Graph Approximation and Clustering on a Budget

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Abstract

We consider the problem of learning from a similarity matrix (such as spectral clustering and low-
dimensional embedding), when computing pairwise similarities are costly, and only a limited number of
entries can be observed. We provide a theoretical analysis using standard notions of graph approximation,
significantly generalizing previous results (which focused on spectral clustering with two clusters). We
also propose a new algorithmic approach based on adaptive sampling, which experimentally matches or
improves on previous methods, while being considerably more general and computationally cheaper.

1 Introduction

Many unsupervised learning algorithms, such as spectral clustering [18], [2] and low-dimensional embedding
via Laplacian eigenmaps and diffusion maps [3], [16], need as input a matrix of pairwise similarities $W$
between the different objects in our data. In some cases, obtaining the full matrix can be a costly matter. For
example, $w_{ij}$ may be based on some expensive-to-compute metric such as W2D [5]; based on some physical
measurement (such as in some computational biology applications); or is given by a human annotator. In
such cases, we would like to have a good approximation of the (initially unknown) matrix, while querying
only a limited number of entries. An alternative but equivalent viewpoint is the problem of approximating
an unknown weighted undirected graph, by querying a limited number of edges.

This question has received previous attention in works such as [17] and [9], which focus on the task of
spectral clustering into two clusters, and assuming two such distinct clusters indeed exist (i.e. that there is
a big gap between the second and third eigenvalues of the Laplacian matrix). In this work we consider, both
theoretically and algorithmically, the question of query-based graph approximation more generally, obtaining
results relevant beyond two clusters and beyond spectral clustering.

When considering graph approximations, the first question is what notion of approximation to consider. One
important notion is cut approximation [14] where we wish for every cut in the approximated graph
to have weight close to the weight of the cut in the original graph up to a multiplicative factor. Many
machine learning algorithms (and many more general algorithms) such as cut based clustering [11], energy
minimization [22], etc. [1] are based on cuts, so this notion of approximation is natural for these uses. A
stronger notion is spectral approximation [19], where we wish to uniformly approximate the quadratic form
defined by the Laplacian up to a multiplicative factor. This approximation is important for algorithms such
as spectral clustering [2], Laplacian eigenmaps [3], diffusion maps [16], etc. that use the connection between
the spectral properties of the Laplacian matrix and the graph.

Our theoretical analysis focuses on the number of queries needed for such approximations. We first
consider the simple and intuitive strategy of sampling edges uniformly at random, and obtain results for
both cut and spectral approximations, under various assumptions. We note that these results are considerably
more general than the theoretical analysis in [17], which focuses on the behavior of the 2nd eigenvector of the
Laplacian matrix, and crucially rely on this large eigengap. We then consider how to extend these results to
more general than the theoretical analysis in [17], which focuses on the behavior of the 2nd eigenvector of the
Laplacian matrix, and crucially rely on this large eigengap. We then consider how to extend these results to
adaptive sampling strategies, and design a generic framework as well as a new adaptive sampling algorithm
for clustering (CLUS2K). Compared to previous approaches, the algorithm is much simpler and avoids doing
a costly full eigen-decomposition at each iteration, yet experimentally appears to obtain equal or even better
performance on a range of datasets.

Our theoretical results build on techniques for graph sparsification ([14], [19]), where the task is to find
a sparse approximation to a given graph $G$. This is somewhat similar to our task, but with two important
differences: First and foremost, we do not have access to the full graph, whereas in graph sparsification the
graph is given, and this full knowledge is used by algorithms for this task (e.g. using the sum of edge weights
associated with each node). Second, our goal is to minimize the number of edge sampled, not the number of
edges in the resulting graph (of course by sampling a smaller number of edges we will get a sparser graph).
Notice that if we wish to end with a sparse graph, one can always use any graph sparsification technique on
our resulting graph and get a graph with guarantees on sparsity.

## 2 A General Graph Approximation Guarantee

For simplicity we will consider all graphs as full weighted graphs (with zero weights at edges that do not
exist) and so any graph will be defined by a set of vertices $V$ and a weight matrix $W$. We will start with a
few basic definitions.

**Definition 2.1.** Let $G = (V,W)$ be a weighted graph and $S \subset V$ a subset of vertices, then the cut defined
by $S$, $|\partial_G S|$, is the sum of all the weights of edges that have exactly one endpoint in $S$.

**Definition 2.2.** Let $G = (V,W)$ and $\tilde{G} = (V,\tilde{W})$ be two graphs on the same set of vertices. $\tilde{G}$ is an $\epsilon$-cut
approximation of $G$ if for any $S \subset V$ we have $(1-\epsilon)|\partial_G S| \leq |\partial_{\tilde{G}} S| \leq (1+\epsilon)|\partial_G S|$

**Definition 2.3.** Let $G = (V,W)$. The graph Laplacian $L_G$ is defined as $L_G = D - W$ where $D$ is a
diagonal matrix with values $D_{ii} = \sum_{1 \leq j \leq n} W_{ij}$. The normalized graph Laplacian $L_G$ is defined as $L_G =
D^{-1/2}(D - W)D^{-1/2} = D^{-1/2}L_G D^{-1/2}$.

The Laplacian holds much information about the graph [4]. One of the main connections of the Laplacian,
and in particular the quadratic form it represents, to the graph is through the equation

$$x^T L_G x = \frac{1}{2} \sum_{i,j=1}^n W_{ij} (x_i - x_j)^2 \quad (1)$$

When $x_i \in \{0,1\}$ this is easily seen to be the value of the cut defined by $x$. Many spectral graph techniques,
such as spectral clustering, can be seen as a relaxation of such a discrete problem to $x \in \mathbb{R}^n$.

**Definition 2.4.** A graph $\tilde{G}$ is an $\epsilon$-spectral approximation of $G$ if

$$\forall x \in \mathbb{R}^n \quad (1-\epsilon)x^T L_G x \leq x^T L_G x \leq (1+\epsilon)x^T L_G x \quad (2)$$

We note that this is different than requiring $\|L_G - L_{\tilde{G}}\| \leq \epsilon$ (using the matrix 2-norm) as we can view it as
a multiplicative error vs. an additive error term. In particular, it implies approximation of eigenvectors (using
the min-max theorem [4]), which is relevant to many spectral algorithms, and includes the approximation of
the 2nd eigenvector (the focus of the analysis in [17]) as a special case. Moreover, it implies cut approximation (via equation [1]), and in fact strictly stronger (see [19] for a simple example of a cut approximation which is not a spectral approximation). Therefore, we will focus on spectral approximation in our theoretical results.

