CONSISTENT BAYESIAN COMMUNITY DETECTION

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Stochastic Block Models (SBMs) are a fundamental tool for community detection in network analysis. But little theoretical work exists on the statistical performance of Bayesian SBMs, especially when the community count is unknown. This paper studies a special class of SBMs whose community-wise connectivity probability matrix is diagonally dominant, i.e., members of the same community are more likely to connect with one another than with members from other communities. The diagonal dominance constraint is embedded within an otherwise weak prior, and, under mild regularity conditions, the resulting posterior distribution is shown to concentrate on the true community count and membership allocation as the network size grows to infinity. A reversible-jump Markov Chain Monte Carlo posterior computation strategy is developed by adapting the allocation sampler of [19]. Finite sample properties are examined via simulation studies in which the proposed method offers competitive estimation accuracy relative to existing methods under a variety of challenging scenarios.

1. Introduction. Community detection is the most basic yet central statistical problem in network analysis. To determine the number of communities, various tests have been constructed based on modularity [29], random matrix theory [4, 17], and likelihood ratio [28]. Methods based on information criteria [25] and network cross-validation [5, 18] have also been designed. In the Bayesian realm, a stochastic block model (SBM) is often employed to jointly infer the number of communities, the connectivity probability matrix, and the membership assignment [22, 19, 8].

Despite clear empirical evidence of good statistical performance [19, 8], theoretical guarantees on Bayesian SBMs are a rarity when the number of communities is unknown. As the only exception, [8] show that the community count may be consistently estimated under the restrictive assumptions of a homogeneous SBM with at most three communities. It is unclear if their calculations generalize to more realistic scenarios. It is also not clear if Bayesian SBMs can consistently recover the true membership allocation.

We study a special class of SBMs whose community-wise connectivity probability matrix is diagonally dominant. This special class offers a stronger encoding of the notion of communities in networks in the sense that nodes within the same community are strictly more likely to connect with each other than with nodes from other communities. Crucially, the diagonal dominance condition enables membership allocations to be fully retrieved from the node-wise connectivity probabilities, as long as each community contains at least two nodes. Of course, the node-wise connectivity probability matrix is estimated from data with statistical error. But as long as it is sufficiently “close” to the truth, it is still possible to precisely recover the membership allocation and the community count.

For a Bayesian estimation of the diagonally-dominant SBM under a modified Nowicki-Snijders prior [22], we show the posterior on the node-wise connectivity matrix contracts...
to the truth in the sup-norm topology. Posterior contraction under sup-norm is necessary to the identification strategy detailed above. [13] establish near minimax optimal posterior contraction rates in the $L_2$ norm for dense networks with the true number of communities assumed known. However, posterior contraction in $L_2$ or other norms that are weaker than the sup-norm do not grant the identification of the number of communities or the membership assignment from node-wise connectivity probabilities. Our sup-norm posterior contraction calculation applies the Schwartz method [10, 11, 12]. The key observation is that the sup-norm is dominated by the Hellinger distance in the special context of SBMs, so the tests required by the Schwartz method exist.

The theoretical gains of the diagonally dominant SBMs come at the price of losing conjugacy with respect to the original Nowicki-Snijders prior. But posterior computation may be carried out with a reasonably efficient reversible-jump Markov chain Monte Carlo (MCMC) algorithm based of the allocation sampler in [19]. Results from extensive numerical studies show that our Bayesian diagonally-dominant SBM offers comparable and competitive statistical performance against various alternatives in estimating the community count and membership assignment.

2. The Diagonally Dominant Stochastic Block Model. Suppose an $n \times n$ binary adjacency matrix $A$ is observed, with entry $A_{ij} = 1$ if node $i$ and node $j$ are connected and $A_{ij} = 0$ otherwise. The stochastic block model (SBM) assumes there are $K \in \mathbb{Z}_+^+$ communities among the $n$ nodes and the connection between nodes exclusively depends on their community membership. The community assignment $Z$ partitions nodes $\{1, ..., n\}$ into $K$ non-empty groups and assigns each node with a community label. Let the community-wise connectivity probability matrix be $P \in [0,1]^{K \times K}$. Then,

$$A_{ij} | Z \sim \text{Ber}(P_{Z(i)Z(j)}) \text{ for } 1 \leq i < j \leq n,$$

and $P(A_{ii} = 0 | Z) = 1$ for $i \in \{1, ..., n\}$, assuming no self-loops. We denote the above SBM model as $SBM(Z, P, n, k)$. Due to its simplicity and expressiveness, SBM and its variants are fundamental tools for community detection [e.g., 15, 2, 23].

2.1. Bayesian SBM with conjugate priors. For Bayesian estimation of the SBM, [22] propose the following conjugate prior: given $K$,

$$P_{ab} \sim U(0, 1), a, b = 1, ..., K$$

$$Z_i \sim MN(\pi), i = 1, ..., n$$

$$\pi \sim \text{Dir}(\alpha).$$

This prior is widely used and adapted to more complicated cases in the Bayesian SBM literature [13, 27, 8, 19].

For the unknown $K$ case, to maintain conjugacy, it is natural to place a Poisson prior on $K$ [19, 8]. With conjugacy, [19] marginalize out $P$ from the posterior $\Pi_n(Z, K, P | A)$ and develop an efficient “allocation sampler” to directly sample from $\Pi_n(Z, K | A)$; [8] adapt the idea of MFM sampler of [20] to the SBM case: marginalize out $K$ from the posterior $\Pi_n(Z, K, P | A)$, and develop a Gibbs sampler sampling from $\Pi_n(Z, P | A)$.

2.2. Our proposal: diagonally dominant SBM. In this paper, we propose to modify the conjugate specification of Nowicki and Snijders’ prior on the connectivity matrix $P$ by imposing a diagonal dominance constraint. The constraint is imposed in two steps: first specify a prior distribution for the diagonal entries of $P$, then conditional on the diagonal entries,
specify a prior distribution on the off-diagonal entries such that the off-diagonal entries are strictly less than their corresponding diagonal entries.

For instance, we specify the following prior:

\[ P_{aa}|K, \delta \sim iid U(\delta, 1], a \in \{1, \ldots, K\}, \]
\[ P_{ab}|K, \delta, \{P_{aa}\}_{a \in \{1, \ldots, K\}} \sim ind U(0, P_{aa} - \delta), a < b \in \{1, \ldots, K\}, \]
\[ \delta \propto \log(n)/n, \]
\[ K \sim Pois(1), \]

where the hyperparameter \( \delta \) is chosen to be a deterministic sequence that goes to 0 as the network size grows to infinity. Uniform distributions in (3) are used for simplicity and can be replaced with other distributions.

In contrast to the Nowicki and Snijders’ priors, our prior specification directly imposes conditional dependence between diagonal entries and off-diagonal entries. The dependence matches the idea of “community” at the price of losing conjugacy.

The modification is mainly for two reasons. Firstly, the prior constraint of diagonal dominance offers a neat identification of the number of communities, and allows us to consistently estimate the number of communities and membership. (See more details in section 3.1.)

Secondly, the resulting posterior under the modified prior is more interpretable. Though the prior specification following [22] is conjugate, off-diagonal entries can be greater than diagonal entries under the prior, that is, nodes can be more likely to be connected to nodes from other communities than nodes from their own community. Such configurations violate the idea of “community”. Consequently, posterior samples of connectivity matrices can violate diagonal dominance and are hard to interpret within the framework of SBM.

2.3. \( L_2 \) minimax rate. This paper studies a special sub-class of SBM. One may wonder if the diagonally dominant (DD) SBM actually solves a simpler community detection problem. To answer this question, we calculate the \( L_2 \) minimax rate of estimation for DD-SBM and compare it with the minimax rates derived in [6].

Now, we define the parameter space of DD-SBM. DD-SBM has the following space of connectivity matrix

\[ S_{k,\delta} = \left\{ P \in [0, 1]^{k \times k} : P^T = P, P_{ii} > \delta + \max_{j \neq i} (P_{ij}), i \in \{1, \ldots, k\} \right\}, \]

where \( \delta \in [0, 1) \) is a constant. The key departure from the literature is the diagonal dominance constraint: \( P_{ii} > \delta + \max_{j \neq i} (P_{ij}), \) for all \( i \in \{1, \ldots, k\}. \) Under this constraint, between community connection probabilities are less than within community connection probabilities by \( \delta. \) The gap is inherited by the node-wise connectivity probability matrix.

Further with the membership assignment \( Z, \) we can define the space for node-wise connectivity probability matrix:

\[ \Theta_{k,\delta} = \left\{ T(ZPZ^T) \in [0, 1]^{n \times n} : P \in S_{k,\delta}, Z \in \mathcal{Z}_{n,k} \right\}, \]

where \( \mathcal{Z}_{n,k} \) denotes the collection of all possible assignment of \( n \) nodes into \( k \) communities which have at least two elements, and \( T(M) := M - \text{diag}(M) \) for any square matrix \( M. \) The node-wise connectivity probability matrix inherits the structural assumption of diagonal dominance. The minimum community size assumption allows recovering community membership from node-wise connectivity probability matrix. It is worthwhile to emphasize that singleton communities are ruled out.
The following $L_2$ minimax result implies that DD-SBM estimation is as difficult as the original SBM estimation problem, as long as the dominance gap is shrinking at certain rate. In our calculation, the gap squared ($\delta^2$) is dominated by the “clustering rate” $\log(k)/n$ \cite{6, 7, 16}.

