Partially Recursive Acceptance Rejection

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Version: January 5, 2017

Abstract

Generating random variates from high-dimensional distributions is often done approximately using Markov chain Monte Carlo. In certain cases, perfect simulation algorithms exist that allow one to draw exactly from the stationary distribution, but most require \(O(n \ln(n))\) time, where \(n\) measures the size of the input. In this work a new protocol for creating perfect simulation algorithms that runs in \(O(n)\) time for a wider range of parameters on several models (such as Strauss, Ising, and random cluster) than was known previously. This work represents an extension of the popping algorithms due to Wilson.

1 Introduction

Partially recursive acceptance rejection (PRAR) is a new protocol for creating algorithms for exactly generating random variates from high dimensional distributions. The method is simple to implement efficiently, and results in algorithms that can be proved to have an expected running time that is linear in problem size over a wider range of parameters than known previously for several problems of interest.

Consider a distribution defined either by an unnormalized weight function \(w(x)\) for discrete spaces, or an unnormalized density function \(f(x)\) for continuous spaces. In the past, techniques for perfect simulation from these distributions have been very different depending on whether the spaces were continuous or discrete. PRAR operates the same way in both situations.

The problems where PRAR is useful often use approximate sampling via Markov chain Monte Carlo (MCMC). However, these are not true algorithms unless the mixing time of the Markov chain being used can be somehow bounded. One such technique for bounding the mixing time of a Markov chain is Dobrushin uniqueness \(\mathbb{E}\) (see also the work on path coupling of Bubley and Dyer \([2]\)). PRAR requires a condition very similar to Dobrushin uniqueness, the difference being that even if Dobrushin uniqueness cannot be shown mathematically, it can be verified algorithmically.
One can prove (up to an arbitrarily small chance of error) that a Markov chain is slowly mixing through computer experiment, however, there is no generally effective way to show that a Markov chain is rapidly mixing. However, with perfect simulation protocols like PRAR, it is possible through computer experiment to verify that the resulting output comes exactly from the target distribution, thereby making them more useful in practice for certain problems than the Markov chain approach.

Our concern here is with fast algorithms that use an expected number of random choices that is linear in the size of the problem. There are currently two protocols for generating samples in expected linear time from these types of problems. The first method is the Clan of Ancestors method of [5]. This method is an extension of the Coupling from the Past [10] protocol or Propp and Wilson. It looks backwards in time at the events that could affect the state in the present. The set of backwards events is called the Clan of Ancestors, which gives the name to the method. This approach has rarely been implemented (see [10] for one such implementation) because unless special care is taken it can be very computationally expensive to keep track of how clans arising from different dimensions interact. One of the advantages of PRAR is that such interactions cannot occur with this approach, making the implementation much easier.

The second linear time method is the Randomness Recycler method of [11, 6]. Like PRAR (and unlike Clan of Ancestors) it is straightforward to implement, however, the range of parameters for which the algorithm is provably linear time is in all known cases more restricted than with PRAR.

The PRAR protocol is illustrated with the following applications.

- For independent sets of a graph with $n$ nodes, maximum degree $\Delta$, and parameter $\lambda$, the method allows $O(n)$ expected sampling time when $\lambda < 1.13/\Delta$, beating the previously best known linear time algorithm which required $\lambda < 1/\Delta$.

- For the continuous state space autonormal model on a graph with $n$ nodes and parameter $\beta$, the method allows $O(n)$ expected sampling time when $\beta < (\Delta-1)\exp(-\beta)$, beating the previously best known linear time algorithm which required $\beta < \Delta\exp(-\beta)$.

- For the random cluster model on a graph with $n$ nodes and maximum degree $\Delta$, and parameters $p$ and $q$, the method allows $O(n)$ expected sampling time when $p < 1/\Delta$.

Of course, if the expected running time is allowed to be $O(n \ln(n))$ rather than linear, other methods with wider parameter ranges exist. For instance, in [11] it was shown using bounding chains and coupling from the past [16] how to sample independent sets in $O(n \ln(n))$ time when $\lambda < 2/(\Delta - 2)$. But for $O(n)$ algorithms, PRAR appears to have the widest bounds.
The rest of the paper is organized as follows. The next section presents the applications, followed by a section describing the theory of the protocol. Then Section 4 applies the protocol to the different applications, proving the running time results listed above. Section 5 then shows how this method can be viewed as a generalization of the popping method of Wilson for sampling directed rooting spanning trees of a graph.

