dots, \boldsymbol{\mu}_r} \sum_{k=1}^r \sum_{\mathbf{y}_j \in S_k} \|\mathbf{y}_j - \boldsymbol{\mu}_k\|^2 \\ &\leq (1 + \varepsilon)(2mr + 2m). \end{aligned}$$

Then if within the inliers there are p misclassified nodes by $\{\check{S}_1, \dots, \check{S}_r\}$, similarly to the previous argument, we get $\frac{p}{n} \leq \frac{(1+\varepsilon)(2r+3)m}{n}$.

When r grows with N , one can also cluster the rows of $\hat{\mathbf{X}}$ in (3.3) based on the ℓ_1 distance. If two inlier nodes belong to the same community, their corresponding rows in $\hat{\mathbf{X}}$ have ℓ_1 distance less than m ; on the other hand, if two inlier nodes belong to different communities, their corresponding rows have ℓ_1 distance greater than $2n_{\min}$. If the number of outliers is far less than the minimum size of the major clusters, for example, $n_{\min} > O(m^2)$, a pairwise comparison between the rows of $\hat{\mathbf{X}}$ can detect the inlier communities accurately even without the knowledge of r . However, this method does not work as effectively as k -means clustering in numerical simulations. An

interesting direction for future research is to figure out whether there is a polynomial time $(1 + \varepsilon)$ approximation k -means clustering for (3.4) when r grows with N .

4. Numerical results. In this section, synthetic data and a real-world network data are employed to demonstrate the efficiency and effectiveness of our community detection procedure: convex optimization (2.3) followed by k -means. As discussed in Section 2, throughout all numerical simulations of the augmented Lagrange multiplier method Algorithm 1, we fix $\alpha = 0$. All simulations were carried out with MATLAB R2014b on a MacBook Pro with a 2.66 GHz Intel Core i7 Processor and 4GB 1067 MHz DDR3 memory. As indicated in Algorithm 1, for the initialization, let $\mathbf{\Lambda}_0 = \mathbf{Z}_0 = \mathbf{0}$. Also, we fix $iter = 100$ and $\rho = 1$. As to the k -means clustering to the normalized columns of $\widehat{\mathbf{X}}$, we use the “kmeans” function in MATLAB with 100 replicates.

4.1. *Synthesized data simulations.* We consider again the synthetic data set used in Section 2. Figure 2 illustrates the adjacency matrix of a concrete realization of the original network. Suppose one knows that there are 2 major clusters, and a GSBM with $r = 2$ clusters is adopted.

We now explain in detail our implementation of Algorithm 1. First, we need to choose the tuning parameter λ between the maximum cross-group density q^+ and the minimum within-group density p^- . Ideal choices of λ are formalized by condition (3.2) in Theorem 3.1. In practice, we propose a simple method to choose λ as the mean connectivity density in a subgraph determined by nodes with “moderate” degrees. If the adjacency matrix of the graph is denoted as \mathbf{A} , and $\mathbf{1}_N$ represents the N -dimensional vector with all coordinates equal to 1, then $\mathbf{A}\mathbf{1}_N$ represents the degrees of the N nodes. The nodes with degrees above the 80th percentile or below the 20th percentile are eliminated from the graph, and λ is chosen as the mean density of the *subgraph* determined by the remaining nodes. The purpose of choosing nodes with moderate degrees is to diminish the influence of the outliers. Notice that the mean density of the subgraph may be very different from the mean of $\mathbf{A}\mathbf{1}_N$, which is usually significantly affected by the outliers.

The convex method is implemented with λ mentioned above. As an illustration, in one realization of the synthetic data set, the solution to convex optimization (2.3), and the community detection result by further implementing k -means clustering with $k = r = 2$ are plotted in Figure 3.

We generated 10 independent graphical data sets, and correspondingly implemented 10 trials of Algorithm 1 followed by k -means clustering, as well as spectral clustering on the graph Laplacians and adjacency matrices. The average misclassification rate among the 1000 inlier nodes of our convex optimization method is 0.0063, which is much smaller than 1 percent. The average time cost for running Algorithm 1 followed by k -means

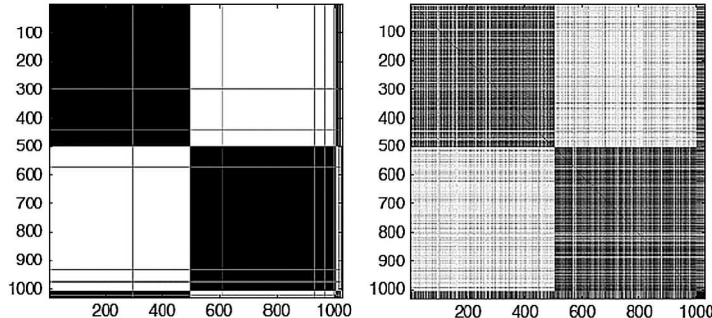


FIG. 3. On the right is the plot of the solution to convex optimization (2.3). Based on it, the community detection result followed by k -means algorithm is shown on the left.

clustering is 87.65 seconds. In contrast, if we apply spectral clustering to the graph Laplacians and adjacency matrices with $k = 2$, respectively, the average misclassification rates among the 1000 inlier nodes are 0.4792 and 0.5000, which are almost equivalent to random guessing. If we treat the 30 outliers as an additional group, and apply spectral clustering to the graph Laplacians and adjacency matrices with $k = 3$, the misclassification rates among all 1030 nodes are correspondingly 0.3083 and 0.4730. Consequently, the misclassification rates are high in terms of detecting the two major clusters.

