Efficient Sampling of SAT Solutions for Testing

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ABSTRACT

In software and hardware testing, generating multiple inputs which satisfy a given set of constraints is an important problem with applications in fuzz testing and stimulus generation. However, it is a challenge to perform the sampling efficiently, while generating a diverse set of inputs which satisfy the constraints. We developed a new algorithm QuickSampler which requires a small number of solver calls to produce millions of samples which satisfy the constraints with high probability. We evaluate QuickSampler on large real-world benchmarks and show that it can produce unique valid solutions orders of magnitude faster than other state-of-the-art sampling tools, with a distribution which is reasonably close to uniform in practice.

CCS CONCEPTS

• **Software and its engineering → Software testing and debugging**; *Formal software verification*; • **Hardware** → Theorem proving and SAT solving;

KEYWORDS

sampling, stimulus generation, constraint-based testing, constrained-random verification

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1 INTRODUCTION

Given a set of constraints, the problem of generating a set of random solutions to the constraints is important both in software and hardware testing and verification. For instance, conventional symbolic execution [13, 25] and dynamic symbolic execution techniques [1–4, 7, 8, 12, 18, 19, 24, 28, 35–40, 42] generate a path constraint for each prefix of feasible execution paths in a program and use a SMT-solver to generate a solution for each such constraint. However, in practice, these techniques face scalability problems because the number of paths for any reasonable program is astronomically large. Instead of generating a single solution for the path constraint of a path prefix, one could generate multiple solutions to randomly test multiple paths having the same prefix. We call this approach *constraint-based fuzzing*. If multiple solutions could be generated efficiently, this would significantly speedup symbolic execution and reap the benefits of random testing [6, 17, 21, 22, 34, 45, 46].

Similar ideas have been proposed and developed in hardware verification. For example, *constrained-random verification* (CRV) [33] has been proposed to generate high-quality inputs for hardware designs. In CRV, verification engineers specify preconditions required by the hardware and other constraints based on domain-specific knowledge [32, 47]. Multiple random inputs satisfying the constraints are then generated using a constraint solver that can sample random solutions from a constraint.

However, despite its importance, the problem of sampling a diverse set of solutions efficiently is still challenging today [9]. There are approaches which give strong guarantees of uniformity [11], but are expensive to run when a large number of samples is required. Other approaches use heuristics for faster sampling [43], but that can make the samples biased towards one portion of the sampling space.

In this work, we specifically focus on the goal of generating random samples to be used as inputs for testing. We assume that the constraints are given as Boolean satisfiability (SAT) problems, since constraints from higher level domains, such as bit-vectors or other satisfiability modulo theories (SMT) problems can be mapped into SAT. Our goal is to efficiently generate lots of random satisfying assignments to SAT formulas, also known as SAT witnesses.

In the testing domain, it is often acceptable to generate invalid solutions some of the time. For example, in constraint-based fuzzing, we may use constraints to direct the execution towards a certain portion of the program, but it is still fine if some samples don't satisfy the constraints and end up executing other program parts. It is also important to notice that, in the testing domain, the most important metric is the number of unique valid solutions generated over time. That is because each unique valid input can help cover new portions of the program and find previously unseen bugs, while repeated samples do not increase coverage.

With that in mind, we have designed QuickSampler, a new technique for efficient sampling. QuickSampler uses a small number of constraint solver calls to generate a large number of samples. QuickSampler works as follows. First, it finds a random assignment to the variables of the Boolean formula (i.e. the constraint). Such an assignment may not satisfy the formula. QuickSampler then uses a MAX-SAT solver to find a solution of the formula that is close to the random satisfying assignment. It then flips the value of each variable in the solution and again uses MAX-SAT to find another close solution of the formula. The difference between the

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original solution and the modified solution is called *an atomic mutation*. For each variable in the formula, this generates at most one atomic mutation. A small bounded number of such atomic mutations are then combined and applied to the original solution to generate a potentially new solution. We found that such combinations of small atomic mutations often results in new valid random solutions. This is because each atomic mutation identifies a small set of variables that are tightly coupled with each other. Whereas the variables from two different atomic mutations are often independent. Therefore, if two such atomic mutations are combined and applied to the original solution, then the resulting solution will often satisfy the formula. The entire process is repeated several times. Since QuickSampler creates lots of solutions by simply combining atomic mutations, it avoids making frequent solver calls (which is often the bottleneck). This in turn results in quick generation of lots of random solutions.

We have implemented QuickSampler as an open-source tool available at https://github.com/RafaelTupynamba/quicksampler/. We use Z3 [14] to solve MAX-SAT queries. The samples generated by QuickSampler are not guaranteed to satisfy a given formula, but our experiments show that they are valid solutions in our benchmarks with high probability (i.e. ≥ 0.75). QuickSampler also produces unique valid solutions orders of magnitude (i.e. ≥ 1000×) faster than other state-of-the-art samplers, while generating a distribution of samples which is still close to uniform. For applications which require only valid solutions, it is also possible to use our technique, by simply checking the samples for validity and filtering out the invalid ones. Our evaluation shows that QuickSampler is still faster than the other samplers, even when including this additional checking.

2 RELATED WORK

There are several different techniques used to tackle the problem of sampling solutions to Boolean constraints [29]. The problem of sampling SAT witnesses is also closely related to the problem of counting the number of solutions, which has #P-complete complexity. Several sampling techniques can be applied to model counting or use some form of model counting internally [16, 30, 44].

One class of sampling methods is based on Markov Chain Monte Carlo (MCMC) algorithms [26, 27]. These include simulated annealing and Metropolis-Hastings which are used to generate samples from a probability space. Those MCMC methods are guaranteed to eventually converge to the desired distribution (such as uniform sampling). However, this convergence is slow in practice for real-world problems, so the algorithms typically employ heuristics which make the sampling more biased [27, 43]. For example, [43] combines Metropolis steps with random walk steps through the assignments to the variables of the formula. In comparison, QuickSampler does not need to wait for a convergence time and covers the search space by finding solutions closest to randomly selected points.

One similar line of work attempts to modify the SAT solver search heuristics in order to generate a more diverse set of solutions [31]. However, unlike QuickSampler, this *diverse* sampling has different goals and does not attempt to cover the whole search space nearly uniformly. QuickSampler also does not modify the inner search strategies of SAT solvers, but instead uses the SAT solvers as an oracle to answer MAX-SAT queries.

$$
\begin{array}{rl}
\sigma : & 0\,1\,0\,0\,0\,1\,0\,1\,1\,0\,1\,1 \\
\delta_a : & 1\,0\,0\,0\,1\,1\,0\,0\,0\,0\,0\,0 \\
\sigma_a = \sigma \oplus \delta_a : & 1\,1\,0\,0\,1\,0\,0\,1\,1\,0\,1\,1 \\
\delta_b : & 0\,1\,0\,0\,0\,1\,1\,0\,1\,0\,0\,0 \\
\sigma_b = \sigma \oplus \delta_b : & 0\,0\,0\,0\,0\,0\,1\,1\,0\,0\,1\,1 \\
(\delta_a \vee \delta_b) : & 1\,1\,0\,0\,1\,1\,1\,0\,1\,0\,0\,0 \\
\tilde{\sigma} = \sigma \oplus (\delta_a \vee \delta_b) : & 1\,0\,0\,0\,1\,0\,1\,1\,0\,0\,1\,1
\end{array}
$$

Figure 1: Combining two mutations.