2 Applications

Each of the applications will be described as an unnormalized density $w(x)$ with respect to a base finite measure $\mu$ from which it is easy to sample from.

2.1 Independent Sets of a Graph

Consider coloring the nodes of a graph $(V, E)$ with either 0 or 1, so the state space is $\Omega = \{0, 1\}^V$. The underlying measure we use has a parameter $\lambda \geq 0$ that controls the average number of nodes in a randomly drawn coloring:

$$\mu(\{x\}) = \lambda \sum_i x(i).$$

Say that $X$ is a Bernoulli random variable with mean $p$ (write $X \sim \text{Bern}(p)$) if $\mathbb{P}(X = 1) = p$ and $\mathbb{P}(X = 0) = 1 - p$. To sample from $\mu$, generate $X(v) \sim \text{Bern}(\lambda/(1 + \lambda))$ independently for all $v \in V$.

We use the convention $0^0 = 1$ so that when $\lambda = 0$ the only state with positive measure is the all 0 coloring, while as $\lambda$ grows the measure favors labelings with more 1’s.

An independent set of a graph is a labeling such that no two adjacent nodes receive a 1. Hence the density of interest is

$$w(x) = \prod_{\{i,j\} \in E} (1 - x(i)x(j)).$$

Note that for all $x \in \Omega$, $w(x) \in \{0, 1\}$ as well.

2.2 Strauss Process

The Strauss process [17] extends the independent set model by allowing two adjacent nodes to both be labeled 1, but assigns a penalty factor of $\alpha \in [0, 1]$ when this occurs. The underlying measure $\mu$ still is defined by (1), now the density becomes

$$w(x) = \prod_{\{i,j\} \in E} \alpha x(i)x(j).$$

With the convention that $0^0 = 1$, then when $\alpha = 0$ this is just the independent set density.
2.3 Autonormal

The autonormal model [1] is a continuous extension of the Ising model [13] used for modeling images and other spatial experiments. For a graph $G = (V, E)$, the state space is $\Omega = [0, 1]^V$, the underlying measure $\mu$ has density

$$f(x) = \exp \left( -J \sum_i (x(i) - y(i))^2 \right)$$

with respect to Lebesgue measure. Here $J \geq 0$ and $y(i)$ are known parameters. To sample from $\mu$, each node label $X(i)$ is independently normal with mean $y(i)$, variance $(2J)^{-1}$, and conditioned to lie in $[0, 1]$. The density is

$$w(x) = \exp \left( - \sum_{\{i,j\} \in E} \beta \cdot (x(i) - x(j))^2 \right),$$

where $\beta$ is another constant.

2.4 Random Cluster

The random cluster model [8] is another way of viewing the Potts model [15], which is itself a different extension of the Ising model [13]. Given a graph $G = (V, E)$ the state space is now a coloring of edges with 0 and 1. Given $x \in \Omega = \{0, 1\}^E$, and parameter $p$, the underlying measure $\mu$ is

$$\mu(\{x\}) = p^{\sum_{e \in E} x(e)}(1 - p)^{\sum_{e \in E}(1 - x(e))}.$$

Again this measure $\mu$ is easy to sample from: draw (for all $e \in E$) $X(e) \sim \text{Bern}(p)$ independently.

A second parameter $q$ controls the density $w$ through the use of $c(x)$, which is the number of connected components in the graph using only the edges with $x(e) = 1$.

$$w(x) = q^{c(x)}.$$  \hspace{1cm} (3)

When $q = 2$, a sample from the random cluster model can be transformed into a sample from the Ising model in linear time [8], and for $q$ an integer greater than 2, it can be transformed in linear time into a sample from the Potts model.

3 Theory

The well-known acceptance rejection method requires two properties to hold:

1. It is easy to sample from the underlying measure $\mu$.  


Figure 1: An illustration of the random cluster model on a 2 by 2 square lattice. Here the state has measure $p(1 - p)^3$ since one edge is included and three edges are not. The density of this state is $q^3$ since the edges of the state break the nodes into 3 connected components. With respect to counting measure, this state has density $p(1 - p)^3q^3$.