Our initial approximation strategy will be to uniformly at random sample a subset $\tilde{E}$ of $m$ edges, i.e., pick $m$ edges without replacement and construct a graph $\tilde{G} = (V, \tilde{W})$ with weights $\tilde{w}_{ij} = \hat{w}_{ij} = \frac{w_{ij}}{p}$ for any $(i,j) \in \tilde{E}$ and zero otherwise, where $p = m/\binom{n}{2}$ is the probability any edge is sampled. It is easy to see that the $E[\tilde{W}] = W$.

We begin by providing a bound on $m$ which ensures an $\epsilon$-spectral approximation. It is based on an adaptation of the work in [19], in which the author considered picking each edge independently. This differs from our setting, where we are interested in picking $m$ edges without replacement, since in this case the probabilities of picking different edges are no longer independent. While this seems like a serious complication, it can be fixed using the notion of negative dependence:

**Definition 2.5.** The random variables $X_1, \ldots, X_n$ are said to be negatively dependent if for all disjoint subset $I, J \subset [n]$ and all nondecreasing functions $f$ and $g$,

$$E[f(X_i, i \in I)g(X_j, j \in J)] \leq E[f(X_i, i \in I)]E[g(X_j, j \in J)]$$

Intuitively, a group of random variables are negatively dependent if when some of them have a high value, the others are more probable to have lower values. If we pick $m$ edges uniformly, each edge that has been picked lowers the chances of the other edges to get picked, so intuitively the probabilities are negatively dependent. The edge picking probabilities have been shown to be indeed negatively dependent in [17].

An important application of negative dependence is that the Chernoff-Hoeffding bounds, which hold for sums of independent random variables, also hold for negatively dependent variables. See supplementary material for details.

We can now state the general spectral approximation theorem:

**Theorem 2.1.** Let $G$ be a graph with weights $w_{ij} \in [0,1]$ and $\tilde{G}$ its approximation after sampling $m$ edges uniformly. Define $\lambda$ as the second smallest eigenvalue of $L_G$ and $k = \max\{\log(\frac{3}{\epsilon}), \log(n)\}$. If $m \geq \binom{n}{2} \left(\frac{16k}{\alpha}\right)^2$ then the probability that $\tilde{G}$ is not an $\epsilon$-spectral approximation is smaller then $\delta$.

**Proof sketch.** The proof is based on an adaptation of part of theorem 6.1 from [19]. The two main differences are that we use negative dependence instead of independence, and a weighted graph instead of an unweighted graph. The proof uses the following lemma:

**Lemma 2.1.** Let $L_G$ be the normalized Laplacian of $G$ with second eigenvalue $\lambda$. If $\|D^{-1/2}(L_G - L_{\tilde{G}})D^{-1/2}\| \leq \epsilon$ then $\tilde{G}$ is an $\sigma$-spectral approximation for $\sigma = \frac{\epsilon \lambda}{\sqrt{2 \alpha}}$.

The next part is to bound $\|D^{-1/2}(L_G - L_{\tilde{G}})D^{-1/2}\|$ using a modified version of the trace method [21] in order to bound this norm. See the supplementary material for more details.

Stating the result in a simplified form, we have that if $\min D_{ii} = \Omega(n^\alpha)$, then one gets an $\epsilon$-approximation guarantee using $m = \mathcal{O}\left(n^{2-\alpha}\left(\frac{\log(n) + \log(1/\delta)}{\epsilon \alpha}\right)^2\right)$ sampled edges.

The main caveat of theorem 2.1 is that it only leads to a non-trivial guarantee ($m \ll n^2$) when $\alpha > 0$ and $\lambda$ is not too small. Most algorithms, such as spectral clustering, assume that the graph has $k \geq 2$ relatively small eigenvalues, in the ideal case (more then one connected component) we even have $\lambda = 0$. Unfortunately, we will now show that this is unavoidable, and that the bound above is essentially optimal (up to log factors) for graphs with bounded $\lambda > C > 0$, i.e. expanders. In the next section, we will show how a few reasonable assumptions allows us to recover non-trivial guarantees even in the regime of small eigenvalues.

Since spectral approximation implies cut approximation, we will use this to find simple bounds on the number of edges needed for both approximations. We will show that a necessary condition for any approximation is that the minimal cut is not too small, the intuition being that that even finding a single edge (for
connectedness) on that cut can be hard, and get a lower bound on the number of samples needed. For this we will need to following simple lemma (which follows directly from the linearity of expectation)

**Lemma 2.2.** Let $X$ be a finite set, and $Y \subset X$. If we pick a subset $Z$ of size $m$ uniformly at random then $E[|Z \cap Y|] = \frac{m|Y|}{|X|}$.

We will now use this to prove a lower bound on the number of edges sampled for binary weighted graphs (i.e. unweighted graph) $w_{ij} \in \{0, 1\}$.

**Theorem 2.2.** Let $G$ be a binary weighted graph with minimal cut weight $c > 0$. Assume $\tilde{G}$ was constructed by sampling $m < \frac{n}{2} \left(1 - \delta\right)$ edges, then for any $\epsilon < 1$, $P\left(\tilde{G} \text{ is not an } \epsilon \text{-cut approximation of } G\right) > \delta$.

**Proof.** Let $Y$ be all the edges in a minimal cut and let $\tilde{E}$ be the edges sampled. Since the weights are binary the weight of this cut in $\tilde{G}$ is the number of edges in $Y \cap \tilde{E}$. From lemma 2.2 we know that $E[|Y \cap \tilde{E}|] = mc/\left(\frac{n}{2}\right) < 1 - \delta$. From the Markov’s inequality we get that $P\left(|Y \cap \tilde{E}| \geq 1\right) < 1 - \delta$. If $|Y \cap \tilde{E}| < 1$ then the intersection is empty and we do not have an $\epsilon$-approximation for any $\epsilon < 1$ proving $P\left(\tilde{G} \text{ is an } \epsilon \text{-cut approximation of } G\right) < 1 - \delta$.

This theorem proves that in order to get any reasonable approximation with a small budget $m$ (at least with uniform sampling) the original graphs minimal cut cannot be too small and that $\Omega\left(\frac{n}{c}\right)$ samples are needed. Comparing this to theorem 2.1 (noticing min $D_{ii} \geq c$) we see that, for graphs with a lower bound on $\lambda$, by sampling within a logarithmic factor of this lower bound is sufficient to ensure a good cut approximation.

### 3 Clusterable Graphs

Clustering algorithms assume a certain structure of the graph, generally they assume $k$ strongly connected components, i.e. the clusters, with weak connections between them (the precise assumptions vary from algorithm to algorithm). While this is a bad scenario for approximation, as this normally means a small minimal cut (and for spectral clustering a small $\lambda$), we will show how approximation can be used (on the inner-cluster graphs) to obtain useful results. We give two results, one geared towards spectral approximation, and the other towards cut approximation.