The closest technique to QuickSampler in literature appears to be SearchTreeSampler [16], which also uses a SAT solver as an oracle. However, SearchTreeSampler performs simple satisfiability queries instead of the MAX-SAT queries by QuickSampler. SearchTreeSampler works by exploring the tree of variable assignments in a breadth-first way, generating *pseudosolutions*, which are partial assignments to the variables that can be completed to a full solution. SearchTreeSampler uses a parameter k which specifies the number of samples computed per level in the tree and can be used to trade-off uniformity and number of solver calls required. On the other hand, QuickSampler uses a different strategy to cover the search space, and also generates a vastly larger number of samples per solver call, by combining learned mutations.

A different class of algorithms is based on universal hashing [15, 30] and can provide strong guarantees of uniformity. These techniques work by adding additional constraints to the formula (known as hash functions) in order to partition the search space uniformly. Those hash functions are typically formed by computing the XOR of a random subset of variables [20]. `UniGen` [11] and UniGen2 [9] are examples of this class, with the latter also employing parallelism to improve performance. In comparison, QuickSampler does not attempt to be perfectly uniform, but only close to uniform in practice. QuickSampler primarily aims for efficiency, using solver calls which are much less expensive to solve than the XOR constraints of hash functions, and generating a large number of samples per solver call.

3 QUICKSAMPLER ALGORITHM

Given a Boolean formula ϕ, the goal of QuickSampler is to generate unique solutions of ϕ efficiently. Another goal of QuickSampler is to make sure that solutions of ϕ are sampled almost uniformly at random. The key idea behind QuickSampler is to make a small number of solver calls to generate a large number of potentially unique solutions of ϕ. The core algorithm behind QuickSampler works as follows. QuickSampler assumes that we are given an initial random solution σ (i.e. a satisfying assignment to ϕ), where σ is a vector of 1s and 0s. Each location in the vector corresponds to a Boolean variable in ϕ and the value at that location in the vector denotes the value assigned to this variable in the solution σ. Let V be the set of all Boolean variables in ϕ. For example, in Figure 1 we show a possible vector σ, in a case where the number of variables is $|V| = 12$.

For each variable $v \in V$, QuickSampler finds a solution σ_v such that σ_v and σ are minimally different and $\sigma_v(v) \neq \sigma(v)$, where $\sigma(v)$ is the value of the variable v in the solution σ. Note that such a solution may not exist for all variables in V. The diff between σ and σ_v, which we will denote using δ_v and which is the XOR of σ and σ_v, is called *an atomic mutation* of σ. That is $\delta_v = \sigma_v \oplus \sigma$. In the example from Figure 1, if the first variable of the formula is a, we might find a new solution σ_a which has the first bit flipped (corresponding to variable a) and additionally other two bits flipped. The corresponding atomic mutation δ_a is also shown in Figure 1. Similarly, if the second variable of the formula is b, we might find a new solution σ_b as shown in Figure 1, which has the second bit (corresponding to variable b) flipped, but also other 3 bits flipped. The corresponding atomic mutation δ_b is again shown in Figure 1.

By definition, the atomic mutation δ_v always ensures that at least $\delta_v(v)$ is one, i.e. σ and σ_v at least differ in the value of the variable v and difference in the values of the remaining variables is minimal. We will later explain how a MAX-SAT query to a SAT solver can be used to find σ_v given ϕ, σ, and v. Given σ, QuickSampler first computes the set of all atomic mutations by going over all the variables $v \in V$. Let us denote the set of all such atomic mutations by Δ^1_σ. Note that given σ and δ_v, we can compute σ_v as $\delta_v \oplus \sigma$.

After computing Δ^1_σ, QuickSampler computes sets of composite mutations Δ^k_σ for $k > 1$, where Δ^k_σ contains the union of all k distinct mutations in Δ^1_σ. For example, if δ_a and δ_b are two mutations in Δ^1_σ such that $a \neq b$, then $\delta_a \vee \delta_b$ is a mutation present in Δ^2_σ. (Since each of δ_a and δ_b are bit-vectors, $\delta_a \vee \delta_b$ is computed by taking bitwise OR of the two bit-vectors.) For example, after computing the atomic mutations $\delta_a, \delta_b \in \Delta^1_\sigma$ from Figure 1, the combined mutation $\delta_a \vee \delta_b$ is added to Δ^2_σ. If we apply the combined mutation to σ, by computing $\sigma \oplus (\delta_a \vee \delta_b)$ we obtain a new assignment $\tilde{\sigma}$, as in Figure 1. Note that $\tilde{\sigma}$ differs from σ on all the bits set in either of the two atomic mutations δ_a and δ_b.

This new assignment $\tilde{\sigma}$ is not guaranteed to be a valid solution, but we have found that it has a high probability of being valid in real benchmarks[1]. This is because the differences δ_a and δ_b consist of a minimal set of bits which can be flipped while still preserving the satisfiability of the formula. So the bits in δ_a are likely to be closely related to each other by some clauses in the formula. It is likely that those clauses would still be satisfied in $\sigma \oplus (\delta_a \vee \delta_b)$, where we flip all the bits from δ_a in addition to the bits from δ_b.

In general, each mutation δ present in a Δ^k_σ denotes a composite mutation and can be XORed with σ to get an assignment $\tilde{\sigma}$ to the variables in ϕ. Such an assignment may or may not be a solution of ϕ. Surprisingly, in our experiments we found that for small values of k (i.e. $k \leq 6$), more than 73% of such assignments obtained by XORing are solutions of ϕ. Let us denote the assignments obtained by applying all the mutations present in Δ^k_σ to σ by Σ^k_σ, i.e.

$$\Sigma^k_\sigma = \left\{ \delta \oplus \sigma \mid \delta \in \Delta^k_\sigma \right\}$$

We let $\Sigma_\sigma = \cup_{1 \leq k \leq 6} \Sigma^k_\sigma$. We found experimentally that over all benchmarks, 75% of the assignments in Σ_σ are solutions of ϕ.