2. The target density is bounded by a known constant $M$.

When these hold (and they do for each of the applications of the previous section), the acceptance rejection (AR) technique is as follows.

| AR | Output: $X$ |
|----|-------------|
| 1) | Randomly draw $X \leftarrow \mu$ |
| 2) | Draw $U$ uniformly from $[0, 1]$ |
| 3) | If $U < w(X)/M$ output $X$ and quit |
| 4) | Else |
| 5) | $X \leftarrow \text{AR}$, output $X$ and quit |

It is well-known [7, 12] that the output is a draw from density $w(x)$ with respect to measure $\mu$.

Now suppose that $x \in C^D$ for color set $C$ and dimension set $D$ (as it is for all of our applications.) Let $(D_1, D_2)$ be a partition of the dimensions $D$. Note that for each of our applications, the product nature of $w(x)$ means that we can write

$$w(x) = w_1(x(D_1))w_2(x(D_2))w_{12}(x(D_1 \cup D_2)),$$

For instance, for the independent sets model, if $(V_1, V_2)$ is a partition of the nodes $V$, then

$$w(x) = \left[ \prod_{(i,j) \in V_1} (1 - x(i)x(j)) \right] \left[ \prod_{(i,j) \in V_2} (1 - x(i)x(j)) \right] \left[ \prod_{i \in V_1, j \in V_2} (1 - x(i)x(j)) \right]$$

and $w(x)$ has been nicely factored into $w_1$, $w_2$, and $w_{12}$.

When for $D_1$ and $D_2$ there is an $M$ such that $w_{12}(x) \leq M$, fully recursive AR is as follows.
### Fully Recursive AR

**Input:** \( S \subseteq D \)

**Output:** \( X(S) \)

1) Parition \( S \) into \( D_1 \) and \( D_2 \)
2) \( X(D_1) \leftarrow \text{Fully Recursive AR}(D_1), X(D_2) \leftarrow \text{Fully Recursive AR}(D_2) \)
3) Draw \( U \) uniformly from \([0,1]\)
4) If \( U < \omega_{12}(X)/M \) output \( X \) and quit
5) Else
6) \( X \leftarrow \text{Fully Recursive AR}(S), \text{output } X(S) \) and quit

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**Lemma 1.** Fully recursive AR generates output \( X \) according to \( \omega \) with respect to \( \mu \).

This is similar to the self-reducibility of Jerrum, Valiant, and Vazirani [14]. More recently, this approach has also been formalized in [12]. The proof follows immediately from the correctness of basic AR and an induction on the number of times line 2 has been used.

#### 3.1 The PRAR protocol

Suppose we desire only to know \( X(v) \) for a single node \( v \). Then first generate \( X(v) \) and \( X(V \setminus \{v\}) \) separately, and then choose to accept or reject the combination. The key idea of PRAR is that sometimes this does not require that we generate \( X(V \setminus \{v\}) \). For example, in the independent set model, if \( X(v) = 0 \), then we accept no matter what \( X(V \setminus \{v\}) \) is. Even if \( X(v) = 1 \), we do not need to know the entirely of \( X(V \setminus \{v\}) \), only those neighbors of \( v \).

The general protocol looks like this.