Now let us study the sensitivity of our algorithm to the choice of λ . To be sure that λ is between $q = 0.11$ and $p = 0.17$, in Figure 4 the community detection results are plotted with $\lambda = 0.11, 0.12, \dots, 0.16$. It is obvious that for our data set the clustering power is robust to λ , unless λ is too close to p . To our surprise, even when $\lambda = q$, the two major clusters are well clustered. This is possibly due to the facts that the graph is relatively sparse and the solution after 100 iterations is still not exactly the solution to (2.3).

On the right of Figure 3, we see that the solution to (2.3) is close to but not exactly equal to what Theorem 3.1 predicts. A possible reason is that the density gap in our synthetic data is not large enough. It is interesting that although the solution does not have exactly the same form as in Theorem 3.1, the k -means in the second step can still successfully cluster the two groups of nodes. We replace the within density $p = 0.17$ with 0.19, 0.21, \dots , 0.29, and the solutions to (2.3) are plotted in Figure 5, respectively. The solutions appear to be closer to the form in Theorem 3.1 as the density gap increases.

4.2. Real data application. In this section, our robust community detection procedure is tested by implementing a modified version of convex optimization (2.3) on a political blogs network data set analyzed in Adamic and Glance (2005). This network data set collected in 2005 is composed of political blogs and their connections by hyperlinks, and it demonstrates the

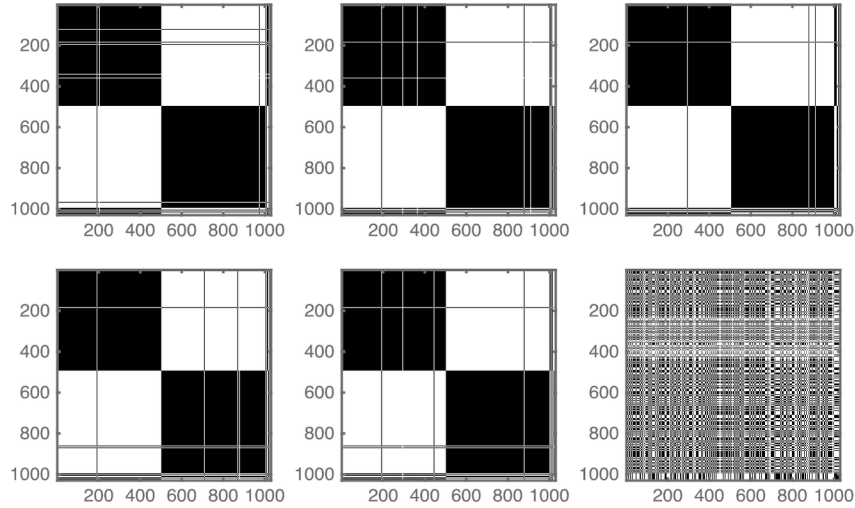


FIG. 4. *The performance of convex community detection with different values of λ .*

division and interaction between the liberal and conservative blogs prior to the 2004 presidential election. By ignoring the directions of the hyperlinks and selecting the largest connected component, there are totally 1222 nodes and 16,714 edges, which implies that the average degree is about 27. As indicated in Zhao, Levina and Zhu (2012), the distribution of the degrees is highly skewed to the right and has high variability. Also, the political memberships of all blogs are clearly studied and labeled manually in Adamic and