**Proposition 1.** For any $k \in \{1, \ldots, n\}$ and $\delta \gtrless \sqrt{\log(k)/n}$,

$$\inf_{\delta} \sup_{\theta \in \Theta_{c, \delta}} \mathbb{E} \left[ \left\| \hat{\theta} - \theta \right\|_2^2 \right] \asymp \frac{k^2}{n^2} + \frac{\log(k)}{n}.$$

**Proof.** The upper bound follows theorem 2.1 of \cite{6} as the diagonally dominant connectivity matrix space is a subset of the unconstrained connectivity matrix space.

The lower bound follows the proof of theorem 2.2 of \cite{6} but their construction violates the diagonally dominant constraint. It turns out a diagonally dominant version of their construction is available. For brevity, we only highlight the differences from the proof in \cite{6}.

For the nonparametric rate, we construct the $Q^\omega$ matrix by $Q^\omega_{ab} = Q^\omega_{ba} = \frac{1}{2} - \delta - \frac{\sqrt{c \log n}}{n} \omega_{ab}$, for $a > b \in \{1, \ldots, k\}$ and $Q^\omega_{aa} = \frac{1}{2}$, for $a \in \{1, \ldots, k\}$. The rest of the proof for the nonparametric rate remains the same.

For the clustering rate, we construct the $Q$ matrix with the following form $\begin{bmatrix} D_1 & B \\ B^T & D_2 \end{bmatrix}$, where $D_1 = \frac{1}{2} I_{k/2}$, $B$ follows the same construction of \cite{6} except that $B_a = \frac{1}{2} - \delta - \sqrt{c \log n} \omega_a$ for $a \in \{1, \ldots, k/2\}$, $D_2 = (\frac{1}{2} - \delta - \sqrt{\frac{\log n}{n}}) I_{k/2} 1_{k/2}^T + (\delta + \sqrt{\frac{\log n}{n}}) I_{k/2}$. As $\delta \gtrless \sqrt{\log(k)/n}$, the KL divergence upper bound remains the same. The rest of the proof for the clustering rate remains the same as the entropy calculation and the volume argument are unaffected.

\subsection{3. Consistent Bayesian Community Detection.}

**3.1. Identification Strategy.** The first consequence of diagonal dominance is that the node-wise connectivity probability matrix spaces of different ranks are non-overlapping. This observation offers a neat partition of the parameter space by the number of communities.

**Lemma 3.1.** Suppose $k \neq k' \in \mathbb{N}$, then $\Theta_{k, \delta} \cap \Theta_{k', \delta'} = \emptyset$ for any $\delta, \delta' \geq 0$.

Secondly, with diagonal dominance, it is possible to exactly identify the number of communities, the membership of every node and the community-wise connectivity probability matrix from node-wise connectivity probability matrix under mild conditions. A more rigorous statement is presented in Lemma 3.2. The recovery is based on checking each node’s connectivity probabilities with other nodes, as each node is connected with nodes from its own community with the highest probability.

**Lemma 3.2.** Suppose $P \in S_{k, \delta}$ for some constant $\delta > 0$, $\theta = T(ZPZ^T)$ for some $Z \in \mathbb{Z}_{n,k}$, $T^{-1}$ recovers both community assignment $Z$ and connectivity matrix $P$ from $\theta$.

**Proof.** Without loss of generality, assume the nodes are ordered by community and we can write $Z = [1_{n_1}, \ldots, 1_{n_k}]$ where $n_j$ denotes the number of nodes in community $j$ and $1_{n_j}$ is a $n \times 1$ vector with entries in the $j^{th}$ block being 1. Therefore, the off-diagonal terms of $\theta$ are the off-diagonal terms of $ZPZ^T$.

Suppose we hope to pin down $i^{th}$ node’s community membership. We take $i^{th}$ row of $\theta$ and it contains the connectivity probabilities of node $i$ and all other nodes. As $Z \in \mathbb{Z}_{n,k}$ whose
minimum community size is two, $C_i \equiv \{ j : \theta_{ij} = \max_\ell \theta_{ij} \}$ is exactly the set of node(s) from the community of node $i$. If $C_i$ contains node(s) from other communities, then the connectivity probabilities of node $i$ with those node(s) are cross-community which are strictly less than the within-community connectivity probability of node $i$, contradicting the construction of $C_i$. If $C_i$ misses node(s) from the community of node $i$, then the connectivity probabilities of node $i$ with those node(s) are within-community which have to match the connectivity probabilities of nodes in $C_i$. Therefore, by enumerating the above procedure for all rows of $\theta$, $Z$ is identified up to a permutation of columns.

To recover $P$ from $\theta$, it suffices to use $Z$ and plug in corresponding values from $\theta$. \hfill \Box

In practice, the exact knowledge of node-wise connectivity probability matrix is not available. However, the precise recovery in Lemma 3.2 is possible with the estimated node-wise connectivity probability matrix. This is formalized in Lemma 3.3. We use sup-norm to characterize the accuracy of the knowledge of node-wise connectivity probability matrix. For any node-wise connectivity matrix $\theta^0$, there exists $Z_0$ and $P^0$ such that $\theta^0 = T(Z_0 P^0 Z_0^T)$. Without loss of generality, we can fix the column ordering of $Z_0$ so that $P^0$ is consequently defined.

**Lemma 3.3.** Suppose $\theta^0 = T(Z_0 P^0 Z_0^T)$ for some $Z_0 \in \mathcal{Z}_{n,k,\delta}$, $P^0 \in S_{k,0,\delta}$ and $\delta > 0$. Then, $\{ \theta = T(ZPZ^T) : ||\theta - \theta^0||_\infty \leq r, Z \in \mathcal{Z}_{n,k}, P \in S_{k,\delta} \} = \{ T(Z_0 PZ_0^T) : ||P - P^0||_\infty \leq r, P \in S_{k,0,\delta} \}$ holds for all $r < \delta/2$.

**Proof.** Pick any $\theta \in \{ \theta = T(ZPZ^T) : ||\theta - \theta^0||_\infty \leq r, Z \in \mathcal{Z}_{n,k}, P \in S_{k,\delta} \}$, define $C_i = \{ j : \theta_{ij} = \max_\ell \theta_{ij} \}$; similarly, for $\theta^0$, define $C^0_i = \{ j : \theta^0_{ij} = \max_\ell \theta^0_{ij} \}$. The statement is equivalent to $C_i = C^0_i$ for all $i \in \{1, ..., n\}$ and all $\theta$.

First, note for any $j \in C^0_i$ and $\ell \in \{1, ..., n\} \setminus C^0_i$, $\theta_{ij} - \theta_{i\ell} = \theta^0_{ij} - \theta^0_{i\ell} > \delta - 2r > 0$. That is, $C^0_i$ identifies a set of nodes with higher connectivity probabilities with node $i$ relative to nodes from $\{1, ..., n\} \setminus C^0_i$. Recall $C_i$ is the collection of nodes with the highest connectivity probability. Then, $C_i \subseteq C^0_i$ for all $i \in \{1, ..., n\}$.

If $C^0_i$ contains nodes from at least two communities of $\theta$, then there exist $j_1, j_2 \in C^0_i$, such that $|\theta_{ij_1} - \theta_{ij_2}| > \delta$ as $P \in S_{k,\delta}$. Note for all $j_1, j_2 \in C^0_i$, $\theta^0_{ij_1} = \theta^0_{ij_2}$, then it follows $|\theta_{ij_1} - \theta_{ij_2}| = |\theta_{ij_1} - \theta^0_{ij_1} + \theta^0_{ij_1} - \theta^0_{ij_2} + \theta^0_{ij_2} - \theta_{ij_2}| \leq |\theta_{ij_1} - \theta^0_{ij_1}| + |\theta^0_{ij_2} - \theta_{ij_2}| \leq 2r < \delta$. Then, the contradiction implies $C_i = C^0_i$ for all $i$. As $\theta$ is arbitrary, $C_i = C^0_i$ for all $i \in \{1, ..., n\}$ and for all $\theta$. \hfill \Box

3.2. **Posterior Concentration.** To study the asymptotic behavior of the diagonally dominated SBM, we make the following assumptions on the prior specification. The prior specification in Assumption 1 and 2 is indexed by $n$, the number of nodes in the network, and can be interpreted as a sequence of prior distributions.

**Assumption 1.** (Prior mass on the parameter space) There exists $\delta \in (0, 1)$ such that for all $0 < \delta < \delta$ and $k > 1$, $\Pi_n \{ S_{k,\delta} | K = k \} \geq 1 - e^{-n^2 \delta}$.

Assumption 1 requires that the prior specification is essentially diagonally dominant. Under Nowicki and Snijders’ prior, conditional on $k$ communities, the prior probability of diagonal dominance is $1/k^k$. Therefore, Nowicki and Snijders’ prior does not satisfy Assumption 1.

**Assumption 2.** (Prior decay rates)
1. (Prior on $P$ conditional on $K$ and $\delta$)
   For $a \in \{1, \ldots, k\}$, diagonal entries \{$P_{aa}$\} are independent with prior density $\pi_n(P_{aa}|K, \delta) \geq e^{-C\log(n)}P_{aa}^{-1}1_{P_{aa}(\in \delta(1))}$ for some positive constant $C$ independent of $a \in \{1, \ldots, k\}$.
   For $a < b \in \{1, \ldots, k\}$, off-diagonal entries \{$P_{ab}\}_{a\in\{1,\ldots,k\}}$ are conditionally independent on diagonal entries with conditional prior density
   \[
   \pi_n\left(P_{ab}|\{P_{aa}\}_{a\in\{1,\ldots,k\}}, \delta, K\right) \geq e^{-C\log(n)}(P_{aa}\wedge P_{ab})1_{\{P_{ab}\in[0,P_{aa}\wedge P_{ab}\wedge \delta]\}}
   \]
   for some positive constant $C$ independent of $a, b \in \{1, \ldots, k\}$.

