On Testing of Samplers

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Abstract

Given a set of items \( F \) and a weight function \( \omega_t : F \rightarrow (0, 1) \), the problem of sampling seeks to sample an item proportional to its weight. Sampling is a fundamental problem in machine learning. The daunting computational complexity of sampling with formal guarantees leads designers to propose heuristics-based techniques for which no rigorous theoretical analysis exists to quantify the quality of generated distributions. This poses a challenge in designing a testing methodology to test whether a sampler under test generates samples according to a given distribution. Only recently, Chakraborty and Meel (2019) designed the first scalable verifier, called Barbarik, for samplers in the special case when the weight function \( \omega_t \) is constant, that is, when the sampler is supposed to sample uniformly from \( F \). The techniques in Barbarik, however, fail to handle general weight functions.

The primary contribution of this paper is an affirmative answer to the above challenge: motivated by Barbarik, but using different techniques and analysis, we design Barbarik2, an algorithm to test whether the distribution generated by a sampler is \( \varepsilon \)-close or \( \eta \)-far from any target distribution. In contrast to black-box sampling techniques that require a number of samples proportional to \(|F|\), Barbarik2 requires only \( \tilde{O}(\text{tilt}(\omega_t, \varphi)^2/\eta(\eta - 6\varepsilon)^3) \) samples, where the tilt is the maximum ratio of weights of two satisfying assignments. Barbarik2 can handle any arbitrary weight function. We present a prototype implementation of Barbarik2 and use it to test three state-of-the-art samplers.

1 Introduction

Motivated by the success of statistical techniques, automated decision-making systems are increasingly employed in critical domains such as medical [19], aeronautics [33], criminal sentencing [20], and military [2]. The potential long-term impact of the ensuing decisions has led to research in the correct-by-construction design of AI-based decision systems. There has been a call for the design of randomized and quantitative formal methods [35] to verify the basic building blocks of the modern AI systems. In this work, we focus on one such core building block: constrained sampling.

Given a set of constraints \( \varphi \) over a set of variables \( X \) and a weight function \( \omega_t \) over assignments to \( X \), the problem of constrained sampling is to sample a satisfying assignment \( \sigma \) of \( \varphi \) with probability proportional to \( \omega_t(\sigma) \). Constrained sampling is a fundamental problem that encapsulates a wide range of sampling formulations [24, 23, 12, 30, 14]. For example, \( \omega_t \) can be used to capture a

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*The accompanying tool, available open source, can be found at https://github.com/meelgroup/barbarik. The Appendix is available in the accompanying supplementary material.
†The authors decided to forgo the old convention of alphabetical ordering of authors in favor of a randomized ordering, denoted by (r). The publicly verifiable record of the randomization is available at https://www.aeaweb.org/journals/policies/random-author-order/search with confirmation code: GH8VZd4mQh. For citation of the work, authors request that the citation guidelines by AEA for random author ordering be followed.

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given prior distribution often represented implicitly through probabilistic models, and \( \phi \) can be used to capture the evidence arising from the observed data, then the problem of constrained sampling models the problem of sampling from the resulting posterior distribution.

The problem of constrained sampling is computationally hard and has witnessed a sustained interest from theoreticians and practitioners, resulting in the proposal of several approximation techniques. Of these, Monte Carlo Markov Chain (MCMC)-based methods form the backbone of modern sampling techniques [3, 7]. The runtime of these techniques depends on the length of the random walk, and the Markov chains that require polynomial walks are called rapidly mixing Markov chains. Unfortunately, for most distributions of practical interest, it is infeasible to design rapidly mixing Markov chains [26], and the practical implementations of such techniques have to resort to the usage of heuristics that violate theoretical guarantees. The developers of such techniques, often and rightly so, strive to demonstrate their effectiveness via empirical behavior in practice [6].

The need for the usage of heuristics to achieve scalability is not restricted to just MCMC methods but is widely observed for other methods such as simulated annealing [29], variational methods [18], and hashing-based techniques [12, 23, 13, 32]. Consequently, a fundamental problem for the designers of sampling techniques is: how can one efficiently test whether a given technique samples from the desired distribution? Most of the existing approaches rely on the computations of statistical metrics such as variation distance and KL-divergence by drawing samples and perform hypothesis testing with a preset q-value. Sound computations of statistical metrics require a large number of samples that is proportional to the support of the posterior distribution [4, 36], which is prohibitively large; it is not uncommon for the distribution support to be significantly larger than \( 2^{70} \). Consequently, the existing approaches tend to estimate the desired quantities using a fraction of the required samples, and such estimates are often without the required confidence. The usage of unsound metrics may lead to unsound conclusions, as demonstrated by a recent study where the usage of unsound metric would lead one to conclude that two samplers were indistinguishable (it is worth mentioning that the authors of the study clearly warn the reader about the unsoundness of the underlying metrics) [21].

The researchers in the sub-field of property testing within theoretical computer science have analyzed the sample complexity of testing under different models of samplers and computation. The resulting frameworks have not witnessed widespread adoption to practice due to a lack of samplers that can precisely fit the models under which results are obtained. In recent work, Chakraborty and Meel [10], building on the concepts developed in the condition sampling model (rf. [1]), designed the first practical algorithmic procedure, called Barbarik, that can rigorously test whether a given sampler samples from the uniform distribution using a constant number of samples, assuming that the given sampler is subquery-consistent (see Definition 9). Empirically, Barbarik was shown to be able to distinguish samplers that were indistinguishable in prior studies based on unsound metrics. While Barbarik made significant progress, it is marred by its ability to handle only the uniform distribution. Therefore, one wonders: Can we design an algorithmic framework to test whether the distribution generated by a given sampler is close to a desired (but arbitrary) posterior distribution of interest?

This paper’s primary contribution is the first efficient algorithmic framework, Barbarik2, to test whether the distribution generated by a sampler is \( \varepsilon \)-close or \( \eta \)-far from the desired distribution specified by the set of constraints \( \phi \) and a weight function \( wt \). In contrast to the statistical techniques that require an exponential or sub-exponential number of samples for samplers whose support can be represented by \( n \) bits, the number of samples required by Barbarik2 depends on the tilt of the distribution, where tilt is defined as the maximum ratio of non-zero weights of two solutions of \( \phi \). Like Barbarik, the key technical idea of Barbarik2 sits at the intersection of property testing and formal methods and uses ideas from conditional sampling and employs chain formulas. However, the key algorithmic framework of Barbarik2 differs significantly from Barbarik, and, as demonstrated, the proof of its correctness and sample complexity requires an entirely new set of technical arguments.

Given access to an ideal sampler \( A \), Barbarik2 accepts every sampler that is \( \varepsilon \)-close to \( A \) while its ability to reject a sampler that is \( \eta \)-far from \( A \) assumes that the sampler under test is subquery consistent. Since Barbarik2 assumes access to an ideal sampler, one might wonder if a tester such as Barbarik2 is needed when we already have access to an ideal sampler. Since sampling is computationally intractable, it is almost always the case that an ideal sampler \( A \) is quite slow and one would prefer to use some other efficient sampler \( G \) instead of \( A \), if \( G \) can be certified to be close to \( A \).
To demonstrate the practical efficiency of Barbarik2, we developed a prototype implementation in Python and performed an experimental evaluation with several samplers. While our framework does not put a restriction on the representation of \( w_t \), we perform empirical validation with weight distributions corresponding to log-linear models, a widely used class of distributions. Our empirical evaluation shows that Barbarik2 returns ACCEPT for the samplers with formal guarantees but returns REJECT for other samplers that are without formal guarantees. Our ability to reject samplers provides evidence in support of our assumption of subquery consistency of samplers. We believe our formalization of testing of samplers and the design of the algorithmic procedure, Barbarik2, contributes to the design of randomized formal methods for verified AI, a principle argued by Seshia et al [35].

## 2 Notations and Preliminaries

A Boolean variable is denoted by a lowercase letter. For a Boolean formula \( \varphi \), the set of variables appearing in \( \varphi \), called the support of \( \varphi \), is denoted by \( \text{Supp}(\varphi) \). An assignment \( \sigma \in \{0, 1\}^{\text{Supp}(\varphi)} \) to the variables of \( \varphi \) is a satisfying assignment or witness if it makes \( \varphi \) evaluate to 1. We denote the set of all satisfying assignments of \( \varphi \) as \( R_\varphi \). For \( S \subseteq \text{Supp}(\varphi) \), we use \( \sigma_{1:S} \) to indicate the projection of \( \sigma \) over the set of variables in \( S \). And we denote by \( R_{\varphi_{1:S}} \) the set \( \{ \sigma_{1:S} \mid \sigma \in R_\varphi \} \).

### Definition 1 (Weight Function)

For a set \( S \) of Boolean variables, a weight function \( w_t : \{0, 1\}^{|S|} \rightarrow \) maps each assignment to some weight.

### Definition 2 (Sampler)

A sampler \( G(\varphi, S, w_t, \tau) \) is a randomized algorithm that takes in a Boolean formula \( \varphi \), a weight function \( w_t \), a set \( S \subseteq \text{Supp}(\varphi) \) and a positive integer \( \tau \) and outputs \( \tau \) independent samples from \( R_{\varphi_{1:S}} \). For brevity of notation we will omit arguments \( \varphi, S, w_t, \tau \), whenever may sometimes refer to a sampler as \( G(\varphi) \) or simply, \( G \).

For any \( \sigma \in \{0, 1\}^{|S|} \) the probability of the sampler \( G \) outputting \( \sigma \) is denoted by \( p_G(\varphi, S, \sigma) \) (or \( p_G(\varphi, \sigma) \)) when the set \( S \) in question is clear from the context.

We use \( D_{G(\varphi, S)} \) to represent the distribution induced by \( G(\varphi, S) \) on \( R_{\varphi_{1:S}} \). When the set \( S \) is understood from the context we will denote \( D_{G(\varphi, S)} \) by \( D_G(\varphi) \).

### Definition 3 (Ideal Sampler)

For a weight function \( w_t \), a sampler \( A(\varphi, S, \tau) \) is called an ideal sampler w.r.t. weight function \( w_t \) if for all \( \sigma \in R_{\varphi_{1:S}} \): \( p_A(\varphi, S, w_t, \sigma) = \frac{w_t(\sigma)}{\sum_{\sigma' \in R_{\varphi_{1:S}}} w_t(\sigma')} \). In the rest of the paper, \( A(\cdot, \cdot, \cdot) \) denotes the ideal sampler. When \( w_t(\sigma) = \frac{1}{|R_{\varphi}|} \) then the ideal sampler is called a uniform sampler.

### Definition 4 (Tilt)

For a Boolean formula \( \varphi \) and weight function \( w_t \), we define \( \text{tilt}(w_t, \varphi) = \max_{\sigma_1, \sigma_2 \in R_\varphi} \frac{w_t(\sigma_1)}{w_t(\sigma_2)} \).

Our goal is to design a program that can test the quality of a sampler with respect to an ideal sampler. We use two different notions of distance of the sampler from the ideal sampler.

### Definition 5 (\( \varepsilon \)-closeness and \( \eta \)-farness)

A sampler \( G \) is \( \varepsilon \)-multiplicative-close (or simply \( \varepsilon \)-close) to an ideal sampler \( A \), if for all \( \varphi \) and all \( \sigma \in R_\varphi \), we have \((1 - \varepsilon) p_A(\varphi, \sigma) \leq p_G(\varphi, \sigma) \leq (1 + \varepsilon) p_A(\varphi, \sigma) \). For a formula \( \varphi \), a sampler \( G(\varphi) \) is \( \eta \)-\( \ell_1 \)-far (or simply \( \eta \)-far) from the ideal sampler \( A(\varphi) \), if \( \sum_{\sigma \in R_\varphi} |p_A(\varphi, \sigma) - p_G(\varphi, \sigma)| \geq \eta \).

It is worth emphasising that the asymmetry in the notions of \( \varepsilon \)-close and \( \eta \)-far stems from the availability of practical samplers. Since the available off-the-shelf solvers with theoretical guarantees provide the guarantee of \( \varepsilon \)-closeness, we are interested in accepting a sampler that is \( \varepsilon \)-close [24, 23, 12, 14]. On the other hand, we would like to be more forgiving to the samplers without guarantees and would like to reject only if they are \( \eta \)-far in \( \ell_1 \) distance, a notion more relaxed than multiplicative closeness.

### Definition 6 ((\( \varepsilon, \eta, \delta \))-tester for samplers)

A (\( \varepsilon, \eta, \delta \))-tester for samplers is a randomized algorithm that takes a sampler \( G \), an ideal sampler \( A \), a tolerance parameter \( \varepsilon \), an intolerance parameter \( \eta \), a guarantee parameter \( \delta \) and a CNF formula \( \varphi \) such that (1) If \( G(\varphi) \) is \( \varepsilon \)-close to \( A(\varphi) \), then the tester returns ACCEPT with probability at least \((1 - \delta) \), and (2) If \( G(\varphi) \) is \( \eta \)-far from \( A(\varphi) \) then the tester returns REJECT with probability at least \((1 - \delta) \).

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2.1 Chain Formula

A crucial component in our algorithm is the chain formula. Chain formulas, introduced in [15], are a special class of Boolean formulas. Given a positive integer \( k \) and \( m \), chain formulas provide an efficient construction of a Boolean formula \( \psi_{k,m} \) with exactly \( k \) satisfying assignments with \( \lceil \log(k) \rceil \leq m \) variables. We employ chain formulas for inverse transform sampling and in the subroutine Barbarik2Kernel.