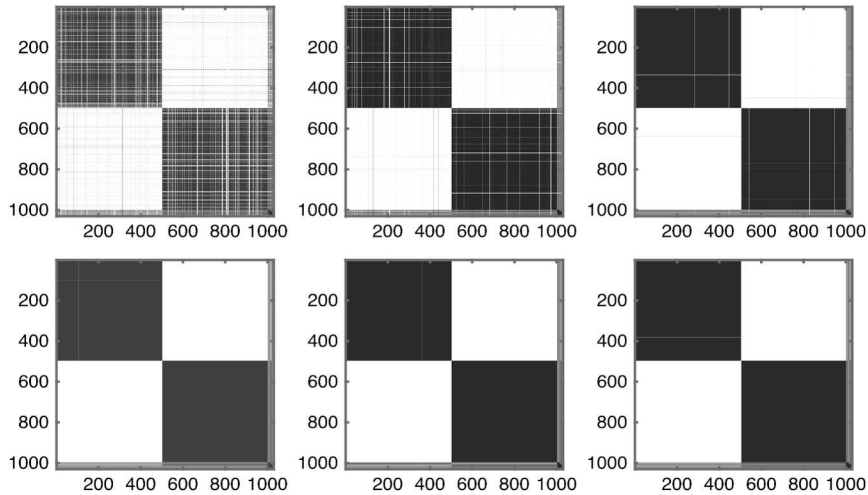


FIG. 5. *The solutions of (2.3) with different values of p .*

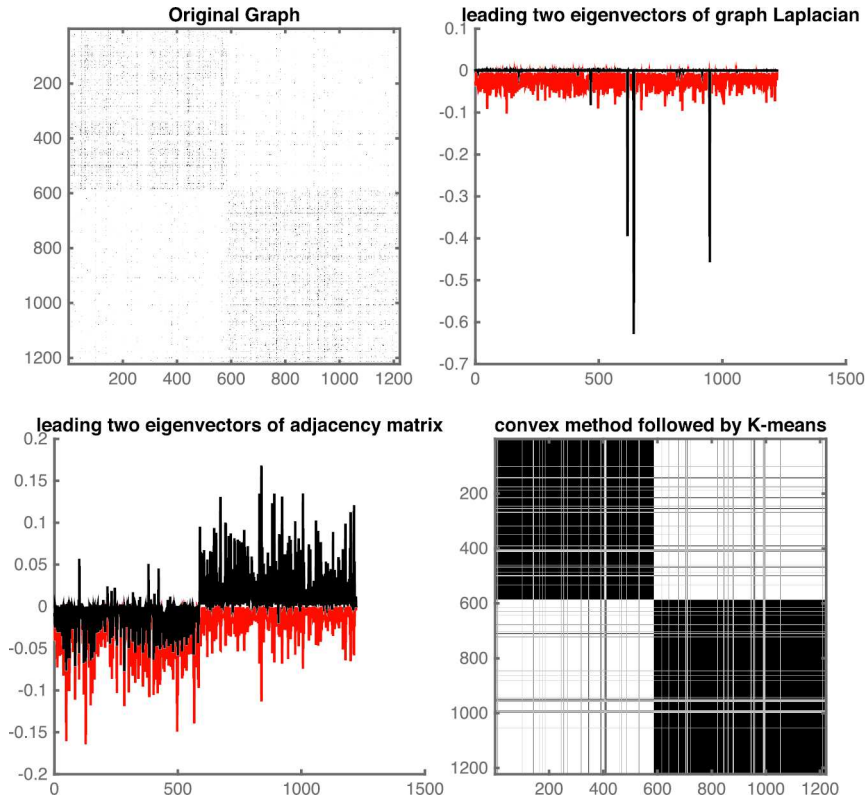


FIG. 6. Political blogs data of two clusters of conservatives and liberals, along with the performance of convex optimization.

Glance (2005), and are treated as the truth for the purpose of evaluating the clustering efficacy of different algorithms. The upper left panel of Figure 6 plots the adjacency matrix of the observed political blogs network.

Since the degrees in this real-world network data have high variability, most community detection methods derived from the simple SBM do not perform well. Instead, algorithms based on the so-called degree-corrected SBM are proposed and proven to work well. For instance, a polynomial time spectral method based on such a model is introduced in Coja-Oghlan and Lanka (2009/10). Back to convex optimization (2.3), modification of the matrix \mathbf{E} is needed to adapt to the heterogeneity of the degrees. As mentioned earlier in Section 4.1 on the synthetic data simulation, λ is chosen data dependently as the mean of the degrees in a trimmed graph. When the degrees have high variability, we propose to change the scalar matrix $\lambda \mathbf{I}_N$ to the diagonal matrix $\mathbf{D} = \text{Diag}(\mathbf{A}\mathbf{1}_N)/N$, the diagonal entries of which are the degrees of all nodes divided by N . In brief, the modified convex

optimization is (2.3) with

$$(4.1) \quad \mathbf{E} := -(\mathbf{I}_N - \mathbf{D})^{1/2} \mathbf{A} (\mathbf{I}_N - \mathbf{D})^{1/2} + \mathbf{D}^{1/2} (\mathbf{J}_N - \mathbf{I}_N - \mathbf{A}) \mathbf{D}^{1/2}.$$

In the second step of our proposed community detection procedure, we choose $k = r = 2$ in the k -means clustering. As a result, our community detection procedure applied to the real-world network data set only costs 137.16 seconds to accurately cluster these 1222 nodes with a misclassification rate about $63/1222 \approx 0.052$. The lower right panel of Figure 6 shows this clustering result by plotting the adjacency matrix of the clustered graph, in which two nodes are connected if and only if they are clustered in the same group.

The misclassification rate is comparable to the best-known results in the literature. The SCORE method proposed in Jin (2015) leads to a misclassification rate of $58/1222$. Profile likelihood method under degree-corrected SBM [Karrer and Newman (2011)] and Newman–Girvan modularity method [Newman and Girvan (2004), Zhao, Levina and Zhu (2012)] usually have misclassification rates about 0.05. However, as indicated in Jin (2015), the tabu algorithm implemented to maximize these criteria is computationally expensive and is numerically unstable due to bad initializations. It is shown in Jin (2015) that the average misclassification of the modularity method is about $105/1222$ based on 100 independent repetitions.

As to classical spectral clustering, the upper right and lower left panels of Figure 6 show that the two eigenvectors of the graph Laplacian/adjacency matrix corresponding to the top two eigenvalues are not capable in detecting and distinguishing the liberal and conservative political blogs. Hence, ordinary spectral clustering does not work when applied to this data set. A data-dependent penalized spectral clustering applied to the graph Laplacian was proposed in Joseph and Yu (2013), but the misclassification rate is nearly 0.2, which is much worse than our result.

5. Discussion. In this paper we introduce the GSBM for robust community detection in the presence of arbitrary outlier nodes, and propose a computationally feasible method using convex optimization. Strong theoretical guarantees are established under mild technical conditions. In particular, when the number of clusters is fixed and the edge density within the inliers is $O(\frac{\log n}{n})$, $O(\log n)$ outliers are allowed; when the edge density within the inliers is on the order of $O(1)$, and the number of clusters grows with n , for example, $O(n^{1/4})$, our method is robust against $O(n^{1/2-\varepsilon})$ adversarial outliers. Under the special case when there is no outlier node, our theoretical result is also consistent with the state-of-the-art results in the literature of computationally feasible community detection under the SBM.

There are a number of possible extensions to the current results. The proposed community detection procedure as well as the theoretical guarantees depend on the assumption $\delta = p^- - q^+ > 0$. Although this assumption is common in the literature of community detection, it is actually a strong assumption which sometimes does not hold in real-world network data applications. For example, suppose there are $r = 3$ clusters, and the connectivity matrix is

$$\begin{bmatrix} 0.4 & 0.2 & 0.05 \\ 0.2 & 0.3 & 0.05 \\ 0.05 & 0.05 & 0.1 \end{bmatrix}.$$

For each node, its associated within-group density is bigger than its associated cross-group densities; however,

$$\max_{1 \leq i < j \leq r} B_{ij} > \min_{1 \leq i \leq r} B_{ii}.$$

Therefore, in the current framework no choice of the tuning parameter λ is capable of the consistent community detection, which implies the matrix \mathbf{E} in the convex optimization step must be modified. In fact, in our simulations, λ is replaced by a data-dependent diagonal matrix based on the degrees of all nodes in order to adapt to high-degree variation. We are interested in justifying this choice under the degree-corrected SBM proposed in Coja-Oghlan and Lanka (2009/10) and analyzed in Karrer and Newman (2011), Zhao, Levina and Zhu (2012), Chaudhuri, Chung and Tsiatas (2012), Jin (2015), Lei and Rinaldo (2015).

