Sampling an Edge in $O(n/\sqrt{m} + \log \varepsilon^{-1})$ Time via Bernoulli Trial Simulation

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Abstract

Sampling edges from a graph in sublinear time is a fundamental problem and a powerful subroutine for designing sublinear-time algorithms. Suppose we have access to the vertices of the graph and know a constant-factor approximation to the number of edges. An algorithm for pointwise $\varepsilon$-approximate edge sampling with complexity $O(n/\sqrt{m})$ has been given by Eden and Rosenbaum [SOSA 2018]. This has been later improved by Tětek and Thorup [STOC 2022] to $O(n \log(\varepsilon^{-1})/\sqrt{m})$. At the same time, $\Omega(n/\sqrt{m})$ time is necessary. We close the problem, under the assumption of knowing $m$ up to a constant factor, for all but very dense graphs by giving an algorithm with complexity $O(n/\sqrt{m} + \log \varepsilon^{-1})$.

Our algorithm is based on a new technique that we call Bernoulli trial simulation. We believe this technique could also be useful for other problems.

Given access to trials of the form $Bern(p)$, this technique allows us to simulate a Bernoulli trial $Bern(f(p) \pm \varepsilon)$ (without knowing $p$), in time complexity $O(\log \varepsilon^{-1})$ for some functions $f$. We specifically use this for $f(p) = 1/(2p)$ for $p \geq 2/3$. Therefore, we can perform rejection sampling, without the algorithm having to know the desired rejection probability. We conjecture that Bernoulli trial simulation for $f(p) = 1/(2p)$ can be done exactly in expected $O(1)$ samples. This would lead to an exact algorithm for sampling an edge with complexity $O(n/\sqrt{m})$, completely resolving the problem of sampling an edge, again assuming rough knowledge of $m$. We consider the problem of removing this assumption to be an interesting open problem.

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1 Introduction

Suppose we have a graph too big to even read the whole input. We then need an algorithm running in time sublinear in the input size. Such algorithms are often called sublinear-time graph algorithms and have recently received a lot of attention. In these settings, one usually has direct access to the vertices of the input graph, but not to the edges. Because of this, one tool commonly used for designing sublinear-time graph algorithms is an algorithm for sampling edges. This allows us to design an algorithm that uses random edge queries, as we can utilize an edge sampling algorithm to simulate the random edge queries.

Formally, we want to sample an edge $\varepsilon$-pointwise-close to uniform. That is, assuming there are $m$ edges, we want to sample each edge with probability in $[\frac{1-\varepsilon}{m}, \frac{1+\varepsilon}{m}]$. We discuss the importance of using pointwise closeness below. We assume that the algorithm may (i) ask for the $i$-th vertex of the input graph, (ii) ask for the degree of a given vertex, and (iii) ask for the $j$-th neighbor of a given vertex. We assume the algorithm has (approximate) knowledge of the number of edges $m$. This assumption of knowing $m$ was not made in the previous work, and we think getting rid of this assumption is a very interesting open problem. This assumption is, however, not a barrier to using our algorithm as a subroutine for implementing random edge queries, as we discuss below.

A number of algorithms for edge sampling are known, with the state-of-the-art complexity for sampling one edge from a distribution $\varepsilon$-pointwise-close to uniform being $O(n \log(\varepsilon^{-1})/\sqrt{m})$ [12]. At the same time, if we have a graph with $n - \Theta(\sqrt{m})$ isolated vertices and a clique over $\Theta(\sqrt{m})$ vertices with $m$ edges, we need to sample $\Omega(n/\sqrt{m})$ vertices before we expect to see a single edge, giving us a simple lower bound. Is it possible to sample an edge in this complexity? We answer this question positively for all but very dense graphs, resolving for these graphs the complexity of sampling an edge up to a constant factor. Specifically, we give an algorithm with complexity $O(n/\sqrt{m} + \log \varepsilon^{-1})$.

The algorithm of Eden and Rosenbaum [3] can be used to sample an edge such that the sampling probabilities of different edges differ by a constant factor. If we knew the precise sampling probability of each edge, we could use rejection sampling to obtain uniform sampling probabilities. The crux of our approach is being able to implement the rejection sampling without knowing what rejection probability we want to use. We do this using a method we call Bernoulli trial simulation.

In the Bernoulli trial simulation problem, we are given a function $f$, a parameter $\varepsilon$, and access to Bernoulli trials $X_i \sim \text{Bern}(p)$, and we are supposed to output $Y \sim \text{Bern}(f(p) \pm \varepsilon)$. We give a solution for $f(p) = 1/(2p)$ for $p \in [2/3, 1]$ with complexity $O(\log \varepsilon^{-1})$. This is the technically most challenging part of our paper. While the analysis is somewhat involved, the algorithm itself is surprisingly simple: if we let $\ell$ to be the number of $X_i$’s that are equal to 0, we output 1 with probability $\max \left( \frac{1}{2} \sum_{t=0}^{\ell} \binom{\ell}{t} / \binom{\ell}{1}, 1 \right)$ and 0 otherwise.