Definition 7. [15] Let \( c_1 c_2 \cdots c_m \) be the \( m \)-bit binary representation of \( k \), where \( c_m \) is the least significant bit. We then construct a chain formula \( \phi_{k,m}(\cdot) \) on \( m \) variables \( a_1, \ldots, a_m \) as follows. For every \( j \) in \( \{1, \ldots, m-1\} \), let \( C_j \) be the connector “\( \lor \)” if \( c_j = 1 \), and the connector “\( \land \)” if \( c_j = 0 \). Define

\[
\phi_{k,m}(a_1, \ldots, a_m) = a_1 C_1 (a_2 C_2 (\cdots (a_{m-1} C_{m-1}(a_{m}) \cdots)),
\]

For example, consider \( k = 11 \) and \( m = 4 \). The binary representation of 11 using 4 bits is 1011. Therefore, \( \phi_{5,4}(a_1, a_2, a_3, a_4) = a_1 \lor (a_2 \land (a_3 \lor a_4)). \)

Lemma 1. [15] Let \( m > 0 \) be a natural number, \( k < 2^m \), and \( \phi_{k,m} \) as defined above. Then \( |\phi_{k,m}| \) is linear in \( m \) and \( \phi_{k,m} \) has exactly \( k \) satisfying assignments. Every chain formula \( \psi \) on \( n \) variables is equivalent to a CNF formula \( \psi_{CNF} \) having at most \( n \) clauses. In addition, \( |\psi_{CNF}| \) is in \( O(n^2) \).

2.2 Barbarik2Kernel and the Subquery Consistency Assumption

Barbarik2Kernel is a crucial subroutine that we use in our algorithm to help us draw conditional samples from \( R_{\phi_S} \). This is similar to the subroutine Kernel used by the Barbarik in [10]. We will now define a collection of functions KernelFamily.

Definition 8. KernelFamily is family of functions that take a Boolean formula \( \varphi \), a set of variables \( S \subseteq \text{Supp}(\varphi) \), and two assignments \( \sigma_1, \sigma_2 \in R_{\varphi_S} \), and return \( \hat{\varphi} \) such that \( R_{\hat{\varphi}_S} = \{\sigma_1, \sigma_2\} \).

[10] introduced the notion of non-adversarial assumption, which was crucial in their analysis. We rename the notion of subquery consistency to better capture its intended properties, defined below.

Definition 9. Let Barbarik2Kernel \( \in \text{KernelFamily} \). A sampler \( G \) is subquery consistent w.r.t. a particular Barbarik2Kernel for \( \varphi \) if for all \( S \subseteq \text{Supp}(\varphi) \), \( \sigma_1, \sigma_2 \in R_{\varphi_S} \), let \( \hat{\varphi} \leftarrow \text{Barbarik2Kernel}(\varphi, S, \sigma_1, \sigma_2) \) then the output of \( G(\hat{\varphi}, \tau, S, \tau) \) is \( \tau \) independent samples from the conditional distribution \( \mathbb{D}_{G(\hat{\varphi})|T} \), where \( T = \{\sigma_1, \sigma_2\} \).

Similar to the usage of non-adversarial assumption in the correctness analysis of Barbarik [10], the notion of subquery consistency would play a crucial role in our analysis. Since each subquery can be viewed as conditioning and given that conditioning is a fundamental operation, one would expect that off the shelf samplers would be subquery consistent. At the same time, in contrast to practical applications, the set \( T \) is arbitrarily chosen, and therefore, it is possible that certain samplers do not satisfy the property of subquery consistency. It is, however, not known how to test whether a sampler is subquery consistent w.r.t a particular Barbarik2Kernel. While our empirical evaluation provides weak evidence to our claim that off the shelf samplers are subquery consistent, we believe checking whether a sampler is subquery consistent is an interesting and important problem for future work.

3 Related Work

Distribution testing involves testing whether an unknown probability distribution is identical or close to a given distribution. This problem has been studied extensively in the property testing literature [11, 8, 36, 37]. The sample space is exponential, and for many fundamental distributions, including uniform, it is prohibitively expensive in terms of samples to verify closeness. This led to the development of the conditional sampling model [11, 8], which can provide sub-linear or even constant sample complexities for the testing of the above-given properties[1, 28, 5, 9, 17]. A detailed discussion on prior work in property testing and their relationship to Barbarik2 is given in Appendix A.

The first practically efficient algorithm for verification of samplers with a formal proof of correctness was presented by Chakraborty and Meel in form of Barbarik [10]. The central idea of Barbarik, building on the work of Chakraborty et al. [11] and Canonne et al. [8], was that if one can have
Barbarik constructs a two-element set $T \subset R_\varphi$, with one element drawn according to the distribution $D_{\hat{G}(\varphi)}$ and one element drawn uniformly at random from the set $R_\varphi$. Using a subroutine Kernel Chakraborty et al. argued that one can draw samples from the conditional distribution $D_{\hat{G}(\varphi)|T}$. Their sample complexity was $\tilde{O}(1/(\eta - 2\varepsilon)^4)$. They proved that if a sampler $G$ is $\varepsilon$-close to a uniform sampler then Barbarik will accept with probability at least $(1 - \delta)$, while if $G(\varphi)$ is $\eta$-far from the uniform sampler and if $G$ is subquery consistent w.r.t Kernel for $\varphi$, then Barbarik rejects with probability at least $(1 - \delta)$. Their underlying assumption was that many samplers that are in use would in fact be subquery consistent and the success of Barbarik in rejecting several samplers provides evidence in support of the aforementioned assumption. They used Barbarik to test the correctness of samplers like STS, Quicksampler, and UniGen.

Note that Barbarik can only distinguish a uniform sampler from a far-from uniform sampler, and the techniques used cannot be generalized easily to the case where the ideal sampler is not necessarily uniform. While Barbarik2, that we present in this paper, does borrow several techniques from Barbarik, including drawing inspiration from the concept of conditional sampling for their design; Barbarik2 is very different from Barbarik both in terms of the algorithmic design and its implementation.

4 An overview of the Barbarik2 Algorithm

In this section, we present the algorithmic framework of Barbarik2, the pseudocode, presented as Algorithm 1, and then the theoretical justification for the algorithm. Barbarik2 takes as input a black-box sampler $G$, a Boolean formula $\varphi$ with the associated weight function $w_\varphi$ and three parameters $(\varepsilon, \eta, \delta)$. It also has access to an ideal sampler $A$. Barbarik2 is an $(\varepsilon, \eta, \delta)$-tester for samplers. Also if Barbarik2 returns REJECT (that is, when $G$ is $\eta$-far from $A$), it provides as witness a new formula $\hat{\varphi}$ which is similar to $\varphi$, except that $\hat{\varphi}$ has only two assignments to the variables in $S$ (namely $\sigma_1$ and $\sigma_2$) that can be extended to satisfying assignments of $\hat{\varphi}$ and the relative probability masses of $\sigma_1$ and $\sigma_2$ in $D_\hat{G}$ are significantly different from that in $D_A$.

The core idea of Barbarik2 is that for verifying the quality of the sampler $G(\varphi)$, we can proceed in two stages. In the first stage, if the sampler is far from the ideal sampler, we hope to find a witness (in the form of two satisfying assignments) for farness with good probability. This can be guaranteed by drawing only one sample each from $D_{\hat{G}(\varphi)}$ and $D_A(\varphi)$. In the second stage, we confirm whether the witness is indeed far. That is, if the witness is the $(\sigma_1, \sigma_2)$ pair, we check that the probability of $\sigma_1$ and $\sigma_2$ in $D_{\hat{G}(\varphi)}$ and $D_A(\varphi)$ are similar or not.

Here Barbarik2 differs from Barbarik in a significant way. Barbarik employs a bucketing strategy. But, Barbarik2 chooses a simpler yet equally effective method to check the similarity between $\sigma_1$ and $\sigma_2$. This is also the most difficult stage of the tester as one may have to draw an exponential number of samples to confirm the similarity. We manage this by drawing samples from the conditional distribution $D_{\hat{G}(\varphi)|\{\sigma_1, \sigma_2\}}$ instead of $D_{\hat{G}(\varphi)}$. Since $D_{\hat{G}(\varphi)|\{\sigma_1, \sigma_2\}}$ is supported on a set of size only two estimating the distance of $D_{\hat{G}(\varphi)|\{\sigma_1, \sigma_2\}}$ from $D_A(\varphi)|\{\sigma_1, \sigma_2\}$ can be done with constant number of samples.

Now since we do not have direct access to the distribution $D_{\hat{G}(\varphi)|\{\sigma_1, \sigma_2\}}$, we circumvent the problem by drawing samples from a new distribution $D_{\hat{\varphi}}$ where $\hat{\varphi}$ is obtained from $\varphi$ and has similar structure as $\varphi$ (with $\text{Supp}(\varphi) \subseteq \text{Supp}(\hat{\varphi})$) and there are only two assignments (namely $\sigma_1$ and $\sigma_2$) to the variables in $\text{Supp}(\hat{\varphi})$ that can be extended to the satisfying assignments of $\hat{\varphi}$. The subroutine Barbarik2Kernel helps us simulate the drawing of samples from $D_{\hat{G}(\varphi)|\{\sigma_1, \sigma_2\}}$ by drawing samples from $D_{\hat{G}(\varphi)}$. The subroutine Bias helps to estimate the distance of $D_{\hat{G}(\varphi)}$ from $D_A(\varphi)$.

Finally, we repeat the whole process for a certain number of rounds, and we argue that if the sampler is indeed far then, with high probability, in at least one round, we will find a witness of farness and confirm that the witness is indeed far. On the other hand, if the sampler is close to ideal, then there does not exist any such witness of farness.

Barbarik2 accesses two subroutines, Bias and Barbarik2Kernel: $\text{Bias}(\hat{\sigma}, \Gamma, S)$ takes as input an assignment $\hat{\sigma}$, a list $\Gamma$ of assignments and a sampling set $S$. It returns the fraction of assignments of $\Gamma$ whose projections on $S$ is equal to $\hat{\sigma}$. Barbarik2Kernel$(\varphi, \sigma_1, \sigma_2)$ is a Barbarik2Kernel subroutine.
Algorithm 1 Barbarik2($G, A, \varepsilon, \eta, \delta, \varphi, \sigma, wt$)

1: $t \leftarrow \ln(1/\delta) \ln \left( \frac{10}{\varepsilon \cdot \theta(0, \sigma)} \right)^{-1}$
2: $n \leftarrow 8n (t/\delta)$
3: $lo = (1 + \varepsilon) / (1 - \varepsilon)$
4: $hi = 1 + (\eta + 6\varepsilon)/4$
5: $\Gamma_1 \leftarrow G(\varphi, S)$
6: $\Gamma_2 \leftarrow A(\varphi, S, t)$
7: for $i = 1$ to $t$
8:    $\sigma_1 \leftarrow \Gamma_1[i]$; $\sigma_2 \leftarrow \Gamma_2[i]$;
9:    if $\sigma_1 = \sigma_2$ then
10:        continue
11:    $\alpha \leftarrow wt(\sigma_1)/wt(\sigma_2)$
12:    $L \leftarrow (\alpha \cdot lo) / (1 + \alpha \cdot lo)$
13:    $H \leftarrow (\alpha \cdot hi) / (1 + \alpha \cdot hi)$
14:    $T = (H + L)/2$
15:    $N \leftarrow n \cdot H/(H - L)^2$
16:    $\hat{\varphi} \leftarrow$ Barbarik2Kernel($\varphi, \sigma_1, \sigma_2$)
17:    $\Gamma_3 \leftarrow \hat{G}(\hat{\varphi}, S, N)$
18:    $Bias \leftarrow Bias(\sigma_1, \Gamma_3, S)$
19:    if $Bias > T$ then
20:        return REJECT
21: return ACCEPT

Algorithm 2 Barbarik2Kernel($\varphi, \sigma_1, \sigma_2$)

1: $m \leftarrow 12$, $k \leftarrow 2^m - 1$
2: $Lits_1 \leftarrow (\sigma_1 \setminus \sigma_2)$
3: $Lits_2 \leftarrow (\sigma_2 \setminus \sigma_1)$
4: $V \leftarrow NewVars(\varphi, m)$
5: $\hat{\varphi} \leftarrow \varphi \land (\sigma_1 \lor \sigma_2)$
6: $l \sim Lits_1 \cup Lits_2$
7: $\hat{\varphi} \leftarrow \hat{\varphi} \land \left( \neg l \rightarrow \psi_{k,m}(V) \right)$
8: $\hat{\varphi} \leftarrow \hat{\varphi} \land \left( l \rightarrow \psi_{k,m}(V) \right)$
9: return $\hat{\varphi}$

Algorithm 3 Bias($\sigma, \Gamma, S$)

1: $count = 0$
2: for $\sigma \in \Gamma$
3:    if $\sigma \setminus S = \sigma$
4:        $count \leftarrow count + 1$
5: return $\frac{count}{|\Gamma|}$

(Definition 8). Its aim is to create a $\hat{\varphi}$ such the behaviour of the sampler on $\hat{\varphi}$ is similar to it’s behaviour on $\varphi$, i.e. $D_{\hat{G}(\hat{\varphi})}^{\hat{\varphi}}(\sigma_1, \sigma_2) \approx D^G(\varphi)$.