In our numerical simulations, contrary to the established theoretical guarantees, the choices of α are much smaller than the number of outlier nodes m . In fact, the procedure works well with the choice $\alpha = 0$. An open question is whether this tuning parameter is actually redundant. In addition, in the second step of our procedure, the number of major inlier clusters r is needed. Since the solution of the convex optimization usually increases the connections within the major groups and diminishes the connections across them, it is natural and interesting to investigate whether r can be inferred exactly from the data. For reasons of space, we leave these as future work.

6. Proofs.

6.1. *Notation.* Throughout the proofs we will use the following notation: the $\ell \times \ell$ identity matrix is denoted by \mathbf{I}_ℓ . An $\ell_1 \times \ell_2$ matrix whose entries all equal to 1 is denoted as $\mathbf{J}_{(\ell_1, \ell_2)}$. For square matrices, we write $\mathbf{J}_\ell := \mathbf{J}_{(\ell, \ell)}$. An ℓ -dimensional vector whose coordinates all equal to 1 is denoted as $\mathbf{1}_\ell$.

If all coordinates of a vector \mathbf{v} are nonnegative, we write $\mathbf{v} \geq \mathbf{0}$. When all coordinates of \mathbf{v} are positive, we write $\mathbf{v} > \mathbf{0}$. We use $\mathbf{u} \geq \mathbf{v}$ to denote

$\mathbf{u} - \mathbf{v} \geq \mathbf{0}$, and similarly, $\mathbf{u} > \mathbf{v}$ denotes $\mathbf{u} - \mathbf{v} > \mathbf{0}$. We also denote by $\|\mathbf{x}\|_\infty$ the maximum absolute values over all coordinates of \mathbf{x} .

Similarly, if all entries of the matrix \mathbf{M} are nonnegative, we write $\mathbf{M} \geq \mathbf{0}$. When all entries of \mathbf{M} are positive, we write $\mathbf{M} > \mathbf{0}$. The inequality $\mathbf{M}_1 \geq \mathbf{M}_2$ denotes $\mathbf{M}_1 - \mathbf{M}_2 \geq \mathbf{0}$, while $\mathbf{M}_1 > \mathbf{M}_2$ denotes $\mathbf{M}_1 - \mathbf{M}_2 > \mathbf{0}$. Denote by $\|\mathbf{M}\|_\infty$ the maximum absolute value over all entries of \mathbf{M} . The norms $\|\cdot\|$ and $\|\cdot\|_F$ represent the operator and Frobenius norms, respectively.

We use $\mathbf{M} \succ \mathbf{0}$ to denote that the symmetric matrix \mathbf{M} is positive definite and use $\mathbf{M} \succeq \mathbf{0}$ to denote that \mathbf{M} is positive semidefinite. Similarly $\mathbf{M}_1 \succ \mathbf{M}_2$ and $\mathbf{M}_1 \succeq \mathbf{M}_2$ represent that $\mathbf{M}_1 - \mathbf{M}_2$ is positive definite and positive semidefinite, respectively.

For any vector $\mathbf{v} \in \mathbb{R}^n$, we denote by $\text{Diag}(\mathbf{v})$ the $n \times n$ diagonal matrix whose diagonal entries are correspondingly the coordinates of \mathbf{v} .

Denote by C, C_0, c , etc. numerical constants, whose values could change from line to line.

6.2. Preliminaries. Before proving Theorem 3.1, we introduce several well-known theorems in linear algebra and probability theory.

LEMMA 6.1 (Weyl [Horn and Johnson (2013), Theorem 4.3.1]). *Let \mathbf{H} and \mathbf{P} be two $n \times n$ Hermitian matrices. Suppose that $\mathbf{H} + \mathbf{P}$, \mathbf{H} and \mathbf{P} have real eigenvalues $\{\lambda_i(\mathbf{H} + \mathbf{P})\}_{i=1}^n$, $\{\lambda_i(\mathbf{H})\}_{i=1}^n$ and $\{\lambda_i(\mathbf{P})\}_{i=1}^n$, each arranged in algebraically nonincreasing order. Then for $i = 1, \dots, n$ we have*

$$\lambda_i(\mathbf{H}) + \lambda_n(\mathbf{P}) \leq \lambda_i(\mathbf{H} + \mathbf{P}) \leq \lambda_i(\mathbf{H}) + \lambda_1(\mathbf{P}).$$

LEMMA 6.2 (Cauchy's interlacing theorem [Horn and Johnson (2013), Theorem 4.3.28]). *Let \mathbf{H} be an $n \times n$ Hermitian matrix and \mathbf{G} its $k \times k$ principal submatrix. Suppose that \mathbf{H} and \mathbf{G} have real eigenvalues $\{\lambda_i(\mathbf{H})\}_{i=1}^n$ and $\{\lambda_i(\mathbf{G})\}_{i=1}^k$, each arranged in algebraically nonincreasing order. Then for $j = 1, \dots, k$ we have*

$$\lambda_j(\mathbf{H}) \geq \lambda_j(\mathbf{G}) \geq \lambda_{j+n-k}(\mathbf{H}).$$