We now make a few interesting and important observations about the set of assignments Σ_σ. QuickSampler needs to make solver calls only to compute Δ^1_σ. Moreover, it is not always necessary to make a solver call while computing the elements of Δ^1_σ—if QuickSampler flips the bit corresponding to the variable v in σ and discovers that the resulting bit-vector is a satisfying assignment to ϕ, then QuickSampler can skip the solver call for δ_v. For the computation of all other Σ^k_σ, QuickSampler needs no solver calls because each element in Σ^k_σ is obtained by applying at most k bitwise Boolean operations. An assignment in Σ^k_σ may or may not be a valid solution, however checking its validity is fast and takes linear time in the size of ϕ. In summary, QuickSampler can potentially make solver calls for the computation of Σ^1_σ, but it makes no solver calls to compute the remaining sets Σ^k_σ. Another observation is that size of Σ^k_σ could grow exponentially with k. This observation combined with the facts that a significant number of assignments in Σ_σ have been empirically found to be solutions of ϕ and that we make at most $|V|$ solver calls suggests that given σ, QuickSampler can rapidly generate lots of unique solutions of ϕ by making very few solver calls. This forms the crux of QuickSampler's core algorithm for sampling.

Given a random solution σ, we described how QuickSampler generates lots of solutions that are small mutations of σ. We next describe how we generate a random solution σ. QuickSampler first chooses a random assignment σ' by picking the values of variables in V uniformly at random. Then it uses a MAX-SAT query to find a closest solution σ to the random assignment σ'. We picked this strategy to make sampling of solutions more uniform. Overall, QuickSampler execution is divided into epochs. In each epoch, QuickSampler generates a random solution σ using the method described above. Then it computes Σ_σ and outputs the elements of Σ_σ that are solutions of ϕ. QuickSampler repeats this process in a loop until it has run out of time budget or it has finished generating a user-specified number of solutions.

Now we describe how MAX-SAT queries can be used to obtain the random solution σ and also to obtain the solutions σ_v for each variable v. The maximum satisfiability problem, or MAX-SAT, is defined as follows: given a set of hard constraints and a set of soft constraints, find a solution which satisfies all the hard constraints and additionally satisfies the maximum possible number of soft constraints. In order to compute the random solution σ, we just need to specify one hard constraint that the formula ϕ must be satisfied and $|V|$ soft constraints indicating that the values of each variable v should preferably be equal to their respective values in the random assignment σ', i.e. $\forall u \in V : \sigma(u) = \sigma'(u)$. In order to compute each solution σ_v, we specify two hard constraints and $|V| - 1$ soft constraints. The hard constraints are that the formula ϕ must be satisfied and that the value of variable v must be flipped, i.e. $\sigma_v(v) \neq \sigma(v)$. The soft constraints are that the values of other variables should preferably remain the same, or $\forall u \in V \backslash \{v\} : \sigma_v(u) = \sigma(u)$.

This completes the general description of the QuickSampler algorithm. However, we have also made some adaptations to this initial algorithm in order to improve its performance. We discuss

[1] Our heuristic to generate samples exploits the clause structure found in real-world benchmarks. We expect it to perform poorly if applied to a randomly-generated SAT formula.

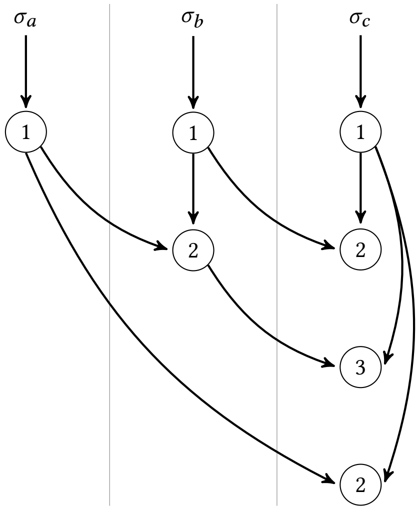


Figure 2: Combining Mutations

in §3.1 the eager generation of samples, in §3.2 the use of the independent support of the formula, and in §3.3 the removal of unsatisfiable variables.

3.1 Eager Generation of Samples

As we have seen, QuickSampler only requires solver calls in order to produce the atomic mutations in Δ^1_σ. After that, the computation of the samples in Σ^k_σ can be performed with simple bitwise operations. However, the solver calls can be expensive for the largest benchmarks. So ideally we would like to leverage each solver call to generate samples as soon as the call is completed, so that we do not need to wait for all solver calls before generating samples.

We have adapted the basic QuickSampler algorithm to generate samples as soon as each solver call is completed. Figure 2 presents an example of this eager generation. Each circle represents one mutation and inside it we indicate the number of atomic mutations used to generate it. When solution σ_a is returned by the solver, we learn one atomic mutation δ_a, represented by the first circle in the figure. Then, as soon as solution σ_b becomes available, we learn the atomic mutation δ_b and also combine it with δ_a to generate a mutation in Δ^2_σ. Then, as soon as solution σ_c becomes available, we learn the mutation δ_c and combine it with the three previously known mutations in order to generate three new mutations.

In conjunction with this eager generation of mutations, we also eliminate duplicate mutations in the current sampling epoch. We found it important to avoid duplicates within one epoch, otherwise we would output too many repeated samples and perform unnecessary work computing them.

We maintain a collection Δ of currently known mutations generated in the current epoch. Whenever we learn a new mutation from a solver call, we combine it with the mutations in Δ. The new generated mutations are added to Δ only if they are previously unseen mutations in this epoch. Also, we only combine the new atomic mutations with mutations from Δ^k_σ for $k < 6$. We do not want to generate mutations composed of more than 6 atomic mutations, because they would have a lower chance of generating valid solutions, according to our experiments.

3.2 Independent Support

Similarly to UniGen2 [9], we can restrict our sampler to only operate over the variables in an independent support S of the formula, instead of generating assignments to all the variables in V. The independent support is a subset of variables which completely determines all the assignments to a formula. More specifically, given an assignment of values to the variables in the independent support S, there is at most one completion of this assignment to the remaining variables which satisfies the formula. So we can think of all other variables being dependent on the variables in the independent support. Knowing an independent support is helpful in reducing the number of variables for which we need to assign values.

In many cases, an independent support arises naturally from the application. For example, when the Tseytin transformation is used to transform a combinatorial logic circuit into a Boolean formula in conjunctive normal form (CNF), auxiliary variables are introduced for all intermediate wires in the circuit. All of those auxiliary variables can be uniquely determined given the inputs to the circuit, so the inputs form an independent support. In cases when an independent support is not known for a formula, there are also methods to compute a minimal independent support for it [23].

3.3 Unsatisfiable variables

If one MAX-SAT query for variable v returns no solutions, we learn that v can only have one truth value in this formula. When this happens in the first epoch, we record the variable v in a set U of unsatisfiable variables. Then, we do not try to flip the value of v again in other epochs. We found that, over all benchmarks, on average 6% of the variables from the independent support were added to the set U. This means that, after the first epoch, all subsequent epochs can work over a reduced sampling set and avoid unnecessary solver calls.