In Barbarik2, in the for loop (in lines 7–20), in each round, the algorithm draws one sample $\sigma_1$ according to the distribution $D_{\hat{G}(\hat{\varphi})}$ and one sample $\sigma_2$ according to the ideal distribution on $R_{\varphi}$ (line 8). In the case that $\sigma_1 = \sigma_2$ it moves to the next iteration (in line 9-10). In line 16, the subroutine Barbarik2Kernel uses $\varphi$, the two samples $\sigma_1$ and $\sigma_2$, to output a new formula $\hat{\varphi}$ such that $Supp(\varphi) \subseteq Supp(\hat{\varphi})$. On line 17, Barbarik2 draws a list, $\Gamma_3$, of $N$ samples according to the distribution $D_{\hat{G}(\hat{\varphi})}$. Barbarik2Kernel ensures that for all $\sigma \in \Gamma_3$, $\sigma \setminus S$ is either $\sigma_1$ or $\sigma_2$. In line 18 Barbarik2 uses Bias to compute the fraction of samples that are equal to $\sigma_1$ (on the variable set $S$), and if the fraction is greater than the threshold then Barbarik2 returns REJECT (in line 20).

Algorithm 2 presents the pseudocode of subroutine Barbarik2Kernel. As stated above, Barbarik2Kernel takes as a Boolean formula $\varphi$, a set $S \subseteq Supp(\varphi)$ and two partial assignments $\sigma_1, \sigma_2 \in R_{\varphi \upharpoonright S}$. Since the set $S$ is implicit from $\sigma_1$ and $\sigma_2$ it may not be explicitly given as an input. Barbarik2Kernel assumes access to subroutine NewVars which takes in two parameters, a formula $\varphi$ and number $m$, and returns a set of $m$ fresh variables that do not appear in $\varphi$. Barbarik2Kernel first constructs two sets of literals, denoted by $Lits_1$ (resp. $Lits_2$), which appear in $\sigma_1$ (resp. $\sigma_2$) but not $\sigma_2$ (resp. $\sigma_1$). The algorithm then constructs the formula $\hat{\varphi}$. First it generates $\varphi \land (\sigma_1 \lor \sigma_2)$ on Line 4, a formula with exactly two solutions. Next, it randomly chooses a literal $l$ from $Lits_1 \cup Lits_2$ and constructs a chain formula $(l \rightarrow \psi_{k,m})$ over the fresh Boolean variables $V[1], V[2] \cdots, V[m]$ where $k$ is the number of satisfying assignments the formula has. Conjuncting the two generated formulas, we get $\hat{\varphi} \equiv \varphi \land (\sigma_1 \lor \sigma_2)$. Therefore, at the end of Barbarik2Kernel, i.e. line 8, $\hat{\varphi}$ has $2k$ solutions. We choose the value of $k$ such that it is odd (see [15]). The chain formula is linked to a random Boolean literal from the given set of literals for two reasons,

1. An ideal or $\varepsilon$-close to ideal sampler would not be affected by the randomization and would generate the same distribution over $\varphi$ as it does over $\varphi \land (\sigma_1 \lor \sigma_2)$.

2. If the sampler under test $G$ is $\eta$-far from ideal, then we want to construct a formula which cannot be easily guessed by $A$. We wish to avoid the scenario where $A$, an $\eta$-far sampler on $\varphi$, somehow behaves as an almost-ideal sampler over $\varphi$ and hence manages to fool Barbarik2.
4.1 Theoretical Analysis

The following theorem gives the mathematical guarantee about the correctness of Barbarik2.

**Theorem 1.** Given sampler \( G \), ideal sampler \( A \), \( \varepsilon < \frac{1}{3} \), \( \eta > 6\varepsilon \), \( \delta \) and weight function \( \omega_t \), Barbarik2 needs at most \( \widetilde{O} \left( \frac{tilt(\omega_t, \varphi)}{\eta(\eta - 6\varepsilon)} \right)^2 \) samples, where \( \widetilde{O} \) hides a poly logarithmic factor of \( 1/\delta \).

- If \( G \) is an \( \varepsilon \)-close to \( A \) then Barbarik2 returns ACCEPT with probability at least \((1 - \delta)\).
- If \( G \) is subquery consistent w.r.t Barbarik2Kernel and if the distribution \( D_{\tilde{G}}(\varphi) \) is \( \eta \)-far from the ideal sampler then Barbarik2 returns REJECT with probability at least \((1 - \delta)\).

Note that if \( G \) is \( \varepsilon \)-close to \( A \) then Barbarik2 accepts (with high probability) even if the sampler \( G \) isn’t subquery consistent w.r.t Barbarik2Kernel. It is also worth noting that Barbarik2 terminates with REJECT as soon as the check in line 19 succeeds. Therefore, we expect Barbarik2 to require significantly less number of samples when it returns REJECT. Furthermore, in the case of ACCEPT, the bound on \( N \), as calculated on line 15 in terms of \( \text{tilt} \), is pessimistic as the probability of observing \( \sigma_1 \) and \( \sigma_2 \) such that \( \alpha \approx \text{tilt} \) for a sampler close to ideal is very small when the tilt is large. The proof of Theorem 1 is presented in Appendix B.

5 Evaluation

The objective of our evaluation was to answer the following questions:

- **RQ1.** Is Barbarik2 able to distinguish between off-the-shelf samplers by returning ACCEPT for samplers \( \varepsilon \)-close to the ideal distribution and REJECT for the \( \eta \)-far samplers?
- **RQ2.** What improvements do we observe over the baseline?
- **RQ3.** How does the required number of samples scale with the \( \text{tilt}(\omega_t, \varphi) \) of the distribution?

To evaluate the runtime performance of Barbarik2 and test the quality of some state of the art samplers, we implemented a prototype of Barbarik2 in Python. Our algorithm utilizes an ideal sampler, for which we use the state of the art sampler WAPS [25]. All experiments were conducted on a high performance computing cluster with 600 E5-2690 v3 @2.60GHz CPU cores. For each benchmark, we use a single core with a timeout of 24 hours. The detailed logs along with list of benchmarks and the runtime code employed to run the experiments are available at [http://doi.org/10.5281/zenodo.4107136](http://doi.org/10.5281/zenodo.4107136).

We focus on the log-linear distributions given their ubiquity of usage in machine learning; a formal description is provided in Appendix C for completeness. Observe that Barbarik2 does not put any restrictions on the representation of the weight distribution. We conducted our experiments on 72 publicly available benchmarks, which have been employed in the evaluation of samplers proposed in the past [13, 21]. The \( \text{tilt} \) of the benchmarks spans many orders of magnitude, between 1 and \( 10^{11} \).

**Samplers Tested** The past few years have witnessed a multitude of sampling techniques ranging from variational methods [38], MCMC-based techniques [27, 31], mutation-based sampling [21], importance sampling-based methods [22], knowledge-compilation techniques [25] and the like. The conceptual simplicity of uniform samplers encourages designers to tune their algorithms for uniform sampling, and the standard technique for weighted sampling employs the well-known method of the inverse transform. For the sake of completeness, we provide a detailed discussion of the transformation technique in Appendix C.

We perform empirical evaluation with the three state of the art samplers wUniGen, wQuicksampler, and wSTS constructed by augmenting inverse sampling with underlying samplers UniGen [13], Quicksampler [21] and STS(SearchTreeSampler) [22] respectively.

While wUniGen is known to have theoretical guarantees of \( \varepsilon \)-closeness, there is no theoretical analysis of the distributions generated by wQuicksampler and wSTS. Of the 72 instances, wUniGen can handle only 35 instances while wQuicksampler and wSTS can handle all the 72 instances. The variation in the number of instances that are amenable to sampling for a particular sampler highlights the trade-off between the runtime performance and theoretical guarantees. It is perhaps worth
Table 1: “A”(resp. “R”) represents Barbarik2 returning ACCEPT(resp. REJECT). maxSamp represents the upper bound on the number of samples required by Barbarik2 to return ACCEPT/REJECT.

| Benchmark          | \(tilt\) (maxSamp) | wUniGen (samples) | wSTS (samples) | wQuicksampler (samples) |
|--------------------|---------------------|-------------------|---------------|------------------------|
| s349_3_2           | 28 (3e+07)          | A (1e+05)         | A (1e+05)     | R (22854)              |
| s820a_3_2          | 37 (5e+07)          | A (96212)         | R (87997)     | A (2e+05)              |
| UserServiceImpl.sk | 140 (6e+08)         | A (1e+05)         | R (1e+05)     | R (4393)               |
| LoginService2.sk   | 232 (2e+09)         | A (1e+05)         | R (38044)     | R (13350)              |
| s349_7_4           | 603 (1e+10)         | A (75555)         | R (4284)      | R (5150)               |
| s344_3_2           | 3300 (3e+11)        | A (1e+05)         | R (59952)     | R (5150)               |
| s420_new_7_4       | 3549 (4e+11)        | A (82312)         | A (96659)     | R (49955)              |
| 54.sk_12_97        | 4e+11 (6e+27)       | DNS               | R (14012)     | R (4627)               |
| s641_7_4           | 9e+07 (3e+20)       | DNS               | R (8747)      | A (1e+06)              |
| s838_3_2           | 2e+08 (1e+21)       | DNS               | R (9504)      | R (4627)               |

emphasizing that wQuicksampler and wSTS are significantly more efficient in runtime performance than the ideal sampler WAPS.

Test Parameters We set tolerance parameter \(\varepsilon\), intolerance parameter \(\eta\), and confidence \(\delta\) for Barbarik2 to be and 0.1, 1.6 and 0.2 respectively. The chosen setting of parameters implies that for a given Boolean formula \(\phi\), if the sampler under test \(\hat{g}(\phi)\) is \(\varepsilon\)-close to the ideal sampler, then Barbarik2 returns ACCEPT with probability at least 0.8, otherwise if the sampler is \(\eta\)-far from ideal sampler then Barbarik2 returns REJECT with probability at least 0.8. Note that, the number of samples required for ACCEPT depends only on the parameters \((\varepsilon, \eta, \delta)\) and \(tilt(wt, \phi)\). We instantiate Barbarik2Kernel with the values \(m = 12\) and \(k = 2^m - 1\). Observe that Theorem 1 does not put restrictions on \(k\) and \(m\).

Description of the table We present the experimental results in Table 1. Due to lack of space, we present results for a subset of benchmarks while the extended table is available in the supplementary material. The first column indicates the name of the benchmark, the second the \(tilt\), and the following columns indicate the outcome of the experiments with wUniGen, wSTS and wQuicksampler in that order. Every cell in the table has two entries. In the second column, the first entry shows the value of \(tilt\) for the corresponding benchmark, while in the other columns, it contains “A” and “R” to indicate the output of Barbarik2 for the corresponding sampler. The second entry for the cells in the column corresponding to \(tilt\) indicates the theoretical upper bound on the samples required for Barbarik2 to terminate, while for rest of the columns, the second entry indicates the number of samples consumed by Barbarik2 for the corresponding instance and the sampler.

RQ1 Our experiments demonstrate that Barbarik2 returns REJECT for wQuicksampler on 68 benchmarks and ACCEPT on the remaining four benchmarks. For wSTS we found Barbarik2 returned REJECT on 62 of the benchmarks and ACCEPT on 7 while it times out on the remaining 3. Since wSTS and wQuicksampler are samplers with no formal guarantees and therefore one may expect them to generation distributions away from the ideal distributions. In this context, the results
in Table 1 provide strong evidence for the reasonableness of the subquery consistency assumption in practice.

In contrast, Barbarik2 returned ACCEPT for wUniGen on all the 35 benchmarks for which wUniGen could sample. Recall, wUniGen formally guarantees $\varepsilon$-closeness of the samples to the required distribution, hence Barbarik2 returning ACCEPT on all the benchmarks provides evidence in support of soundness of Barbarik2.

**RQ2** We also computed the number of samples required by the baseline approach owing to [4]. Since the number of samples is so large that exhaustive experimentation is infeasible, we had to resort to estimating the average time taken by a sampler for a given instance. Based on the estimated time, we can estimate the time taken by the baseline for our benchmark set. We observe that the time taken by the baseline would be over $10^6$ seconds for 43, 42 and 16 benchmarks for wQuicksampler, wSTS and wUniGen respectively. In this context, it is worth highlighting that Barbarik2 terminates within 24 hours for all the instances for all the samplers. We observe that the geometric means of the speedups over the baseline approach are $10^{5.0}, 10^{20.2}$ and 58 for wSTS, wQuicksampler and, wUniGen respectively. The lower speedup in the case of wUniGen owes to its ability to handle only small benchmarks, for which the number of models was not very large. The extended results are available in Appendix D.

**RQ3** The number of trials required (indicated by the variable $t$ as on Line 7 of Algorithm 1) depends only on $(\varepsilon, \eta, \delta)$, so for the values we use, $(0.1, 1.6, 0.2)$, we find that we require $t = 14$ trials. The analysis of the algorithm reveals an upper bound on the sample complexity of the tester (See Section 4, Theorem 1) which is quadratic in terms of the tilt($\omega$, $\varphi$). We now return to Table 1 and observe that the number of samples required by Barbarik2 before returning ACCEPT were significantly lower than the theoretical bound provided in the second column. Furthermore, as noted earlier, the number of samples required before Barbarik2 returns REJECT is typically significantly less than the worst case – a trend demonstrated in Table 1.