Pointwise and total variation distances. For use in sublinear-time algorithms, it is important that we consider sampling under pointwise distance. To see why, consider the following example. Suppose each edge $e$ has a weight $w(e)$ and we want to estimate the average weight of an edge. We use an edge sampling algorithm to sample edges and return their average weight as our estimate. If we were only able to sample close to uniformly in total variation distance, it could be that the sampling error is greater than $\varepsilon/n$ on the edges with large weights. Sampling $\varepsilon$-close to uniform in total variation distance would then be insufficient to get a $(1 + O(\varepsilon))$-approximation of the average edge weight. Similarly, sampling close to uniform in $\ell_p$ is not sufficient for $p < \infty$. The case of $\ell_\infty$ is equivalent to pointwise close for the uniform distribution.

\footnote{In general, we say distribution $D_1$ is $\varepsilon$-pointwise-close to distribution $D_2$ if, for any measurable $S$, it holds $1 - \varepsilon \leq D_1(S)/D_2(S) \leq 1 + \varepsilon$}
Using our algorithm as a subroutine and the necessity of knowing \( m \). Suppose we have an algorithm \( A \) that performs random edge queries. We may then use our algorithm in a black box manner to implement these queries (unlike, for example, the algorithm for sampling multiple edges from [8] which has polynomial dependency on \( \varepsilon \)). Specifically, if \( A \) uses \( q \) random edge queries, then we may set \( \varepsilon = 1/(10q) \) and it will only decrease the success probability of \( A \) by at most \( 1/10 \).

If the goal is to get an algorithm with a constant success probability (which can then be amplified) that uses our edge sampling algorithm as a subroutine, then we may remove the need for having an a priori constant-factor approximation \( \tilde{m} \) of \( m \) by computing it using the algorithm from [9], only adding a constant to the failure probability. The algorithm from [9] has expected complexity \( O(n/\sqrt{m}) \). The complexity of our algorithm will also still be as desired: it follows from our analysis that the complexity is \( O(\frac{n\sqrt{m}}{m} + \log \varepsilon^{-1}) \). It holds by the Jensen inequality that \( \mathbb{E}[\frac{n\sqrt{m}}{m} + \log \varepsilon^{-1}] \leq \frac{n\sqrt{\mathbb{E}[m]}}{m} + \log \varepsilon^{-1} = O(n/\sqrt{m} + \log \varepsilon^{-1}) \) since it holds \( \mathbb{E}[\tilde{m}] = O(m) \).

To summarize, we may remove the assumption of a priori knowledge of \( m \) when sampling multiple edges at the cost of adding a constant failure probability. This means that we may use our algorithm as a subroutine in an algorithm with constant probability of error, even without knowing \( m \) a priori.

1.1 Technical overview

The starting point of our algorithm is the algorithm by Eden and Rosenbaum [6], which we now shortly recall. We then describe how Bernoulli trial simulation can be used to get a more efficient algorithm. We describe the techniques behind the Bernoulli trial simulation – our main technical contribution – at the end of this section.

The algorithm by Eden and Rosenbaum [6].

Consider each undirected edge as two directed edges, and let \( \theta \) be a degree threshold. We refer to vertices with degree at most \( \theta \) as light vertices, and to all other vertices as heavy. We refer to edges originating in light vertices as light edges, and to all other edges as heavy edges. Using rejection sampling, light edges can be sampled with probability exactly \( \frac{1}{d_i} \): by sampling a uniform vertex \( v \), then sampling one of its incident edges u.a.r., and then returning that edge with probability \( \frac{d_i(v)}{\theta} \). Sampling heavy vertices is done by first sampling a light edge \( uv \) as described above, and if the second endpoint \( v \) of the sampled light edge is heavy, sampling one of its incident edges. This procedure results in every heavy edge \( vw \) being sampled with probability \( \frac{d_i(v)}{n\theta} \cdot \frac{1}{d_i(v)} \), where \( d_i(v) \) is the number of light neighbors of \( v \). In Eden and Rosenbaum [6], \( \theta \) is set to \( \sqrt{2m/\varepsilon} \) which implies that for every heavy vertex \( v \), \( d_i(v) \in [(1-\varepsilon)d(v), d(v)] \). Hence, each (heavy) edge is sampled with probability \( \frac{(1-\varepsilon)m}{n\theta} \cdot \frac{1}{d_i(v)} \). The total probability of sampling some edge (with the algorithm failing otherwise) is thus at least \( \frac{(1-\varepsilon)m}{n\theta} \cdot \sqrt{\frac{m}{n}} \). We thus need \( O(\frac{n}{\sqrt{m}}) \) attempts before we expect to sample an edge, leading to a multiplicative dependence on \( \varepsilon \).

Achieving an additive dependency on \( \varepsilon \).