4 IMPLEMENTATION

We have implemented[2] the technique in C++, using Z3 [14] as the underlying solver. QuickSampler uses the Z3 optimization subsystem *vZ* [5] in order to solve the MAX-SAT queries. We also use the *push*() and *pop*() interfaces to efficiently add and remove constraints from a single solving context.

QuickSampler takes as input a SAT formula in conjunctive normal form (CNF), represented in the DIMACS file format. The formula includes a list of variables which compose its independent support.

Our implementation outputs the samples generated to a file without checking if they are valid solutions. If desirable, it is possible to add a posterior check which verifies if the samples are valid or not (and possibly filters out the invalid ones). We also do not check for duplicates, which can appear between different epochs in the sampling algorithm. This global check for uniqueness could also be added, but it would require an additional time and memory

[2] The source code is available at https://github.com/RafaelTupynamba/quicksampler.

overhead. Some applications might prefer not to keep all generated samples in memory, and allow the generation of repeated samples instead.

We have implemented an offline analysis to check if the samples are valid and generate histograms that count how many times each solution has been sampled. We record the time taken by the sample generation and also the time taken by the checking phase. The checking phase is not heavily optimized and for most benchmarks it was more expensive than the sampling phase. We believe there is still room for improvement in the checking phase, since all it needs to do is to propagate the values of the independent support to the remaining variables and check if all clauses are satisfied.

5 EVALUATION

We evaluate QuickSampler by comparing against two state-of-the-art samplers UniGen2 [9] and SearchTreeSampler [16]. UniGen2 provides strong uniformity guarantees, by using hash functions composed of XOR constraints in order to partition the search space into similar-sized bins.

SearchTreeSampler, on the other hand, uses the SAT solver to find pseudosolutions (partial assignments to the first few variables) and progressively augments the pseudosolutions into real solutions. SearchTreeSampler is only approximately uniform. The uniformity can be increased with a higher number of samples per level k, but at a cost of also increasing the number of solver calls required. In our experiments, we used the default value of $k = 50$.

Both QuickSampler and UniGen2 can leverage the knowledge of an independent support of the formula to improve sampling performance. So in order to make for a fair comparison, we modified SearchTreeSampler to use this additional information. We reorder the variables of the formula in order to place first the ones which are part of the independent support. And we additionally tell SearchTreeSampler to finish sampling after processing those variables and output pseudosolutions (assignments to the variables of the independent support) that it has produced so far. Since an assignment to the independent support can only be completed to one solution, there is no need to find assignments to the remaining variables.

For the evaluation, we use the set of benchmarks from the UniGen2 paper [9] available online[3]. From the benchmarks listed in [9], we found 173 on the online repo. The benchmarks include bit-blasted versions of SMTLib benchmarks, ISCAS89 circuits augmented with parity conditions on randomly chosen subsets of outputs and next-state variables, problems arising from automated program synthesis and constraints arising in bounded model checking. Thus, they are representative of the kinds of constraints that might appear in SMT formulas for software testing or circuit constraints for hardware.

On 10 benchmarks[4], UniGen2 reported an error because the specified independent support is not really an independent support for the formula. In all those benchmarks, we verified that the number of solutions computed by the exact model counter sharpSAT [41] is larger than $2^{|S|}$, which should not happen if S is a real independent support for the formula. So we decided to exclude those benchmarks from our results. The results in this paper include the remaining 163 benchmarks.

Table 1: Correctness statistics for the samples produced in one epoch of QuickSampler (average among all benchmarks)

Atomic mutations	Total	Valid	%
0	1	1	100%
1	32	32	100%
2	511	492	96%
3	5619	5208	93%
4	47493	42179	89%
5	346367	282860	82%
6	2143385	1571553	73%
Total	2543409	1902325	75%

On 3 benchmarks, UniGen2 could not estimate the number of solutions: on parity.sk_11_11, UniGen2 raised a floating point exception and on isolateRightmost.sk_7_481 and listReverse.sk_11_43, the ApproxMC [10] model counter used by UniGen2 couldn't finish even in 40 hours. On 2 benchmarks, UniGen2 estimated the number of solutions but couldn't produce any samples: on doublyLinkedList.sk_8_37 it timed out and on diagStencilClean.sk_41_36 it ran out of memory.

The experiments were conducted on a 12-core, 3.50GHz Intel Core i7-5930K CPU. For each benchmark, each of the algorithms was given one core and 1.5 GB of memory. For QuickSampler and SearchTreeSampler, we allowed a maximum timeout of 1 hour, or 2 hours on the hardest benchmarks. We also stopped the sampling after a large number of samples had been produced (at least 10 million samples).

For UniGen2, we requested the generation of 1000 samples for most benchmarks, allowing up to 20 hours to produce them. For the hardest benchmarks, we reduced the number of requested samples to 500. For all the benchmarks in which UniGen2 failed to produce any samples, it times out after 20 hours even when the number of requested samples was 1.

5.1 Correctness of Samples

On Table 1, we list the average number of samples produced and how many of those were valid, on one epoch of the sampling algorithm. The results were averaged across all 163 benchmarks. They are classified according to the number of individual atomic mutations which compose the mutation. The base solution used in the epoch is the one with 0 atomic mutations and the neighbors of the base solution obtained when flipping each bit correspond to 1 atomic mutation. Those are always valid solutions to the formula, since they are obtained as the result of solver calls.

From 2 to 6 atomic mutations, we see that the fraction of valid solutions decreases from 96% to 73%. And overall, 75% of all samples produced were valid, when we allow a maximum of 6 atomic mutations. Table 1 shows that, by adjusting this maximum, we can

[3] Benchmarks and source code for UniGen2 were obtained from https://bitbucket.org/kuldeepmeel/unigen.

[4] GuidanceService2.sk_2_27, GuidanceService.sk_4_27, IssueServiceImpl.sk_8_30, PhaseService.sk_14_27, ActivityService.sk_11_27, IterationService.sk_12_27, ActivityService2.sk_10_27, ConcreteActivityService.sk_13_28, NotificationServiceImpl2.sk_10_36, LoginService.sk_20_34.

change the accuracy of the sampling. For example, with a maximum of 5 atomic mutations instead of 6, the fraction of valid samples would increase to 83%. However, there would be a substantial decrease in the quantity of samples produced. We have chosen to use the maximum number of 6 atomic mutations to allow the generation of millions of samples, while still having a reasonably good accuracy of 75%.

If n is the number of atomic mutations, then the number of mutations of level 6 can go up to $\binom{n}{6}$, a sixth-degree polynomial in n. This explains why we can generate millions of samples from only tens of atomic mutations.

5.2 Performance Comparison

For the performance comparison, we define t_q, t_s, t_u to be the average time taken by QuickSampler, SearchTreeSampler and UniGen2, respectively to produce a valid sample. t_q was computed as $t_q = T_q/(s_q \cdot p)$, where T_q is the total execution time, s_q is the total number of samples produced and p is the fraction of samples which are valid for QuickSampler. We additionally define t_q^* to be the estimated time per valid sample that QuickSampler would require if it also checked all samples for validity. t_q^* was computed as $t_q^* = (T_q + T_c)/(s_q \cdot p)$, where T_c is the total time taken to check the validity of all s_q produced samples.