6 Conclusion

In this paper, we study the problem of verifying whether a probabilistic sampler samples from a given discrete distribution. Existing approaches require samples linear in the size of the sampling set, which is commonly exponentially large. We present a conditional sampling technique that can verify the sampler in sample complexity constant in terms of the sampling set. We also test a prototype implementation of our algorithm against three state-of-the-art samplers.

We noticed that the analytical upper bound on the sample complexity is significantly weak compared to our observed values; this suggests that the bounds could be further tightened. Our algorithm can only deal with those discrete distributions for which the relative probabilities of any two points is easily computable. Since our algorithm does not deal with all possible discrete distributions, extending the approach to other distributions would enable the testing of a broader set of samplers.

**Broader Impact**

The recent advances in machine learning techniques have led to increased adoption of the said techniques in safety-critical domains. The usage of a technique in a safety-critical domain necessitates appropriate verification methodology. This paper seeks to take a step in this direction and focused on one core component. Our analysis is probabilistic, and therefore, practical adoption of such techniques requires careful design of frameworks to handle failures.

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Appendix

A Relationship of Barbarik2 with Property Testing

Testing of samplers is basically testing if two distributions $D_{\mathcal{G}(\varphi)}$ and $A_{\mathcal{G}(\varphi)}$ are similar, where $\mathcal{G}$ is the sampler under test and $A$ is the ideal sampler. As stated in the Introduction and the Related Work section, the sub-field of property testing in theoretical computer science has been studying this problem for over two decades and our tester Barbarik2 draws ideas from some of the latest research in this area.

In understanding the closeness between two distributions one may consider a variety of different distance measures. The variation distance (also called the $\ell_1$ distance) is possibly most commonly used. In property testing the problem is to distinguish between the case where the two distributions are $\varepsilon$-close in $\ell_1$ distance from the case where the distributions are $\eta$-far from each other in $\ell_1$ distance. An easier question, called the “equivalence testing of distributions” considers the problem of distinguish identical distributions from distributions that are $\eta$-far from each other in $\ell_1$ distance. The former question, often referred to as the tolerant version of equivalence testing of distributions or estimation of variation distance, is more suitable for various applications. The goal in all the settings is to minimize the sample complexity. The time complexity or other complexity measures are usually not considered in property testing literature.

The problem of equivalence testing of distributions was first considered by [4] and they (along with [37]) showed that the sample complexity was $\Theta(N^{2/3})$, where $N$ is the size of the support of the distributions. Note that, in the setting of samplers, $N$ is exponential in the input size and hence the number is prohibitively large. The tolerant version of the problem was proved to have even higher sample complexity of $\Theta(N)$ ([37, 36]). This was a significant bottleneck is practicality of these property testing algorithms and the tight lower bounds implied that no improvement was possible for algorithms that has only blackbox access to the distributions. Even the much simpler problem of testing if a distribution is uniform requires $\Omega(\sqrt{N})$ samples.

In [11, 8] a new model for sampling was introduced called the conditional sampling. This model allowed access to the distributions that the standard sampling method (or the blackbox access to the distributions) could not give. It allowed a kind of grey-box access to the distributions. It was shown that in this model only $O(1/\varepsilon^2)$ conditional samples were needed to test if a distribution is uniform or $\varepsilon$-far from uniform. In fact similar conditional sample complexity is sufficient for the non-tolerant version of the equivalence testing of distributions. For the tolerant version of equivalence testing of distributions it was shown that polynomial in $\log(N)$ number of conditional samples suffice. Although this brings down the sample complexity drastically but still it was quite high for practical implementations. On top of that a major obstacle was whether the conditional samples were at all practical and were they implementable.

In [10] they successfully used the idea from the conditional sampling testing to test if samplers are uniform. They crucially used a special kind of conditional sampling. In [8] a concept of pair-conditioning (they called PCOND) was introduced to define a restricted version of the conditional sampling model. A normal conditional sample is obtained by specifying a subset $S$ of the domain of the distribution $D$ and then drawing a random sample from the conditional distribution $D|_S$. A PCOND-sample is a normal conditional sample where the subset $S$ is of size 2. In [10] it was shown how this kind of restricted samples can be successfully implemented using a clever use of chain-formulas.

When it come to the more general problems of non-tolerant version of equivalence testing of distributions it can be shown that the sample complexity in the PCOND-model is at least polynomial in $\log N$. The tolerant version has even higher PCOND-sample complexity. Since our primary objective was to have a tester that can be practical and implementable we had to circumvent the problem of high sample complexity and also of implementational issues of conditional sampling. In our tester Barbarik2 we addressed these problems by using another trick from [10], that of, using two different notions of distance $\ell_1$ for farness and $\ell_\infty$ for closeness. In Barbarik2 we re-designed the sampler and give a proof of correctness in this paradigm using very different techniques as compare to that used in [10].
It is worth noting here that recently conditional sampling and its various variants has been used to design efficient testing and learning algorithms for various other properties of distributions ([1, 28, 5, 9, 17]). Many of these have the potential to be used more efficient and sophisticated testing of samplers and related questions. But the major question is the practicality of the models and the implementability of the algorithms.

B Proof of Correctness of Barbarik2

In this section, we present the theoretical analysis of Barbarik2, and the proof of Theorem 1. The proof clearly follows from the the following three lemmas.

**Lemma 2.** If a sampler \( G \) is \( \varepsilon \)-close to the ideal sampler \( A \) then Barbarik2 returns ACCEPT with probability at least \((1 - \delta)\).

**Lemma 3.** If \( G \) is subquery consistent w.r.t Barbarik2Kernel and if the distribution \( D_G(\varphi) \) is \( \eta \)-far from the ideal sampler then Barbarik2 returns REJECT with probability at least \((1 - \delta)\).

**Lemma 4.** Given \( \varepsilon, \eta \) and \( \delta \), Barbarik2 needs at most \( \tilde{O}\left(\frac{\text{tilt}(\varphi, \psi \psi)}{\eta (\eta - 6 \varepsilon)}\right) \) samples for any input formula \( \varphi \) and weight function \( \psi \), where the tilde hides a poly logarithmic factor of \( 1/\delta, 1/\eta \) and \( 1/(\eta - 6 \varepsilon) \).

We will present the proofs of Lemma 2, Lemma 3 and Lemma 4 in Section B.1, Section B.2 and Section B.3 respectively.

In the rest of this section we will use the following notations:

- We use \( \mathbb{1}(E) \) to represent the indicator variable for the event \( E \).
- We use \( R_i \) to denote the event that Barbarik2 returns REJECT in iteration \( i \).

For the proof of correctness of our algorithm, we need some standard concentration inequalities. The following versions of the Chernoff Bound will be used.

**Lemma 5.** Let \( Y_1, Y_2, \ldots, Y_n \) be i.i.d 0-1 random variables.

1. If \( \mathbb{E}[Y_i] \geq \theta \geq 0 \), then for any \( t \leq \theta \),

\[
\Pr \left[ \sum_{j \in [n]} \frac{Y_j}{n} \leq t \right] < \exp \left( -\frac{(\theta - t)^2n}{2\theta} \right)
\]

2. If \( \mathbb{E}[Y_i] \leq \theta \), then for any \( t \geq \theta \),

\[
\Pr \left[ \sum_{j \in [n]} \frac{Y_j}{n} \geq t \right] < \exp \left( -\frac{(t - \theta)^2n}{2t} \right)
\]

We are now ready to present the proofs of Lemma 2, Lemma 3 and Lemma 4.

B.1 Proof of Lemma 2

**Lemma 2.** If a sampler \( G \) is \( \varepsilon \)-close to the ideal sampler \( A \) then Barbarik2 returns ACCEPT with probability at least \((1 - \delta)\).

For the proof of Lemma 2 we will firstly show (in Lemma 6) that in each iteration of the loop, the probability that Barbarik2 returns REJECT is less than \( \delta/t \) and then the proof of Lemma 2 follows by the application of the Chernoff Bound. Recall that \( R_i \) denotes the event that Barbarik2 returns REJECT in iteration \( i \).

---

\(^3\)for any \( \varepsilon < \frac{1}{3} \) and \( \eta > 6 \varepsilon \)

\(^4\)for any \( \varepsilon < \frac{1}{3} \) and \( \eta > 6 \varepsilon \)
Lemma 6. If sampler $\mathcal{G}$ is $\varepsilon$-close to an ideal sampler $\mathcal{A}$ then the probability that Barbarik2 returns REJECT in any particular iteration of the loop, is at most $\delta/t$. Then

$$\Pr \left[ R_i \mid \bigwedge_{j \in [i-1]} R_j \right] \geq \left( 1 - \frac{\delta}{T} \right)$$

Proof. (of Lemma 6) Barbarik2 returns REJECT in the $i$th iteration if the $Bias$ (in the $i$th iteration) is more than $T$, where $T = \frac{L_H}{\delta}$ with

$$L = \frac{(1 + \varepsilon)p_A(\varphi, S, \sigma_1)}{(1 + \varepsilon)p_A(\varphi, S, \sigma_1) + (1 - \varepsilon)p_A(\varphi, S, \sigma_2)}$$

And since, by definition, all the elements in $\Gamma_1$, $\Gamma_2$ and $\Gamma_3$ are obtained by drawing independent samples from $D_{\mathcal{G}(\varphi)}$, $D_{\mathcal{A}(\varphi)}$ and $D_{\mathcal{G}(\hat{\varphi})}$ respectively so

$$\Pr \left[ R_i \mid \bigwedge_{j \in [i-1]} R_j \right] = \Pr [ Bias \leq T \text{ in the } i\text{th iteration}] = 1 - \Pr [ Bias > T \text{ in the } i\text{th iteration}]$$

$$= 1 - \Pr \left[ \sum_{j \in [N]} \mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_1) > T \right]$$

Note that the random variables $\mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_1)$ are an i.i.d 0-1 random variable. And since the sampler $\mathcal{G}$ is assumed to be $\varepsilon$-close to the ideal sampler so we have

$$(1 - \varepsilon)p_A(\hat{\varphi}, \Gamma_3[j]) \leq p_\mathcal{G}(\hat{\varphi}, \Gamma_3[j]) \leq (1 + \varepsilon)p_A(\hat{\varphi}, \Gamma_3[j]).$$

Thus we have,

$$E[\mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_1)] = p_\mathcal{G}(\hat{\varphi}, S, \sigma_1) \leq (1 + \varepsilon)p_A(\hat{\varphi}, S, \sigma_1)$$

Now, since $p_A(\hat{\varphi}, S, \sigma_1) = \frac{p_A(\varphi, S, \sigma_1)}{p_A(\varphi, S, \sigma_1) + p_A(\varphi, S, \sigma_2)}$ we have

$$E[\mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_1)] = p_\mathcal{G}(\hat{\varphi}, S, \sigma_1) \leq \frac{(1 + \varepsilon)p_A(\varphi, S, \sigma_1)}{p_A(\varphi, S, \sigma_1) + p_A(\varphi, S, \sigma_2)} \quad (1)$$

Similarly, we have that

$$E[\mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_2)] = p_\mathcal{G}(\hat{\varphi}, S, \sigma_2) \geq \frac{(1 - \varepsilon)p_A(\varphi, S, \sigma_2)}{p_A(\varphi, S, \sigma_1) + p_A(\varphi, S, \sigma_2)} \quad (2)$$

Now we consider two cases depending on whether $p_A(\varphi, S, \sigma_1)$ is greater or lesser than $p_A(\varphi, S, \sigma_2)$. If $p_A(\varphi, S, \sigma_1) \leq p_A(\varphi, S, \sigma_2)$ then from Equation 1 we have

$$E[\mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_1)] = p_A(\hat{\varphi}, S, \sigma_1)$$

$$\leq \frac{(1 + \varepsilon)p_A(\varphi, S, \sigma_1)}{p_A(\varphi, S, \sigma_1) + p_A(\varphi, S, \sigma_2)}$$

$$\leq \frac{(1 + \varepsilon)p_A(\varphi, S, \sigma_1)}{(1 + \varepsilon)p_A(\varphi, S, \sigma_1) + (1 - \varepsilon)p_A(\varphi, S, \sigma_2)} = L \quad (3)$$

But if $p_A(\varphi, S, \sigma_1) \geq p_A(\varphi, S, \sigma_2)$ then from Equation 1 we have

$$E[\mathbb{I}(\Gamma_3[j] \downarrow S = \sigma_2)] = p_A(\hat{\varphi}, S, \sigma_2)$$

$$\geq \frac{(1 - \varepsilon)p_A(\varphi, S, \sigma_2)}{p_A(\varphi, S, \sigma_1) + p_A(\varphi, S, \sigma_2)}$$

$$\geq \frac{(1 - \varepsilon)p_A(\varphi, S, \sigma_2)}{(1 + \varepsilon)p_A(\varphi, S, \sigma_1) + (1 - \varepsilon)p_A(\varphi, S, \sigma_2)}$$
And in that case since \( p_A(\hat{\varphi}, S, \sigma_1) + p_A(\hat{\varphi}, S, \sigma_2) = 1 \) we have

\[
E[\mathbb{1}(\Gamma_3[j]_4S = \sigma_1)] = p_A(\hat{\varphi}, S, \sigma_1)
= 1 - p_A(\hat{\varphi}, S, \sigma_2)
\leq 1 - \left(1 - \frac{(1 - \varepsilon)p_A(\varphi, S, \sigma_2) + (1 - \varepsilon)p_A(\varphi, S, \sigma_2)}{1 + \varepsilon} \right)
\leq \frac{(1 + \varepsilon)p_A(\varphi, S, \sigma_1) + (1 - \varepsilon)p_A(\varphi, S, \sigma_2)}{1 + \varepsilon} = L \tag{4}
\]

Thus in either case, from Equation (3) and Equation (4) we have \( E[\mathbb{1}(\Gamma_3[j]_4S = \sigma_1)] \leq L \). Now applying the Chernoff bound from Lemma 5 we have

\[
\Pr[\text{Bias} \geq T] = \Pr \left[ \sum_{j \in [N]} \frac{\mathbb{1}(\Gamma_3[j]_4S = \sigma_1)}{N} > T \right]
= \exp \left( - \frac{(T - L)^2N}{2L} \right) = \exp \left( - \frac{(H - L)^2N}{8L} \right)
\leq \exp \left( - \frac{(H - L)^2N}{8H} \right) \quad \text{Because } [H \geq L] \tag{5}
\]

\[
\leq \frac{\delta}{t}, \tag{6}
\]

where the inequality in line (5) follows because \( H \geq L \) when \( \varepsilon \leq 1/3 \) and \( \eta \geq 6\varepsilon^5 \) and last inequality follows because \( N = n.H/(H - L)^2 \) where \( n = 8 \log(t/\delta) \).