#### 3.1 Spectral Approximation

**Definition 3.1.** Assume a graph $G = (V, W)$ consists of $k$ clusters, define $W^{in}$ as the block diagonal matrix consisting of the similarity scores between same-cluster elements.

$$W^{in} = \begin{bmatrix} W^1 & 0 & \cdots & 0 \\ 0 & W^2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & W^k \end{bmatrix}$$

and $W^{out} = W - W^{in}$ the off-diagonal elements.

**Assumption 3.1.** Define $\lambda^{in} = \min_{1 \leq i \leq k} \lambda_2(L^i)$, the smallest of all the second normalized eigenvalues over all $L^i = L_{W^i}$. Assume $\lambda^{in} > C > 0$ for some constant $C$.

**Assumption 3.2.** $\min D^{in}_{ii} = \Omega\left(n^\alpha\right)$ where $D^{in}_{ii} = \sum_j W^{in}_{ij}$ for some $\alpha > 0$.

**Assumption 3.3.** Assume that $||W^{out}|| = \mathcal{O}\left(n^\beta\right)$ for some $\beta < \alpha$. 


Assumption 3.1 implies well connected clusters, while assumption 3.2 excludes sparse, well-connected graphs, which we have already shown earlier to be hard to approximate. Assumption 3.3 essentially requires the between-cluster connections to be relatively weaker than the within-cluster connections.

Under these assumptions, the next theorem proves the clusters can be found.

**Theorem 3.1.** Let $P$ be the zero eigenspace of $L^\text{in} = D^\text{in} - W^\text{in}$ corresponding to the $k$ clusters, $\tilde{L}$ the Laplacian of the graph we get by sampling $m = \tilde{O}(n^{2-\gamma})$ edges for $\beta \leq \gamma \leq \alpha$, and $Q$ the space spanned by the first $k$ eigenvectors of $\tilde{L}$. Under previous assumptions, $||\sin(\Theta(P,Q))|| = O(\frac{n^\beta + n^\gamma}{n^\alpha})$.

We simplified the statement in order not to get overwhelmed by notation. $\Theta(P,Q)$ is a diagonal matrix whose diagonal values correspond to the canonical angles between the subspaces $P$ and $Q$, and $||\sin(\Theta(P,Q))||$ is a common way to measure distance between subspaces.

**Proof sketch.** If $\gamma = 0$, i.e. $Q$ was spanned by eigenvectors of the full $L$, then the theorem would be true by the sin-theta theorem [6] using our assumptions. We need to show that this theorem can be used with $\tilde{L}$. The sin-theta theorem states that $||\sin(\Theta(P,Q))|| \leq \frac{||L^\text{out}||}{\bar{\mu}_2}$ where $||L^\text{out}||$ the "noise" factor, and $\bar{\mu}_2$ the unnormalized second eigenvalue of $L^\text{in}$ the "signal" factor. Using theorem 2.1 and our first two assumptions we can approximate each $L^W_i$ and use to show that $\bar{\mu}_2 = \Omega(n^\alpha)$. We now only need to show $||L^\text{out}|| = O(n^{\beta} + n^\gamma)$. This can be done using the matrix Chernoff inequality [20], by applying a result in [12] that shows how it can be adapted to sampling without replacements. We note that the result in [12] is limited to sampling without replacements as negative dependence has no obvious extension to random matrices. For further details see the supplementary material.

This gives us a tradeoff between the number of edges sampled and the error. The theoretical guarantee from the sin-theta theorem for the complete graph is $O(n^\beta/n^\alpha)$ so for $\gamma = \beta$ we have the same guarantee as if we used the full graph. For $n$ large enough one can get $||\sin(\Theta(P,Q))||$ as small as desired by using $\gamma = \alpha - \epsilon$.

### 3.2 Cut Approximation

Cut based clustering, such as [11], have a different natural notion of "clusterable". We will assume nothing on eigenvalues, making this more general than the previous section.

**Assumption 3.4.** Assume $G$ can be partitioned into $k$ clusters, within which the minimal cut is at least $c^\text{in}_i$. Furthermore, assume that any cut separating between the clusters of $G$ (but does not split same cluster elements) is smaller than $c^\text{out}$, and that $c^\text{in}_i > 4c^\text{out}$.

These assumptions basically require the inner-cluster connections to be relatively stronger than between-cluster connections.

**Theorem 3.2.** Let $G$ be a graph with weights $w_{ij} \in [0,1]$ and $\tilde{G}$ its approximation after observing $m$ edges. Under previous assumptions if $m = \tilde{\Omega} \left( \frac{n^2}{c^\text{in}_i k [\ln(\frac{1}{\delta})]} \right)$ then the cuts separating the clusters are smaller then any cut that cuts into one of the clusters.

**Proof Sketch.** We can use cut approximation for the clusters themselves so $c^\text{in}_i \geq c^\text{in}/2$. Using the Chernoff bound and union bound for the $2^k$ cuts between clusters, we get that none of them is greater than $c^\text{in}/2$. See the supplementary material for full proof.

In the supplementary material, we provide a more in-depth analysis of cut approximation including an analog of theorem 2.1.
4 Adaptive Sampling and the Clus2K Algorithm

Theorem 2.2 states that, with uniform sampling and no prior assumptions of the graph structure, we need at least $\Omega(\frac{n^2}{c})$ where $c$ is the weight of the smallest cut. What if we had an adaptive algorithm instead of just uniform sampling? It is easy to see that for some graphs the same (up to a constant) lower bound holds. Think of a graph with $2n$ vertices, consisting of two cliques that have $c$ randomly chosen edges connecting them. Let’s assume further that some oracle told us which vertex is in which clique, so any sensible algorithm would sample only edges connecting the cliques. As the edges are random, it would take $\Theta(\frac{n^2}{c})$ tries just to hit one edge needed for any good approximation. However, in some cases an adaptive scheme can reduce the number of samples, as we now turn to discuss in the context of clustering.

Consider a similar toy problem - we have a graph which is known to consist of two connected components, each a clique of size $n$ and we wish to find these clusters. We can run the uniform sampling algorithm until we have only two connected components and return them. How many edges do we need to sample until we get only two connected components? If we look only at one clique, then basic results in random graph theory show that with high probability, the number of edges added before we get a connected graph is $\Theta(n \log(n))$, which lower bounds the number of samples needed. To improve on this we can use an adaptive algorithm with the following scheme: at each iteration, pick an edge at random connecting the smallest connected component to some other connected component. At each step we have at least a probability of $\frac{1}{2}$ to connect two connected components. This is because there are $n$ nodes in the wrong cluster, and at least $\frac{n}{2}$ in the right cluster (since we pick the smallest connected component). Therefore with high probability the number of steps needed to decrease the number of connected components from $2n$ to two is $\Theta(n)$.