In order to avoid the multiplicative dependency in \( \varepsilon \), we instead set the threshold \( \theta \) to \( \sqrt{c\tilde{m}} \) for some constant \( c \). Considering the same sampling procedures as before, light edges can still be sampled with probability exactly \( \frac{1}{d_i} \). This holds because the total variation distance from uniform of each query is at most \( 1/(10q) \), so the total variation distance from uniform of the sequence of \( q \) queries is at most \( 1/10 \), meaning that the output from the algorithm has total variation distance at most \( 1/10 \) from the distribution the output would have if the queries were answered exactly.

Suppose we refer to edges originating in light vertices as light edges, and to all other edges as heavy edges. Using rejection sampling, light edges can be sampled with probability exactly \( \frac{1}{d_i} \): by sampling a uniform vertex \( v \), then sampling one of its incident edges u.a.r., and then returning that edge with probability \( \frac{d_i(v)}{\theta} \). Sampling heavy vertices is done by first sampling a light edge \( uv \) as described above, and if the second endpoint \( v \) of the sampled light edge is heavy, sampling one of its incident edges. This procedure results in every heavy edge \( vw \) being sampled with probability \( \frac{d_i(v)}{n\theta} \cdot \frac{1}{d_i(v)} \), where \( d_i(v) \) is the number of light neighbors of \( v \). In Eden and Rosenbaum [6], \( \theta \) is set to \( \sqrt{2m/\varepsilon} \) which implies that for every heavy vertex \( v \), \( d_i(v) \in [(1-\varepsilon)d(v), d(v)] \). Hence, each (heavy) edge is sampled with probability \( \frac{(1-\varepsilon)m}{n\theta} \cdot \frac{1}{d_i(v)} \). The total probability of sampling some edge (with the algorithm failing otherwise) is thus at least \( \frac{(1-\varepsilon)m}{n\theta} \cdot \sqrt{\frac{m}{n}} \). We thus need \( O(\frac{n}{\sqrt{m}}) \) attempts before we expect to sample an edge, leading to a multiplicative dependence on \( \varepsilon \).
sampled with probability exactly $\frac{1}{\epsilon}$. For heavy edges, however, the values $d_v(v)/d(v)$ can vary up to a constant factor between the different heavy vertices, leading to a large bias towards heavy edges originating in vertices $v$ with higher values of $\frac{d_v(v)}{d(v)}$. If for each vertex $v$, we knew the value of $d_v(v)$, we could use rejection sampling with probability $q$ that is inversely proportional to $p = \frac{d_v(v)}{d(v)}$, e.g., $q = \frac{d_v(v)}{2d_v(v)} = \frac{1}{2p}$ (we may assume that, say, $p \geq 2/3$ and thus $q < 1$, by making $c$ large enough). This would result in each heavy edge being sampled with exactly equal probability $\frac{d_v(v)}{\epsilon^2} \cdot \frac{d(v)}{2d(v)} = \frac{1}{2p\theta}$.

While we do not know the exact value of $d_v(v)$, we can approximate it up to a $(1 \pm \Theta(\epsilon))$-multiplicative factor using $O(1/\epsilon^2)$ neighbor queries. This results in $(1 \pm \Theta(\epsilon))$-approximation of $q$ and thus leads to a distribution $\epsilon$-close to uniform. Note that we only need to approximate $q$ when the algorithm samples a heavy edge. Moreover, when we do that, we return the edge with constant probability. Thus, in expectation, we only need to approximate $q$ a constant number of times. This means that the total expected time complexity is $O(n/\sqrt{m} + 1/\epsilon^2)$.

We now reach the main contribution of the paper, which is achieving an additive logarithmic dependency. The crux of the approach is that we do not actually need to (approximately) learn the value of $p$, in order to reject with probability proportional to $q = 1/(2p)$. Rather, we “simulate” a Bernoulli trial that succeeds with probability $q \approx \frac{1}{2p}$ by using the results of only $\Theta(\log \epsilon^{-1})$ many Bern$(p)$ trials.

When we sample a uniform neighbor of a heavy vertex $v$, we see a light neighbor of $v$ with probability exactly $p = \frac{d_v(v)}{d(v)}$ where, as discussed above, we can set $\theta$ so that $p > 2/3$. Therefore, we have access to a Bernoulli trial that succeeds with probability Bern$(p)$ for $p > 2/3$. As previously explained, in order to achieve closeness to uniformity, we need to perform rejection sampling (corresponding to a Bernoulli trial) that succeeds with probability $\approx q = \frac{1}{2p}$. We prove that we can simulate Bern$(1/(2p) \pm \epsilon)$ by relying on the results of $\Theta(\log \epsilon^{-1})$ independent copies of Bern$(p)$. Namely, we perform $\Theta(\log \epsilon^{-1})$ neighbor queries where each results in a light neighbor with probability $p$, giving us an independent copy of a random variable distributed as Bern$(p)$. Relying on the number of light and heavy neighbors we observe in these trials, we explain below how to decide whether to reject the given edge or not, in a way that results in a rejection probability $\frac{1}{2p} \pm \Theta(\epsilon)$.