\textbf{Proof.} (of Lemma 2) Let \( R_i \) denote the event that Barbarik2 returns REJECT in iteration \( i \) and \( \overline{R} \) denote the event that Barbarik2 returns ACCEPT. Thus \( \overline{R} = \bigcap_i \overline{R}_i \).

In the \( i^{th} \) iteration if the bias is less than the threshold, Barbarik2 fails to REJECT. Thus from Lemma 6 if the sampler \( \mathcal{G} \) is \( \varepsilon \)-close to the ideal sampler \( A \) then

\[
\Pr \left[ \overline{R}_i \bigcap \bigwedge_{j \in [i-1]} \overline{R}_j \right] \geq 1 - \frac{\delta}{t}
\]

If Barbarik2 has not returned REJECT in any of the iteration then after the last iteration Barbarik2 returns ACCEPT. The probability of Barbarik2 returning ACCEPT (event \( \overline{R} \)) is

\[
\Pr[\overline{R}] \geq \prod_{i \in [t]} \Pr \left[ \overline{R}_i \bigcap \bigwedge_{j \in [i-1]} \overline{R}_j \right] \geq \left( 1 - \frac{\delta}{t} \right)^t \geq 1 - \delta
\]

\( \square \)

\textbf{B.2 Proof of Lemma 3}

\textbf{Lemma 3.} If \( \mathcal{G} \) is subquery consistent w.r.t Barbarik2Kernel and if the distribution \( D_{\mathcal{G}(\varphi)} \) is \( \eta \)-far from the ideal sampler then Barbarik2 returns REJECT with probability at least \( (1 - \delta) \).

\textbf{Proof.} To prove the Lemma, we will start by splitting the set \( R_\varphi \) into disjoint subsets depending on the distribution \( D_{\mathcal{G}(\varphi)} \).

\textbf{Definition 10.} We define the following sets for use in the soundness proof:

\[
\bullet \ D = \{ x \in R_\varphi : p_\mathcal{G}(\varphi, x) \leq p_A(\varphi, x) \}
\]

\( \hat{H} \geq L \text{ if } h \geq \hat{t} \text{ that is } (6\varepsilon + \eta)/4 \geq (2\varepsilon)/(1 - \varepsilon) \)

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• $U = R_\varphi \setminus D$
• $U_0 = \{x \in R_\varphi : p_A(\varphi, x) < p_\varphi(\varphi, x) \leq (1 + \frac{\eta + 6\varepsilon}{4}) p_A(\varphi, x)\}$
• $U_1 = \{x \in R_\varphi : (1 + \frac{\eta + 6\varepsilon}{4}) p_A(\varphi, x) < p_\varphi(\varphi, x)\}$

Recall, $R_i$ is the event that Barbarik2 returns REJECT in the $i$th iteration of the for loop. Then the following lemmas helps us to lower bound the probability of $\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D$ and the probability of $R_i$ under the condition that $\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D$.

**Lemma 7.** If the sampler $G$ is $\eta$-far from the ideal sampler then

$$\Pr \left[ R_i \mid (\bigwedge_{j \in [i-1]} R_j) \land (\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D) \right] \geq \frac{4}{5}.$$  

**Lemma 8.** If the sampler $G$ is $\eta$-far from the ideal sampler on input $\varphi$ then

$$\Pr [\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D] \geq \frac{\eta(\eta - 6\varepsilon)}{8}.$$  

And now using Lemmas 8 and 7 we can complete the proof of soundness. The probability that Barbarik2 returns REJECT in the $i$th iteration of the for loop is

$$\Pr \left[ R_i \mid (\bigwedge_{j \in [i-1]} \overline{R}_j) \land (\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D) \right] \cdot \Pr [\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D] \geq \frac{4}{5} \frac{\eta(\eta - 6\varepsilon)}{8} \quad \text{[From Lemma 8 and Lemma 7]}$$

(7)

The probability of Barbarik2 returning REJECT in any iteration (event $R$) is given by

$$\Pr [\bigcup_i R_i] = 1 - \prod_{i \in [t]} \Pr \left[ \overline{R}_i \mid (\bigwedge_{j \in [i-1]} \overline{R}_j) \right] \geq 1 - \prod_{i \in [t]} \left(1 - \frac{\eta(\eta - 6\varepsilon)}{10}\right) \quad \text{[Using Equation (7)]}$$

$$\geq 1 - \left(1 - \frac{\eta(\eta - 6\varepsilon)}{10}\right)^t$$

Substituting $t, \quad \geq 1 - \delta$  

Now to complete the proof of Lemma 3 we have to prove the Lemma 7 and Lemma 8. They are presented next.

**Lemma 7.** If the sampler $G$ is $\eta$-far from the ideal sampler then

$$\Pr \left[ R_i \mid (\bigwedge_{j \in [i-1]} \overline{R}_j) \land (\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D) \right] \geq \frac{4}{5}.$$  

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Proof. (of Lemma 7) Let us assume \( \Gamma_1[i] \in U_1 \) and \( \Gamma_2[i] \in D \). That is, we have \( p_G(\varphi, S, \Gamma_2[i]) \leq p_A(\varphi, S, \Gamma_2[i]) \) and \( p_G(\varphi, S, \Gamma_1[i]) > (1 + \frac{a}{b} \frac{\epsilon}{n}) p_A(\varphi, S, \Gamma_1[i]) \). It follows that

\[
\frac{p_G(\varphi, S, \Gamma_1[i])}{p_G(\varphi, S, \Gamma_2[i])} \geq \left( 1 + \frac{6\epsilon + \eta}{4} \right) \frac{p_A(\varphi, S, \Gamma_1[i])}{p_A(\varphi, S, \Gamma_2[i])}.
\]

Since \( x > 0, a/b > x \implies a/(a + b) > x/(x + 1) \), we have from Equation 8

\[
\frac{p_G(\varphi, S, \Gamma_1[i])}{p_G(\varphi, S, \Gamma_2[i]) + p_G(\varphi, S, \Gamma_1[i])} \geq \left( 1 + \frac{6\epsilon + \eta}{4} \right) \cdot \left( 1 + \frac{6\epsilon + \eta}{4} \right) \cdot \frac{p_A(\varphi, S, \Gamma_1[i])}{p_A(\varphi, S, \Gamma_2[i])}^{-1}.
\]

Thus we have

\[
E[1(\Gamma_3[j]_1S = \sigma_1)] = p_G(\varphi, S, \Gamma_1[i])
\]

\[
= \frac{p_G(\varphi, S, \Gamma_2[i]) + p_G(\varphi, S, \Gamma_1[i])}{p_G(\varphi, S, \Gamma_2[i])} \text{ [by subquery consistent sampler assumption]}
\]

\[
\geq \left( 1 + \frac{6\epsilon + \eta}{4} \right) \cdot \frac{p_A(\varphi, S, \Gamma_1[i])}{p_A(\varphi, S, \Gamma_2[i])} \cdot \left( 1 + \frac{6\epsilon + \eta}{4} \right) \cdot \frac{p_A(\varphi, S, \Gamma_1[i])}{p_A(\varphi, S, \Gamma_2[i])}^{-1}.
\]

\[
= H \text{ [By definition of } H]\]

Barbarik2 returns REJECT in the \( t \)th iteration if the Biases (in the \( t \)th iteration) is more than \( T \), where \( T = \frac{L + H}{2} \) with

\[
H = \frac{(1 + \frac{6\epsilon + \eta}{4})p_A(\varphi, S, \sigma_1)}{(1 + \frac{6\epsilon + \eta}{4})p_A(\varphi, S, \sigma_1) + p_A(\varphi, S, \sigma_2)}.
\]

And since, by definition, all the elements in \( \Gamma_1, \Gamma_2 \) and \( \Gamma_3 \) are obtained by drawing independent samples from \( D_{G(\varphi)} \), \( D_{A(\varphi)} \) and \( D_{G(\varphi)} \) respectively so

\[
\Pr \left[ R_i \mid (\bigwedge_{j \in [i-1]} \bar{R_j}) \wedge (\Gamma_1[i] \in U_1 \wedge \Gamma_2[i] \in D) \right]
\]

\[
= \Pr [Bias > T \text{ in the } t \text{th iteration} \mid (\Gamma_1[i] \in U_1 \wedge \Gamma_2[i] \in D)]
\]

\[
= \Pr \left[ \sum_{j \in [N]} \frac{1(\Gamma_3[j]_1S = \sigma_1)}{N} \geq T \mid (\Gamma_1[i] \in U_1 \wedge \Gamma_2[i] \in D) \right]
\]

Now since \( \frac{1(\Gamma_3[j]_1S = \sigma_1)}{N} \) are i.i.d 0-1 random variables and since \( \Gamma_1[i] \in U_1 \) and \( \Gamma_2[i] \in D \) implies \( E[1(\Gamma_3[j]_1S = \sigma_1)] \geq H \) (from Equation 9) by applying Chernoff bound from Lemma 5 we have:

\[
\Pr \left[ \frac{1}{N} \sum_{j \in [N]} \frac{1(\Gamma_3[j]_1S = \sigma_1)}{N} \geq T \right] \leq \exp \left( -\frac{(H - T)^2N}{8H} \right)
\]

by the choice of \( N \leq \frac{\delta}{t} \)

since \( \delta < 0.5 \) and \( t \geq 3 \leq 1/5 \)

\[\square\]

**Lemma 8.** If the sampler \( G \) is \( \eta \)-far from the ideal sampler on input \( \varphi \) then

\[
\Pr [\Gamma_1[i] \in U_1 \wedge \Gamma_2[i] \in D] \geq \frac{\eta(\eta - 6\epsilon)}{8}.
\]

Proof. of Lemma 8) Since the sampler \( G \) is \( \epsilon \)-far from the ideal sampler on input \( \varphi \) so, the \( \ell_1 \) distance between \( D_G(\varphi) \) and \( D_A(\varphi) \) is at least \( \eta \). By the definition of sets \( U \) and \( D \) we have,

\[
\sum_{x \in U} (p_G(\varphi, x) - p_A(\varphi, x)) = \sum_{x \in D} (p_A(\varphi, x) - p_G(\varphi, x)) \geq \frac{\eta}{2} \tag{10}
\]
Now by definition of $U_0$, we have
\[ \sum_{x \in U_0} (p_G(\varphi, x) - p_A(\varphi, x)) < \frac{\eta + 6\varepsilon}{4} \sum_{x \in U_0} p_A(\varphi, x) < \frac{\eta + 6\varepsilon}{4} \] (11)

As $U = U_0 \cup U_1$,
\[ \sum_{x \in U_1} (p_G(\varphi, x) - p_A(\varphi, x)) \]
\[ \quad = \sum_{x \in U} (p_G(\varphi, x) - p_A(\varphi, x)) - \sum_{x \in U_0} (p_G(\varphi, x) - p_A(\varphi, x)) \] (12)

Substituting Equation (11) and Equation (10) in Equation (12) we get:-
\[ \sum_{x \in U_1} (p_G(\varphi, x) - p_A(\varphi, x)) \geq \frac{\eta}{2} - \frac{\eta + 6\varepsilon}{4} = \frac{\eta - 6\varepsilon}{4} \]

Therefore, \[ \sum_{x \in U_1} p_G(\varphi, x) \geq \frac{\eta - 6\varepsilon}{4} \]

Thus we have,
\[ \Pr [\Gamma_1[i] \in U_1] = \sum_{x \in U_1} p_G(\varphi, x) \geq \frac{\eta - 6\varepsilon}{4} \] (13)

From Equation (10) we know that,
\[ \Pr [\Gamma_2[i] \in D] = \sum_{x \in D} p_A(\varphi, x) \geq \frac{\eta}{2} \] (14)

Since $\Gamma_1[i] \in U_1$ and $\Gamma_2[i] \in D$ are independent events, putting together Equation (13) and Equation (14), we see that
\[ \Pr [\Gamma_1[i] \in U_1 \land \Gamma_2[i] \in D] \geq \frac{\eta(\eta - 6\varepsilon)}{8} \]

\[ \square \]

B.3 Proof of Lemma 4

Lemma 4. Given $\varepsilon$, $\eta$ and $\delta$, Barbarik2 needs at most $\tilde{O}\left(\frac{\text{tilt}(\varphi)}{\eta(\eta - 6\varepsilon)}\right)^2$ samples for any input formula $\varphi$ and weight function $wt$, where the tilde hides a poly logarithmic factor of $1/\delta$, $1/\eta$ and $1/(\eta - 6\varepsilon)$.