LEMMA 6.3 (Chernoff's inequality [Chernoff (1981)]). *Let X_1, \dots, X_n be independent random variables with*

$$\mathbb{P}(X_i = 1) = p_i, \quad \mathbb{P}(X_i = 0) = 1 - p_i.$$

Then the sum $X = \sum_{i=1}^n X_i$ has expectation $\mathbb{E}(X) = \sum_{i=1}^n p_i$, and we have

$$\begin{aligned} \mathbb{P}(X \leq \mathbb{E}(X) - \lambda) &\leq e^{-\lambda^2/(2\mathbb{E}(X))}, \\ \mathbb{P}(X \geq \mathbb{E}(X) + \lambda) &\leq e^{-\lambda^2/(2(\mathbb{E}(X) + \lambda/3))}. \end{aligned}$$

Finally, we consider the following problem: suppose that $\mathbf{A} = (a_{ij})_{1 \leq i, j \leq n}$ is a random symmetric matrix, whose diagonal entries are all zeros, while $a_{ij}, 1 \leq i < j \leq n$ are independent zero-mean Bernoulli random variables obeying $|a_{ij}| \leq 1$ and $\text{Var}(a_{ij}) \leq \sigma^2$. Can we prove that with high probability, $\|\mathbf{A}\| \leq C(\sigma\sqrt{n \log n} + \log n)$ for some numerical constant C ? In the sequel, this upper bound is derived by applying the following matrix Bernstein inequality, which is an improvement of Ahlswede and Winter (2002):

LEMMA 6.4 [Tropp (2012), Theorem 6.1]. *Consider a finite sequence $\{\mathbf{X}_k\}$ of independent, random, self-adjoint matrices with dimension d . Assume that*

$$\mathbb{E}\mathbf{X}_k = \mathbf{0} \quad \text{and} \quad \|\mathbf{X}_k\| \leq R.$$

If the norm of the total variance satisfies

$$\left\| \sum_k \mathbb{E}(\mathbf{X}_k^2) \right\| \leq M^2,$$

then the following inequality holds for all $t \geq 0$:

$$\mathbb{P}\left\{ \left\| \sum_k \mathbf{X}_k \right\| \geq t \right\} \leq 2d \exp\left(\frac{-t^2/2}{M^2 + Rt/3} \right).$$

COROLLARY 6.5. *Let $\mathbf{A} = (a_{ij})_{1 \leq i, j \leq n}$ be a symmetric random matrix whose diagonal entries are all zeros. Moreover, suppose $a_{ij}, 1 \leq i < j \leq n$ are independent zero-mean random variables satisfying $|a_{ij}| \leq 1$ and $\text{Var}(a_{ij}) \leq \sigma^2$. Then, with probability at least $1 - \frac{c}{n^4}$, we have*

$$\|\mathbf{A}\| \leq C_0(\sigma\sqrt{n \log n} + \log n)$$

for some numerical constants c and C_0 .

PROOF. For each pair $(i, j): 1 \leq i < j \leq n$, let \mathbf{X}_{ij} be the matrix whose (i, j) and (j, i) entries are both a_{ij} , whereas other entries are zeros. Then we have

$$\mathbf{A} = \sum_{1 \leq i < j \leq n} \mathbf{X}_{ij}.$$

Moreover, we can easily have $\mathbb{E}\mathbf{X}_{ij} = \mathbf{0}$, $\|\mathbf{X}_{ij}\| \leq 1$ and

$$\mathbf{0} \preceq \sum_{1 \leq i < j \leq n} \mathbb{E}\mathbf{X}_{ij}^2 \preceq (n-1)\sigma^2\mathbf{I}_n.$$

They by applying Lemma 6.4, the proof is complete. \square

6.3. *Supporting lemmas.* Notice that optimization (2.3) is determined by the adjacency matrix \mathbf{A} . Here we derive some properties of \mathbf{A} and leave the detailed proofs in the supplemental article Cai and Li (2015). More precisely, we give some properties of the random matrix \mathbf{K} , which is a principal submatrix of \mathbf{A} ; see (1.3).

LEMMA 6.6. *Recall that $p^- = \min_{1 \leq i \leq r} B_{ii}$, $q^+ = \max_{1 \leq i < j \leq r} B_{ij}$ and $\delta = p^- - q^+$. If*

$$(6.1) \quad \delta > C \left(\sqrt{\frac{q^+ \log n}{n_{\min}}} + \frac{\log n}{n_{\min}} \right),$$

for some sufficiently large numerical constant C , then with probability at least $1 - \frac{2}{n} - \frac{2r}{n^2}$, for all $i = 1, \dots, r$ and $1 \leq j < k \leq r$, we have

$$(6.2) \quad \mathbf{K}_{ii} \mathbf{1}_{l_i} \geq ((l_i - 1)B_{ii} - 2\sqrt{(l_i - 1)B_{ii} \log n}) \mathbf{1}_{l_i},$$

$$(6.3) \quad \mathbf{K}_{jk} \mathbf{1}_{l_k} \leq \left(B_{jk} + \frac{\delta}{16} \right) l_k \mathbf{1}_{l_j},$$

$$(6.4) \quad \mathbf{K}_{jk}^\top \mathbf{1}_{l_j} \leq \left(B_{jk} + \frac{\delta}{16} \right) l_j \mathbf{1}_{l_k},$$

$$(6.5) \quad \mathbf{1}_{l_j}^\top \mathbf{K}_{jk} \mathbf{1}_{l_k} \geq \left(B_{jk} - \frac{\delta}{16} \right) l_k l_j.$$