Bernoulli trial simulation.

In the Bernoulli trial simulation problem, we are given a function $f$, a parameter $\epsilon$, and access to Bernoulli trials $X_i \sim$ Bern$(f)$, and we are supposed to output $Y \sim$ Bern$(f(p) \pm \epsilon)$ for some given function $f$. We give a solution for $f(p) = 1/(2p)$ for $p \in [2/3, 1]$ with complexity $\Theta(\log \epsilon^{-1})$. That is, in order to simulate a Bernoulli trial that succeeds with probability $1/(2p)$, we perform $\Theta(\log \epsilon^{-1})$ trials of Bern$(p)$ (where clearly if we knew $p$, this could be done using no additional queries). This is the technically most challenging part of our paper. While the analysis is somewhat involved, the algorithm itself is surprisingly simple: let $k = \Theta(\log \epsilon^{-1})$ denote the number of Bernoulli trials we invoke, and let $\ell$ to be the number of $X_i$’s that are equal to 0. We output 1 with probability $\max\left(\frac{1}{2} \sum_{t=0}^{\ell} \binom{\ell}{t} / \binom{k}{t}, 1\right)$ and 0 otherwise.

By the symmetry of the $k$ samples $x_1, \ldots, x_k \sim$ Bern$(p)$, a natural attempt would be to output 1 with a probability that only depends on the number of 1’s that we see. In other words, if exactly $\ell$ of the values $x_1, \ldots, x_k$ equal 1, we output 1 with some probability $p_{k, \ell}$. So overall, we can successfully simulate a Bernoulli trial with bias $\sum_{\ell=0}^{k} p_{k, \ell} \cdot \binom{k}{\ell} p^{\ell} (1 - p)^{k-\ell}$, since the probability of seeing exactly $\ell$ many 1’s is precisely $\binom{k}{\ell} p^{\ell} (1 - p)^{k-\ell}$. Hence, our goal is to set the values $p_{k, \ell}$ so that the sum is approximately $\frac{1}{2p}$.

Before we attempt this approach, we try simulating a simpler Bernoulli trial, such as Bern$(p^a)$ for some $0 \leq a \leq k$. Ordinarily, this is trivial, as one can just consider whether the first $a$ samples are all 1 and ignore the rest, but our goal is to use all $k$ samples and only depend on
the number of samples that are 1 rather than which ones are 1. We fix this by noting that if we permute the \( k \) samples randomly and then look at the first \( a \) samples, the probability they are all 1 is precisely \( \binom{\ell}{a}/\binom{k}{a} \), which only depends on the number \( \ell \) of samples that are 1. So, by outputting 1 with this probability, we can simulate \( \text{Bern}(p^\ell) \).

Overall, our goal is to sample \( \text{Bern}(\frac{1}{2p}) \), and we can approximate \( \frac{1}{2p} \) using a Taylor series as 
\[
\frac{1}{2p} (1 + (1 - p) + (1 - p)^2 + \cdots + (1 - p)^k).
\]
As long as \( p \geq \frac{2}{3} \), and for \( k = \Theta(\log \epsilon^{-1}) \), this will be accurate up to error \( \epsilon \). Since we can flip 1’s and 0’s, it is equivalent to sample from a distribution with probability
\[
\frac{1}{2} (1 + p + p^2 + \cdots + p^k) = \sum_{a=0}^{k} p^a,
\]
as long as \( p \leq \frac{1}{2} \). Indeed, by adding up the probabilities for each \( p^a \), we get it suffices to sample with probability \( p_{k, \ell} = \frac{1}{2} \sum_{a=0}^{\ell} \binom{\ell}{a} / \binom{k}{a} \), if we see \( \ell \) 1’s. This is not always possible and can be more than 1, for instance, if \( \ell > \frac{k}{2} \). However, since we assume \( p \leq \frac{1}{4} \), the probability of seeing \( \ell \geq \frac{k}{2} \) is exponentially small in \( k \) by a Chernoff bound, so we can simply truncate the probability \( p_{k, \ell} \) by 1 without suffering much error. Indeed, as long as \( k \geq C \log \epsilon^{-1} \) for a fixed constant \( C \), the simulation will still be accurate up to error \( \epsilon \).

1.2 Related work

Using uniform edge samples as a basic query in the sublinear time setting was first suggested by Aliakbarpour et al. \[2\] in the context of estimating the number of \( s \)-stars in a graph, where they showed that this access allows to circumvent lower bounds that hold in the standard adjacency list access. It was later used for the more general tasks of estimating and uniformly sampling arbitrary subgraphs in sublinear time \[3\ 11\ 5\ 12\].