Proof. From Algorithm 1, line 1, we see that the number of trials is:
\[ t = \frac{\ln(1/\delta)}{\ln(\frac{10}{10 - \eta(\eta - 6\varepsilon)})} \]
\[ (\ln(x) \leq x - 1) \quad t \leq \frac{\ln(1/\delta)}{\ln(\frac{10}{\eta(\eta - 6\varepsilon)})} \]

In every iteration we calculate a value $N$ according to the expression:
\[ N = 8\ln\left(\frac{t}{\delta}\right) \cdot \frac{\alpha \cdot hi}{1 + \alpha \cdot hi} \cdot \left(\frac{\alpha \cdot hi}{1 + \alpha \cdot hi} - \frac{\alpha \cdot lo}{1 + \alpha \cdot lo}\right)^{-2} \]
\[ = 8\ln\left(\frac{t}{\delta}\right) \cdot \left(\frac{1}{hi - lo}\right)^2 \cdot hi \cdot \frac{1 + \alpha \cdot hi}{\alpha} \cdot (1 + \alpha \cdot lo)^2 \]
\[ (1 < lo < hi < 2) \quad < 8\ln\left(\frac{t}{\delta}\right) \cdot \left(\frac{1}{hi - lo}\right)^2 \cdot 2 \cdot \frac{1 + \alpha \cdot 2}{\alpha} \cdot (1 + \alpha \cdot 2)^2 \]
On Line (11) in Algorithm 1 we define:
\[
\alpha = \frac{\text{wt}(\sigma_1)}{\text{wt}(\sigma_2)}
\]
(Definition 4) \(\tilde{\text{tilt}}(\text{wt}, \varphi) = \max_{\sigma_1, \sigma_2 \in R_\varphi} \frac{\text{wt}(\sigma_1)}{\text{wt}(\sigma_2)}\)

Thus, \(\alpha \leq \tilde{\text{tilt}}(\text{wt}, \varphi)\). Substituting the values of \(\alpha\), \(lo\) and \(hi\), we get:
\[
N < 8\ln \left(\frac{t}{\delta}\right) \cdot \left(\frac{\tilde{\text{tilt}}(\text{wt}, \varphi)}{\eta - 6\varepsilon}\right)^2
\]

The maximum number of samples drawn after \(t\) trials is:
\[
2t + tN < 2tN
\]
(Substituting for \(t, N\))
\[
< 8\ln \left(\frac{1}{\delta} \cdot \frac{10 \cdot \ln(1/\delta)}{\eta(\eta - 6\varepsilon)}\right) \times \frac{10 \cdot \ln(1/\delta)}{\eta(\eta - 6\varepsilon)} \times \frac{\tilde{\text{tilt}}(\text{wt}, \varphi)^2}{(\eta - 6\varepsilon)^2}
\]
\[
= \tilde{O} \left(\frac{\tilde{\text{tilt}}(\text{wt}, \varphi)^2}{(\eta - 6\varepsilon)^2}\right)
\]
\(\square\)

C Log-Linear Distributions and Inverse Transform Sampling

Log-linear models capture wide class of distributions of interest including those arising from graphical models, conditional random fields, skip-gram models [34]. Formally, for \(\sigma \in \{0, 1\}^n\), we define
\[
\Pr[\sigma | \theta] \propto e^{\theta \cdot \sigma}
\]

Following Chavira and Darwiche [16], we describe the following equivalent representation, called literal-weighted functions, of log-linear models.

**Definition 11 (Literal-Weighted Functions).** For a CNF formula \(\varphi\) and set \(S \subseteq \text{Supp}(\varphi)\), a weight function \(\text{wt} : \{0, 1\}^{\lvert S \rvert} \rightarrow (0, 1)\) is called a literal-weighted function if there is a map \(\hat{\varphi} : S \rightarrow (0, 1)\) such that for any assignment \(\sigma \in R_{\varphi,S}\)
\[
\text{wt}(\sigma) = \prod_{x \in \sigma} \hat{\varphi}(x) \quad \text{if} \quad x = 1
\]
\[
\text{wt}(\sigma) = \prod_{x \in \sigma} (1 - \hat{\varphi}(x)) \quad \text{if} \quad x = 0
\]

In this case we call \(\text{wt}\) a literal-weighted function w.r.t. \(\hat{\varphi}\). And note that we have \(\Pr[\sigma | \theta] \propto \text{wt}(\sigma)\).

We now discuss the standard technique of inverse transform sampling for completeness. For completeness, we follow the description due to Chakraborty et al [15].

**Lemma 9.** For any \(\varepsilon\)-close uniform sampler \(V\), any CNF formula \(\varphi\) with support \(S\) and a literal-weighted function \(\text{wt} : \{0, 1\}^{\lvert S \rvert} \rightarrow (0, 1)\), we can construct a \(\hat{\varphi}\) s.t.
\[
\forall_{\sigma \in R_{\varphi}}, \frac{(1 - \varepsilon)\text{wt}(\sigma)}{\sum_{\sigma' \in R_{\varphi}} \text{wt}(\sigma')} \leq p_V(\hat{\varphi}, S, \sigma) \leq \frac{(1 + \varepsilon)\text{wt}(\sigma)}{\sum_{\sigma' \in R_{\varphi}} \text{wt}(\sigma')}
\]

**Proof.** Let \(S_i = \{x_{i,1}, \ldots, x_{i,m_i}\}\) be a set of \(m_i\) “fresh” variables (i.e. variables that were not used before) for each \(x_i \in S\). Given any integer \(m_i > 0\) and a positive odd number \(k_i < 2^{m_i}\), we construct \(\varphi_{k_i,m_i}(x_{i,1}, \ldots, x_{i,m_i})\) using the chain formula construction in [15] such that \(\lvert R_{\varphi_{k_i,m_i}} \rvert = k\). For notational clarity, we simply write \(\varphi_{k_i,m_i}\) when the arguments of the chain formula are clear from context. For each variable \(x_i \in S\), such that \(\hat{\varphi}(x_i^1) = \frac{1}{2^{m_i}}\) and \(\hat{\varphi}(x_i^0) = 1 - \hat{\varphi}(x_i)\), let \((x_i \leftrightarrow \varphi_{k_i,m_i})\) be the representative clause. Thus let \(\varphi^{\text{CNF}} = \bigwedge_{i \in S}(x_i \leftrightarrow \varphi_{k_i,m_i})\). We then define the formula \(\hat{\varphi}\) as follows:
\[
\hat{\varphi} = \varphi \land \varphi^{\text{CNF}}
\]
We can see that model count of the formula $|R_{\hat{\varphi}}|$ can be given by:

$$|R_{\hat{\varphi}}| = \sum_{\hat{\sigma} \in R_{\hat{\varphi}}} 1 = \sum_{\sigma \in R_{\varphi}} \sum_{\hat{\sigma} \in R_{\hat{\varphi}}: \hat{\sigma} = \sigma} 1 \quad (15)$$

Since the representative formula of every variable uses a fresh set of variables, we have from the structure of $\hat{\varphi}$ that if $\sigma$ is a witness of $\varphi$ then:

$$\sum_{(\hat{\sigma} \in R_{\hat{\varphi}}: \hat{\sigma} = \sigma)} 1 = \prod_{i \in \sigma_1} (2^{m_i} - k_i) \prod_{i \in \sigma_1} k_i \quad (16)$$

For any $\sigma \in R_{\varphi}$:

$$p_V(\hat{\varphi}, S, \sigma) = \sum_{(\hat{\sigma} \in R_{\hat{\varphi}}: \hat{\sigma} = \sigma)} 1 = \sum_{(\hat{\sigma} \in R_{\hat{\varphi}}: \hat{\sigma} = \sigma)} \frac{1}{|R_{\hat{\varphi}}|} \quad (17)$$

Using (15),

$$= \frac{\sum_{\sigma' \in R_{\varphi}} \sum_{(\hat{\sigma} \in R_{\hat{\varphi}}: \hat{\sigma} = \sigma')} 1}{\prod_{i \in \sigma_0} (2^{m_i} - k_i) \prod_{i \in \sigma_1} k_i} \quad \text{Using (16)}$$

$$= \frac{\prod_{i \in \sigma_0} (2^{m_i} - k_i) \prod_{i \in \sigma_1} k_i}{\prod_{i \in S} 2^{m_i}} \frac{\prod_{i \in \sigma_0} (2^{m_i} - k_i) \prod_{i \in \sigma_1} k_i}{\prod_{i \in S} 2^{m_i}} \frac{\sum_{\sigma' \in R_{\hat{\varphi}}} \sum_{(\hat{\sigma} \in R_{\hat{\varphi}}: \hat{\sigma} = \sigma')} \frac{1}{|R_{\hat{\varphi}}|}}{\sum_{\sigma' \in R_{\varphi}} \frac{1}{|R_{\varphi}|}}$$

From the definition of $\varepsilon$-additive closeness (Def. 5) we have:

$$(1 - \varepsilon)p_V(\varphi, S, \sigma) \leq p_V(\varphi, S, \sigma) \leq (1 + \varepsilon)p_V(\varphi, S, \sigma)$$

Substituting into 17, we get:

$$\forall \sigma \in R_{\varphi}, \frac{(1 - \varepsilon)\frac{1}{|R_{\varphi}|}}{\sum_{\sigma' \in R_{\varphi}} \frac{1}{|R_{\varphi}|}} \frac{1}{|R_{\varphi}|} \leq p_V(\hat{\varphi}, S, \sigma) \leq \frac{(1 + \varepsilon)\frac{1}{|R_{\varphi}|}}{\sum_{\sigma' \in R_{\varphi}} \frac{1}{|R_{\varphi}|}} \frac{1}{|R_{\varphi}|}$$

Remark 1. It is worth noting that Lemma 9 implies that if $\mathcal{V}$ is $\varepsilon$-close uniform sampler $\mathcal{V}$ then it can be used as a blackbox to obtain a $\varepsilon$-close to an ideal sampler w.r.t any literal-weighted function wt. It should also be noted that Lemma 9 does not imply that if $\mathcal{V}$ is $\eta$-close from a uniform sampler, then the new sampler (obtained using the above transformation) is also $\varepsilon$-close from the ideal sampler w.r.t wt. Therefore, to test whether $p_V(\hat{\varphi}, S, \sigma)$ is close to ideal sampler, one can not rely on merely testing uniformity of $\mathcal{V}$.

D Extended Tables of Results

D.1 Comparing sample complexity.

“A” (“R”) represent Barbarik2 returning ACCEPT(REJECT). “DNS” is used against those instances on which the indicated sampler Did Not Sample. “-” indicates that Barbarik2 timed out on that particular instance on the indicated sampler. Note that “DNS” is different from “-” as “DNS” indicates the failure of the underlying sampler to sample the initial set of samples, while “-” indicates the failure of Barbarik2 to finish within the timeout period. The timeout was set to 50,000 seconds for wSTS and wQuicksampler, while for wUniGen it was 24 hours.
Table 2: The Extended Table

| Benchmark          | $t_{ill}$ (maxSamp) | wUniGen (samples) | wSTS (samples) | wQuicksampler (samples) |
|--------------------|---------------------|-------------------|----------------|-------------------------|
| 107.sk_3_90        | $\frac{1}{2e+05}$  | DNS R (5146)      | DNS R (6009)   |                         |
| tableBasedAddition.sk | $\frac{1}{2e+05}$  | DNS R (6009)      | DNS R (24534)  |                         |
| 55.sk_3_46         | $\frac{1}{2e+05}$  | DNS R (8911)      | DNS R (4354)   |                         |
| 111.sk_2_36        | $\frac{1}{2e+05}$  | DNS R (23543)     | DNS R (5150)   |                         |
| 17.sk_3_45         | $\frac{1}{2e+05}$  | DNS R (1e+05)     | DNS R (4677)   |                         |
| 80.sk_2_48         | $\frac{1}{2e+05}$  | DNS R (4284)      | DNS R (4627)   |                         |
| 27.sk_3_32         | $\frac{1}{2e+05}$  | A R (25329)       | DNS R (6009)   |                         |
| 70.sk_3_40         | $\frac{1}{2e+05}$  | A R (10402)       | DNS R (17704)  |                         |
| 32.sk_4_38         | $\frac{1}{2e+05}$  | A R (18081)       | DNS R (14682)  |                         |
| 84.sk_4_77         | $\frac{1}{2e+05}$  | DNS R (5146)      | DNS R (4354)   |                         |
| 53.sk_4_32         | $\frac{1}{2e+05}$  | A R (35618)       | A R (6009)     |                         |
| s35932_3_2         | 3 (6e+05)           | DNS TO R (11756)  |                     |                         |
| s35932_7_4         | 3 (6e+05)           | DNS TO R (11756)  |                     |                         |
| s832a_3_2          | 3 (6e+05)           | A R (8708)        | A R (54138)     |                         |
| 109.sk_4_36        | 8 (3e+06)           | A R (26218)       | A R (6009)      |                         |
| 77.sk_3_44         | 11 (5e+06)          | DNS R (47582)     | DNS R (47907)   |                         |
| s35932_15_7        | 12 (6e+06)          | DNS TO R (4354)   |                     |                         |
| s832a_7_4          | 15 (8e+06)          | A R (4393)        | A R (13350)     |                         |
| 51.sk_4_38         | 18 (1e+07)          | A R (78661)       | A R (4627)      |                         |
| 29.sk_3_45         | 26 (2e+07)          | DNS R (4284)      | DNS R (55989)   |                         |
| 81.sk_5_51         | 27 (3e+07)          | DNS R (28409)     | A R (2e+05)     |                         |
| s349_3_2           | 28 (3e+07)          | A R (1e+05)       | A R (22854)     |                         |