This argument leads us to consider adaptive sampling schemes, which iteratively sample edges according to a non-uniform distribution. Intuitively, such a distribution should place more weight on edges which may be more helpful in approximating the structure of the original graph. We first discuss how we can incorporate arbitrary non-uniform distributions into our framework. We then propose a specific non-uniform distribution, motivated by the toy example above, leading to a new algorithm for our setting in the context of clustering.

One approach to incorporate non-uniform distributions is by unbiased sampling, where we re-scale the weights according to the sampling probability. This means that the weights are unbiased estimates of the actual weights. Unfortunately, this re-scaling is not easy to compute in general when sampling without replacement, as the probability of sampling an edge is a marginal distribution over all the algorithm’s possible trajectories. Sampling with replacement is much easier, since it only depends on the sampling probability in the current iteration. Moreover, as long as we sample only a small part of all edges, the risk of re-sampling an already-sampled edge is negligible. Finally, one can show that whatever the non-uniform distribution, a simple modification (adding with probability half a uniform sample) suffices for cut approximation to hold. Unfortunately, we found this approach to work poorly in practice, as it was unstable and oscillated between good and bad clustering long after a good clustering is initially found.

Due to these issues, we consider a biased sampling without replacement approach, where we mix the non-uniform distribution with a uniform distribution (as proposed earlier) on unseen edges, but do not attempt to re-scale of weights. More specifically, consider any adaptive sampling algorithm which picks an unseen edge at step $i + 1$ with probability $p(e; \tilde{G}_i)$ that depends on the graph $\tilde{G}_i$ seen so far. We will consider a modified distribution that with probability $0.5$ picks an unseen edge uniformly, and with probability $0.5$ picks it according to $p(e; \tilde{G}_i)$. While biased sampling can ruin approximation guarantees, in the clustering scenarios one can show similar results to theorem 3.2 (under stronger conditions) for any adaptive sampling scheme. The theoretical guarantees for adaptive sampling are in the supplementary material.

4.1 CLUS2K Algorithm

We now turn to consider a specific algorithmic instantiation, in the context of clustering. Motivated by the toy example from earlier, we consider a non-uniform distribution which iteratively attempts to connect clusters in the currently-observed graph, by picking edges between them. These clusters are determined by the clustering algorithm we wish to use on the approximated graph, and are incrementally updated after
each iteration. Inspired by the common practice (in computer vision) of over-segmentation, we use more clusters than the desired number of clusters \( k \) \((2k \text{ in our case})\). Moreover, as discussed earlier, we mix this distribution with a uniform distribution. The resulting algorithm, which we denote as CLUS2K, appears as Algorithm 1 below.

**Algorithm 1 CLUS2K**

**Input:** budget \( b \), number of clusters \( k \)

**Initialize:** \( S = \{(i,j) \in \{1,\ldots,n\}^2 : i < j \}, \hat{W} \) the zero matrix.

**for** \( t = 1, \ldots, b \) **do**

- With probability \( 1/2 \) pick \((i,j) \in S\) uniformly;
- Otherwise:
  - \( C_1, \ldots, C_{2k} \leftarrow \) cluster \( \hat{W} \) into \( 2k \) clusters;
  - pick two distinct clusters \( C_l \) and \( C_m \) uniformly at random;
  - pick \((i,j) \in S\) connecting \( C_l \) and \( C_m \) uniformly at random;
- Set \( \hat{w}_{ij} = \hat{w}_{ji} = w_{ij} \); \( S = S \setminus (i,j) \);

**end for**

For the setting of budget-constrained clustering, the two most relevant algorithms we are aware of is the algorithm of [17] (hereby denoted as S&T), and the IU_RED algorithm of [9]. These algorithms are somewhat similar to our approach, in that they interleave uniform sampling and a non-uniform sampling scheme. However, the sampling scheme is very different than ours, and focuses on finding the edge to which the derivative of the 2nd Laplacian eigenvector is most sensitive. This has two drawbacks. First, it is specifically designed for spectral clustering and the case of \( k = 2 \) clusters, which is based on the 2nd Laplacian eigenvector. Extending this to more than 2 clusters requires either recursive partitioning (which can be suboptimal), or considering sensitivity w.r.t. \( k - 1 \) eigenvectors, and it is not clear what is the best way to do so. Second, computing eigenvector derivatives requires a full spectral decomposition at each iteration, which can be quite costly or impractical for large matrices. In contrast, our algorithm does not compute derivatives. Therefore, when used with spectral clustering methods, which require only the smallest \( 2k \) eigenvectors, we have a significant gain.

It is possible to speed up implementation even further, in the context of spectral clustering. Since only a single edge is added per iteration, one can use the previously computed eigenvectors as an initial value for fast iterative eigenvector solvers (although restarting every couple of steps is advised). Another possible option is to pick several edges from this distribution at each step, which makes this process parallelizable.

## 5 Experiments

We tested our CLUS2K algorithm on several datasets, and compared it to the S&T and IU_RED discussed earlier (other alternatives were tested in [17] and shown to be inferior). It is important to note that S&T and IU_RED were designed specifically for \( k = 2 \) and spectral clustering using the unnormalized Laplacian \( L_G \), while we also tested for various values of \( k \), and using the normalized Laplacian \( L_G \) as well [18]. The IU_RED performed badly (perhaps because it relies substantially on the \( k = 2 \) assumption) in these cases while S&T performed surprisingly well (yet still inferior to CLUS2K ). Clustering was measured by cluster purity. The purity of a single cluster is the percent of the most frequent class in the cluster. The purity of a clustering is a weighted average of its single cluster purity, weighted by the number of elements in each cluster. The purity shown is averaged over 5 runs.

### 5.1 Synthetic Data

The synthetic experiments were performed on two datasets - The two half circles dataset, and a dataset comprising of four well separated Gaussians, both experiments used unnormalized spectral clustering (see figure 5.1) using a gaussian weight matrix. The two half circles is a classic clustering dataset with \( k = 2 \).
clusters. The Gaussian dataset shows how the various algorithms handle an easy $k > 2$ dataset, and IU_RED performs worse than uniform sampling in this case.