As mentioned in the introduction, sampling edges from a distribution that is pointwise close to uniform in sublinear time was first suggested by Eden and Rosenbaum \[6\] who gave an algorithm with complexity \( O(n/\sqrt{\epsilon m}) \). This was later improved by Tétek and Thorup \[12\] to an algorithm with complexity \( O(n \log(\epsilon^{-1})/\sqrt{m}) \). They also considered two additional access models (full neighborhood access and hash-ordered access) and gave new lower and upper bounds for these settings. In \[8\], Eden, Mossel, and Rubinfeld gave an upper bound for the problem of sampling \( k \) edges from a pointwise close to uniform distribution. The complexity of their algorithm is \( O \left( \sqrt{k} \cdot \frac{n}{\sqrt{m}} \cdot \frac{\log^2 n}{\epsilon^2} + k \right) \). This was later shown to be essentially optimal (i.e., up to the dependencies on \( \epsilon \) and \( \log n \)) by \[12\]. In \[7\], Eden, Ron and Rosenbaum gave an \( O \left( \frac{nn}{m} \cdot \frac{\log^2 n}{\epsilon} \right) \) algorithm for sampling edges in graphs with arboricity at most \( \alpha \). They also showed their algorithm is optimal up to the \( \text{poly}(\log n, \epsilon^{-1}) \) dependencies.

The task of sampling close to uniform edges was also recently considered in the setting where the access to the graph is given via Bipartite Independent Set (BIS) queries \[11\ 4\ 14\].

2 Preliminaries

The query model: Since we do not have time to read the whole input (and thus to change its representation), it matters how exactly we are able to query it. Throughout this paper, we assume that the graphs’ vertices are labeled arbitrarily in \([n]\), the edges of every vertex \( v \) are labeled arbitrarily by \([d(v)]\), and that the algorithm knows \( n \). We then assume the following standard set of queries:

- **Uniform vertex queries:** given \( i \in [n] \), return the \( i \)-th vertex
- **Degree queries:** given a vertex \( v \), return its degree \( d(v) \)
- **Neighbor queries:** given a vertex \( v \) and \( j \in [d(v)] \), return the \( j \)-th neighbor of \( v \)

This setting has been previously called the adjacency list or indexed neighbor access model and is among the most-studied settings for sublinear-time algorithms.
A model with an additional query

- **Uniform edge queries**: given \( i \in [m] \), return vertices \( u, v \) such that \( uv \) is the \( i \)-th edge of the graph

has also been considered. Our algorithm can be thought of as a reduction between the two models. One can show (by randomly permuting the edges) that up to a logarithmic factor this setting is equivalent to just assuming random edge queries (with replacement). Our algorithm then allows us to simulate random edge queries in the indexed neighborhood access model.

### 3 Bernoulli trial simulation

In this section, we describe our algorithm to simulate a Bernoulli random variable with expectation roughly \( \frac{1}{2p} \), given i.i.d. samples from Bernoulli random variables with expectation \( p \). Specifically, we show that one can simulate a random variable with expectation between \( \frac{1}{2p} - \varepsilon \) and \( \frac{1}{2p} + \varepsilon \) using only \( O(\log \frac{1}{\varepsilon}) \) queries, as long as \( p \geq \frac{2}{3} \).

Our algorithm is very simple and described below in Algorithm 1. We prove the accuracy of the algorithm in Lemma 1. We prove the accuracy of the algorithm in Lemma 1.

**Algorithm 1**: Simulate a Bernoulli trial with probability \( 1/(2p) \pm \varepsilon \)

- **input**: \( X_1, \ldots, X_k \) for \( k = \Theta(\log \frac{1}{\varepsilon}) \) and \( X_i \sim \text{Bern}(p) \) for \( p \geq 2/3 \)
- **output**: \( Y \sim \text{Bern}(q) \) for \( q = 1/(2p) \pm \varepsilon \)

1. \( \ell \leftarrow \sum_{i=1}^k (1 - X_i) \)
2. \( p_{k,\ell} := \max \left( \frac{1}{2} \sum_{t=0}^\ell \left( \begin{array}{c} \ell \\ t \end{array} \right) / \left( \begin{array}{c} \ell \\ t \end{array} \right), 1 \right) \)
3. With probability \( p_{k,\ell} \), let \( Y = 1 \), otherwise \( Y = 0 \)
4. return \( Y \)

**Lemma 1.** Let \( p \in [2/3, 1] \) be unknown. When Algorithm 1 is given \( k \geq \Omega(\log \frac{1}{\varepsilon}) \) i.i.d. samples from Bern\((p)\), it returns \( Y \sim \text{Bern}(q) \), where \( q \in \left[ \frac{1}{2p} - \varepsilon, \frac{1}{2p} + \varepsilon \right] \).