continued...
| Benchmark            | tilt (maxSamp) | wUniGen (samples) | wSTS (samples) | wQuickSampler (samples) |
|----------------------|---------------|-------------------|----------------|--------------------------|
| s298_3_2             | 32 (3e+07)    | A (1e+05)         | R (80883)      | R (26491)                |
| s820a_3_2            | 37 (5e+07)    | A (96212)         | R (87997)      | A (2e+05)                |
| s298_15_7            | 44 (6e+07)    | A (1e+05)         | R (42520)      | R (53107)                |
| 63.sk_3_64           | 58 (1e+08)    | DNS               | R (4393)       | R (4677)                 |
| s820a_15_7           | 79 (2e+08)    | A (84310)         | R (2e+05)      | R (16714)                |
| s1488_15_7           | 110 (4e+08)   | A (86152)         | R (17168)      | R (7341)                 |
| s1488_3_2            | 132 (6e+08)   | A (89686)         | R (89236)      | R (7341)                 |
| s382_15_7            | 138 (6e+08)   | A (92159)         | R (2e+05)      | R (6009)                 |
| UserServiceImpl.sk_8_32 | 140 (6e+08)  | A (95566)         | R (1e+05)      | R (4393)                 |
| 20.sk_1_51           | 144 (7e+08)   | DNS               | R (30895)      | R (5146)                 |
| s820a_7_4            | 167 (9e+08)   | A (96984)         | A (1e+05)      | R (6009)                 |
| s832a_15_7           | 194 (1e+09)   | A (90183)         | R (9434)       | R (13350)                |
| s1488_7_4            | 206 (1e+09)   | A (95566)         | R (4677)       | R (4627)                 |
| s344_15_7            | 218 (2e+09)   | A (96984)         | R (94481)      | R (4354)                 |
| LoginService2.sk_23_36 | 232 (2e+09)  | A (1e+05)         | R (38044)      | R (13350)                |
| s420_new1_15_7       | 265 (2e+09)   | DNS               | R (19224)      | A (3e+05)                |
| s349_15_7            | 412 (5e+09)   | A (99215)         | R (28400)      | R (14682)                |
| s444_15_7            | 501 (8e+09)   | A (1e+05)         | A (1e+05)      | R (26627)                |
| s349_7_4             | 603 (1e+10)   | A (75555)         | R (4284)       | R (5150)                 |
| s444_7_4             | 644 (1e+10)   | DNS               | R (4393)       | R (4354)                 |
| s420_new1_7_4        | 982 (3e+10)   | A (1e+05)         | R (4354)       | R (18473)                |
| s298_7_4             | 986 (3e+10)   | A (83681)         | R (8638)       | R (6009)                 |
| s420_new1_3_2        | 1226 (5e+10)  | DNS               | A (1e+05)      | R (5150)                 |

continued...
| Benchmark     | \( t\text{ilt} \) (maxSamp) | wUniGen (samples) | wSTS (samples) | wQuicksampler (samples) |
|---------------|---------------------------|------------------|---------------|------------------------|
| s382_7_4      | 1283 (5e+10)              | A (92307)        | R (26491)     | R (7341)               |
| s420_3_2      | 1552 (8e+10)              | A (1e+05)        | R (14756)     | R (48983)              |
| s1238a_7_4    | 1856 (1e+11)              | A (95095)        | R (5150)      | R (7341)               |
| s1238a_3_2    | 1965 (1e+11)              | A (1e+05)        | R (28848)     | R (4627)               |
| s444_3_2      | 2028 (1e+11)              | A (1e+05)        | R (2e+05)     | R (9500)               |
| s1238a_15_7   | 2317 (2e+11)              | DNS              | R (9020)      | R (88233)              |
| s420_new_15_7 | 2317 (2e+11)              | A (99198)        | R (1e+05)     | R (4393)               |
| 30.sk_5_76    | 2453 (2e+11)              | DNS              | R (5216)      | R (4677)               |
| s344_7_4      | 2607 (2e+11)              | A (1e+05)        | R (14170)     | R (16818)              |
| s344_3_2      | 3300 (3e+11)              | A (1e+05)        | R (59952)     | R (5150)               |
| s420_new_7_4  | 3549 (4e+11)              | A (82312)        | A (96659)     | R (49955)              |
| s953a_7_4     | 8984 (3e+12)              | DNS              | A (2e+05)     | R (4627)               |
| s953a_15_7    | 10596 (4e+12)             | DNS              | R (11734)     | R (59735)              |
| 10.sk_1_46    | 15268 (7e+12)             | DNS              | R (35179)     | R (1e+05)              |
| s420_new_3_2  | 17449 (1e+13)             | A (1e+05)        | R (44937)     | R (5150)               |
| 19.sk_3_48    | 18253 (1e+13)             | DNS              | R (59014)     | R (4627)               |
| s953a_3_2     | 20860 (1e+13)             | DNS              | R (51161)     | R (1e+05)              |
| s641_3_2      | 1e+06 (5e+16)             | DNS              | R (14454)     | R (4627)               |
| ProjectService3.sk_12_55 | 5e+06 (7e+17) | DNS | R (9020) | R (4393) |
| 71.sk_3_65    | 1e+07 (3e+18)             | DNS              | R (1e+05)     | R (4284)               |
| s838_7_4      | 1e+07 (5e+18)             | DNS              | R (4393)      | R (4284)               |
| s838_15_7     | 3e+07 (3e+19)             | DNS              | R (5150)      | R (4393)               |
| s713_3_2      | 6e+07 (1e+20)             | DNS              | R (56386)     | R (5827)               |

continued...
| Benchmark   | $tilt$ (maxSamp) | Barbarik2 | wUniGen (samples) | wSTS (samples) | wQuicksampler (samples) |
|-------------|------------------|-----------|-------------------|----------------|------------------------|
| s713_7_4    | 6e+07 (1e+20)   | DNS       | R (5827)          | R (37419)      |
| s641_7_4    | 9e+07 (3e+20)   | DNS       | R (8747)          | A (1e+06)      |
| s838_3_2    | 2e+08 (1e+21)   | DNS       | R (9504)          | R (4627)       |
| 54.sk_12_97 | 4e+11 (6e+27)   | DNS       | R (14012)         | R (4627)       |
D.2 Comparing the runtime performance of Barbarik2 against the baseline approach

In each of the following tables we compare the runtime of Barbarik2 against the runtime of the baseline approach. The runtime of Barbarik2 on REJECT instances depends on which iteration the tester terminated on. The runtime of the baseline is extrapolated from the expected number of samples and the average sampling rate of the sampler. To do this we use the $\ell_1$-testing algorithm given in [4]. In the context of this paper, the algorithm assumes black box sample access to a uniform sampler over the models of a Boolean formula $\varphi$, and the sampler under test, and requires $O(\#\varphi^{2/3}(\eta - \varepsilon)^{-8/3} \log(\#\varphi/\delta))$ samples, where $\#\varphi$ is the model count, $(\varepsilon, \eta)$ are the closeness and farness parameters, and $\delta$ is the confidence parameter.

D.2.1 Comparision with baseline for wSTS

Table 3: Extended table comparing the baseline tester for wSTS with Barbarik2

| Benchmark   | Baseline       | Barbarik2(s) | Speedup |
|-------------|----------------|--------------|---------|
| s349_7_4    | 16457.21       | 5            | 3428.58 |
| s420_new1_7_4 | 5.4E+6      | 6            | 8.6E+5  |
| s298_7_4    | 705.13         | 8            | 94.02   |
| s444_7_4    | 1.1E+7         | 8            | 1.3E+6  |
| s832a_7_4   | 3725.35        | 10           | 372.53  |
| s1488_7_4   | 184.99         | 12           | 15.16   |
| s344_7_4    | 24751.45       | 15           | 1683.77 |
| s420_3_2    | 2.2E+6         | 17           | 1.3E+5  |
| s1238a_7_4  | 1.4E+6         | 20           | 66538.64|
| s832a_3_2   | 2149.58        | 22           | 98.60   |
| s832a_15_7  | 15121.66       | 24           | 622.29  |
| s838_15_7   | 2.9E+13        | 27           | 1.1E+12 |
| s349_15_7   | 16457.21       | 28           | 587.76  |
| s838_7_4    | 3.7E+13        | 29           | 1.3E+12 |
| s382_7_4    | 14915.27       | 32           | 469.03  |
| s298_15_7   | 384.62         | 32           | 12.09   |
| s420_new1_15_7 | 4.1E+6      | 33           | 1.3E+5  |
| 27.sk_3_32  | 79531.43       | 34           | 2346.06 |
| s1238a_15_7 | 1.8E+6         | 37           | 49906.05|
| 111.sk_2_36 | 2.9E+8         | 42           | 6.8E+6  |
| 51.sk_4_38  | 2.0E+6         | 44           | 45904.52|
| 80.sk_2_48  | 6.0E+7         | 46           | 1.3E+6  |
| s1488_15_7  | 128.69         | 48           | 2.67    |
| s953a_15_7  | 1.1E+9         | 49           | 2.2E+7  |
| s344_3_2    | 15750.92       | 51           | 309.45  |
| s298_3_2    | 229.07         | 52           | 4.42    |
| s838_3_2    | 2.7E+13        | 57           | 4.8E+11 |
| s420_new_3_2 | 2.9E+6      | 65           | 44288.35|
| 84.sk_4_77  | 3.4E+13        | 68           | 5.0E+11 |
| 65.sk_3_46  | 4.1E+10        | 70           | 5.9E+8  |
| s349_3_2    | 30563.39       | 73           | 416.96  |
| 107.sk_3_90 | 1.7E+13        | 86           | 1.9E+13 |
| s1238a_3_2  | 2.2E+6         | 87           | 25824.41|
| s344_15_7   | 24751.45       | 91           | 271.10  |
| 32.sk_4_38  | 5.8E+5         | 94           | 6228.23 |
| 10.sk_1_46  | 6.5E+7         | 112          | 5.8E+5  |
| 29.sk_3_45  | 2.2E+8         | 150          | 1.5E+6  |
| s420_new_7_4 | 4.1E+6      | 152          | 27272.30|
| s1488_3_2   | 52.52          | 163          | 0.32    |
| s953a_3_2   | 6.4E+8         | 165          | 3.9E+6  |
Table 3: Extended table comparing the baseline tester for wSTS with Barbarik2

| Benchmark                        | Baseline | Barbarik2(s) | Speedup   |
|----------------------------------|----------|--------------|-----------|
| s420_new_15_7                    | 4.5E+6   | 186          | 24014.34  |
| 70.sk_3_40                       | 2.9E+6   | 201          | 14544.89  |
| s444_15_7                        | 13470.05 | 202          | 66.82     |
| s420_new1_3_2                    | 2.6E+6   | 211          | 12084.36  |
| s820a_3_2                        | 2189.81  | 221          | 9.91      |
| s444_3_2                         | 11186.45 | 247          | 45.22     |
| s713_3_2                         | 8.8E+10  | 255          | 3.5E+8    |
| 109.sk_4_36                      | 6.6E+5   | 269          | 2459.36   |
| s820a_7_4                        | 4240.22  | 277          | 15.33     |
| s63.sk_3_64                      | 5.8E+11  | 282          | 2.1E+9    |
| s641_7_4                         | 8.2E+10  | 311          | 2.6E+8    |
| s382_15_7                        | 33182.79 | 343          | 96.86     |
| s820a_15_7                       | 4154.77  | 370          | 11.23     |
| ProjectService3.sk_12_55         | 1.3E+10  | 458          | 2.9E+7    |
| s35932_3_2                       | 3.6E+2   | TO           | -         |
| s35932_7_4                       | 3.6E+2   | TO           | -         |
| s35932_15_7                      | 3.6E+2   | TO           | -         |
| s953a_7_4                        | 5.7E+8   | 689          | 8.3E+5    |
| UserServiceImpl.sk_8_32          | 479.33   | 720          | 0.67      |
| s30.sk_5_76                      | 7.0E+14  | 1116         | 6.2E+11   |
| s77.sk_3_44                      | 5.3E+6   | 1687         | 3156.66   |
| tableBasedAddition.sk_240_1024  | 3.8E+14  | 1832         | 2.1E+11   |
| s81.sk_5_51                      | 5.0E+9   | 2099         | 2.4E+6    |
| LoginService2.sk_23_36           | 12951.33 | 2368         | 5.47      |
| 20.sk_1_51                       | 1.1E+10  | 2568         | 4.1E+6    |
| 19.sk_3_48                       | 3.1E+8   | 2760         | 1.1E+5    |
| 17.sk_3_45                       | 4.3E+7   | 3016         | 14948.13  |
| 71.sk_3_65                       | 4.7E+12  | 4365         | 1.1E+9    |
| s4.sk_12_97                      | 2.7E+18  | 4688         | 5.8E+14   |
Table 4: Extended table comparing the baseline tester for wQuicksampler with Barbarik2