2. (Prior on $Z$ conditional on $K$)
   The prior on the membership assignment $Z$ satisfies $\Pi_n(Z = z|K = k) \geq e^{-Cn\log(k)}$ for all $z \in \mathcal{Z}_{n,k}$ and for some universal positive constant $C$.

3. (Prior on $K$)
   The support of $K$ is $[K_n]$ with $K_n \lesssim \sqrt{n}$. For $k \in [K_n]$, the prior on $K$ satisfies $\Pi_n(K = k) \geq e^{-Ck\log(k)}$ for some universal positive constant $C$.

Assumption 2 makes more specific decay rate assumptions on the prior mass of connectivity matrix $P$, the assignment $Z$, and the number of communities $K$. The rate assumption of the prior on $P$ given $K$ and $\delta$ essentially requires the prior density on $P$ is lower bounded away from 0. For instance, the uniform prior on $P$ and the Poisson prior on $K$ in (3) satisfy Assumption 2.

**Theorem 3.4.** Suppose adjacency matrix $A \sim SBM(Z_0, P^0, n, k_0)$, let $\theta^0 = T(Z_0P^0Z_0^T)$, $P^0 \in \Theta_{k_0, \delta_0}$ for some $k_0 \lesssim \sqrt{n}$ and $\delta_0 > 0$, and the number of zero and one entries of $\theta^0$ is at most $O(n^2\varepsilon_n)$ where $\varepsilon_n^2 \approx \frac{\log(k_0)}{n}$. The prior $\Pi_n$ satisfies Assumption 1 and 2. Then, for all sufficiently large $M$,
   \[
   \mathbb{P}_{0,n}\Pi_n\left(\theta : ||\theta - \theta^0||_\infty \geq M\varepsilon_n|A\right) \to 0.
   \]

The proof of Theorem 3.4 follows Schwartz method [26, 3, 9, 11]. Details of the proof are deferred to Section 3.3.

Though exact $L_\infty$ minimax rates of SBM or DD SBM are unknown, $L_\infty$ minimax rates are lower bounded by $L_2$ minimax rates. The $L_2$ minimax rate calculation of DD SBM in Proposition 1 can be useful for judging the sharpness of the posterior contraction rate in Theorem 3.4. As we assume $k_0 \lesssim \sqrt{n}$, the posterior contraction rate in $|| \cdot ||_\infty$ matches the $L_2$ minimax rates in Proposition 1, and the posterior contraction rate is minimax-optimal.

With Theorem 3.4 and Lemma 3.3, we can establish the consistent estimation of the true number of communities and true membership assignment. The main result is summarized as follows.

**Theorem 3.5.** Under the same assumptions of Theorem 3.4,
   \[
   \mathbb{P}_{0,n}\left[\Pi_n\left(\{K = k_0\} \cap \{Z = Z_0\}|A\right)\right] \to 1.
   \]

**Proof.** In light of Theorem 3.4, the posterior mass is essentially on $\{\theta : ||\theta - \theta^0||_\infty \leq \varepsilon_n\}$. Therefore, we leverage Lemma 3.3 to identify $k_0$ and $Z_0$ on the set.

Define $E_0 = \{K = k_0\} \cap \{Z = Z_0\}$. Note the decomposition
   \[
   E_0^c = (E_0^c \cap \{||\theta - \theta^0||_\infty \leq \varepsilon_n\}) \cup (E_0^c \cap \{||\theta - \theta^0||_\infty > \varepsilon_n\})
   \]
   for some $\varepsilon_n$, then
   \[
   \Pi_n(E_0^c|A) \leq \Pi_n(E_0^c, ||\theta - \theta^0||_\infty \leq \varepsilon_n|A) + \Pi_n(||\theta - \theta^0||_\infty > \varepsilon_n|A)
   \]
where \( \varepsilon_n \to 0 \) is chosen to match the posterior contraction rate in sup-norm.

Then, the posterior probability of choosing wrong number of communities or wrong membership assignment can be upper bounded via the identification assumption and convergence of the posterior distribution of \( \theta \). For the first part of Equation (8), the \( \delta \) gap assumption of \( \theta^0 \) satisfies \( \delta_0 \gtrsim \varepsilon_n \). Then, by Lemma 3.3, for all sufficiently small \( \varepsilon_n \), \( \{||\theta - \theta^0||_\infty \leq \varepsilon_n \} \) is the same as its \( Z_0 \) slice where the implied number of communities is \( k_0 \).

For the second part, Theorem 3.4 implies \( \mathbb{P}_0[\Pi_n (||\theta - \theta^0||_\infty > \varepsilon_n | A)] \to 0. \)

### 3.3. Proof of Theorem 3.4

Pioneered by [26] and further developed by [3, 9, 11], Schwartz method is the major tool to study posterior concentration properties of Bayesian procedures as sample size grows to infinity [12]. Schwartz method seeks for two sufficient conditions to guarantee posterior concentration: the existence of certain tests and prior mass condition. The existence of certain tests often reduces to the construction of certain sieves and an entropy condition associated with the sieve, if the metric under which we wish to obtain posterior contraction is dominated by Hellinger distance. The prior mass condition requires sufficient amount of prior mass on some KL neighborhood near the truth.

Establishing convergence in \( || \cdot ||_\infty \) via the general framework of Schwartz method requires \( || \cdot ||_\infty \) to be dominated by Hellinger distance. In general, \( || \cdot ||_\infty \) is (weakly) stronger than Hellinger distance and not dominated by Hellinger distance. However, in the special case of SBM, the parameter space is constrained and the desired dominance holds. This observation is shown in Lemma 3.6.

**Lemma 3.6.** Suppose \( A_{ij}|\theta^0 \overset{\text{Ind}}{\sim} \text{Ber}(\theta_{ij}) \) for \( i < j \) and \( i, j \in \{1, ..., n\} \), then \( || \cdot ||_\infty \) is dominated by Hellinger distance: \( ||\theta^0 - \theta^1||_\infty \leq 2H(\mathbb{P}_{\theta^0}, \mathbb{P}_{\theta^1}) \).

With the norm dominance, the existence of certain tests reduces to construct a suitable sieve which charges sufficient prior mass and whose metric entropy is under control. In our proof, the sieve is constructed as the set of all well separated node-wise connectivity probability matrices: \( \bigcup_{k=1}^{K_n} \Theta_{k, \delta_n} \) for some carefully chosen \( \delta_n \) and \( K_n \).

In light of Lemma 3.1, the metric entropy of the sieve can be neatly bounded. The entropy calculation is summarized in Lemma 3.7.

**Lemma 3.7.** Suppose \( \varepsilon_n \to 0 \) as \( n \to \infty \), and \( \varepsilon_n \lesssim \delta_n \), then metric entropy satisfies

\[
\log N\left(\varepsilon_n, \bigcup_{k=1}^{K_n} \Theta_{k, \delta_n}, || \cdot ||_\infty \right) \lesssim (n + 1) \log K_n + \frac{1}{2} K_n (K_n + 1) \log (1/\varepsilon_n).
\]

The prior mass condition in terms of KL divergence can be reduced to a prior mass condition in terms of \( || \cdot ||_\infty \) norm. This observation is summarized in Lemma 3.8.

**Lemma 3.8.** The observation model is \( A_{ij}|\theta^0 \overset{\text{Ind}}{\sim} \text{Ber}(\theta_{ij}) \) for \( i < j \) and \( i, j \in \{1, ..., n\} \). Suppose \( C_0 = \min_{i < j \in \mathcal{E}_0} \theta_{ij} > 0 \), and the number of zero and one entries of \( \theta^0 \) is less than \( O(n^2 \varepsilon_n) \) for some \( \varepsilon_n \to 0 \) such that \( n^2 \varepsilon_n \to \infty \). If \( ||\theta - \theta^0||_\infty \leq \varepsilon_n \), then \( KL(\mathbb{P}_{\theta^0}, \mathbb{P}_\theta) \lesssim C_0^{-1} n^2 \varepsilon_n^2 \), and \( V_{2,0}(\mathbb{P}_{\theta^0}, \mathbb{P}_\theta) \lesssim C_0^{-1} n^2 \varepsilon_n^2 \).

Lemma 3.8 simplifies the prior mass condition to element-wise probability calculation. Immediately with Assumption 2, we obtain the following prior mass calculation.
LEMMA 3.9 (prior mass condition). Suppose \( P^0 \in S_{k_0, \delta_0} \) for some \( k_0 \lesssim \sqrt{n} \) and constant \( \delta_0 \in (0, 1) \), and \( \varepsilon_n^2 \propto \log(k_0)/n \), then under Assumption 2, there exists a constant \( C \) only dependent on \( P^0 \) and \( C_0 \) such that
\[
\Pi_n \left( P : ||P - P^0||_\infty < C_0 \varepsilon_n; Z = Z_0; K = k_0|\delta \right) \geq e^{-Cn^2 \varepsilon_n^2}
\]
holds for all sufficiently large \( n \).

With the above preparation, the proof of Theorem 3.4 is as follows. The structure of the proof follows [11].