### 5.2 Real Data

We tested on three further datasets - the iris and glass UCI datasets (both with $k>2$ clusters) using a gaussian weight matrix, and the Caltech-7 dataset, a subset of the Caltech-101 images datasets with 7 clusters gathered by [15], using the similarity matrix suggested by [10]. We tested each dataset using both the normalized and unnormalized Laplacian for clustering. The results are presented in figure 5.2

Overall, the experiments show that the CLUS2K algorithm performs as good or better than previous algorithms for budget-constrained clustering, while being significantly computationally cheaper as well as more general.
Figure 2: UCI datasets results
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A  Proof of Theorem 2.1

We will need to Hoeffding-Chernoff bound for negative dependence:

**Theorem A.1.** Assume $X_i \in [0,1]$ are negatively dependent variables and define $X = \sum_{i=1}^{n} X_i$ then

$$P \left( |X - E[X]| \geq \epsilon E[X] \right) \leq 2 \exp \left( -\frac{\epsilon^2 E[X]^3}{3} \right)$$

See [7] 1.6 and 3.1 for details.

First it is important to note a change in notation from [19] in order to be consistent with notation used in [14]. A $\epsilon$-spectral approximation in our paper is weaker than a $(1 + \epsilon)$-spectral approximation in [19].

We will now go over the main changes needed to prove Theorem 6.1 in [19] (disregarding S.2) with negatively dependent sampling of edges and weights $w_{ij} \in [0,1]$.

The proof of Claim 6.5 is quite straightforward. The claim of Lemma 6.6 needs to be changed to

$$E[\Delta^k_t \Delta^l_t] \leq w_{r,t}^{-1} \gamma^k + l - 1 \gamma^r$$

instead of $E[\Delta^k_t \Delta^l_t] \leq \gamma^k + l - 1 \gamma^r$. The changes to the proof are again straightforward (remembering $w_{ij} \in [0,1]$).

The main change is to Lemma 6.4. Using the modified Lemma 6.6 and substituting negative dependents for independence one can prove

$$\sum_{\sigma \text{ valid for } T, \tau} \prod_{s \in T} \Delta_{v_s-1,v_s} \prod_{i: \tau(i)=s} \Delta_{v_i-1,v_i} \leq \frac{1}{\gamma^{|T|-|T|}} \sum_{\sigma \text{ valid for } T, \tau} \prod_{s \in T} \frac{w_{v_s-1,v_s}}{d_{v_s-1}}$$

instead of equation 10 in the paper. The last change is to pick $\sigma(s)$ proportional to $w_{v_s-1,v_s}$ instead of uniformly to prove that

$$\sum_{\sigma \text{ valid for } T, \tau} \prod_{s \in T} \frac{w_{v_s-1,v_s}}{d_{v_s-1}} \leq 1$$

instead of equation 11. From there on all changes are straightforward.

B  Proof of Theorem 3.1

Let $\tilde{L} = \tilde{L}^{in} + \tilde{L}^{out}$. Let $P$ be the zeros eigenspace of $\tilde{L}^{in}$, which is the same as the zero eigenspace of $L^{in}$, if all the $W^j$ are connected. Let $Q$ be the space spanned by the first $k$ eigenvectors of $\tilde{L}$. According to the Sin-Theta theorem [8], $||\sin(\Theta(P,Q))|| \leq \frac{||\tilde{L}^{out}||}{\mu_2^{in}}$ where $|| \cdot ||$ is the spectral norm of $\tilde{L}^{out}$ and $\mu_2^{in}$ is the second smallest unnormalized eigenvalue of $\tilde{L}^{in}$. To prove the theorem we will show that $\mu_2^{in} = \Omega(n^\alpha)$ and that $||\tilde{L}^{out}|| = O(n^\beta + n^\gamma)$.

The first claim is through using the first two assumptions and the following lemma

**Lemma B.1.** Let $\lambda_2$ and $\mu_2$ be the second smallest normalized and unnormalized eigenvalues of $L$, and $d = \min_i D_{ii}$ then $\mu_2 \geq \lambda_2 \cdot d$. 

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\textbf{Proof.} From the min-max theorem we have
\[
\mu_2 = \min_{U: \dim(U) = 2} \left\{ \max_{x \in U \setminus \{0\}} \frac{x^T L x}{||x||^2} \right\} \\
\lambda_2 = \min_{U: \dim(U) = 2} \left\{ \max_{x \in U \setminus \{0\}} \frac{x^T L x}{x^T D x} \right\}
\]
and the lemma follows from the fact that \(x^T D x \geq d ||x||^2\).

Let \(m_1\) be the number of edges needed in order to have an \(\epsilon\)-spectral approximation of each inner-cluster matrix \(W^i\) for \(\epsilon = 3/4\) with probability \(\delta/2\), then by theorem 2.1 we have that \(m_1 = \tilde{O}(n^{2-\alpha})\). Using this fact, the first two assumptions and lemma 3.1, it is easy to see that \(\mu_2^n = \Omega(n^\alpha)\).

We now need to show that \(||\bar{L}^{\text{out}}|| = O(n^\beta + n^\gamma)\). The main tool would be the matrix Chernoff inequality for sampling matrices without replacements.

\textbf{Theorem B.1.} Consider a finite sequence of Hermitian matrices \(X_1, \ldots, X_k\) sampled uniformly without replacements from a finite set of matrices of dimension \(n\). Assume that
\[
X_k \succeq 0 \quad ||X_i|| \leq R.
\]
Define \(Y = \sum_{i=1}^k X_i\) then
\[
P(||Y|| \geq (1+\epsilon)||E[Y]||) \leq n \cdot \left(\frac{e^\epsilon}{(1+\epsilon)^{1+\epsilon}}\right)^{||E[Y]||/R}
\]

\textbf{Proof.} This is an adaptation of theorem 5.1.1 from [27] replacing the independence requirement to sampling without replacements. In order to adapt the proof we notice that the only place where independence is used in lemma 3.5.1 (subadditivity of the matrix cumulant generating functions) where we need to prove that
\[
\forall \theta \in \mathbb{R} \quad E \left[ Tr \left( \exp \left( \sum \theta X_i \right) \right) \right] \leq Tr \left( \exp \left( \sum \log E e^{\theta X_i} \right) \right) \tag{3}
\]
Using the result of [42], if \(X_i\) are sampled uniformly at random without replacements for a finite set, and \(Y_i\) are sampled with the same probability with replacements then
\[
E \left[ Tr \left( \exp \left( \sum \theta X_i \right) \right) \right] \leq E \left[ Tr \left( \exp \left( \sum \theta Y_i \right) \right) \right] \tag{4}
\]
so we can conclude that
\[
E \left[ Tr \left( \exp \left( \sum \theta X_i \right) \right) \right] \leq E \left[ Tr \left( \exp \left( \sum \theta Y_i \right) \right) \right] \leq \leq Tr \left( \exp \left( \sum \log E e^{\theta Y_i} \right) \right) = Tr \left( \exp \left( \sum \log E e^{\theta X_i} \right) \right)
\]
where the second inequality is from \(3\) as \(Y_i\) are independent.