| Benchmark       | Baseline (s) | Barbarik2(s) | Speedup |
|-----------------|--------------|--------------|---------|
| s344_3_2        | 24751.45     | 3            | 8534.98 |
| s344_15_7       | 24751.45     | 4            | 7071.84 |
| s349_7_4        | 28212.36     | 4            | 7624.96 |
| s298_7_4        | 512.82       | 4            | 119.26  |
| s420_new1_3_2   | 5.1E+6       | 4            | 1.2E+6  |
| s420_new_3_2    | 2.2E+6       | 4            | 5.1E+5  |
| s420_new_15_7   | 3.5E+6       | 4            | 7.8E+5  |
| s382_7_4        | 12429.39     | 5            | 2589.46 |
| s444_7_4        | 51980.83     | 5            | 10192.32|
| s820a_7_4       | 2283.19      | 5            | 430.79  |
| s1488_7_4       | 128.07       | 6            | 20.99   |
| s444_3_2        | 8700.57      | 6            | 1359.46 |
| s838_7_4        | 1.3E+13      | 7            | 1.8E+12 |
| s838a_3_2       | 4.8942.42    | 7            | 6.975.56|
| s1238a_3_2      | 1.6E+6       | 7            | 2.2E+5  |
| s953a_7_4       | 6.6E+8       | 8            | 8.8E+7  |
| s1488_3_2       | 65.65        | 8            | 8.31    |
| s838_3_2        | 1.9E+13      | 8            | 2.4E+12 |
| s1488_15_7      | 60.36        | 9            | 6.80    |
| s349_7_4        | 35265.44     | 9            | 3833.20 |
| s344_3_2        | 22501.32     | 9            | 2393.76 |
| s349_3_2        | 14016.18     | 10           | 1424.87 |
| s5.52_3_46      | 4.3E+7       | 10           | 4.3E+6  |
| s1238a_7_4      | 1.1E+6       | 11           | 97431.59|
| s298_3_2        | 534.49       | 11           | 46.89   |
| s832a_7_4       | 4139.28      | 12           | 344.94  |
| s1488_15_7      | 60.36        | 12           | 41613.34|
| s349_7_4        | 326.81       | 14           | 23.68   |
| s444_3_2        | 91761.04     | 15           | 1859.56 |
| s620a_15_7      | 56653.59     | 16           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 17           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 17           | 1011.79 |
| s832a_7_4       | 4139.28      | 18           | 344.94  |
| s1488_15_7      | 60.36        | 19           | 6.80    |
| s349_7_4        | 326.81       | 20           | 23.68   |
| s444_3_2        | 91761.04     | 21           | 1859.56 |
| s620a_15_7      | 56653.59     | 22           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 23           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 24           | 1011.79 |
| s832a_7_4       | 4139.28      | 25           | 344.94  |
| s1488_15_7      | 60.36        | 26           | 6.80    |
| s349_7_4        | 326.81       | 27           | 23.68   |
| s444_3_2        | 91761.04     | 28           | 1859.56 |
| s620a_15_7      | 56653.59     | 29           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 30           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 31           | 1011.79 |
| s832a_7_4       | 4139.28      | 32           | 344.94  |
| s1488_15_7      | 60.36        | 33           | 6.80    |
| s349_7_4        | 326.81       | 34           | 23.68   |
| s444_3_2        | 91761.04     | 35           | 1859.56 |
| s620a_15_7      | 56653.59     | 36           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 37           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 38           | 1011.79 |
| s832a_7_4       | 4139.28      | 39           | 344.94  |
| s1488_15_7      | 60.36        | 40           | 6.80    |
| s349_7_4        | 326.81       | 41           | 23.68   |
| s444_3_2        | 91761.04     | 42           | 1859.56 |
| s620a_15_7      | 56653.59     | 43           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 44           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 45           | 1011.79 |
| s832a_7_4       | 4139.28      | 46           | 344.94  |
| s1488_15_7      | 60.36        | 47           | 6.80    |
| s349_7_4        | 326.81       | 48           | 23.68   |
| s444_3_2        | 91761.04     | 49           | 1859.56 |
| s620a_15_7      | 56653.59     | 50           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 51           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 52           | 1011.79 |
| s832a_7_4       | 4139.28      | 53           | 344.94  |
| s1488_15_7      | 60.36        | 54           | 6.80    |
| s349_7_4        | 326.81       | 55           | 23.68   |
| s444_3_2        | 91761.04     | 56           | 1859.56 |
| s620a_15_7      | 56653.59     | 57           | 5595.55 |
| s420_new1_7_4   | 2.2E+6       | 58           | 1.2E+12 |
| s832a_15_7      | 13861.52     | 59           | 1011.79 |
| s832a_7_4       | 4139.28      | 60           | 344.94  |
Table 4: Extended table comparing the baseline tester for wQuicksampler with Barbarik2

| Benchmark                  | Baseline | Barbarik2(s) | Speedup |
|----------------------------|----------|--------------|---------|
| 20.sk_1_51                 | 4.0E+9   | 82           | 4.8E+7  |
| 70.sk_3_40                 | 4.3E+6   | 101          | 4247.10 |
| s1238a_15_7                | 1.0E+6   | 107          | 9614.31 |
| 10.sk_1_46                 | 7.1E+7   | 128          | 3.1E+6  |
| s953a_3_2                  | 3.4E+8   | 132          | 2.6E+6  |
| s820a_3_2                  | 1167.90  | 137          | 8.54    |
| 30.sk_5_76                 | 3.0E+14  | 210          | 1.4E+12 |
| ProjectService3.sk_12_55   | 6.4E+9   | 219          | 2.9E+7  |
| LoginService2.sk_23_36     | 12692.30 | 229          | 55.52   |
| s420_new1_15_7             | 5.2E+6   | 232          | 13726.91|
| 77.sk_3_44                 | 1.2E+7   | 409          | 30125.88|
| 29.sk_3_45                 | 1.3E+8   | 658          | 2.0E+5  |
| 54.sk_12_97                | 4.0E+17  | 690          | 5.8E+14 |
| s641_7_4                   | 6.8E+10  | 1117         | 6.1E+7  |
| s35932_15_7                | 1.4E+356 | 1182         | 1.2E+353|
| tableBasedAddition.sk_240_1024 | 3.0E+13 | 1430         | 2.1E+10 |
| s35932_7_4                 | 1.2E+356 | 2227         | 5.5E+352|
| s35932_3_2                 | 1.1E+356 | 2346         | 4.5E+352|
| 81.sk_5_51                 | 2.0E+9   | 2461         | 8.3E+5  |
### D.4 wUniGen

| Benchmark           | Baseline | Barbarik2(s) | Speedup |
|---------------------|----------|--------------|---------|
| s1488_3_2           | 229.78   | 6648         | 0.03    |
| s298_7_4            | 7564.11  | 10758        | 0.70    |
| s1488_15_7          | 643.45   | 11493        | 0.06    |
| s298_15_7           | 2948.72  | 12325        | 0.24    |
| s349_7_4            | 1.8E+06  | 12858        | 1.36    |
| s820a_15_7          | 48724.11 | 14070        | 3.46    |
| s344_15_7           | 3.8E+05  | 14074        | 27.18   |
| s1488_7_4           | 853.78   | 15049        | 0.06    |
| s820a_7_4           | 42728.33 | 16124        | 2.65    |
| s349_15_7           | 3.9E+05  | 17690        | 21.80   |
| s382_7_4            | 9.7E+05  | 21785        | 44.45   |
| s349_3_2            | 3.0E+05  | 22395        | 13.54   |
| s832a_15_7          | 5.6E+05  | 23036        | 24.45   |
| s420_new_7_4        | 4.0E+09  | 24092        | 1.7E+5  |
| s344_7_4            | 1.7E+06  | 26423        | 64.55   |
| s382_15_7           | 2.7E+09  | 26612        | 1.0E+5  |
| s344_3_2            | 2.3E+05  | 27408        | 8.47    |
| s382_3_2            | 2061.62  | 30262        | 0.07    |
| s344_3_2            | 5.0E+05  | 32378        | 15.29   |
| s1238a_7_4          | 1.5E+09  | 33689        | 45.408  |
| s32a_7_4            | 1.0E+07  | 34315        | 2.24    |
| s382_15_7           | 1.0E+07  | 39024        | 263.98  |
| s1238a_3_2          | 7.1E+08  | 40406        | 175.75  |
| s420_new_15_7       | 4.9E+09  | 40725        | 1.2E+5  |
| 27.sk_3_32          | 7.4E+06  | 41997        | 176.26  |
| s332a_3_2           | 7.4E+04  | 42696        | 1.75    |
| UserServiceImpl.sk_8_32 | 21547.88 | 45090       | 0.48    |
| 32.sk_4_38          | 4.9E+08  | 45126        | 10872.8 |
| s420_new1_7_4       | 2.8E+08  | 48911        | 5639.38 |
| s444_3_2            | 1.9E+06  | 55017        | 34.61   |
| LoginService2.sk_23_36 | 1.3E+06  | 56229        | 22.38   |
| s420_3_2            | 2.3E+09  | 68048        | 33247.5 |
| 53.sk_4_32          | 2.2E+07  | 70590        | 312.87  |
| s420_new_3_2        | 1.2E+10  | 75284        | 1.6E+5  |
### D.5 Number of samples required for baseline approach

Table 6: Number of samples required for baseline tester

| Benchmark       | Number of samples |
|-----------------|-------------------|
| s344_3_2        | 2E+6              |
| s344_15_7       | 2E+6              |
| s349_7_4        | 2E+6              |
| s298_7_4        | 6E+4              |
| s420_new1_3_2   | 3E+8              |
| s420_new_3_2    | 3E+8              |
| s420_new_15_7   | 3E+8              |
| s382_7_4        | 1E+6              |
| s444_7_4        | 4E+6              |
| s820a_7_4       | 3E+5              |
| s1488_7_4       | 1E+4              |
| s444_3_2        | 1E+6              |
| s838_7_4        | 2E+15             |
| 27.sk_3_32      | 6E+6              |
| s1238a_3_2      | 1E+8              |
| s953a_7_4       | 4E+10             |
| s1488_3_2       | 7E+3              |
| s838_3_2        | 2E+15             |
| s1488_15_7      | 8E+3              |
| s349_15_7       | 2E+6              |
| s344_7_4        | 2E+6              |
| s349_3_2        | 2E+6              |
| 55.sk_3_46      | 2E+9              |
| s1238a_7_4      | 1E+8              |
| s298_3_2        | 4E+4              |
| s832a_7_4       | 4E+5              |
| 111.sk_2_36     | 3E+7              |
| s838_15_7       | 2E+15             |
| s420_new1_7_4   | 3E+8              |
| s832a_15_7      | 1E+6              |
| UserServiceImpl.sk_8_32 | 2E+4        |
| s382_15_7       | 3E+6              |
| 53.sk_4_32      | 6E+6              |
| s820a_15_7      | 4E+5              |
| 84.sk_4_77      | 1E+15             |
| 51.sk_4_38      | 8E+7              |
| s444_15_7       | 1E+6              |
| 109.sk_4_36     | 4E+7              |
| 107.sk_3_90     | 7E+16             |
| 71.sk_3_65      | 5E+13             |
| s641_3_2        | 3E+12             |
| s298_15_7       | 6E+4              |
| 32.sk_4_38      | 7E+7              |
| s420_3_2        | 3E+8              |
| s420_new_7_4    | 3E+8              |
| 80.sk_2_48      | 6E+9              |
| s832a_3_2       | 2E+5              |
| 19.sk_3_48      | 1E+10             |
| 63.sk_3_64      | 5E+12             |
| 17.sk_3_45      | 2E+9              |
| s713_3_2        | 6E+12             |
Table 6: Number of samples required for baseline tester

| Benchmark                | Number of samples |
|--------------------------|-------------------|
| s953a_15_7               | 5E+10             |
| 20.sk_1_51               | 7E+10             |
| 70.sk_3_40               | 2E+8              |
| s1238a_15_7              | 1E+8              |
| 10.sk_1_46               | 6E+9              |
| s953a_3_2                | 4E+10             |
| s820a_3_2                | 1E+5              |
| 30.sk_5_76               | 2E+15             |
| ProjectService3.sk_12_55 | 2E+11             |
| LoginService2.sk_23_36   | 1E+5              |
| s420_new1_15_7           | 3E+8              |
| 77.sk_3_44               | 3E+8              |
| 29.sk_3_45               | 3E+9              |
| 54.sk_12_97              | 4E+18             |
| s641_7_4                | 5E+12             |
| s35932_15_7              | 1E+357            |
| tableBasedAddition.sk_240_1024 | 1E+15 |
| s35932_7_4              | 1E+357            |
| s35932_3_2              | 1E+357            |
| 81.sk_5_51              | 4E+10             |