**Proof.** Suppose we have \( k \) i.i.d. samples generated from Bern\((p)\), of which \( \ell \) are 0 and \( k - \ell \) are 1. We consider a general class of algorithms including the one described in the lemma statement. Suppose the algorithm chooses constants \( c_0, c_1, c_2, \ldots, c_k \), and a threshold \( k' \leq k \) independently of the samples (we will eventually choose \( k' = \lfloor k/2 \rfloor \) and \( c_0 = c_1 = \cdots = c_k = \frac{1}{2} \)). Then, if \( \ell \leq k' \), the algorithm outputs 1 with probability

\[
\sum_{t=0}^\ell \left( c_t \cdot \frac{\left( \begin{array}{c} \ell \\ t \end{array} \right)}{\left( \begin{array}{c} \ell \\ t \end{array} \right)} \right)
\]

and 0 otherwise. Else, if \( \ell > k' \), the algorithm outputs 1 with some probability \( p_{k,\ell} \) which can be arbitrary in the range \([0, 1]\).

We start by only assuming that \( c_0 = \frac{1}{2} \) and \( |c_t| \leq \frac{1}{2} \) for all \( 1 \leq t \leq k \). We also ignore the threshold parameter \( k' \) and just suppose that the algorithm outputs 1 with probability \( \sum_{t=0}^\ell \left( c_t \cdot \frac{\left( \begin{array}{c} \ell \\ t \end{array} \right)}{\left( \begin{array}{c} \ell \\ t \end{array} \right)} \right) \) for any \( 0 \leq \ell \leq k \). This technically may not be possible, as this value may either be negative or exceed 1, but we will ignore this issue for now.

We start by determining the probability that this modified (and perhaps impossible) algorithm outputs 1. Let \( \tau = 1 - p \leq 1/3 \). Because the probability of seeing exactly \( \ell \) 0’s is \( \left( \begin{array}{c} k \\ \ell \end{array} \right) \cdot \tau^\ell (1 - \tau)^{k - \ell} \), we can write the overall probability that the algorithm outputs 1 as

\[
\sum_{\ell=0}^k \left[ \left( \begin{array}{c} k \\ \ell \end{array} \right) \cdot \tau^\ell (1 - \tau)^{k - \ell} \cdot \sum_{t=0}^\ell \left( c_t \cdot \frac{\left( \begin{array}{c} \ell \\ t \end{array} \right)}{\left( \begin{array}{c} \ell \\ t \end{array} \right)} \right) \right].
\] (1)
We can now rewrite Equation (1) as

\[
\sum_{\ell=0}^{k} \sum_{t=0}^{\ell} \binom{k}{\ell} \cdot \tau^\ell (1 - \tau)^{k - \ell} \cdot c_t \cdot \frac{(t)}{k} = \sum_{\ell=0}^{k} \sum_{t=0}^{\ell} c_t \cdot \tau^\ell (1 - \tau)^{k - \ell} \cdot \frac{(t)}{k} \\
= \sum_{\ell=0}^{k} \sum_{t=0}^{\ell} c_t \cdot \tau^\ell (1 - \tau)^{k - \ell} \cdot \frac{(t)}{k} \\
= \sum_{\ell=0}^{k} \sum_{t=0}^{\ell} c_t \cdot \tau^\ell (1 - \tau)^{k - \ell} \cdot \binom{k - t}{k - \ell}.
\]

Next, we expand out \((1 - \tau)^{k - \ell}\) using the binomial theorem, to rewrite the above sum as

\[
\sum_{\ell=0}^{k} \sum_{t=0}^{\ell} \sum_{s=0}^{k - \ell} c_t \cdot \tau^{\ell + s} (-1)^s \binom{k - \ell}{s} \binom{k - t}{k - \ell}.
\]

Now, let \(u = \ell + s\) and \(v = \ell + s - t\). In this case, we can rewrite this sum over the triple \((u, v, s)\). Assuming that we only know \(\ell, s, t\) are integers and \(k\) is a nonnegative integer, the conditions that \(0 \leq \ell \leq k\), \(0 \leq t \leq \ell\), and \(0 \leq s \leq k - \ell\) are equivalent to \(0 \leq s \leq v \leq u \leq k\). Therefore, we can write the above sum (2) as

\[
\sum_{u=0}^{k} \sum_{v=0}^{u} \sum_{s=0}^{v} c_{u-v} \cdot u^u \cdot (-1)^s \binom{k - u + s}{s} \binom{k - u + v}{k - u + s}.
\]

Note that the innermost sum above is simply the alternating sum of binomial coefficients, which equals 1 if \(v = 0\) and is 0 if \(v > 0\). So, we can simplify this sum by only considering when \(v = 0\) and replacing the innermost sum by 1, which gives us

\[
\sum_{u=0}^{k} \tau^u \cdot u^u \cdot \binom{k - u + 0}{k - u} \
= \sum_{u=0}^{k} \tau^u \cdot u^u \cdot \binom{k - u + 0}{k - u} \cdot 1 = \sum_{u=0}^{k} c_u \cdot \tau^u.
\]