PROOF. We first verify prior mass condition. By Lemma 3.8, the set
\[
\left\{ \theta \in \bigcup_{k=1}^{K_n} \Theta_{k,0} : KL \left( P_{\theta_n^0}, P_{\theta} \right) < n^2 \varepsilon_n^2, V_{2,0} \left( P_{\theta_n^0}, P_{\theta} \right) < n^2 \varepsilon_n^2 \right\}
\]
contains a sup-norm ball \( \left\{ \theta \in \bigcup_{k=1}^{K_n} \Theta_{k,0} : ||\theta - \theta^0||_\infty < C_0 \varepsilon_n \right\} \) for some constant \( C_0 \) only dependent on \( \theta^0 \). Choose \( 1 > \tau_n \sim \varepsilon_n \), the sup-norm ball further contains the following sup-norm ball \( \left\{ \theta \in \Theta_{k_0,\tau_n} : ||\theta - \theta^0||_\infty < C_0 \varepsilon_n \right\} \). By Lemma 3.3, the sup-norm ball is essentially its \( Z_0 \) slice which reduces to
\[
\Pi_n \left( P \in S_{k_0, \tau_n} : ||P - P^0||_\infty < C \varepsilon_n; Z = Z_0; K = k_0 \right).
\]
By Lemma 3.9, the prior mass is further lower bounded by \( e^{-Cn^2 \varepsilon_n^2} \) for some constant \( C \) only dependent on \( P^0 \) and \( C_0 \).

Next, we check the existence of tests. The existence of tests boils down to metric entropy condition and prior mass condition of the sieve. The sieve is constructed as \( \bigcup_{k=1}^{K_n} \Theta_{k,n} \) with \( 1 > \delta_n \sim \varepsilon_n^2 \).

Metric entropy condition of the sieve requires the metric entropy is upper bounded by \( Cn^2 \varepsilon_n^2 \). Clearly, this is satisfied by Lemma 3.7.

It is left to show the prior mass on the sieve. Note \( \Pi_n \left( \left( \bigcup_{k=1}^{K_n} \Theta_{k,n} \right)^c \right) \leq \Pi_n \left( \Theta_{K_n,n}^c \right) = \Pi_n \left( \Theta_{K_n,n}^c | K = K_n \right) \Pi_n (K = K_n) \), then the prior mass on the sieve is also satisfied by a union bound:
\[
\Pi_n \left( \Theta_{k,n}^c | K = k \right) \leq \sum_{z \in \mathcal{Z}_n,k} \Pi_n \left( \Theta_{k,n}^c | Z = z, K = k \right) \Pi_n (Z = z | K = k) \\
\leq \max_{z \in \mathcal{Z}_n,k} \Pi_n \left( \Theta_{k,n}^c | Z = z, K = k \right) \\
= \max_{z \in \mathcal{Z}_n,k} \Pi_n (\mathbf{T}^c(zPz^T) : P \in S_{k,n}^c | Z = z, K = k) \\
\leq \Pi_n \left( S_{k,n}^c | K = k \right) \\
\lesssim e^{-n^2 \delta_n} \lesssim e^{-Cn^2 \varepsilon_n^2}
\]
for some constant \( C \).

4. Posterior Sampler and Inference.

4.1. Reversible-jump MCMC algorithm. Under the diagonally dominant prior (3), the posterior distribution is as follows,
\[
\Pi_n (Z, K, P | A) \propto \Pi (A | Z, P) \Pi_n (P | Z) \Pi_n (Z | K) \Pi_n (K)
\]
with
\[
\Pi(A|Z, P) = \prod_{1 \leq a \leq b \leq K} P_{ab}^{O_{ab}(Z)} (1 - P_{ab})^{n_{ab}(Z) - O_{ab}(Z)} \]
\[
\Pi_n(P|Z, K, \delta_n) = \prod_{1 \leq a < b \leq K} \frac{1_{(p_{ab} \leq (p_{ab} + n_{ab} - 1) \leq \delta_n)}}{(p_{ab} + n_{ab} - 1)} \]
\[
\Pi_n(Z|K) = \frac{\Gamma(K)}{\Gamma(n+K)} \prod_{1 \leq c \leq K} \Gamma(n_c(Z) + 1) \]
\[
\Pi_n(K) \propto \prod_{K} 1_{1 \leq K \leq K_n}. \]

For comparison, the Nowicki and Snijders’ prior is conjugate and the community-wise connectivity probability matrix \(P\) can be marginalized out in the posterior distribution. Therefore, posterior inference on \(K\) is directly based on posterior draws from \(\Pi_n(Z, K|A)\). However, the truncated Nowicki and Snijders’ prior loses conjugacy. Our posterior inference needs to sample from \(\Pi_n(P, Z, K|A)\).

We propose an Metropolis-Hastings algorithm to sample from (11). The proposal \((Z^*, K^*, P^*)\) is accepted with probability
\[
\min \left( 1, \frac{\Pi_n(Z^*, K^*, P^*|A) \Pi_{prop}(Z, K, P|Z^*, K^*, P^*)}{\Pi_n(Z, K, P|A) \Pi_{prop}(Z^*, K^*, P^*|Z, K, P)} \right)
\]
where \(\Pi_{prop}\) denotes the density function of the proposal distribution and \((Z, K, P)\) denotes the current iteration.

To be specific, the proposal distribution is adapted from the allocation sampler developed in [19]. For each iteration of the sampler, the proposal distribution first sample \((Z, K)\) in the spirit of the allocation sampler, then sample \(P\) given \((Z, K)\). The proposal distribution is decomposed into two parts: conditional on the previous draw \((P, Z, K)\) and data matrix \(A\),
\[
\Pi_{prop}(Z^*, K^*, P^*|Z, K, P, A) \propto \Pi_{prop}(P^*|Z^*, A) \Pi_{prop}(Z^*, K^*|Z, K, P, A)
\]
where \(P^*|Z, A \sim^{ind} Beta(O_{ab}^* + 1, n_{ab}^* - O_{ab}^* + 1)\) with \(O_{ab}^* \equiv O_{ab}(Z^*)\) and \(n_{ab}^* \equiv n_{ab}(Z^*)\), and \((Z^*, K^*)|(Z, K, P, A)\) are simulated in the spirit of the allocation sampler developed in [19, 21].

The proposal distribution of \((Z^*, K^*)|(Z, K, P, A)\) follows the allocation sampler of [19] but it is different in the way that connectivity probability matrix \(P\) is involved and used for likelihood evaluation. In contrast, the allocation sampler of [19] explores the \((Z, K)\) space with \(P\) marginalized out. Details of the posterior sampler are in the Supplement.

The expectation of the proposal distribution \(\Pi_{prop}(P^*|(Z^*, A))\) is the ordinary block constant least squares estimator which is widely used to estimate the connectivity probability matrix in the literature [see 6, 16, 27, for instance]. As the proposal density matches the likelihood component \(\Pi(A|P^*, Z^*)\), the acceptance rate is a product of prior density ratios and proposal density ratios.

4.2. Posterior Inference. Under the 0-1 loss function \(\ell(k, k_0) = 1_{k = k_0}\), the Bayes estimate of \(K\) is its posterior mode. As in the Metropolis-Hastings sampler, \(K\) communities may contain empty communities, we compute the effective number of communities based on samples of \(Z\).

The community assignment is identified up to a label switching. In our matrix formulation, the assignment \(Z\) is identified up to a column permutation. That is, \(ZZ^T\) is invariant to column permutations. If the \((i, j)th\) entry of \(ZZ^T\) is 1, node \(i\) and node \(j\) are classified into the same community by \(Z\). In addition, the node-wise connectivity \(\theta\) is also identified without relabelling concerns. With the 0-1 loss function \(\ell(Z, Z_0) = 1_{(ZZ^T = Z_0Z_0^T)}\), Bayes estimate of \(Z\) is its posterior mode. To pin down the posterior mode of \(Z\), we can find the posterior mode of \(ZZ^T\) and the corresponding \(Z\) is the posterior mode of \(Z\).
5. Numerical Experiments. Section 3 presents asymptotic properties of Bayesian SBM with diagonally dominant priors which is henceforth abbreviated as “DD-SBM”. This section assesses finite sample properties of DD-SBM under various settings.

5.1. Simulation design. We perform simulation studies for different configurations of the number of communities, network size, and overall sparsity of connectivity. In particular, we choose \((k_0, n, \rho) \in \{3, 5, 7\} \times \{50, 75\} \times \{\frac{1}{4}, 1\}\), and for each \((k_0, n, \rho)\) configuration, 100 networks are generated from \(SBM(Z_0, \rho P^0, n, k_0)\).

To control the source of variation in the synthetic networks, the 100 networks share the same community structure \(Z_0\) where nodes are deterministically and uniformly assigned to \(k_0\) communities; the 100 networks also share the same connectivity matrix \(\rho P^0\). The randomness in the 100 synthetic networks is only from the stochastic generation of Bernoulli trials of \(SBM(Z_0, \rho P^0, n, k_0)\).

We choose the following cases for \(P^0\).

- **Case 1:** \(P^0 = 0.6 \times I_{k_0} + 0.2 \times 1_{k_0}1_{k_0}^T\),
- **Case 2:** \(P^0 = 0.2 \times I_{k_0} + 0.6 \times 1_{k_0}1_{k_0}^T\),
- **Case 3:** \(P^0 = 0.4 \times I_{k_0} + 0.4 \times 1_{k_0}1_{k_0}^T\),
- **Case 4:** \(P^0 = 0.2 \times I_{k_0} + 0.2 \times 1_{k_0}1_{k_0}^T + 0.4 \times 1_{k_0}1_{k_0}^T1_{k_0}1_{k_0/2}1_{k_0/2}^T\),

where \(I_k\) denotes identity matrix of rank \(k\), \(1_k\) denotes the \(k\)-dimensional vector of ones, and \(1_{n,k}\) denotes the \(n\)-dimensional vector with the first \(k\) elements being 1 and the rest \((n-k)\) elements being 0.