We define for each edge \(e\) connecting nodes in different clusters the matrix \(X_e\) that is equal to zero with probability \(1-p\) and is equal to \(\frac{1}{p} L_e\) with probability \(p\), where \(L_e\) is the Laplacian of a single edge graph with weight \(w_e\). Then \(L^{\text{out}} = \sum_{e \in S^{\text{out}}} X_e, E[L^{\text{out}}] = L^{\text{out}}, X_e \succeq 0\) and \(||X_e|| \leq 1/p\).

If we use the matrix Chernoff inequality with \(1+\epsilon = 2e \cdot n^{\gamma-\beta}\) then
\[
P(||\bar{L}^{\text{out}}|| \geq 2en^\gamma) \leq n \left(\frac{1}{2n^{\gamma-\beta}}\right)^{2en^\gamma p}
\]
So if \(p = m/\binom{n}{2} = \mathcal{O}\left(\frac{\log(n)}{n^\gamma}\right)\) we get that \(P(||\bar{L}^{\text{out}}|| \geq 2en^\gamma) < \delta/2\) for large enough \(n\).
C Cut Approximation

We will start by proving an analog of theorem 2.1 in the paper. We will use the following lemma from [13]:

**Lemma C.1.** Let $G$ be an undirected graph with $n$ vertices and minimal cut $c > 0$. For all $\alpha \geq 1$ the number of cuts with weight smaller or equal to $\alpha c$ is less then $n^{2\alpha}$.

The lemma is proven in [13] for graphs with integer weights, but the extension to any positive weights is trivial by scaling and rounding. We can now state and prove the theorem guaranteeing good cut approximations.

**Theorem C.1.** Let $G$ be a graph with weights $w_{ij} \in [0, 1]$, with minimal cut $c > 0$, and $G^*$ its approximation after sampling $m$ edges uniformly. If $m \geq \binom{n}{2}^{2(\ln(n) + \ln(\delta) + k)}$ where $k = \ln(2 + 4\ln(n))$, then the probability that $G^*$ is not an $\epsilon$-cut approximation is smaller then $\delta$.

**Proof.** This is an adaptation of the proof in [14] - consider a cut with weight $\alpha c$. Let $p = m/\binom{n}{2}$ the probability to sample a single edge. Let $Y_c = X_c \cdot w_c$ where $X_c$ is an indicator whether edge $e$ on the cut was sampled and $w_e$ its weight. Define $Y$ the sum of $Y_c$ on all the edges along the cut, then by the fact that edges are negatively dependent and theorem [A.7] the probability that the cut is not an $\epsilon$ approximation is smaller then

$$2 \exp \left( -\frac{\epsilon^2 \mathbb{E}[Y]}{3} \right) = 2 \exp \left( -\frac{\epsilon^2 \alpha p}{3} \right) \leq 2 \exp \left( -\left( \ln \left( \frac{1}{\delta} \right) + k \right) \alpha \right) \cdot n^{-2\alpha}$$

Define $P(\alpha) = 2 \exp \left( -\left( \ln \left( \frac{1}{\delta} \right) + k \right) \alpha \right) \cdot n^{-2\alpha}$ and let $f(\alpha)$ the number of cuts with value $\alpha c$ in the original graph. By the union bound the probability that some cut is not an $\epsilon$ approximation is less then $\sum_{\alpha \geq 1} f(\alpha)P(\alpha)$ (notice that this sum is well defined since $f(\alpha)$ is non zero only in a finite number of $\alpha$ values). Defining $F(\alpha) = \sum_{\alpha \geq x} f(\alpha)$ then by the previous lemma $F(\alpha) \leq n^{2\alpha}$. Let $g$ be any measure on $[1, \infty)$ such that $G(\alpha) = \int_1^\infty g(x) \, dx \leq n^{2\alpha}$, then the integral $\int_1^\infty P(x) \, dx$ is maximized when $G(\alpha) = n^{2\alpha}$. This is due to the fact that $P$ is a monotonically decreasing function, so if the inequality is not tight at some point $x_1$ we could increase the value by picking $\tilde{g}(x) = g(x) + \delta (x - x_1) - \delta \delta(x - x_2)$ for some appropriate $x_2 > x_1$ and $\delta$ (where $\delta$ is the Dirac delta function). From this we can conclude that the probability of some cut not being an $\epsilon$-approximation is bounded by

$$n^2 P(1) + \int_1^\infty P(\alpha) \frac{dn^{2\alpha}}{d\alpha} \, d\alpha = 2 \delta e^{-k} + 4 \delta \ln(n) e^{-k} \frac{\ln(\frac{1}{\delta}) + k}{ln(\frac{1}{\delta}) + k} \leq \delta (2 + 4\ln(n)) \exp(-k) = \delta$$

A drawback is that the theorem gives a bound that depends on the minimal cut, which we do not know, and unlike the situation in [14] we cannot approximate it using the full graph. We can prove a bound that uses only known data about the graph. The following theorem shows we can lower bound $c$.

**Lemma C.2.** Let $G$ be a graph with weights $w_{ij} \in [0, 1]$, with minimal cut $c$, and $G^*$ its approximation after sampling $m$ edges with minimal cut $\tilde{c} > 0$. Define $p = m/\binom{n}{2}$ the probability to sample a single edge. Also define $l = \frac{3\ln(\frac{1}{\delta})}{4}$ and $\beta = \sqrt{1 + \frac{l}{pe}} - \sqrt{\frac{l}{pe}}$. With probability greater then $1 - \delta$ the following inequality holds - $c \geq \tilde{c} \cdot \beta^2$. 