Finally, we need to deal with the fact that when \(\ell > k\), the algorithm outputs 1 with some arbitrary probability \(p_{k, \ell} \in [0, 1]\), rather than with probability exactly \(\sum_{\ell=0}^{k} \binom{c_t \cdot (t)}{k} \binom{(t)}{k}\). If \(|c_t| \leq 1\) for all \(t\), then \(\sum_{\ell=0}^{k} \binom{c_t \cdot (t)}{k} \binom{(t)}{k} \leq k + 1\) for all \(\ell\). This means that setting the output to 1 with probability \(p_{k, \ell}\) when we see that \(\ell > k\) zeroes have been sampled, does not change the output probability by more than \((k + 2) \cdot \mathbb{P}(\ell > k)\). If we set \(k' = \lfloor k/2 \rfloor\), then \((k + 2) \cdot \mathbb{P}(\ell > k') = e^{-\Omega(k)}\) by a simple application of the Chernoff bound (since \(p \geq \frac{3}{4}\)). Therefore, the overall algorithm outputs 1 with probability \(\sum_{u=0}^{k} c_u \cdot \tau^u \pm e^{-\Omega(k)}\).

Finally, we must ensure that this algorithm is feasible, i.e., that \(0 \leq \sum_{\ell=0}^{k} \binom{c_t \cdot (t)}{k} \binom{(t)}{k} \leq 1\) for all \(\ell \leq \lfloor k/2 \rfloor\), as long as \(c_0 = \frac{1}{2}\) and \(|c_t| \leq \frac{1}{2}\) for all \(1 \leq t \leq k\). Note that \(\binom{n}{0} = \binom{n}{n} = 1\), and moreover, for general \(t\) and \(\ell \leq \lfloor k/2 \rfloor\), \(\binom{t}{k} / \binom{k}{k} \leq (\ell/k)^t \leq 2^{-t}\). So, we can write
Algorithm 2: Sample an edge pointwise $\Theta(1)$-close to uniform

1. $u \leftarrow$ uniformly random vertex
2. $j \leftarrow \text{Unif}([\sqrt{6m}])$
3. Fail if $d(v) > \lfloor \sqrt{6m} \rfloor$ or $d(v) \leq j$
4. $v \leftarrow j$-th neighbor of $u$
5. $B \sim \text{Bern}(1/3)$
6. if $B = 1$ then
   7. return $uv$
8. else if $B = 0$ and $v$ is heavy then
   9. $w \leftarrow$ random neighbor of $v$
10. return $vw$
11. end
12. return Fail

$\sum_{i=0}^{\ell} \left( c_i \cdot \binom{\ell}{i} j^i (\ell-j)^{\ell-i} \right)$ as being in the range $c_0 \pm \left( \sum_{i=1}^{\ell} |c_i| \cdot 2^{-i} \right) \subset \frac{1}{2} \pm \left( \sum_{i=1}^{\ell} 2^{-(i+1)} \right) \subset \frac{1}{2} \pm \frac{1}{2} = [0, 1]$. Hence, all probabilities are valid.

Therefore, by setting $c_u = \frac{1}{2}$ for all $0 \leq u \leq k$, we can simulate a draw from $\frac{1}{2} \cdot \frac{1}{1-\tau} = \frac{1}{2p}$ up to error $e^{-\Omega(k)}$, using only $k$ samples. Setting $k = \Omega(\log \epsilon^{-1})$, the conclusion follows. \qed

4 Sampling an edge

In this section, we give our algorithm for sampling an edge. We first give an algorithm for $\Theta(1)$-approximate edge sampling. The algorithm closely follows the approach from [6] but uses Bernoulli trial simulation to reduce the sampling error in a way much more efficient than the one used in [6]. Throughout this section, we assume for sake of simplicity, that we know the number of edges exactly. The analysis of correctness only uses that we have an upper bound, while the analysis of the complexity needs that we have a lower bound up to a constant factor. Putting this together, it is in fact sufficient to have a constant-factor approximation.

Lemma 2. Let $e$ be the edge returned by Algorithm 2 if successful. Then for any light edge $e'$, it holds $\mathbb{P}(e = e') = 1/(3n\theta)$, and for any heavy edge it holds $\mathbb{P}(e = e') = \frac{2}{3} \cdot \frac{d(v)}{d(e')} \cdot \frac{1}{n\theta}$.

Proof. Fix a light edge $e' = uv$. Recall that by definition, $uv$ is light iff $d(u) \leq \theta$ for $\theta = \lfloor \sqrt{6m} \rfloor$. The edge $uv$ is returned only in the case that (1) $u$ is sampled in Step 1, (2) the chosen index $j$ in Step 2 is the label of $v$, and (3) $B = 1$ in Step 5. Therefore, $\mathbb{P}[e = e'] = \frac{1}{n} \cdot \frac{1}{\sqrt{6m}} \cdot \frac{1}{3} = \frac{1}{3n\theta}$.