In the four cases, within community connectivity probabilities are all 0.8. For simplicity, the between community connectivity probabilities are the same for Case 1-3; in Case 1, cross community connectivity is weak; in Case 2, cross community connectivity is strong; and in Case 3, cross community connectivity is medium. Case 4 combines the structure of Case 1 and Case 3 and half of the cross community connectivity is strong.

The reasons for choosing \(n \in \{50, 75\}\) are as follows. Firstly, many networks in natural and social sciences are often of moderate size. Secondly, asymptotically consistent estimators can perform poorly when sample size is moderate. It is more informative to compare methods for networks of moderate size than that for networks with thousands of nodes. Thirdly, MCMC algorithms are computationally expensive, and the computation bottleneck prevents us from networks with more than thousands of nodes.

As the number of parameters in the SBM grows in the order of \(O(k_0^2)\), the difficulty of community detection increases as \(k_0\) grows. The case of \(k_0 = 7\) imitates the situation of many communities, while the cases of \(k_0 \in \{3, 5\}\) imitate networks with moderately many communities.

5.2. Simulation results. For comparison, we also implement Bayesian SBM with the Nowicki and Snijders’ prior [21, 8], composite likelihood BIC method [25], and network cross-validation [5]. Two posterior samplers for the Nowicki and Snijders’ prior are available in the literature: the allocation sampler of [19], and the MFM adapted MCMC algorithm of [8]. We use the code provided in the supplementary materials of [8] and choose default values for the hyperparameters in their algorithm. The Bayesian SBM of [8, 19] is henceforth denoted as “c-SBM” (Bayesian SBM with conjugate priors). [25] propose composite likelihood BIC to choose the number of communities, and this method is henceforth denoted as “CLBIC”. [5] design a cross-validation strategy to choose the number of communities for SBM, and it is henceforth denoted as “NCV”.
Compared with c-SBM, DD-SBM achieves similar accuracy across different configurations. To be specific, when \( k_0 = 3 \), DD-SBM tends to over-estimate the number of communities; when \( \rho = \frac{1}{2} \) and \( k_0 \in \{ 5, 7 \} \), DD-SBM is slightly more accurate than c-SBM in Case 1 and 3 and similarly accurate to c-SBM in Case 2 and 4. When the posterior samples of connectivity matrix of c-SBM are also diagonally dominant, c-SBM is essentially DD-SBM. Therefore, it is reasonable to expect DD-SBM and c-SBM have similar accuracy in networks generated from diagonally dominant SBM.

Compared with CLBIC, DD-SBM is less accurate in most cases. This is due to the design of \( P^0 \) in Case 1 - 3, such that the working likelihood of CLBIC is close to the true likelihood. In Case 4, the true likelihood is more complicated than the working likelihood of CLBIC, and the advantage of CLBIC over DD-SBM is less obvious.

Compared with NCV, DD-SBM is more accurate in most cases. To be specific, when \( k_0 = 3 \) and \( \rho = \frac{1}{2} \), DD-SBM tends to over-estimate the number of communities; in other configurations, DD-SBM is more accurate than NCV.

Case 2 is the most difficult as the between community connectivity probability is very close to within community connectivity probability. Indeed, the methods nearly uniformly choose one big community, except that CLBIC sometimes chooses two communities.

To assess the membership assignment accuracy, we use the Hubert-Arabie adjusted Rand index [14, 24] to measure the agreement between two clustering assignments. The index is expected to be 0 if two independent assignments are compared, and is 1 if two equivalent assignments are compared. Though the adjusted Rand index tends to capture the disagreement
among large clusters, community sizes in our simulation study are about the same and the adjusted Rand index is still a meaningful metric.

| $k_0$ | $\rho$ | $n$ | Case 1 | Case 2 | Case 3 | Case 4 |
|-------|-------|----|--------|--------|--------|--------|
| 3     | $\frac{1}{2}$ | 50 | 0.62   | 0.63   | 0.00   | 0.00   |
|       |       | 75 | 0.87   | 0.91   | 0.00   | 0.00   |
|       |       | 50 | 0.97   | 0.98   | 0.01   | 0.01   |
|       |       | 75 | 0.99   | 0.99   | 0.03   | 0.03   |
| 5     | $\frac{1}{2}$ | 50 | 0.10   | 0.03   | 0.00   | 0.00   |
|       |       | 75 | 0.25   | 0.11   | 0.00   | 0.00   |
|       |       | 50 | 0.83   | 0.86   | 0.00   | 0.00   |
|       |       | 75 | 0.94   | 0.99   | 0.00   | 0.00   |
| 7     | $\frac{1}{2}$ | 50 | 0.03   | 0.00   | 0.00   | 0.00   |
|       |       | 75 | 0.07   | 0.01   | 0.00   | 0.00   |
|       |       | 50 | 0.24   | 0.12   | 0.00   | 0.00   |
|       |       | 75 | 0.57   | 0.43   | 0.00   | 0.00   |

**Table 2**

Adjusted Rand index

Given a synthetic network $A$ and draws from the posterior distribution $\Pi(\cdot | A)$, we can compute the adjusted Rand index of posterior draws of $Z$ against $Z_0$ and use their mean as the accuracy metric for $\Pi(\cdot | A)$. Like the adjusted Rand index for two clustering assignments, the averaged index assesses the agreement of the posterior distribution of $Z$ against the truth $Z_0$.

Table 2 presents the average of adjusted Rand indices of the 100 synthetic networks under different $(k_0, \rho, n)$ configurations in the four cases. Overall, the average adjusted Rand index of DD-SBM is similar to that of c-SBM. This echoes the similar estimation accuracy of $k$ of DD-SBM and c-SBM, as community detection is highly sensitive to the number of communities. When $\rho = \frac{1}{2}$ and $k_0 \in \{5, 7\}$, DD-SBM is slightly better than c-SBM in Case 1 and 3. When data is less informative, the regularity in the prior of DD-SBM improves estimation accuracy over c-SBM. The advantage disappears in Case 2 and 4 where cross community connectivity is close to within community connectivity.

6. Sparse Networks. The framework in Section 3 can be extended to sparse networks whose overall connectivity probability shrinks to 0 as network size increases [e.g. 16, 7]. We state the posterior contraction rates and the posterior consistency results for those sparse networks as follows. Their proofs follow exactly the same argument except that the derivations involve the sparse factor $\rho_n$.

**Theorem 6.1.** Suppose adjacency matrix $A \in \{0, 1\}^{n \times n}$ is generated from the SBM with $\theta_n = \rho_n T(Z_0 P^0 Z_0^T)$, $\log(k_0)/n \geq \rho_n \geq 1$, $P^0 \in \Theta_{k_0, \delta_0}$ for some $k_0 \geq \sqrt{n}$ and $\delta_0 > 0$, and the number of zero and one entries of $T(Z_0 P^0 Z_0^T)$ is at most $O(n^2 \varepsilon_n)$ where $\varepsilon_n^2 \sim \frac{\log(k_0)}{n}$. The prior $\Pi_n$ satisfies Assumption 2. Then, for all sufficiently large $M$,

$$P_{\theta_0, n} \Pi_n \left( \theta : \| \theta - \theta_0 \|_\infty \geq M \varepsilon_n \right) \rightarrow 0.$$  

The posterior contraction rate in Theorem 6.1 is independent of the sparsity level. In contrast, $L_2$ minimax rates of error derived in [16, 7] are proportional to the sparsity level. We conjecture that $L_\infty$ minimax rates of error are also proportional to the sparsity level. It is likely that the posterior contraction rate in Theorem 6.1 is sub-optimal.
THEOREM 6.2. Under the same assumptions of Theorem 6.1 except that the sparsity level satisfies $\log(k_0)/n \gtrsim \rho_n^2 \gtrsim 1$, then

$$\mathbb{P}_{0,n} [\Pi_n (\{K = k_0\} \cap \{Z = Z_0\}|A)] \to 1.$$ 

In the sparse network setting, the diagonal dominance gap also vanishes at the rate of $\rho_n$. Our identification strategy for the number of communities requires $\rho_n \delta_0 \gtrsim \epsilon_n \asymp \sqrt{\log(k_0)/n}$ to guarantee consistent community detection. In contrast, some work in the sparse network literature works for networks with sparser sparsity levels [e.g. 1, for a recent survey]. The Bayesian model outlined in (3) may need additional modifications to adapt to networks at various sparse levels.

7. Concluding Remarks. In this paper, we have shown Bayesian SBM can consistently estimate the number of communities and the membership assignment. Towards this end, we propose the diagonally dominant Nowicki-Snijders’ prior and trade conjugacy of Nowicki-Snijders’ prior for simpler and clearer asymptotic analysis. In the simulation studies, c-SBM has similar finite sample estimation accuracy to DD-SBM. We conjecture that c-SBM can also consistently estimate the number of communities and the membership assignment for networks generated from diagonally dominant SBM. However, the proof technique adopted in this paper cannot be applied to c-SBM.

The price of losing conjugacy is on the computation side. The posterior sampler in [8] is much faster than our allocation sampler as they successfully adapt the idea of MFM sampler of [20] to the SBM case. It remains unclear if the MFM idea can be applied to the non-conjugate case.

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**SUPPLEMENTARY MATERIAL**

Supplement to “Consistent Bayesian Community Detection”. This Supplement contains additional results and proofs in the text.


Supplement to “Consistent Bayesian Community Detection”

The supplement file contains complete proofs for Lemma 3.1, 3.6, 3.7, 3.8 and 3.9, details of the sampler, and complete simulation results for all configurations.