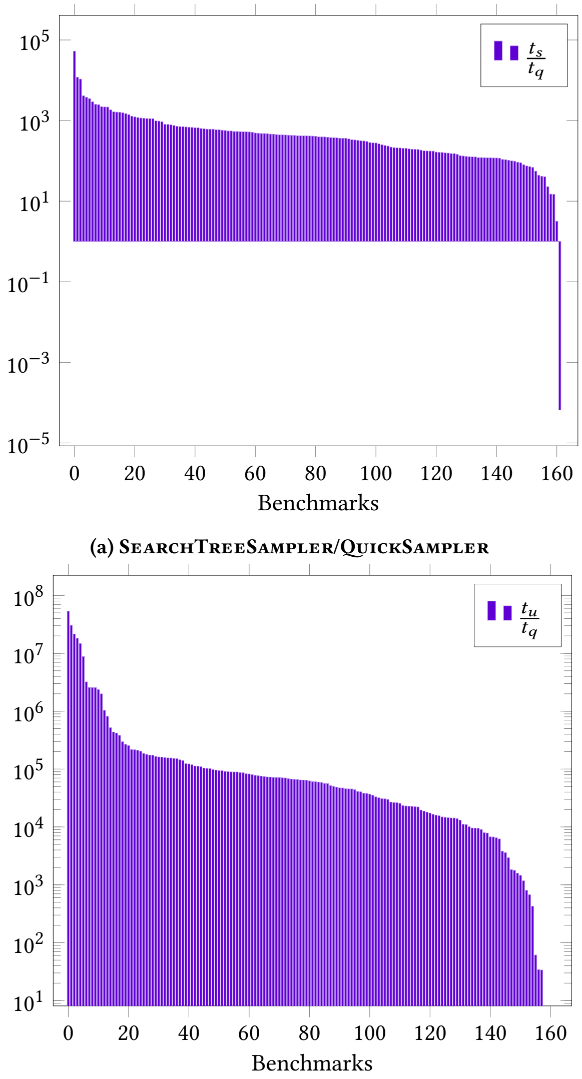
Table 2 shows the performance comparison among a selected set of benchmarks. We have included the largest benchmarks (more than 4000 variables), the benchmarks which were listed as representative benchmarks in [9] and the benchmarks used for uniformity plots in §5.3. This includes the benchmarks which QuickSampler or SearchTreeSampler found hard.

The first group of columns in Table 2 shows basic information about the benchmarks: size of the independent support, number of variables, clauses and solutions. The number of solutions was obtained from UniGen2. On most benchmarks, an exact number of solutions is known, while for some we only know an approximation (represented with ≈) and on some UniGen2 failed completely to compute the number of solutions.

The second group of columns shows results for QuickSampler: the number of epochs completed, number of MAX-SAT solver calls, number of samples generated, fraction of samples which are valid and the average times per valid sample t_q and t_q^*, in microseconds. The third and fourth group of columns present results for SearchTreeSampler and UniGen2: the number of samples produced and the average time per sample, taken in comparison with the QuickSampler time t_q.

The mean value for some ratios of interest is shown on Table 3. For example, $t_s/t_q \approx 10^{2.5 \pm 0.8}$. This was computed by taking the average and the standard deviation of $\log_{10}(t_s/t_q)$ across all benchmarks.

Figure 3 shows a comparison of the average time per valid sample, against SearchTreeSampler and UniGen2. As reported in Table 3, QuickSampler was on average 2.5 orders of magnitude faster than SearchTreeSampler and 4.7 orders of magnitude faster than UniGen2. Overall, QuickSampler was only slower than SearchTreeSampler on the benchmark diagStencilClean.sk_41_36, with $t_s/t_q = 6.6 \cdot 10^{-5}$. We believe QuickSampler did not do well on diagStencilClean.sk_41_36 because the Z3 solver used in our implementation did not perform well on this formula. In comparison, MiniSAT, the solver used by SearchTreeSampler, was much faster on this benchmark. The opposite effect can be seen, for example, on parity.sk_11_11, where MiniSAT was only able to complete a small number of solver calls.



(a) SearchTreeSampler/QuickSampler

(b) UniGen2/QuickSampler

Figure 3: Average time per valid sample

Next we present graphs of the same metrics, but now also taking into account the time that would be required for QuickSampler to check if the samples are valid. This should only be needed if the application cannot deal with invalid samples. Figures 4a and 4b show the comparison with SearchTreeSampler and UniGen2, respectively. We see that QuickSampler is still 1 order of magnitude faster than SearchTreeSampler and 3.2 orders of magnitude faster than UniGen2, even when including this checking time. QuickSampler was only slower than SearchTreeSampler on three benchmarks,