LEMMA 6.7. *Suppose $p^- \geq C \left(\frac{\log n}{n_{\min}} \right)$. With probability at least $1 - c \frac{r}{n_{\min}^4}$, we have*

$$(6.6) \quad \|B_{ii}(\mathbf{J}_{l_i} - \mathbf{I}_{l_i}) - \mathbf{K}_{ii}\| \leq C_0 \sqrt{l_i B_{ii} \log l_i}, \quad 1 \leq i \leq r$$

and

$$(6.7) \quad \|\mathbf{U}\| \leq C_0 (\sqrt{nq^+ \log n} + \log n),$$

where \mathbf{U} is an $n \times n$ symmetric matrix defined as

$$\mathbf{U} := \begin{bmatrix} \mathbf{0} & \dots & B_{1r} \mathbf{J}_{(l_1, l_r)} - \mathbf{K}_{1r} \\ \vdots & \ddots & \vdots \\ B_{1r} \mathbf{J}_{(l_1, l_r)} - \mathbf{K}_{1r}^\top & \dots & \mathbf{0} \end{bmatrix}$$

whose diagonal blocks are all $\mathbf{0}$'s. Here C , C_0 and c are some numerical constants.

It is worth noting that by applying a very recent result Vu [(2014), Lemma 8], which is an improvement of Füredi and Komlós (1981), Vu (2007),

we can prove $\|\mathbf{U}\| \leq C_0(\sqrt{nq^+} + \sqrt{\log n})$. Condition (3.1) in Theorem 3.1 can then be relaxed to

$$\delta > C \left(\sqrt{\frac{p^- \log n}{n_{\min}}} + \frac{\alpha}{n_{\min}} + \frac{\sqrt{nq^+}}{n_{\min}} + \frac{m\sqrt{r}}{n_{\min}} + \frac{nmp^-}{(\alpha - 2m)n_{\min}} \right).$$

The benefit is that when $m = O(1)$, $p^- = O(1)$, $q^+ = O(1)$ and $\delta = O(1)$, n_{\min} can be as small as $O(\sqrt{N})$ by letting $\alpha = \sqrt{N}$. In particular, if there is no outlier node, that is, the ordinary SBM, this is consistent with the state-of-the-art result in the literature of computationally feasible community detection.

6.4. *Proof of Theorem 3.1.* In this section, we will rigorously prove Theorem 3.1. First, to simplify the calculations, we can assume the permutation matrix \mathbf{P} to be the identity matrix \mathbf{I}_N . This suggestion is formalized by the following lemma:

LEMMA 6.8. *If Theorem 3.1 is true for $\mathbf{P} = \mathbf{I}_N$, it is also true for any permutation matrix \mathbf{P} .*

The proof is given in the supplemental article Cai and Li (2015). Lemma 6.8 guarantees that in order to prove Theorem 3.1, we can assume without loss of generality that $\mathbf{P} = \mathbf{I}$, that is, $\mathbf{A} = \begin{bmatrix} \mathbf{K} & \mathbf{Z} \\ \mathbf{Z}^\top & \mathbf{W} \end{bmatrix}$.

In the following, we will prove Theorem 3.1 based on the following idea: In order to analyze a solution $\hat{\mathbf{X}}$ to (2.3), we need to explore several inequalities that it satisfies. The obvious ones are $\hat{\mathbf{X}} \succeq \mathbf{0}$ and $\mathbf{0} \leq \hat{\mathbf{X}} \leq \mathbf{J}_N$ as the feasibility conditions in (2.3). However, the optimality condition of $\hat{\mathbf{X}}$ implies that for any feasible $\tilde{\mathbf{X}}$, we have $\langle \hat{\mathbf{X}}, \mathbf{E} \rangle \leq \langle \tilde{\mathbf{X}}, \mathbf{E} \rangle$. To sufficiently utilize this condition, we need to construct a feasible matrix \mathbf{X} , such that $\langle \hat{\mathbf{X}}, \mathbf{E} \rangle \leq \langle \mathbf{X}, \mathbf{E} \rangle$ is a tight constraint. In Section 6.4.1 we will show how to construct this \mathbf{X} .

After establishing these inequalities for any solution $\hat{\mathbf{X}}$, we give in Section 6.4.2 a sufficient condition which guarantees that $\hat{\mathbf{X}}$ has the form (3.3) (with $\mathbf{P} = \mathbf{I}$), and then in Section 6.4.3 we prove that with high probability this sufficient condition is true by using the supporting lemmas proven previously. Consequently, these three steps imply Theorem 3.1.

6.4.1. *Solution candidate.* In this section, we will construct a candidate solution \mathbf{X} feasible to (2.3). Denote

$$\mathbf{E} = \alpha \mathbf{I}_N + \lambda(\mathbf{J}_N - \mathbf{I}_N) - \mathbf{A}$$

$$:= \begin{bmatrix} (\alpha - \lambda)\mathbf{I}_{l_1} + \lambda\mathbf{J}_{l_1} - \mathbf{K}_{11} & \dots & \lambda\mathbf{J}_{(l_1, l_r)} - \mathbf{K}_{1r} & \tilde{\mathbf{Z}}_1 \\ \vdots & \ddots & \vdots & \vdots \\ \lambda\mathbf{J}_{(l_r, l_1)} - \mathbf{K}_{1r}^\top & \dots & (\alpha - \lambda)\mathbf{I}_{l_r} + \lambda\mathbf{J}_{l_r} - \mathbf{K}_{rr} & \tilde{\mathbf{Z}}_r \\ \tilde{\mathbf{Z}}_1^\top & \dots & \tilde{\mathbf{Z}}_r^\top & \tilde{\mathbf{W}} \end{bmatrix},$$

which is equivalent to defining

$$(6.8) \quad \tilde{\mathbf{Z}}_i = \lambda\mathbf{J}_{(l_i, m)} - \mathbf{Z}_i, \quad i = 1, \dots, r,$$

$$(6.9) \quad \tilde{\mathbf{W}} = (\alpha - \lambda)\mathbf{I}_m + \lambda\mathbf{J}_m - \mathbf{W}.$$