8. Proofs.

8.0.0.1. Proof of Lemma 3.1.

PROOF. Suppose \( \theta \in \Theta_{k,\delta} \), it suffices to show \( \theta \not\in \Theta_{k',\delta'} \) for all \( k' < k \) and \( \delta' \geq 0 \). Now prove the statement by contradiction.

If \( \theta \in \Theta_{k',\delta'} \) for some \( k' < k \) and \( \delta' \geq 0 \), then some nodes from some communities implied by \( \theta \) are merged. But by construction of \( \Theta_{k,\delta} \), between-community connectivity probabilities of \( \theta \) are strictly less than corresponding within community connectivity probabilities. Therefore, once merged, the connectivity probabilities of the merged block are not identical. This is a contradiction.

\( \square \)

8.0.0.2. Proof of Lemma 3.6.

PROOF. The Hellinger distance between two Bernoulli random variables satisfies

\[
H^2 \left( \mathbb{P}_{\theta_{ij}}, \mathbb{P}_{\theta_{ij}} \right) = \frac{1}{2} \left[ \left( \sqrt{\theta_{ij}^0} - \sqrt{\theta_{ij}^1} \right)^2 + \left( \sqrt{1 - \theta_{ij}^0} - \sqrt{1 - \theta_{ij}^1} \right)^2 \right]
\]

\[
= \frac{1}{4} \left[ \left( \frac{1}{2} \right)^2 \left( \theta_{ij}^0 - \theta_{ij}^1 \right)^2 + \left( \frac{1}{2} \right)^2 \left( 1 - \theta_{ij}^0 - 1 + \theta_{ij}^1 \right)^2 \right]
\]

\[
\geq \frac{1}{4} \left( \theta_{ij}^0 - \theta_{ij}^1 \right)^2
\]

as \( \theta_{ij}^0 \) and \( \theta_{ij}^1 \) are in \([0,1]\), \( |\sqrt{\theta_{ij}^0} + \sqrt{\theta_{ij}^1}| \leq 2 \) and \( |\sqrt{1 - \theta_{ij}^0} + \sqrt{1 - \theta_{ij}^1}| \leq 2 \).

By independence, \( P_\theta = \otimes_{i<j} P_{\theta_{ij}} \). Then, the Hellinger distance between \( \mathbb{P}_{\theta^0} \) and \( \mathbb{P}_{\theta^1} \) satisfies

\[
H^2 \left( P_{\theta^0}, P_{\theta^1} \right) = 2 - 2 \prod_{i<j} \left( 1 - \frac{1}{2} H^2 \left( P_{\theta_{ij}^0}, P_{\theta_{ij}^1} \right) \right)
\]

\[
\geq 2 - 2 \prod_{i<j} \left( 1 - \frac{1}{8} \left( \theta_{ij}^0 - \theta_{ij}^1 \right)^2 \right)
\]

\[
\geq 2 - 2 \min_{i<j} \left( 1 - \frac{1}{8} \left( \theta_{ij}^0 - \theta_{ij}^1 \right)^2 \right)
\]

\[
= \frac{1}{4} \max_{i<j} \left( \theta_{ij}^0 - \theta_{ij}^1 \right)^2
\]

\[
= \frac{1}{4} \| \theta^0 - \theta^1 \|_\infty^2.
\]

\( \square \)

8.0.0.3. Proof of Lemma 3.7.

PROOF. Note \( \Theta_{k,\delta_n} = \bigcup_{Z \in Z_{n,k}} \Theta^Z_{k,\delta_n} \), where \( \Theta^Z_{k,\delta_n} = \{ T(ZPZ^T) : P \in S_{k,\delta_n} \} \) denotes the \( Z \) slice of the parameter space.

By Lemma 3.3 and the assumption on \( \delta_n \) and \( \varepsilon_n \), node-wise connectivity probability matrix space can be simplified via \( \{ \theta : \| \theta - \theta^0 \|_\infty < \varepsilon_n \} = \{ T(Z_0PZ_0^T) : \| P - P^0 \|_\infty < \varepsilon_n \} \).

This relation implies the covering number \( N \left( \varepsilon_n, \Theta^Z_{k,\delta_n}, \| \cdot \|_\infty \right) \leq (1/\varepsilon_n)^{k(k+1)/2} \), and then union bound implies the covering number \( N \left( \varepsilon_n, \Theta_{k,\delta_n}, \| \cdot \|_\infty \right) \leq k^n (1/\varepsilon_n)^{k(k+1)/2} \).

...
By Lemma 3.1, $\Theta_{k, \delta}$ are non-overlapping for different $k$, then another union bound implies the statement (9). \hfill \Box

8.0.0.4. Proof of Lemma 3.8.

PROOF. First recall some basic expansions from calculus. For $x_0 \in (0, 1)$, define $f(x) = -x_0 \log \frac{x}{x_0} - (1 - x_0) \log \frac{1 - x}{1 - x_0}$ for $x \in [0, 1]$. Taylor expand $f(x)$ around $x_0$:

$$f(x) = f(x_0) + f'(x_0)(x - x_0) + \frac{1}{2}f''(x_0)(x - x_0)^2 + O \left((x - x_0)^3\right)$$

$$= \frac{1}{2x_0(1-x_0)}(x - x_0)^2 + O \left((|x - x_0|^3)\right).$$

For $x_0 = 0$, the above $f(x) = -\log(1 - x)$ with the convention $0 \log 0 = 0$. Its Taylor expansion around 0 is $f(x) = -\log(1 - x) = x + O \left(x^2\right)$. For $x_0 = 1$, the above $f(x) = -\log(x)$ also with the convention $0 \log 0 = 0$. Its Taylor expansion around 1 is $f(x) = -\log(x) = 1 - x + O \left((1 - x)^2\right)$.

With $||\theta - \theta^0||_\infty \leq \varepsilon_n$ and the assumption on $\theta^0$, expand KL divergence at $\theta^0$,

$$KL(\mathbb{P}_{\theta^0}, \mathbb{P}_\theta) = -\sum_{i<j: \theta^0_{ij} > 0 \theta_{ij} \log \frac{\theta_{ij}}{\theta^0_{ij}} - \sum_{i<j: \theta^0_{ij} < 1} \left(1 - \theta^0_{ij}\right) \log \frac{1 - \theta_{ij}}{1 - \theta^0_{ij}}$$

$$\leq (N_0 + N_1) \left(\varepsilon_n + O \left(\varepsilon_n^2\right)\right) + \frac{n(n-1)}{2} C_0^{-1} \left(\varepsilon_n^2 + O \left(|\varepsilon_n|^3\right)\right)$$

where $N_0 = \# \{ (i, j): \theta^0_{ij} = 0, i < j \}$ denotes the number of zero entries in $\theta^0$, and $N_1 = \# \{ (i, j): \theta^0_{ij} = 1, i < j \}$ denotes the number of one entries in $\theta^0$.

To bound $V_{2,0}$, note the Taylor expansion of $f(x) = \log \frac{x}{1-x}$ around $x_0 \in (0, 1)$ satisfies $f(x) = \log \frac{x}{1-x} = \log \frac{x_0}{1-x_0} + \frac{x_0}{x_0(1-x_0)}(x-x_0) + O \left((x-x_0)^2\right)$.

By independence of different entries and with $||\theta - \theta^0||_\infty \leq \varepsilon_n$, KL variation can be bounded similarly by an expansion of $f(x) = \log(x/(1-x))$:

$$V_{2,0}(\mathbb{P}_{\theta^0}, \mathbb{P}_\theta) = \mathbb{P}_0 \left\{ \left[ \sum_{i<j} \left( A_{ij} \log \frac{\theta_{ij}}{\theta^0_{ij}} + (1 - A_{ij}) \log \frac{1 - \theta_{ij}}{1 - \theta^0_{ij}} \right) + KL(\mathbb{P}_{\theta^0}, \mathbb{P}_\theta) \right] \right\}^2$$

$$= \sum_{i<j} \mathbb{P}_0 \left\{ \left( A_{ij} \log \frac{\theta_{ij}}{\theta^0_{ij}} + (1 - A_{ij}) \log \frac{1 - \theta_{ij}}{1 - \theta^0_{ij}} \right) + KL\left(\mathbb{P}_{\theta^0_{ij}}, \mathbb{P}_{\theta_{ij}}\right) \right\}^2$$

$$\leq \sum_{i<j} \frac{\theta^0_{ij} \theta_{ij}}{\theta^0_{ij} + (1 - \theta^0_{ij})} \left( \log \frac{\theta_{ij}}{\theta^0_{ij}} - \log \frac{1 - \theta_{ij}}{1 - \theta^0_{ij}} \right)^2$$

$$\lesssim \sum_{i<j} \frac{\theta^0_{ij} \theta_{ij}}{\theta^0_{ij} + (1 - \theta^0_{ij})} \varepsilon_n^2$$

$$\lesssim n^2 \varepsilon_n^2 / C_0 \hfill \Box

8.0.0.5. Proof of Lemma 3.9.

PROOF. By the dependence assumption made in Assumption 2, the prior mass has the factorization

$$\Pi_n \left( P: ||P - P^0||_\infty < C_0 \varepsilon_n | K = k_0 \right) \Pi_n \left( Z = Z_0 | K = k_0 \right) \Pi_n \left( K = k_0 \right).$$

Next, we bound individual components of (13) respectively.
To bound the first component of (13), the conditional indepence of the off-diagonal entries of $P$ on the diagonal entries of $P$ suggests the following factorization,
\[
\Pi_n \left( P : \|P - P^0\|_\infty < C_0 \varepsilon_n | K = k_0 \right) = \Pi_n \left( \bigcap_{1 \leq a < b \leq k_0} E_{n,ab} | K = k_0 \right) = \Pi_{1 \leq a \leq k_0} \left\{ \prod_{1 \leq a < b \leq k_0} \Pi_n \left( E_{n,ab} | \{P_{aa}\}, K = k_0 \right) \right\} d\Pi_n (P_{aa} | K = k_0) \]
where $E_{n,ab} = \{ P_{ab} : |P_{ab} - P^0_{ab}| < C_0 \varepsilon_n \}$. As $\varepsilon_n = o(1)$ and $P^0 \in S_{k_0,\delta_0}$, (conditional) prior density of $P_{ab}$ is positive on $E_{n,ab}$ for all $a, b \in [k_0]$.