Table 2: Comparison of sampling algorithms

					QuickSampler						SearchTreeSampler		UniGen2	
Benchmark	$\lvert S \rvert$	Vars	Clauses	Solutions	n	Calls	Samples	Valid	t_q (μs)	t_q^* (μs)	Samples	t_s/t_q	Samples	t_u/t_q
blasted_case47	28	118	328	262144	244	6616	10010929	0.564	7.5	26	11694350	41.3	3932170	426
blasted_case110	17	287	1263	16384	1387	22208	10001202	0.822	28.3	29	8502350	14.9	245762	34
s820a_7_4	23	616	1703	591872	128	3093	10002673	0.770	5.9	34	4007950	151.6	2959363	802
s820a_15_7	23	685	1987	722944	114	2759	10014350	0.674	9.0	66	3875900	103.2	3614721	674
s1238a_3_2	32	686	1850	2466250752	9	328	10140047	0.936	2.7	211	1917850	707.2	1001	60515
s1196a_3_2	32	690	1805	1038090240	11	393	10077447	0.803	3.2	246	1848850	609.1	1001	60320
s832a_15_7	23	693	2017	3713024	83	2014	10017640	0.818	6.4	100	2742600	204.4	1001	3803
blasted_case_1_b12_2	45	827	2725	274877906944	1	89	10021799	0.739	2.9	305	1001600	1235.7	1001	71769
blasted_squaring16	72	1627	5835	1865275930882	0	65	10304220	0.209	15.8	1961	285450	799.7	1001	215680
blasted_squaring7	72	1628	5837	274408144896	0	68	11344920	0.112	32.1	3788	255750	438.1	1001	22186
70.sk_3_40	40	4670	15864	8589934592	8	304	10134785	1.000	5.8	1236	4091950	151.2	1001	109854
ProcessBean.sk_8_64	64	4768	14458	≈7009386627072	1	86	10011221	0.906	4.1	1294	297900	2932.3	1001	179418
56.sk_6_38	38	4842	17828	3690987520	9	334	10049283	0.930	5.3	694	1685350	406.3	1001	71623
35.sk_3_52	52	4915	10547	4398046511104	2	95	10717156	1.000	2.3	229	2348300	664.6	1001	435883
80.sk_2_48	48	4969	17060	1099511627776	2	126	10252598	1.000	4.0	1399	2572650	350.5	1001	103909
7.sk_4_50	50	6683	24816	2199023255552	2	124	10139607	1.000	4.9	1778	1717250	429.5	1001	296687
doublyLinkedList.sk_8_37	37	6890	26918	2038431744	106	3425	10003513	0.267	678.4	6308	231850	22.9	0	-
19.sk_3_48	48	6993	23867	2959802892288	1	89	10198861	0.937	4.1	2010	756400	1156.1	1001	814253
29.sk_3_45	45	8866	31557	347892350976	2	120	10045170	0.855	6.7	2772	215450	2483.0	1001	1995316
isolateRightmost.sk_7_481	481	10057	35275	-	0	59	11191269	0.878	11.3	3293	6000	52789.2	0	-
17.sk_3_45	45	10090	27056	274877906944	3	157	10181716	1.000	5.7	2374	1600150	392.8	1001	3207452
81.sk_5_51	51	10775	38006	18141941858304	1	52	11099585	0.867	4.0	3863	75850	11859.7	1001	1035125
LoginService2.sk_23_36*	36	11511	41411	≈163840	272	6019	10001533	0.724	680.3	3212	1593200	14.8	778250	34
sort.sk_8_52	52	12125	49611	≈88046829568	2	105	10563617	0.625	31.1	7354	30650	3775.2	1001	155253
parity.sk_11_11*	11	13116	47506	-	68	615	3833	0.809	2322699.9	3535813	462	3.2	0	-
77.sk_3_44	44	14535	27573	18253611008	6	249	10014904	0.966	5.8	1580	1478300	420.4	1001	2552683
20.sk_1_51	51	15475	60994	37108517437440	1	52	11126152	0.910	4.0	3751	84250	10695.1	1001	2360454
enqueueSeqSK.sk_10_42	42	16466	58515	≈3355443200	4	207	10008980	0.762	34.8	21412	29450	3512.4	1001	30830
karatsuba.sk_7_41*	41	19594	82417	≈1245184	2	86	670641	0.088	125504.0	203615	50	1116.2	1001	61
diagStencilClean.sk_41_36*	36	378131	2110471	≈13	5	66	87	0.701	120336466	120397476	908868	0.000066	0	-
tutorial3.sk_4_31*	31	486193	2598178	≈49283072	6	193	2114947	0.798	4281.2	362747	1200	693.2	506	18783

Table 3: Mean ratio comparisons across all benchmarks

Ratio	Mean
t_s/t_q	$10^{2.5\pm0.8}$
t_u/t_q	$10^{4.7\pm1.0}$
t_s/t_q^*	$10^{1.0\pm0.5}$
t_u/t_q^*	$10^{3.2\pm0.7}$
u_q/u_s	$10^{2.3\pm0.7}$
u_q/u_u	$10^{4.4\pm1.1}$

where the ratio t_s/t_q^* was 0.95 for 17.sk_3_45, 0.71 for 70.sk_3_40 and $6.6 \cdot 10^{-5}$ for diagStencilClean.sk_41_36.

Those results show clearly that QuickSampler is capable of generating valid solutions orders of magnitude faster than the other techniques. However, we believe that an even more important metric is the number of *unique* valid solutions generated over time, since repeated solutions do not help uncover new behavior in the test program. So we performed an experiment to evaluate the number of unique valid solutions generated.

All three algorithms were allowed to run until they produced 10 million samples or reached 1 hour of execution. If their execution times are T_q, T_s, T_u, we define $T = \min\{T_q, T_s, T_u\}$ and look at the number of unique valid solutions that each algorithm could produce in time T and represent those numbers as u_q, u_s, u_u. We found out that on most benchmarks QuickSampler was able to produce 10 million samples before 1 hour and it was the fastest algorithm to finish. So the uniqueness comparison is performed at time T_q. On six benchmarks, neither of the algorithms could produce 10 million samples before 1 hour, so the uniqueness comparison is performed at 1 hour. The names of those benchmarks are marked with an asterisk in Table 2.

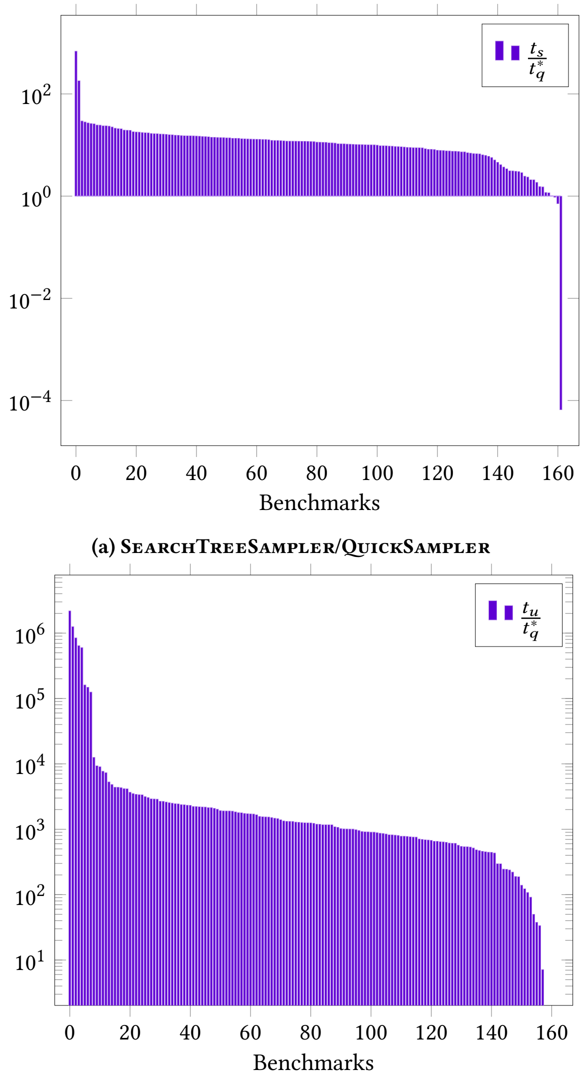
Figure 5a compares unique solutions produced by QuickSampler and SearchTreeSampler. On average, the number of unique solutions produced by QuickSampler was 2.3 orders of magnitude larger, as seen in Table 3. On only one benchmark it was lower (karatsuba.sk_7_41, with $u_q/u_s = 0.76$).