### Partially Recursive AR

**Input:** \( S \) and \( D \) where \( S \subseteq D \)

**Output:** \([X(S'), S']\) where \( X \) is a draw from \( w \) over dimensions \( D \) and \( S \subseteq S' \)

1) If \( S = \emptyset \) then output \([\emptyset, \emptyset]\)
2) Else
3) Let \( d \) be any element of \( S \), let \( D_1 \leftarrow \{d\} \)
4) Draw \( X(d) \) randomly from \( \omega_1 \) over \( \mu \)
5) Draw \( U \) uniformly from \([0,1]\)
6) If \( U \leq \min_{x(D \setminus \{d\})} \omega_{12}(X(D_1), x(D \setminus D_1))/M \)
7) \( [X(S'''), S'''] \leftarrow \text{Partially Recursive AR}(S \setminus \{d\}, D \setminus \{d\}) \)
8) \( S' \leftarrow S'' \cup \{d\} \), output \([X(S'), S']\) and quit
9) Else
10) Let \( D_3 \) be the smallest set such that \( \omega_{12}(X(D_1 \cup D_3)) \) determines \( \omega_{12}(X) \)
11) \([X(S'''), S'''] \leftarrow \text{Partially Recursive AR}(D_3, D \setminus \{d\}) \)
12) If \( U \leq \omega_{12}(X(D_1 \cup D_3))/M \), then \( S' \leftarrow S'' \cup \{d\} \), output \([X(S'), S']\)
13) Else let \([X(S'), S] \leftarrow \text{Partially Recursive AR}(S, D) \) and output \([X(S'), S']\)
Lemma 2. Suppose \texttt{PartiallyRecursiveAR}(S, D) terminates with probability 1 with output \((X(S), D)\). Then \(X(S)\) has the same distribution as the coordinates of \(S\) from \(X\) where \(X\) is a complete draw from density \(w\) with respect to \(\mu\) over dimensions \(D\).

Proof. The Fundamental Theorem of Perfect Simulation [12, 9] says that if the algorithm terminates with probability 1, then we assume that lines 1, 6, 11, and 13 have the correct output when proving that the overall algorithm is correct.

With that assumption, lines 7 and 11 are drawing a state \(X\), and then reporting \(X(S'')\) for some set of dimensions \(S''\) that contain \(S\). So the algorithm’s output has the same distribution as \texttt{FullyRecursiveAR}, but not all coordinates of \(X\) are reported in the output.

It is the analysis of the running time where we see a Dobrushin like condition.

Lemma 3. Let \(c_1 < 1\) be the probability that line 13 is reached. Let \(p(d)\) denote the probability that line 10 is reached given \(D_1 = d\). Suppose for all \(d \in D\), there exists \(B\) with \(\mathbb{E}[\#(D_3)\mid d] \leq B\), and that \(\mathbb{E}[\#(D_3)\mid d]p(d) \leq c_2 < 1\). Given \(S\) then the expected number of times line 4 is called (or equivalently line 5) is at most \((1 - c_1)^{-1}(1 - c_2)^{-1}\#(S)\).

Proof. Consider two temporary changes to the algorithm. First, at line 13, change it to \texttt{Else}, output \([\emptyset, \emptyset]\) and quit. Second, at line 3, add \(S \leftarrow S \setminus \{d\}\) to the end. Because of our previous change to line 13, this does not alter the algorithm any further.

Consider the expected time needed to either reach our new line 13, or to quit. Then there might be several recursive calls to \texttt{ParitallyRecursiveAR} over the run of the algorithm. Let \(N_t\) be the number of dimensions in the union of the \(S\) sets after \(t\) recursive calls to the algorithm. Then \(N_0 = \#(S)\).

Now consider \(N_{t+1}\) given \(N_t\). Two things can happen. If lines 7 and 8 activate, then \(N_{t+1} = N_t - 1\). If lines 10 and 11 activate, then \(N_{t+1} = N_t - 1 + \#(D_3)\). This second event happens with probability \(p(d)\). So \(\mathbb{E}[N_{t+1}\mid N_t, d] = N_t - 1 + p(d)\mathbb{E}[\#(D_3)\mid d]\).

When this right hand side is at most \(N_t - (1 - c_2)\), standard martingale theory (see for instance [4]) gives that the expected amount of time for the \(N_t\) process to reach 0 is \(N_0/(1 - c_2)\).

Now consider what happens if line 13 is changed back. Then the expected time between reaching line 13 is \(\#(S)(1 - c_2)^{-1}\). Each time through the algorithm there is at least a \(1 - c_1\) chance line 13 is not executed and the algorithm does not recurse further. Therefore, the total expected number of steps taken is at most \((1 - c_1)^{-1}(1 - c_2)^{-1}\#(S)\). □
4 Applications

4.1 Independent sets of a graph

Independent sets of a graph label each node either 0 or 1. In this case where there are only two colors, the general PRAR can be simplified. If the label of a node is 0, then the node is immediately accepted. But if the label is 1, then all the neighbors of the node must also be 0. If a neighbor is 1, then we can immediately track down its neighbors to ensure that they are all 0, and so on.