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Proof. Let \( S \) be a subset of vertices such that \(|\partial_G S| = c\) then from the Chernoff-Hoeffding inequality (the one-sided version)

\[
P (|\partial_G S| \geq (1 + \epsilon)|\partial_G S|) = P (p|\partial_G S| \geq (1 + \epsilon)p|\partial_G S|) 
\leq \exp \left(-\frac{\epsilon^2 pc}{3}\right)
\]

Where we multiply by \( p \) to have all the elements bounded by 1. Setting \( \epsilon = \sqrt{\frac{3 \ln(\frac{1}{\delta})}{pc}} \) we get that with probability greater then \( 1 - \delta \) that

\[
pc \left(1 + \sqrt{\frac{3 \ln(\frac{1}{\delta})}{pc}}\right) = pc + \sqrt{3 \ln(\frac{1}{\delta}) \sqrt{pc}} \geq |\partial_G S| \geq \hat{c}.
\]

By completing the square we get that

\[
\left(\sqrt{pc} + \sqrt{\frac{3 \ln(\frac{1}{\delta})}{4}}\right)^2 = (\sqrt{pc} + \sqrt{\delta})^2 \geq \hat{c} + 1
\]

which means (after some simple algebraic manipulation) that

\[
c \geq \hat{c} \beta^2
\]

We can combine these to theorems and get

**Theorem C.2.** Let \( G \) be a graph with weights \( w_{ij} \in [0, 1] \) and \( \hat{G} \) its approximation after sampling \( m \) edges with minimal cut \( \hat{c} > 0 \). Define \( \beta \) and \( k \) as in previous theorems. If \( m \geq (n) \frac{3(2 \ln(n) + \ln(\frac{1}{\delta}) + k)}{\epsilon^2 \beta^2} \) then the probability that \( \hat{G} \) is not an \( \epsilon \)-cut approximation is smaller then \( \delta \).

**Proof.** This is just using lemma C.1 with error probability \( \frac{\delta}{2} \) and using that \( c \) for theorem C.1 with the same error probability and the union bound.

This theorem gives a high probability bound that depends only on observable quantities. While the notation is a bit cumbersome, it is easy to see that if \( \hat{p} \hat{c} \gg \ln(\frac{1}{\delta}) \), i.e. the unscaled weight of the smallest cut is not too small, then \( \beta \approx 1 \) and we have a bound that is almost as good as if we knew the real \( c \).

We will now prove theorem 3.2 in the paper.

**Theorem 3.2.** Let \( G \) be a graph with weights \( w_{ij} \in [0, 1] \) and \( \hat{G} \) its approximation after observing \( m \) edges. Assume \( G \) is partitioned into \( \ell \) clusters each has minimal cut greater or equal to \( c_{in} \), and the cuts separating clusters from the others is smaller then \( c_{out} \). Furthermore assume \( c_{in} > 4c_{out} \). If \( m \geq \frac{12n^2}{c_{in}} (2 \ln(n) + \ell \ln(\frac{2}{\delta}) + k) \) then the cuts separating the clusters are smaller then any cut that cuts into one of the clusters.

**Proof.** After seeing \( m \) edges, the probability for sampling any edge inside any cluster is \( p = m/(\binom{n}{2}) \). By theorem C.1 we have that if \( m \geq \frac{12n^2}{c_{in}} (2 \ln(n) + \ell \ln(\frac{2}{\delta}) + k) \) then the probability of any cut in a single cluster being smaller then \( \frac{c_{out}}{2} \) is smaller then \( \frac{\delta}{2} \), with the union bound we have that with probability greater then \( 1 - \frac{\delta}{2} \) all cuts in any cluster (and therefore any cut in \( \hat{G} \) that cuts some cluster) have weights greater or equal to \( \frac{c_{out}}{2} \).

We now need to show that the cuts separating the clusters are not too large. Consider a cut separating some clusters from the others. If the weight of this cut is \( c \) we need to show that with probability greater then \( 1 - \frac{\delta}{4\ell} \) we have \( \hat{c} < \frac{c}{2} \). This means that we want to show that \( \hat{c} < (1 + \hat{c})c < (1 + \hat{c})c_{out} = \frac{c}{2} \), i.e. we can use the negatively dependent Chernoff-Hoeffding inequality (theorem A.1) with \( \hat{c} = \frac{c_{in}}{2c_{out}} - 1 > \frac{c_{in}}{4c_{out}} \) (using the fact that \( c_{in} > 4c_{out} \)) and get that the \( P(p\hat{c} - pc > (1 + \hat{c})pc_{out}) \leq \exp \left(-\frac{\epsilon^2 pc_{out}}{3}\right) \leq \exp \left(-\frac{pc_{in}}{12}\right) \). As \( m \geq \frac{12n^2}{c_{in}} \ln(\frac{2}{\delta}) \) we can finish the proof.
D Adaptive Sampling with replacement

While we found that adaptive sampling with replacements did not perform as well as without replacements in practice, for completeness we will present her a proof that it has the same theoretical guarantees as uniform sampling for cut approximation.

Let \( G_i \) be the graph build at step \( i \), an adaptive sampling algorithm is an algorithm who picks an edge at step \( i + 1 \) with probability \( p(e; G_i) \) that depends on \( G_i \). In order to prove that with high probability \( \tilde{G} = \tilde{G}_m \) is a \( \epsilon \)-approximation of \( G \) for \( m = o(n^2) \) we need that \( p(e; \tilde{G}_i) \) isn’t too small on any edge. This can be easily done by sampling according to a modified distribution - with probability 0.5 pick an edge uniformly, and with probability 0.5 pick it according to \( p(e; H_i) \). The new distribution satisfies \( \tilde{p}(e; \tilde{G}_i) = \frac{1}{2} p(e; \tilde{G}_i) + \frac{n(n-1)}{2} > \frac{1}{2} \).

The graphs \( \tilde{G}_i \) are by no means independent. Although one can view (after subtracting the mean) them as a martingale process, using the method of bounded differences \cite{7} will not suffice, as it depends on the square of the bounding constant, so we will have a \( n^4 \) factor that only gives a trivial bound. We will next show that a high probability bound does exists.

Consider a cut with weight \( c \) that contains the edges \( e_1, ..., e_l \) and consider any bounded adaptive sampling algorithm with replacements with \( m \) steps. Define \( X_{ik} \) with \( 1 \leq i \leq l \) and \( 1 \leq k \leq m \) to be the random variable that has value \( \frac{w(e_i)}{\tilde{p}(e_i)} \) if the edge \( e_i \) was chosen at step \( k \) and zero otherwise. Define \( Y_k = \sum_{i=1}^{l} X_{ik}, Y_k \) is the weight added to the cut at step \( k \) and its expectation is \( c \).