Now fix a heavy edge $e' = vw$. The edge $vw$ is returned in the event that (1) the sampled vertex $u$ in Step 1 is a light neighbor of $v$, (2) the chosen index $j$ in Step 2 is the label of $v$, (3) $B = 0$ in Step 5, and (4) $w$ is the sampled neighbor in Step 9. Therefore, if we define $\Gamma_L(v)$ to be the set of light neighbors of $v$, then $\mathbb{P}[e = e'] = \sum_{u \in \Gamma_L(v)} \frac{1}{n} \cdot \frac{1}{\sqrt{6m}} \cdot \frac{2}{3} \cdot \frac{1}{d(v)} = \frac{2}{3} \cdot \frac{d(v)}{d(e')} \cdot \frac{1}{n\theta}$. \qed

We are now able to give an algorithm for sampling an edge $1 \pm \epsilon$-pointwise-close to uniformly. Simply re-running the above algorithm until it succeeds would result in $\Theta(1)$-pointwise close to uniform sampling. The algorithm below differs in that if Algorithm 2 returns a heavy edge (which has some bias), we use rejection sampling based on Bernoulli trial simulation to reduce the bias.

Theorem 3. Assume $\epsilon \leq 1/2$. Algorithm 3 returns an edge from a pointwise $\epsilon$-close to uniform distribution. Its expected complexity is $O(n/\sqrt{m} + \log \epsilon^{-1})$.
Algorithm 3: Sample an edge $1 \pm \varepsilon$-pointwise-close to uniform

```plaintext
1 repeat
2     $vw \leftarrow \text{Algorithm 2}$
3     if $v$ is light then
4         return $vw$
5     end
6     if $v$ is heavy then
7         $w_1, \ldots, w_k \leftarrow$ random neighbors of $v$ for $k = \Theta(\log \varepsilon^{-1})$
8         $Y \leftarrow \text{Algorithm 1}$ where each $X_i$ is the indicator of $[d(w_i) \leq \sqrt{6m}]$
9         if $Y = 0$ then
10            return $vw$
11        end
12     end
13 end
```

Proof. We start with proving the correctness of the algorithm. By Lemma 1, each invocation of Algorithm 2 returns each light edge with probability $\frac{1}{3d(v)}$, and each heavy edge with probability $\frac{2}{3} \cdot \frac{d(v)}{d(v)} \cdot \frac{1}{3d(v)}$. If Algorithm 2 returns a heavy edge $vw$, then for every $w_i$ sampled in Step 7 in Algorithm 3, it holds that the indicator of the event $[d(w_i) \leq \sqrt{6m}]$ is the result of a Bernoulli trial $\text{Bern}(p)$ with $p = \frac{d(v)}{d(v)}$. Let $H$ denote the set of vertices with degree greater than $\lceil \sqrt{6m} \rceil$. Then $\text{deg}_H(v) \leq |H| \leq \frac{2m}{\sqrt{6m}} \leq \frac{2}{3}m \leq \frac{1}{3}d(v)$, where the last is since $v$ is heavy (so $d(v) > \lceil \sqrt{6m} \rceil$). Therefore, $p = \frac{d(v)}{d(v)} \in \left[\frac{2}{3}, 1\right]$. Hence, by Lemma 1, the value $Y$ returned by Algorithm 1 is such that $Y \sim \text{Bern}(q)$, where $q = \left[\frac{1}{2p} - \varepsilon/8, \frac{1}{2p} + \varepsilon/8\right]$ (for the constant in $\Theta$ in the $\Theta(\log \varepsilon^{-1})$ being large enough). Therefore, in a single iteration of the repeat loop, every fixed heavy edge $vw$ is returned with probability $\frac{2}{3} \cdot \frac{d(v)}{d(v)} \cdot \frac{1}{3d(v)} \cdot \left(\frac{1}{2p} \pm \varepsilon/8\right) \in \frac{1+\varepsilon/4}{3d(v)}$.

The ratio of sampling probabilities of any pair of edges is thus at most $(1+\varepsilon/4)/(1-\varepsilon/4) \leq 1+\varepsilon$ (using the assumption $\varepsilon \leq 1/2$). Therefore, conditioning on an edge being returned, each edge is returned with probability in $\frac{1+\varepsilon/4}{3d(v)}$, as claimed.

We turn to analyze the complexity of the algorithm. By the above analysis, every invocation of the loop returns an edge with probability at least $\frac{(1-\varepsilon)2m}{3d(v)\sqrt{m}} \geq \sqrt{\frac{m}{10m}}$. Therefore, the expected number of iterations until an edge is returned is $O(n/\sqrt{m})$. Furthermore, each invocation of Algorithm 2 takes a constant number of queries. Therefore, an iteration where no edge is returned by Algorithm 2 takes a constant number of queries. If Algorithm 2 does return an edge, and it is heavy, then sampling the $w_i$ neighbors in Step 7 takes $\Theta(\log \varepsilon^{-1})$ queries. Observe that if indeed such an edge is returned by Algorithm 2, then by Lemma 1, it is returned by the algorithm with probability $\frac{1}{2p} \geq \frac{1}{2}$ (since $p \in [2/3, 1])$. Therefore, the expected number of times we execute Algorithm 1 is constant. Hence, the expected query complexity is $\Theta\left(n/\sqrt{m} + \log \varepsilon^{-1}\right)$.

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9