So if a neighbor of the end of the backbone is labeled 1, that increases the length of the backbone by 1. On the other hand, if all the neighbors of the end of the backbone at labeled 0, then the node that is the end of the backbone accepts its label of 1. If the backbone had length 1, then we are done. Otherwise, that meant the the second to the end node in the backbone rejects—because it comes into conflict with the end of the backbone that is labeled 1. Therefore the last two nodes in backbone are removed from the backbone and return to being unresolved. The process then starts over again.

This gives us a connected sequence of nodes labeled 1 that grows and shrinks in length. Call this sequence the backbone of the current state, and the method Backbone_PRAR. See Figure 2 for an illustration.

![Figure 2: Backbone PRAR for independent sets. Here white stands for label 0 and black for label 1. For instance, at step 7 the bottom center node was labeled 0. This meant that the bottom right node was accepted, which then meant that the right center node was rejected, so both were removed at Step 8. By step 12 the backbone has resolved and the upper left labeling of 1 is accepted.](image)

This idea of a backbone works on other applications with two colors, such as the Ising model and the Strauss model.
Lemma 4. The backbone method for independent sets only requires an independent, identically distributed stream of Bernoulli random variables with mean $\lambda/(1+\lambda)$. Let $\Delta$ be the maximum degree of the graph and

$$\gamma = \frac{\lambda}{1+\lambda} \sum_{i=1}^{\Delta-1} \left(1 - \frac{\lambda}{(1+\lambda)(\lambda+\Delta)}\right)^{i-1}.$$ 

If $\gamma < 1$, then the expected number of Bernoulli’s needed to resolve one node is bounded above by $C = 1 + \lambda \Delta \Delta^{-1}/(1 - \gamma)$. Since this is a constant with respect to the size of the graph, the time needed to generate a sample over the entire graph is at most $Cn$.

Proof. When the backbone resolves, it resolves either as an acceptance or a rejection. The number of resolutions until acceptance is stochastically bounded above by a geometric random variable with parameter $1/(1+\lambda)$. Therefore, the expected number of resolutions of the backbone is at most $1 + \lambda + \lambda/(1+\lambda) - 1 = \lambda$.

How many draws does it take to resolve a node? It certainly takes one to determine the label for the node. So if $T$ is the resolution time, then $\mathbb{E}[T] \leq 1 + \Delta R$, where $R$ is an upper bound on the expected resolution time for subsequent nodes. These subsequent nodes have maximum degree at most $\Delta - 1$. The first neighbor takes at most $R$ expected time.

On to the second neighbor. Note that the second neighbor only needs to be resolved if the first neighbor resolved to a 0. If the first neighbor had resolved to a 1, then the original node is rejected, there is no need for further action. The chance that a neighbor resolves to 1 is at least $c = \lambda/(1+\lambda)[\lambda/(1+\lambda)]^{\Delta-1}$. So the second neighbor is only activated with probability $1 - c$.

Similarly, the third neighbor can also take time distributed as $R$, but only if the first two neighbors fail. Adding this up over the (up to $\Delta - 1$) neighbors gives

$$R \leq 1 + \frac{\lambda}{1+\lambda} \sum_{i=1}^{\Delta-1} R \left[1 - \left(\frac{\lambda}{1+\lambda}\right)\left(\frac{1}{1+\lambda}\right)^{\Delta-1}\right]^{i-1},$$

which gives the result.

It is straightforward to verify that for $\lambda < 1.13/(\Delta - 2)$ we have $\gamma < 1$. This gives the result presented in Section 1.

Call the value of $\lambda$ where $\gamma = 1$ the critical value of $\lambda$, and denote it $\lambda_c$. For $\lambda < \lambda_c$, the algorithm is guaranteed to generate samples in polynomial time. For $\lambda \geq \lambda_c$, the algorithm might operate in polynomial time, or it might not.

### 4.2 Strauss process

Now consider what happens in the Strauss process. Again consider drawing an initial node and accepting or rejecting based upon the neighbors of the node.
If the node is labeled 0, then we always accept as before. If the node is labeled 1, then the chance of accepting is $\alpha$ raised to the power of each of the neighbors of the node labeled 1.