In Figure 5b, we present the ratio of unique solutions between QuickSampler and UniGen2. Again, the ratio was lower only on karatsuba.sk_7_41, with $u_q/u_u = 0.08$. On average, u_q was 4.4 orders of magnitude higher than u_u. We found that QuickSampler performed poorly on karatsuba.sk_7_41 because it had not completed one sampling epoch within the first hour of execution, and most of the samples are generated towards the end of the sampling epoch. However, within 2 hours, QuickSampler was able to complete 2 sampling epochs, generating a vastly larger amount of samples, as reported in Table 2.

5.3 Uniformity of Coverage

The results from §5.2 show that QuickSampler can produce unique valid solutions very fast, which was our primary goal. But we would still like to check if the distribution of samples produced is similar to uniform, because we don’t want to be missing a large portion of the solution space, while focusing on a very biased subset of solutions. We have designed our main sampling function to start from a random point in the space of possible variable assignments in order to make our coverage more uniform. This also guarantees that any solution has a positive probability of being output by our algorithm.

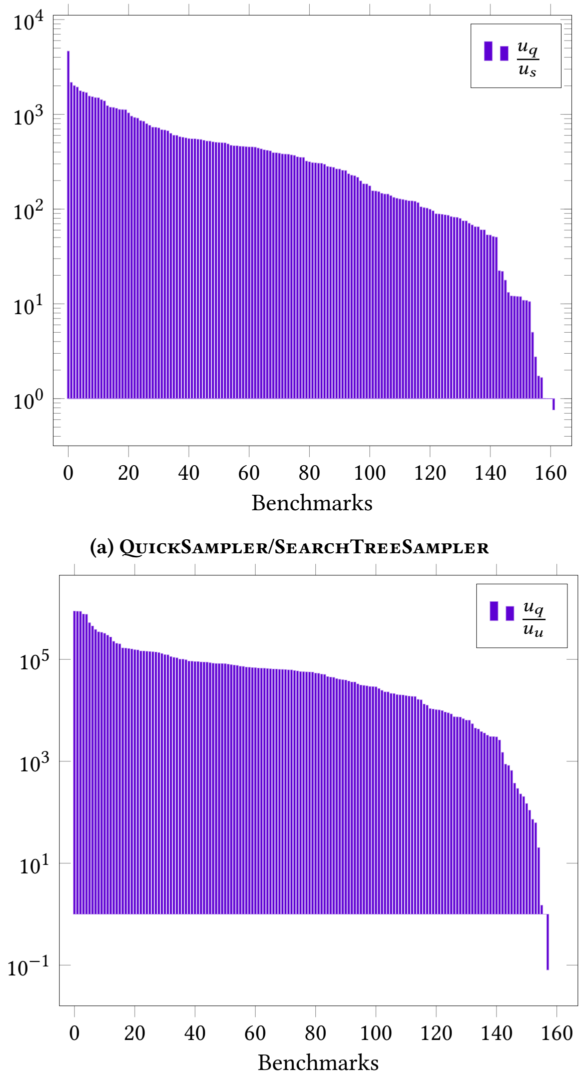
In order to empirically evaluate the uniformity of QuickSampler, we compare its distribution of solutions with the ones from the



(a) SearchTreeSampler/QuickSampler

(b) UniGen2/QuickSampler

Figure 4: Average time per valid sample, including time to check validity



(a) QuickSampler/SearchTreeSampler

(b) QuickSampler/UniGen2

Figure 5: Unique solutions produced over same amount of time

two other samplers SearchTreeSampler, UniGen2 as well as a distribution from a perfect uniform sampler. Only the valid samples are considered in this analysis. We compare on the benchmarks for which the number of samples generated by UniGen2 in a time limit of 10 hours was at least five times the total number of solutions. It is important for statistical significance that each solution be sampled on average at least five times. For each of the benchmarks, let s_q, s_s, s_u be the number of valid samples generated by each algorithm and $s = \min\{s_q, s_s, s_u\}$. We subsample uniformly s samples from the valid samples produced by each algorithm and we also generate s samples from a perfectly uniform distribution, using the total number of solutions provided by UniGen2.

Figures 6 to 10 show the results of the comparison on all benchmarks for which the number of generated samples s can be at least

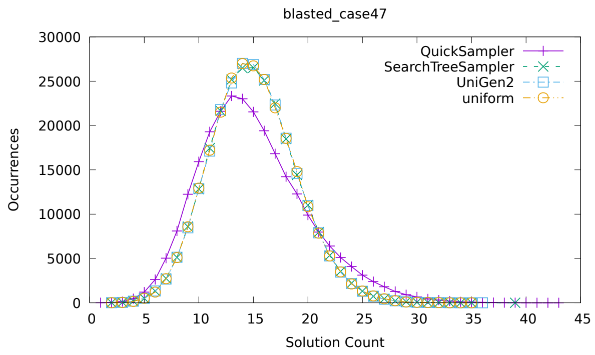


Figure 6: blasted_case47 histogram

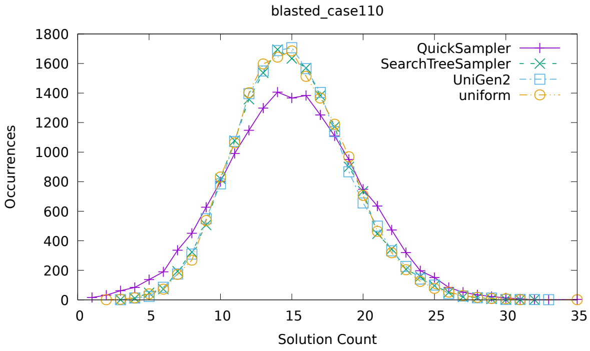


Figure 7: blasted_case110 histogram

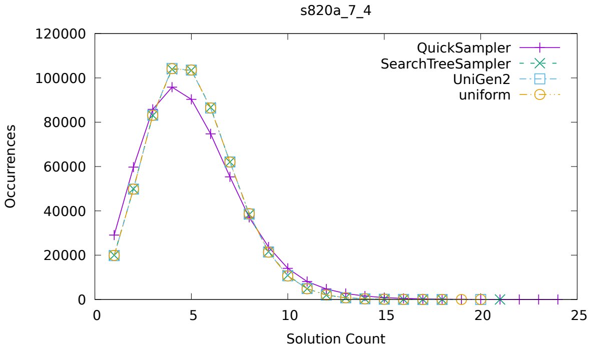


Figure 8: s820a_7_4 histogram

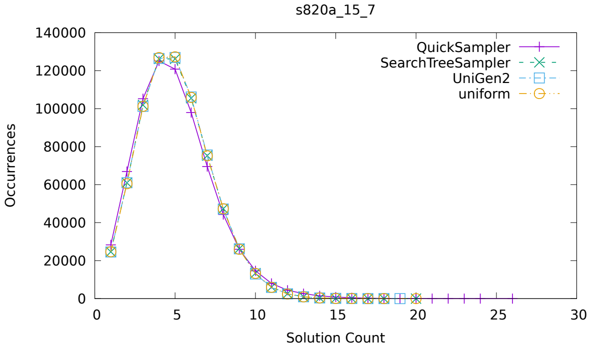


Figure 9: s820a_15_7 histogram

five times the number of solutions before the timeout is reached. The x axis represents the number of times each solution has been sampled and the y axis represents the quantity of solutions which have been sampled x times. We can see that SearchTreeSampler and UniGen2 are usually indistinguishable from uniform, but QuickSampler is also very close to uniform behavior.