By Assumption 2 (2), for $a < b \in [k_0]$, the prior probability $\Pi_n (E_{n,ab} | \{P_{aa}\}, K = k_0) \geq |E_{n,ab}| \min_{P_{ab} \in E_{n,ab}} \pi_n (P_{ab} | \{P_{aa}\}, K = k_0, \delta) \gtrsim \varepsilon_n e^{-C\log(n)(P_{aa} \cup P_{bb})}$ for some universal constant $C$. As $P_{aa} \in E_{n,aa}$ for $a \in [k_0]$, $P_{aa} \cup P_{bb} \leq (P^0_{aa} \cup P^0_{bb}) + C_0 \varepsilon_n \leq \|P^0\|_\infty + C_0 \varepsilon_n$, which gives a bound independent of $\{P_{aa}\}$.

Similarly, Assumption 2 (2) implies $\Pi_n (E_{n,aa} | K = k_0) \gtrsim \varepsilon_n e^{-C\log(n)(P^0_{aa} + C_0 \varepsilon_n)}$.

Therefore, combining the bounds for $P_{ab}$’s gives
\[
\Pi_n \left( P : \|P - P^0\|_\infty < C_0 \varepsilon_n | K = k_0 \right) \gtrsim e^{Ck_0^2 \log(1/\varepsilon_n) - Ck_0^2 \log(n) + ||P^0||_\infty + C_0 \varepsilon_n}
\]
where $k_0^2$ has the same order as $1/2(k_0(k_0 + 1))$ and is used for simpler notation, and the constant $C$ is universal.

As $\varepsilon_n^2 \asymp \log(k_0)/n$ and $1 \asymp \log(k_0)/n$, $\log(n) \asymp -\log(\varepsilon_n)$.
As $k_0 \asymp \sqrt{n}$, $k_0^2 \log(n) \asymp n \log(k_0)$. Then, $\Pi_n \left( P : \|P - P^0\|_\infty < C_0 \varepsilon_n | K = k_0 \right) \gtrsim e^{-Cn\log(k_0)}$ for some constant $C$ dependent on $P^0$.

To bound the second and the third component of (13), by Assumption 2 (3) and (4), there exists a universal constant $C$ such that $\Pi_n (Z = Z_0 | K = k_0) \geq e^{-Cn\log(k_0)}$ and $\Pi_n (K = k_0) \geq e^{-Cn\log(k_0)}$.

Note $n^2 \varepsilon_n^2 \asymp n \log(k_0)$, the right hand side of the inequality (10) can be replaced with $e^{-Cn\log(k_0)}$ and (10) holds for some constant $C$ dependent on $P^0$.

\[
\square
\]

9. Posterior Sampler. This section presents details of the Metropolis-Hastings algorithm used to draw posterior samples from (11). The proposal has two stages: in the first stage, sample $(Z, K)$; in the second stage, sample $P$ given $(Z, K)$. The first stage is adapted from the allocation sampler [19].

At $t$th iteration, the proposal $\Pi_{prop} (Z^*, K^* | A, Z^{(t)}, K^{(t)}, P^{(t)})$ consists of the four steps MK, GS, M3 and AE with equal probability $\frac{1}{4}$. With proposal $(Z^*, K^*)$, sample $P^* | (Z^*, A)$ by independently sampling each entry of $P^*$ from the Beta distribution $Beta(O_{ab} + 1, n_{ab} - O_{ab} + 1)$. With proposal $(P^*, Z^*, K^*)$, the acceptance rates in the allocation sampler regimes are computed.

9.1. MK. MK: choose “add” or “delete” one empty cluster with probability $1/2$. If “add” move is chosen, randomly pick one community identifier from $[K + 1]$ for the new empty community and rename the others as necessary; if “delete” move is chosen, randomly pick one community from $[K]$, delete the community if it is empty and abandon the MK move if it is not empty.

In the step MK, if “add” one empty community is chosen, accept the proposal with probability $\min \left( 1, \frac{\Pi_n (P^* | Z^*) K^*}{\Pi_n (P^{(t)} | Z^{(t)}) (n + K)} \right)$; if “delete” one empty community is chosen, accept the proposal with probability $\min \left( 1, \frac{\Pi_n (P^* | Z^*) K^*}{\Pi_n (P^{(t)} | Z^{(t)}) (n + K - 1)} \right)$. 
9.2. GS. GS: relabel a random node. First randomly pick \( i \) then generate \( Z^*(i) \) according to \( \Pi_{prop}(Z^*(i) = k) \propto \beta(Z^*,A)^{-1} \Pi(Z^*|K^*) \) where \( K^* = K^{(i)} \), the prior probability \( \Pi(Z^*|K^*) = \int \Pi(Z^*|\alpha,K^*) \Pi(\alpha|K^*) d\alpha = \frac{\Gamma(K^*)}{(n+K)^{n+K}} \prod_{1 \leq i \leq K} \Gamma(n^*_i + 1) \) due to multinomial-Dirichlet conjugacy, and \( \beta(Z^*,A) = \prod_{1 \leq a \leq b \leq K} \Gamma(O_{ab} + 1) / \Gamma(n^*_a - O_{ab} + 1) \) is the coefficient corresponding to the proposal distribution of \( P \). Clearly, \( Z^*(j) = Z(j) \) for all \( j \neq i \in [n] \).

In the step GS, suppose node \( i \) is chosen and its original label \( c_1 \) is relabeled with \( c_2 \), then accept the proposal with probability \( \min(1, \frac{\Pi_n(P^*|Z^*)}{\Pi_n(P^m|Z^*)}) \).

9.3. M3. M3: randomly pick two communities \( c_1, c_2 \in [K] \), reassign nodes \( \{ i : Z(i) \in \{ c_1, c_2 \} \} \) to \( \{ c_1, c_2 \} \) sequentially according to the following scheme. Start with \( B_0 = B_1 = \emptyset \) and \( A_0 \) being the sub-network without nodes from community \( c_1 \) and \( c_2 \), define the assignment \( B_h = \{ Z^*(x_i) \}_{i=1}^{h-1} \) with \( x_i \) being the node index of the \( i \)-th element in \( \{ i : Z(i) \in \{ c_1, c_2 \} \} \), define the sub-network \( A_h = A_{h-1} \cup \{ x_h \} \) by appending one more node, define the assignment \( Z_{B_h}^* \) for the sub-network \( A_h \) as the assignment with the node \( x_h \) assigned to \( c_j \), and define the size of communities in the sub-network \( A_{h-1} \) as \( \{ n_{c_1,c_2} \}_{c \in [K]} \). For \( i \in [n_c] \), assign the \( i \)-th node of \( \{ i : Z(i) \in \{ c_1, c_2 \} \} \) to \( c_1 \) with probability \( p_{B_1}^{i,1} \) and to \( c_2 \) with probability \( p_{B_1}^{i,2} \equiv 1 - p_{B_1}^{i,1} \), where

\[
p_{B_1}^{i,c} = \frac{\Pi(A_i|Z_{B_1}^*,K,P)}{\Pi(A_i|Z_{B_1}^*,P)} = \frac{\Pi(A_i|P,Z_{B_1}^*) \Pi(P|Z_{B_1}^*,K) \Pi(Z_{B_1}^*) \Pi(K)}{\Pi(A_i|P) \Pi(P) \Pi(K)}.
\]

To improve mixing, once \( c_1 \) and \( c_2 \) are drawn, shuffle \( \{ i : Z(i) \in \{ c_1, c_2 \} \} \) before the sequential reassignment. Therefore, the ordering of node indices in the sequential reassignment is random.

In the step M3, suppose community \( c_1 \) and \( c_2 \) are chosen, then accept the proposal with probability \( \min(1, \frac{\Pi_n(P^*|Z^*)}{\Pi_n(P^m|Z^*)} \frac{\prod_{i=1}^{n_c} p_{B_1}^{Z(i)} \Gamma(n^*_1 + 1) \Gamma(n^*_2 + 1) \beta(Z^*,A)}{\prod_{i=1}^{n_c} p_{B_1}^{Z(i)} \Gamma(n^*_1 + 1) \Gamma(n^*_2 + 1) \beta(Z^*,A)}) \), where \( n_c = n_{c_1} + n_{c_2} \).

9.4. AE. AE: merge two random clusters or split one cluster into two clusters with probability \( 1/2 \). If “merge” is chosen, randomly merge two clusters \( c_1 \) and \( c_2 \) with \( Z^*(i) = c_1 \) for all \( i \in \{ j : Z(j) \in \{ c_1, c_2 \} \} \) and \( Z^*(i) = Z(i) \) for all \( i \notin \{ j : Z(j) \in \{ c_1, c_2 \} \} \). The proposal probability is \( \left( n_c \right)^{K-1} \). If “split” is chosen, randomly pick two cluster identifiers \( \{ c_1, c_2 \} \) from \( [K+1] \), renaming others’ identifiers as necessary, and assign the nodes in cluster \( c_1 \) to the cluster \( c_2 \) with the random probability \( p_c \sim U(0,1) \). By integrating out \( p_c \), the proposal probability is \( \frac{\Gamma(n_{c_2}+1) \Gamma(n_{c_1}+1)}{\Gamma(n_{c_1}+n_{c_2})} \).