The following lemma, the proof of which is given in the supplemental article Cai and Li (2015), guarantees the existence of r vectors $\mathbf{x}_1, \dots, \mathbf{x}_r \in \mathbb{R}^m$, which will be employed to construct a candidate solution:

LEMMA 6.9. *If $\alpha \geq 2m$ and $0 < \lambda < 1$, the solution to*

$$(6.10) \quad \begin{aligned} \min \quad & \sum_{i=1}^r \langle \mathbf{x}_i, \tilde{\mathbf{Z}}_i^\top \mathbf{1}_{l_i} \rangle + \frac{1}{2} \sum_{i=1}^r \mathbf{x}_i^\top \tilde{\mathbf{W}} \mathbf{x}_i \\ \text{subject to} \quad & \mathbf{x}_i \geq \mathbf{0} \quad \text{for } 1 \leq i \leq r, \\ & \sum_{i=1}^r \mathbf{x}_i^\top (\mathbf{e}_j \mathbf{e}_j^\top) \mathbf{x}_i \leq 1 \quad \text{for } 1 \leq j \leq m, \end{aligned}$$

exists uniquely. Moreover, denote the solutions by $\mathbf{x}_1, \dots, \mathbf{x}_r \in \mathbb{R}^m$, which by definition satisfy $\|\mathbf{x}_i\|_\infty \leq 1$. Then there are nonnegative vectors $\beta_1, \dots, \beta_r \in \mathbb{R}^m$ and an $m \times m$ nonnegative diagonal matrix

$$\Xi = \text{diag}(\xi_1, \dots, \xi_m),$$

such that

$$(6.11) \quad \tilde{\mathbf{W}} \mathbf{x}_i + \tilde{\mathbf{Z}}_i^\top \mathbf{1}_{l_i} = \beta_i - \Xi \mathbf{x}_i,$$

$$(6.12) \quad \xi_j \left(1 - \sum_{i=1}^r \mathbf{x}_i^\top (\mathbf{e}_j \mathbf{e}_j^\top) \mathbf{x}_i \right) = 0, \quad j = 1, \dots, m$$

and

$$(6.13) \quad \langle \mathbf{x}_i, \beta_i \rangle = 0, \quad i = 1, \dots, r.$$

For all $1 \leq j, k \leq r$, there holds

$$(6.14) \quad \mathbf{x}_j^\top (\tilde{\mathbf{W}} + \Xi) \mathbf{x}_k \leq m \sqrt{l_j l_k}.$$

Furthermore, for all $i = 1, \dots, r$ and $j = 1, \dots, m$, we have

$$(6.15) \quad \beta_{i_j} + \mathbf{e}_j^\top \mathbf{Z}_i^\top \mathbf{1}_{l_i} \leq (\alpha - \lambda + \xi_j)x_{i_j} + \lambda l_i + \lambda \sum_{k=1}^m x_{i_k}.$$

Finally, for all $i = 1, \dots, r$,

$$(6.16) \quad \mathbf{0} \leq \beta_i \leq (m + l_i - 1)\mathbf{1}_m.$$

Throughout the paper, we define

$$\mathbf{V} := [\mathbf{v}_1, \dots, \mathbf{v}_r] := \begin{bmatrix} \mathbf{1}_{l_1} & \mathbf{0} & \dots & \mathbf{0} \\ \mathbf{0} & \mathbf{1}_{l_2} & \dots & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \dots & \mathbf{1}_{l_r} \\ \mathbf{x}_1 & \mathbf{x}_2 & \dots & \mathbf{x}_r \end{bmatrix}$$

and

$$\mathbf{X} = \mathbf{V}\mathbf{V}^\top = \begin{bmatrix} \mathbf{J}_{l_1} & \dots & \mathbf{0} & \mathbf{1}_{l_1}\mathbf{x}_1^\top \\ \vdots & \ddots & \vdots & \vdots \\ \mathbf{0} & \dots & \mathbf{J}_{l_r} & \mathbf{1}_{l_r}\mathbf{x}_r^\top \\ \mathbf{x}_1\mathbf{1}_{l_1}^\top & \dots & \mathbf{x}_r\mathbf{1}_{l_r}^\top & \mathbf{x}_1\mathbf{x}_1^\top + \dots + \mathbf{x}_r\mathbf{x}_r^\top \end{bmatrix}.$$

Since \mathbf{x}_i 's are feasible to optimization (6.10), we can easily see that \mathbf{X} is feasible to optimization (2.3). We aim to prove that under mild technical conditions, \mathbf{X} is actually a solution to optimization (2.3).

6.4.2. *Sufficient condition for the optimality of \mathbf{X} .* In this section, we propose a condition which guarantees that any solution $\widehat{\mathbf{X}}$ to (2.3) must be in the form of (3.3) with $\mathbf{P} = \mathbf{I}_N$. This sufficient condition is equivalent to constructing a matrix $\mathbf{\Lambda}$ satisfying a series of equalities and inequalities as indicated in the following lemma. We call it a dual certificate. In Section 6.4.3, we will show that with high probability, this dual certificate can be constructed in an explicit way.