**Lemma D.1.** If \( \forall i, l: \tilde{p}(e_i) \geq \rho \) and \( w(e_i) \leq 1 \) then

\[
E[\exp(tpY_k)|\tilde{G}_{k-1}] \leq \exp(c p(e^t - 1))
\]

**Proof.** Since at most one of the positive variables \( X_{ik} \) is nonzero for a constant \( k \) then they are negatively dependent when conditioned by \( \tilde{G}_{k-1} \). This implies that \( E[\exp(tpY_k)|\tilde{G}_{k-1}] \leq \prod_{i=1}^{l} E[\exp(tpX_{ik})|\tilde{G}_{k-1}] \). By definition of \( X_{ik} \) we get that

\[
E[\exp(tpX_{ik})|\tilde{G}_{k-1}] = \tilde{p}(e_i) \cdot \exp \left( \frac{tpw(e_i)}{\tilde{p}(e_i)} \right) + (1 - \tilde{p}(e_i))
\]

One can easily verify that the right hand side of equation \[5\] decreases monotonically with \( \tilde{p}(e_i) \), so the fact that \( \rho < \tilde{p}(e_i) \) and \( w(e_i) \leq 1 \) implies that

\[
E[\exp(tpX_{ik})|\tilde{G}_{k-1}] \leq \rho w(e_i) e^{t} + (1 - \rho w(e_i)) = \\
= \rho w(e_i) (e^{t} - 1) + 1 \leq \exp(\rho w(e_i)(e^{t} - 1))
\]

Where the last inequality is due to the fact that for \( 1 + x < e^{x} \). We can finish the proof since

\[
E[\exp(tpY_k)|\tilde{G}_{k-1}] \leq \prod_{i=1}^{l} E[\exp(tpX_{ik})|\tilde{G}_{k-1}]
\]

\[
\leq \exp(\rho c (e^{t} - 1)) \]

as \( \sum w(e_i) = c \).

We can now prove the concentration of measure bound for a single cut

**Theorem D.1.** Let \( G \) be a graph such that \( w(e_i) \leq 1 \) and \( \tilde{G} = \tilde{G}_m \) the output of a bounded adaptive sampling algorithm with replacements such that \( \tilde{p}(e_i) \geq \rho \) then the probability that a cut with weight \( c \) in \( \tilde{G}_m \) is not a \( \epsilon \)-approximation is bounded by \( 2 \exp \left( -\frac{2pcm}{\epsilon} \right) \).

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Proof. We need to show that

\[ P \left( \left| \sum_{k=1}^{m} Y_k - mc \right| > \epsilon mc \right) \leq 2 \exp \left( -\frac{\epsilon^2 pmc}{3} \right) \]

The proof is similar to the proof of the Chernoff bound, replacing independence with lemma D.1. First look at \( P \left( \sum_{k=1}^{m} Y_k > (1 + \epsilon) mc \right) \). Using the standard trick for all \( t > 0 \)

\[ P \left( \sum_{k=1}^{m} Y_k > (1 + \epsilon) mc \right) = P \left( \exp \left( t \rho \sum_{k=1}^{m} Y_k \right) > \exp(t(1 + \epsilon) pmc) \right) \]

By the Markov inequality this is bounded by \( \frac{E \left[ \exp \left( t \rho \sum_{k=1}^{m} Y_k \right) \right]}{\exp(t(1 + \epsilon) pmc)} \). The law of total expectation states that

\[ E \left[ \exp \left( t \rho \sum_{k=1}^{m} Y_k \right) \right] = E \left[ E \left[ \exp \left( t \rho \sum_{k=1}^{m} Y_k \right) \mid \tilde{G}_{m-1} \right] \right] \]

As \( \sum_{k=1}^{m} Y_k \) is a deterministic function of \( \tilde{G}_{m-1} \) this is equal to

\[ E \left[ E \left[ \exp \left( t \rho \sum_{k=1}^{m} Y_k \right) \mid \tilde{G}_{m-1} \right] \exp \left( t \rho \sum_{k=1}^{m-1} Y_k \right) \right] \]

\[ \leq E \left[ \exp \left( t \rho \sum_{k=1}^{m-1} Y_k \right) \right] \exp(\rho c(e^t - 1)). \]

Using lemma D.1. By induction we can conclude that the expectation is smaller then \( \exp(\rho mc(e^t - 1)) \). We have shown that

\[ P \left( \sum_{k=1}^{m} Y_k > (1 + \epsilon) mc \right) \leq \frac{\exp(\rho mc(e^t - 1))}{\exp(t(1 + \epsilon) pmc)} \]

Following the steps as in the standard Chernoff bound proof one can show that this is smaller (for the right \( t \)) then \( \exp \left( -\frac{\epsilon^2 pmc}{3} \right) \). The proof for this bound on \( P \left( \sum_{k=1}^{m} Y_k < (1 - \epsilon) mc \right) \) is done in a similar fashion, and using the union bound we finish our proof.

Using \( \rho = \frac{1}{n^2} \) one can now show similar theorems to what we shown in the previous section with this theorem replacing the (negatively dependent) Chernoff bound.

E  Adaptive Sampling without Replacements

For a specific graph one can always design a bad biased sampling scheme. Consider an adversarial scheme that always samples the largest weight edge between two constant clusters, it is easy to see that this can lead to bad cut clustering. To circumvent this we will consider graphs where the edge weights between the clusters, which we regard as noise, are picked randomly.

Assumption E.1. Assume \( G \) can be partitioned into \( k \) clusters of size \( \Omega(n) \), within which the minimal cut is at least \( c_{in} = \Omega(n^\alpha) \).

Assumption E.2. Assume that the weights of edges between the clusters are 0, besides \( c_{out} = o(n^\alpha) \) edges chosen uniformly at randomly (without replacement) between any two clusters that have weight 1.
Theorem E.1. Let $\tilde{G}$ be the graph after sampling $m = \tilde{\Omega}(n^{\alpha-\beta} k \ln(\frac{1}{\delta}))$ edges without replacements (with probability $1/2$ of sampling uniformly) with $\beta < \alpha$. Let $\tilde{c}_{\text{in}}$ and $\tilde{c}_{\text{out}}$ be the minimal cut weight inside any cluster and the maximal cut weight between clusters, under previous assumptions the probability that $\tilde{c}_{\text{in}} < \tilde{c}_{\text{out}}$ is smaller than $\delta$.

Proof. Using theorem C.1 on the edges sampled uniformly (remembering that the biased sampling can only increase the cut weight) we get that with probability greater than $\delta/2$, $\tilde{c}_{\text{in}} = \tilde{\Omega}(\frac{m}{n} c_{\text{in}}) = \tilde{\Omega}(n^{\alpha-\beta})$. If we consider the weight of any cut between clusters, then the key observation is that because the edges are picked uniformly at random, then whatever the algorithm does is equivalent to running a uniform sampling of a constant edge set. We then get that the expected minimal cut weight is $\tilde{O}(\frac{m}{n} c_{\text{out}}) = o(n^{\alpha-\beta})$ using lemma 2.2 (the upper bound is by looking as if all edges were picked from this cut). We can now use the Markov inequality to show $P(\tilde{c}_{\text{out}}/\tilde{c}_{\text{in}} < 1) = \frac{o(n^{\alpha-\beta})}{\tilde{O}(n^{\alpha-\beta})} < \delta/2$.

It is simple to generalize this theorem to any uniform weighting that has $o(c_{\text{out}})$ expected cut weights.