In the step AE, if “merge” two communities is chosen, accept the proposal with probability \( \min(1, \frac{\Pi_n(P^*|Z^*)}{\Pi_n(P^m|Z^*)} \frac{\prod_{i=1}^{n_c} p_{B_1}^{Z(i)} \Gamma(n^*_1 + 1) \Gamma(n^*_2 + 1) \beta(Z^*,A)^{K+n}}{\prod_{i=1}^{n_c} p_{B_1}^{Z(i)} \Gamma(n^*_1 + 1) \Gamma(n^*_2 + 1) \beta(Z^*,A)^{K+n}}) \); if “split” is chosen, accept the proposal with probability \( \min(1, \frac{\Pi_n(P^*|Z^*)}{\Pi_n(P^m|Z^*)} \frac{\prod_{i=1}^{n_c} p_{B_1}^{Z(i)} \Gamma(n^*_1 + 1) \Gamma(n^*_2 + 1) \beta(Z^*,A)^{K+n}}{\prod_{i=1}^{n_c} p_{B_1}^{Z(i)} \Gamma(n^*_1 + 1) \Gamma(n^*_2 + 1) \beta(Z^*,A)^{K+n}}) \).

10. Complete simulation results. This section provides complete simulation results. We choose \( \{k_0, n, \rho\} \in \{3,5,7\} \times \{50,75\} \times \{\frac{1}{2},1\} \), and for each \( \{k_0, n, \rho\} \) configuration, 100 networks are generated from \( SBM(0, \rho \beta^*, n, k_0) \).

To reduce Monte Carlo error and reach reasonable mixing, the Metropolis-Hastings algorithm and the allocation sampler collect \( 2 \times 10^4 \) posterior draws for each synthetic dataset after discarding first \( 10^4 \) draws as burn-in. Both algorithms are initialized at \( K = 2 \) and random membership assignment.
| $k_0$ | $n$ | $\rho$ | Method   | Bias Case 1 | RMSE Case 1 | Bias Case 2 | RMSE Case 2 | Bias Case 3 | RMSE Case 3 | Bias Case 4 | RMSE Case 4 |
|-------|-----|------|----------|------------|-------------|------------|-------------|------------|-------------|------------|-------------|
| 3     | 50  | 1/2  | DD-SBM   | 1.3        | 1.8         | -1.9       | 1.9         | -1.6       | 1.8         | 0.0        | 1.3         |
|       |     |      | c-SBM    | -0.5       | 0.8         | -1.9       | 1.9         | -1.8       | 1.9         | -1.0       | 1.0         |
|       |     |      | CLBIC    | -0.2       | 0.5         | -1.2       | 1.3         | -1.2       | 1.3         | -1.1       | 1.3         |
|       |     |      | NCV      | -0.0       | 0.9         | -2.0       | 2.0         | -2.0       | 2.0         | -2.0       | 2.0         |
| 3     | 75  | 1/2  | DD-SBM   | 0.1        | 0.3         | -1.9       | 2.0         | 0.1        | 0.3         | -0.6       | 1.0         |
|       |     |      | c-SBM    | -0.0       | 0.2         | -1.9       | 1.9         | -0.1       | 0.6         | -0.8       | 0.9         |
|       |     |      | CLBIC    | 0.0        | 0.0         | -1.3       | 1.4         | -0.3       | 0.6         | -0.9       | 1.0         |
|       |     |      | NCV      | 0.0        | 0.0         | -2.0       | 2.0         | -0.3       | 0.9         | -0.8       | 0.9         |
| 3     | 50  | 1/2  | DD-SBM   | 0.5        | 1.0         | -1.9       | 2.0         | -1.1       | 1.6         | -0.6       | 1.1         |
|       |     |      | c-SBM    | -0.1       | 0.5         | -1.9       | 2.0         | -1.3       | 1.6         | -1.0       | 1.0         |
|       |     |      | CLBIC    | 0.0        | 0.0         | -1.0       | 1.0         | -0.8       | 0.9         | -0.9       | 1.0         |
|       |     |      | NCV      | 0.0        | 0.1         | -2.0       | 2.0         | -1.9       | 1.9         | -1.9       | 2.0         |
| 5     | 50  | 1/2  | DD-SBM   | 0.0        | 0.1         | -1.9       | 1.9         | 0.0        | 0.2         | -0.7       | 0.9         |
|       |     |      | c-SBM    | 0.0        | 0.3         | -1.6       | 1.8         | 0.0        | 0.4         | -0.8       | 0.9         |
|       |     |      | CLBIC    | 0.0        | 0.0         | -1.0       | 1.0         | 0.0        | 0.0         | -0.9       | 1.0         |
|       |     |      | NCV      | 0.0        | 0.0         | -2.0       | 2.0         | 0.0        | 0.0         | -0.9       | 1.0         |
| 5     | 75  | 1/2  | DD-SBM   | 0.7        | 1.2         | -4.0       | 4.0         | -3.6       | 3.6         | -2.7       | 2.8         |
|       |     |      | c-SBM    | -1.0       | 1.4         | -3.9       | 3.9         | -3.7       | 3.8         | -2.9       | 2.9         |
|       |     |      | CLBIC    | -1.6       | 1.9         | -3.3       | 3.4         | -3.2       | 3.2         | -2.8       | 2.9         |
|       |     |      | NCV      | -1.5       | 2.0         | -4.0       | 4.0         | -4.0       | 4.0         | -3.0       | 3.2         |
| 5     | 50  | 1/2  | DD-SBM   | -1.1       | 2.0         | -3.9       | 3.9         | -3.9       | 3.9         | -2.4       | 2.6         |
|       |     |      | c-SBM    | -2.5       | 2.7         | -4.0       | 4.0         | -4.0       | 4.0         | -3.0       | 3.0         |
|       |     |      | CLBIC    | -2.5       | 2.6         | -3.0       | 3.0         | -3.0       | 3.0         | -2.9       | 2.9         |
|       |     |      | NCV      | -3.8       | 3.9         | -4.0       | 4.0         | -4.0       | 4.0         | -3.9       | 3.9         |
| 5     | 75  | 1/2  | DD-SBM   | 0.0        | 0.5         | -4.0       | 4.0         | -2.0       | 2.3         | -2.8       | 2.9         |
|       |     |      | c-SBM    | -0.3       | 0.8         | -3.9       | 4.0         | -2.0       | 2.3         | -2.9       | 2.9         |
|       |     |      | CLBIC    | 0.0        | 0.0         | -3.0       | 3.0         | -2.8       | 2.8         | -2.7       | 2.7         |
|       |     |      | NCV      | 0.0        | 0.0         | -4.0       | 4.0         | -3.8       | 3.9         | -2.6       | 2.7         |
| 7     | 50  | 1/2  | DD-SBM   | -5.5       | 5.6         | -5.9       | 5.9         | -5.9       | 5.9         | -3.9       | 4.1         |
|       |     |      | c-SBM    | -5.9       | 5.9         | -5.9       | 5.9         | -6.0       | 6.0         | -5.0       | 5.1         |
|       |     |      | CLBIC    | -5.2       | 5.2         | -5.3       | 5.3         | -5.3       | 5.3         | -5.4       | 5.5         |
|       |     |      | NCV      | -6.0       | 6.0         | -6.0       | 6.0         | -6.0       | 6.0         | -6.0       | 6.0         |
| 7     | 75  | 1/2  | DD-SBM   | -3.1       | 3.5         | -6.0       | 6.0         | -6.0       | 6.0         | -4.5       | 4.6         |
|       |     |      | c-SBM    | -4.7       | 4.8         | -5.9       | 6.0         | -5.9       | 5.9         | -4.9       | 5.0         |
|       |     |      | CLBIC    | -4.8       | 4.9         | -5.3       | 5.3         | -5.3       | 5.3         | -4.8       | 4.9         |
|       |     |      | NCV      | -6.0       | 6.0         | -6.0       | 6.0         | -6.0       | 6.0         | -5.5       | 5.6         |
| 7     | 75  | 1/2  | DD-SBM   | -4.6       | 4.7         | -6.0       | 6.0         | -5.9       | 6.0         | -4.3       | 4.4         |
|       |     |      | c-SBM    | -5.4       | 5.4         | -5.9       | 5.9         | -5.9       | 5.9         | -5.0       | 5.0         |
|       |     |      | CLBIC    | -4.8       | 4.9         | -5.0       | 5.0         | -5.0       | 5.0         | -4.8       | 4.9         |
|       |     |      | NCV      | -6.0       | 6.0         | -6.0       | 6.0         | -6.0       | 6.0         | -5.5       | 5.6         |
| 7     | 75  | 1/2  | DD-SBM   | -1.4       | 2.0         | -5.9       | 6.0         | -5.5       | 5.5         | -4.8       | 4.8         |
|       |     |      | c-SBM    | -2.3       | 2.6         | -5.9       | 5.9         | -5.3       | 5.4         | -5.0       | 5.0         |
|       |     |      | CLBIC    | -3.4       | 3.5         | -5.0       | 5.0         | -5.0       | 5.0         | -4.7       | 4.7         |
|       |     |      | NCV      | -3.2       | 3.5         | -6.0       | 6.0         | -6.0       | 6.0         | -4.8       | 4.8         |

Table 3: Bias and RMSE of $\hat{K}$. 