Another way to view this, is to, for each edge adjacent to the original node, draw a $\text{Bern}(\alpha)$ random variable. If this variable is 1, then the neighbor does not matter. If this variable is 0, then the neighbor does matter, and recursion needs to be used to find out its value.

This changes the expected number of neighbors to be considered from $\Delta - 1$ to $(\Delta - 1)\alpha$. The chance of a node being labeled 1 is strictly greater in the recursion, therefore, the new value of $\gamma_\alpha$ is at most

$$\gamma_\alpha = \frac{\lambda}{1 + \lambda} \alpha(\Delta - 1).$$

Note that $\gamma_\alpha < 1$ is equivalent to $\lambda < 1/[\alpha(\Delta - 1) - 1]$, so a similar argument to the previous section gives the following result.

**Lemma 5.** When $\lambda < [\alpha(\Delta - 1) - 1]^{-1}$, then PRAR generates a sample from the Strauss process using $O(n)$ expected number of Bernoulli draws.

### 4.3 Autonormal

As with the independent set density, the idea is to consider what happens when a single node is drawn, the rest of the graph is drawn, and the combination is either accepted or rejected. The value that $U$ from line 6 in the general protocol must fall below is the product of the chance of rejecting because of each of the neighboring edges.

That is, in order to determine if node $v$ can be combined with the state of $x(V \setminus \{v\})$, it is necessary to independently draw a uniform $[0, 1]$ random variable for each of the neighbors $w$ of $v$. Only if every edge accepts can the entire state be said to accept.

If the single node $v$ is assigned value $x(v)$, the chance of rejecting based on $w$ is at most

$$\exp(-\beta(x(v) - x(w)^2) \leq \exp(-\beta \max\{1 - x(i), x(i)\}^2),$$

| $\Delta$ | $\lambda_c$ for RR | $\lambda_c$ for CoA | $\lambda_c$ for PRAR |
|---------|---------------------|---------------------|---------------------|
| 3       | 0.2                 | 0.5                 | 1.13224...          |
| 4       | 0.142857...         | 0.333...            | 0.57833...          |
| 5       | 0.111111...         | 0.25                | 0.29315...          |

Figure 3: Range of critical $\lambda$ compared to $\Delta$. Since expected sampling time is guaranteed linear for $\lambda < \lambda_c$, higher is better. Column for $\lambda_c$ for the Randomness Recycler (RR) comes from Theorem 1 of [6]. Column for $\lambda_c$ for Clan of Ancestors (CoA) comes from a branching process analysis.
where the upper bound on the right hand side does not depend on $x(w)$!

Therefore, only if $U_w \geq \exp(-\beta \max\{1-x(i), x(i)\})$ does the value $x(w)$ need to be determined. Therefore, the expected number of neighbors of the original node $v$ that need to be found out is bounded above by

\[ \Delta (1 - \exp(-\beta \max\{1-x(i), x(i)\}^2)). \]

The original node $v$ might have had up to $\Delta$ neighbors, but subsequent nodes will only have at most $\Delta - 1$ neighbors. Therefore, if $(\Delta - 1)(1 - \exp(-\beta \max\{1-x(i), x(i)\}^2)) < 1$, then on average the number of new nodes to consider generated by a node will be negative, and PRAR will terminate after a finite number of steps. This argument yields the following lemma.

**Lemma 6.** Let $\gamma = (\Delta - 1)\exp(-\beta)$. If $\gamma < 1$, then PRAR can generate a sample from the Autonormal model in $O(n)$ random choices on a graph with $n$ nodes and maximum degree $\Delta$.

A similar analysis for the Clan of Ancestors approach requires $\Delta \exp(-\beta) < 1$, therefore the parameter range with guaranteed performance here is slightly wider.

### 4.4 Random Cluster

Suppose that $q > 1$ in the random cluster model with density given by (3). Then the density of a configuration gains a factor of $q$ for each connected component in the graph.

Viewed as a penalty, this means that for a particular edge, there is a penalty of $1/q$ if it connects two previously disconnected components in the rest of the graph. In other words, if $c = (1/q)^n$, where $n$ is the number of nodes in the graph, then the density can be written as

\[ w_2(x) = cw(x) = (1/q)^{n-c(x)}. \]

Now consider a single edge $\{i, j\}$ chosen from the underlying measure. If the edge is labeled 0 (which happens with probability $1 - p$), then the edge is accepted regardless of the rest of the components. If the edge is labeled 1 (which happens with probability $p$), then the edge is accepted with probability $1/q$ if the rest of the state does not connect nodes $i$ and $j$, and accepted with probability 1 otherwise.