LEMMA 6.10. *Suppose Ξ and β_1, \dots, β_r are defined as in Lemma 6.9. If there exist symmetric matrices $\mathbf{\Lambda} \in \mathbb{R}^{N \times N}$, $\Psi_{jj} \in \mathbb{R}^{l_j \times l_j}$ ($1 \leq j \leq r$) and*

matrices $\Phi_{jk} \in \mathbb{R}^{l_j \times l_k}$ ($1 \leq j < k \leq r$), such that

$$(6.17) \quad \Lambda = \begin{bmatrix} (\alpha - \lambda)\mathbf{I}_{l_1} + \lambda\mathbf{J}_{l_1} - \mathbf{K}_{11} + \Psi_{11} & \dots & \lambda\mathbf{J}_{(l_1, l_r)} - \mathbf{K}_{1r} - \Phi_{1r} & \tilde{\mathbf{Z}}_1 - \frac{1}{l_1}\mathbf{1}_{l_1}\beta_1^\top \\ \vdots & \ddots & \vdots & \vdots \\ \lambda\mathbf{J}_{l_r, l_1} - \mathbf{K}_{1r}^\top - \Phi_{1r}^\top & \dots & (\alpha - \lambda)\mathbf{I}_{l_r} + \lambda\mathbf{J}_{l_r} - \mathbf{K}_{rr} + \Psi_{rr} & \tilde{\mathbf{Z}}_r - \frac{1}{l_r}\mathbf{1}_{l_r}\beta_r^\top \\ \tilde{\mathbf{Z}}_1^\top - \frac{1}{l_1}\beta_1\mathbf{1}_{l_1}^\top & \dots & \tilde{\mathbf{Z}}_r^\top - \frac{1}{l_r}\beta_r\mathbf{1}_{l_r}^\top & \tilde{\mathbf{W}} + \Xi \end{bmatrix}$$

satisfies $\Psi_{ii} > \mathbf{0}$, $\Phi_{jk} > \mathbf{0}$, $\Lambda\mathbf{V} = \mathbf{0}$ and $\Lambda \succeq \mathbf{0}$, then any minimizer $\hat{\mathbf{X}}$ to (2.3) must be of the form

$$\hat{\mathbf{X}} = \begin{bmatrix} \mathbf{J}_{l_1} & \dots & \mathbf{0} & \mathbf{1}_{l_1}\mathbf{x}_1^\top + \mathbf{H}_1 \\ \vdots & \ddots & \vdots & \vdots \\ \mathbf{0} & \dots & \mathbf{J}_{l_r} & \mathbf{1}_{l_r}\mathbf{x}_r^\top + \mathbf{H}_r \\ \mathbf{x}_1\mathbf{1}_{l_1}^\top + \mathbf{H}_1^\top & \dots & \mathbf{x}_r\mathbf{1}_{l_r}^\top + \mathbf{H}_r^\top & \mathbf{x}_1\mathbf{x}_1^\top + \dots + \mathbf{x}_r\mathbf{x}_r^\top + \mathbf{H}_0 \end{bmatrix},$$

which is the same as (3.3). Moreover, \mathbf{X} is a solution to (2.3).

An intuition behind the theorem and the rigorous proof are given in the supplemental article Cai and Li (2015). It is noteworthy that the condition on Λ is weaker if the number of clusters r gets smaller. The reason is that the equality condition is $\Lambda\mathbf{V} = \mathbf{0}$. Obviously when r gets smaller, \mathbf{V} has fewer columns, and hence the equality constraint becomes milder. We emphasize that the choices of Ψ_{ii} and Φ_{ij} are intended to fit the equality constraint of Λ , that is, $\Lambda\mathbf{V} = \mathbf{0}$. To make sure $\Lambda \succeq \mathbf{0}$, we need to first project Λ onto the orthogonal compliment of \mathbf{V} , and then show the projection is positive definite. This is based on the spectral norm bound as indicated in Lemma 6.7, which provides a concentration inequality for a random matrix.

6.4.3. *Construction of dual certificate.* It suffices to construct a matrix Λ in the form of (6.17) in Lemma 6.10, which satisfies $\Lambda\mathbf{V} = \mathbf{0}$, $\Psi_{ii} > \mathbf{0}$, $\Phi_{jk} > \mathbf{0}$ and $\Lambda \succeq \mathbf{0}$. The following lemma guarantees the existence of such Λ , and its proof is given in the supplemental article Cai and Li (2015).

LEMMA 6.11. *Suppose $p^- \geq C(\frac{\log n}{n_{\min}})$, $q^+ + \frac{\delta}{4} < \lambda < p^- - \frac{\delta}{4}$ and $\alpha \geq 3m$. Moreover, assume*

$$(6.18) \quad \delta > C \left(\sqrt{\frac{p^- \log n}{n_{\min}}} + \frac{\alpha}{n_{\min}} + \frac{\sqrt{nq^+ \log n}}{n_{\min}} + \frac{m\sqrt{r}}{n_{\min}} + \frac{nmp^-}{(\alpha - 2m)n_{\min}} \right)$$

for some sufficiently large numerical constant C . Then, with probability at least $1 - \frac{1}{n} - \frac{2r}{n^2} - \frac{cr}{n_{\min}^4}$, there exist matrices Ψ_{ii} 's and Φ_{jk} 's satisfying $\Psi_{ii} > \mathbf{0}$, $\Phi_{jk} > \mathbf{0}$ and the matrix Λ defined by Ψ_{ii} 's and Φ_{jk} 's obey $\Lambda\mathbf{V} = \mathbf{0}$ and $\Lambda \succeq \mathbf{0}$.

SUPPLEMENTARY MATERIAL

Supplemental materials to “Robust and computationally feasible community detection in the presence of arbitrary outliers nodes”

(DOI: [10.1214/14-AOS1290SUPP](https://doi.org/10.1214/14-AOS1290SUPP); .pdf). We give in the supplement proofs to Lemmas [6.6](#), [6.7](#), [6.8](#), [6.9](#), [6.10](#) and [6.11](#).

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