We have also applied Pearson's chi-squared test to the s samples obtained from each algorithm. We compute the χ^2 statistic and the corresponding p-value using the known number of solutions to

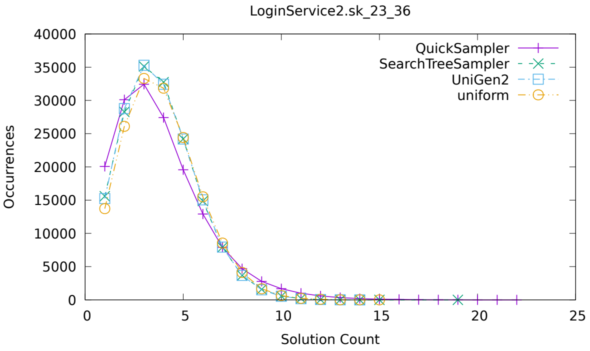


Figure 10: LoginService2.sk_23_36 histogram

Table 4: Chi-squared Uniformity Test

	Not Rejected	Rejected
QuickSampler	149	11
SearchTreeSampler	153	7
UniGen2	155	5

the formula. We reject the null hypothesis that the distribution is uniform if the p-value is lower than the confidence level of 0.05. This gives a bound on the type I error rate (i.e., the probability that a uniform distribution is mistakenly rejected as non-uniform)[5]. Table 4 show the results of applying this test to the 160 benchmarks for which we know an estimate of the number of solutions. We can see that SearchTreeSampler and UniGen2 are more uniform, but QuickSampler is still close to uniform on most benchmarks. However, this result should be taken with care, since the uniformity test is not very reliable on benchmarks where QuickSampler completed a small number of epochs or when the number of produced samples is too low.

Besides analyzing the uniformity of the distribution, we also measured the number of unique valid solutions generated. This is arguably more important than the histograms of solution counts, because we want unique solutions to increase coverage in testing.

We computed the number u of unique valid solutions generated by QuickSampler and also the number $\bar{u}$ of unique solutions that should be generated if the sampling was perfectly uniform. We record the ratio $u/\bar{u}$ for all benchmarks for which we have an estimate of the number of solutions. The ratio $u/\bar{u}$ had an average value of 0.981, with standard deviation of 0.052. Besides one benchmark (doublyLinkedList.sk_8_37, with value 0.41), all other benchmarks had $u/\bar{u} > 0.87$. In comparison, for SearchTreeSampler, the average was 0.996 and standard deviation 0.038. SearchTreeSampler also performed worst on the benchmark doublyLinkedList.sk_8_37, with value 0.538, and all other benchmarks having $u/\bar{u} > 0.92$. UniGen2 obtained an average of 1.000 and a standard deviation of 0.002, with a minimum value of 0.999. On doublyLinkedList.sk_8_37, UniGen2 timed out, so we cannot compare on this benchmark.

[5] We could not perform power analysis to estimate the type II error rate because that would require a specific alternative hypothesis and we did not see any natural alternative hypothesis for the distribution of samples.

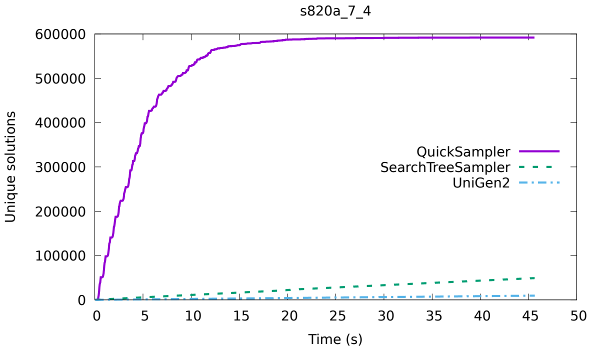


Figure 11: s820a_7_4 unique solutions

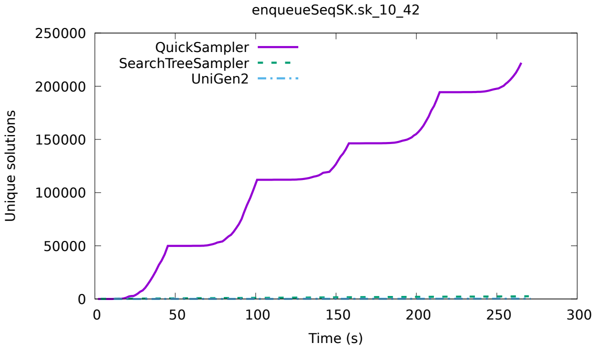


Figure 12: enqueueSeqSK.sk_10_42 unique solutions

We also present plots of the number of unique solutions produced over time, for two representative benchmarks. In Figure 11 we show the graph for benchmark s820a_7_4, where the number of samples produced is larger than the total number of solutions. We see that the number of unique solutions grows very fast initially, and then stabilizes as we approach complete coverage of all solutions. SearchTreeSampler and UniGen2, on the other hand, produce solutions at a much slower rate. In Figure 12 we show benchmark enqueueSeqSK.sk_10_42, where the number of valid samples produced is much smaller than the total number of solutions. We can see that QuickSampler is able to generate unique solutions orders of magnitude faster than SearchTreeSampler and UniGen2. We also notice a distinctive step pattern in the graph. This happens because we produce the largest number of samples at the end of each sampling epoch, when the collection of known mutations is the largest.

In summary, we see that SearchTreeSampler and UniGen2 are a bit closer to uniform sampling, but QuickSampler is still very close. In almost all cases the number of unique solutions generated was very close to the number that would be expected if the sampling was uniform and we are able to produce new unique solutions at a faster rate than the other techniques.

6 CONCLUSION

We have developed a new technique to sample solutions to Boolean constraints, with the goal of applying it to constrained-random verification and fuzz testing. For those applications, it is typically acceptable to produce a small number of invalid inputs, so we allow our technique to output samples which are not guaranteed to be valid. By leveraging a small number of MAX-SAT solver calls, QuickSampler can generate millions of samples.

Our experiments show that the produced samples are valid with an average probability of 75% on a set of large, real-world benchmarks. Moreover, QuickSampler is more than 2 orders of magnitude faster at producing valid samples, when compared to other state-of-the-art samplers. It is also more than 2 orders of magnitude faster at producing *unique* valid samples, which is specially important to increase testing coverage. We have also verified that QuickSampler is still 1 order of magnitude faster even when it takes the additional time to verify that the generated solutions are valid. Finally, the distribution of samples produced is close to uniform on most of the benchmarks.

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