Suppose that $x(\{i, j\})$ is randomly chosen to be 1. Then draw $U$ uniformly over $[0, 1]$. If $U < 1/q$, then the edge $\{i, j\}$ is accepted regardless of the rest of the state and the edge value becomes known. Otherwise, recursion must be used to determine enough of the rest of the state in order to determine if the nodes $\{i, j\}$ are connected or not.

The first edge $\{i, j\}$ can be connected to as many as $2(\Delta - 1)$ different edges, each of which must be considered to determine if $x(\{i, j\}) = 1$. Let $e$ be one of these edges (either of the form $\{i, k\}$ or $\{j, k\}$ for some nodes $k$.)
If \( e \) is chosen to be labeled 0 in the recursion, then it is removed from the “needs a value” list. Otherwise, it is adjacent to at most \( \Delta - 1 \) new edges that might need a value. Hence the expected change of the size of the number of edges that need values is bounded above by
\[
(-1)(1 - p) + p(\Delta - 1) = \Delta p - 1.
\]
If this quantity is less than 0, then the number of edges to be considered drops (on average) at each step, and the expected number of steps is bounded. This gives the following lemma.

**Lemma 7.** Let \( G \) be a graph with \( n \) nodes, \( m \) edges, and maximum degree \( \Delta \). If \( p < 1/\Delta \), then the expected number of random choices made in the algorithm is \( O(m) \).

## 5 Connection to popping

This PRAR protocol can be viewed as an extension of the cycle popping algorithm of Wilson for uniformly generating from rooted trees in a directed graph.

Consider a graph \( (V, E) \), and construct a directed graph by taking each edge \( \{i, j\} \) and adding directed arcs \( (i, j) \) and \( (j, i) \). Designate a special node \( r \in V \) known as the root of the graph. Then let a configuration consist of a \( \{0, 1\} \) labeling of arcs such that every node \( v \neq r \) has exactly one outgoing edge \( (v, w) \) labeled 1.

Let \( \mu \) be the underlying measure that is uniform over all such labelings. Then it is easy to sample from \( \mu \): independently for each node \( i \) select a neighbor \( j \) uniformly at random and label that outgoing arc 1, and all other outgoing arcs from \( i \) label 0.

The density \( w(x) \) then is 1 if every node has a directed path using edges labeled 1 to the root, and is 0 otherwise. When \( w(x) \) is 1, say that \( x \) encodes a directed rooted tree in the original graph.

Then Wilson [18] presented a simple algorithm for generating from \( w(x) \) over \( \mu \). Start with an arbitrary node \( i \), and uniformly choose a neighbor \( j \). From \( j \) choose neighbor \( k \), and continue until one of two things happens.

If the directed path reaches a node already examined, then there is a loop. Erase the loop and continue onwards. For instance, if the choices where \( a \rightarrow b \rightarrow c \rightarrow d \rightarrow b \), then \( (b, c, d, b) \) forms a loop, and the next step would start with \( a \rightarrow b \). The other thing that can happen is that the directed path reaches \( r \). In this case, fix the labeling for all nodes along the path.

Now choose another node in the graph and repeat, choosing random neighbors, erasing loops as they form, and stopping when reaching either \( r \) or a previously fixed node.

This algorithm is just PRAR with the backbone method applied to \( \mu \) and \( w \)!

At each step of the algorithm we are recursively moving deeper into the graph in order to determine if acceptance should occur. If a loop forms, then rejection occurs, and all the edges in the loop are eliminated. But if the path should encounter a previously
fixed path, then acceptance occurs not only for the original edge but all along the path as well.

Wilson gave a proof tailored for his algorithm. Because this is also a PRAR algorithm, we immediately have correctness for the loop-erased random walk method of uniformly generating rooted trees.

Acknowledgements

An earlier version of this technique appears in [12] (without the backbone method, connection to popping, and the general running time bound given here.) The recent development of this method was supported by NSF grant DMS-1418495.

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