Faster SAT Solving for Software with Repeated Structures
(with Case Studies on Software Test Suite Minimization)

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Abstract

Theorem provers has been used extensively in software engineering for software testing or verification. However, software is now so large and complex that additional architecture is needed to guide theorem provers as they try to generate test suites. The Snap test suite generator (introduced in this paper) combines the Z3 theorem prover with the following tactic: cluster some candidate tests, then search for valid tests by proposing small mutations to the cluster centroids. This technique effectively removes repeated structures in the tests since many repeated structures can be replaced with one centroid. In practice, Snap is remarkably effective. For 27 real-world programs with up to half a million variables, Snap found test suites which were 10 to 750 smaller times than those found by the prior state-of-the-art. Also, Snap ran orders of magnitude faster and (unlike prior work) generated 100% valid tests.

Keywords: SAT solvers, Test suite generation, Mutation

1. Introduction

Many software problems can be transformed into “SAT”; i.e. a propositional satisfiability problem \([1, 2, 3, 4, 5, 6, 7]\). For example, Fig. [1] shows the different branches of program being translated into a propositional formula. Test cases can be automatically generated by theorem provers that solve for the constraints in those formula. After decades of research, such theorem provers can process impressively complex formula. As Micheal Lowry said at a panel at ASE’15:

“It used to be that reduction to SAT proved a problem’s intractability. But with the new SAT solvers, that reduction now demonstrates practicality.”

However, in practice, there is a problem. General SAT solvers, such as the Z3 \([8]\), MathSAT \([9]\), vZ \([10]\) et al., are challenged by the complexity of real-world software models. For example, the largest benchmark for SAT Competition 2017 \([11]\) had 58,000 variables – which is far smaller than (e.g.) the 300,000 variable problems seen in the recent SE testing literature \([12]\).

We diagnosis the problem with SAT solvers as follows: they are looking too closely at specific details. Recent work, presented in \([12, 13]\) suggests that modern software systems contain many repeated structures. If so, we would expect test suite generators to waste time generating many very similar solutions. This is indeed the case. For example, in one sample of 10 million tests generated from the blasted_case47 (a problem described later in this paper), the QuickSampler tool from ICSE’18 \([12]\), only found 26,000 unique valid solutions. That is, 99% of the tests QuickSampler was repeating other tests.

This paper asks if structural replication can be used to design better solvers for SE tasks. Our case study will be test suite minimization. The Snap test suite generator (introduced in this paper) combines Z3 with the following tactic:

Cluster candidate tests, then search for valid tests by via small mutations to the cluster centroids.

This technique effectively removes repeated structures in the tests since many repeated structures can be replaced with one centroid. In practice, Snap is remarkably effective. For 27 real-world programs with up to half a million variables, Snap found test suites which were 10 to 750 smaller times than those found by the prior state-of-the-art. Also, Snap ran orders of magnitude faster and (unlike prior work) generated 100% valid tests. Note that:

- This document will use the terms “tests”, “test cases”, or “SAT solutions” interchangeably since we address the software testing task as a (transformed) SAT task.
- An open-source version of Snap (and all SE models used in this paper) is freely available on-line \([2]\).

2. Background

2.1. Why Explore Test Suite Minimization?

When changing software, it is useful to test if the new work damages old functionality. For this reason, testing and re-testing code is widely applied in both open-source projects and closed-source projects \([15, 16, 17]\).

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\(^1\)A propositional formula is constructed from simple propositions, such as “five is greater than three” or propositional variables such as \(P\) and \(Q\), using connectives or logical operators such as \(\text{not, AND, OR},\) or \(\text{IMPLIES}\); for example: \((P \text{ AND NOT } Q) \text{ IMPLIES } (P \text{ OR } Q)\).

\(^2\)http://github.com/ai-se/SatSpaceExpo
When developers extend a code base, test suites let them check that their new work does not harm old functionality. Such tests mean that developers can find and fix more faults, sooner. Hence, better tests enable faster code modification [15, 16, 18].

By minimizing the number of tests executed, we also minimize the developer efforts required to specify the expected behavior associated with each test execution [19]. If testing for (e.g.) core dumps, then specifying off-nominal behavior is trivial (just look for a core dump file). But in many other cases, specifying what should (and should not) be seen when a test executes is a time-consuming task requiring a deep understanding of the purpose and context of the software.

Smaller tests suites are also cheaper to run. The industrial experience is that excessive testing can be onerously expensive, especially when run after each modification to software [19]. Such high-frequency testing can grow to 80% of the software maintenance effort [19, 20]. Many current organizations spend tens of millions of dollars each year (or more) on cloud-based facilities to run large tests suites [19]. The fewer the tests those organizations have to run, the cheaper their testing.

Smaller test suites are faster to execute. If minimal and effective test suites can be generated, within a fixed time limit, more faults can be found and fixed [19]. Faster test execution means that software teams can certify a new release, quicker. This is important for organizations using continuous integration since faster test suites mean they can make more releases each day – which means that clients can sooner receive new (or fixed) features [21].

Generating test suites can be difficult. Good test suite generators must struggle to achieve several goals:
1. Terminate quickly;
2. Scale to large programs;
3. Return small test suites that contain valid tests;
4. Cover most program branches;
5. Minimize test suite redundancy.

In practice, the test suite generation problem is a complex problem that requires extra machinery to guide the theorem provers. For example, Snap’s extra machinery knows how to avoid repeated structures. As a result, Snap runs very fast, and generates such small test suites.

### 2.2. Repeated Structures in Software

This section presents evidence of structural repetition in software. Historically, this evidence lead to the design of Snap.

A repeated observation is that apparently complex software can be controlled by just a few key variables. Just to say the obvious, controlling a system containing a few keys is just a simple matter of finding the keys then changing each of the key’s settings. More specifically, when applied to test case generation, test suites get smaller if they only use the key variables.

One way to see how many keys are in a software system is to ask how many “prototypes” (minimum number of exemplars) are required to model that system. If the keys are few, a few examples are enough to model a system; e.g. software with 8 binary keys only needs $2^8 = 256$ examples. There are many different ways to find those exemplars [22] but in a result that endorses keys, the number of required exemplars is often very small, even for seemingly complex systems. For example, we have successfully modelled security violations in 28,750 Mozilla functions with 271 exemplars and 6000 commits from Github using 300 exemplars [23]. And even in the deep learning world, there are very recent results [24] with “less than one”-short learning suggesting that it is possible and useful to synthesize a small number of artificial exemplars by aggregating across multiple examples.

The presence of keys illustrate why a few variables can be enough to model software (e.g. in the tiny test suites generated later in this article). For example, effective defect prediction or effort estimation is possible using less than half a dozen variables [24, 25]. Additionally, configuring complex systems is often remarkably simple and effective and can be achieved using very small decision trees that only require a few variables [26]. Further, by generating tests only for the main branches in the code, even applications that process large cloud databases can be tested via just a few dozen inputs [27]. As to what causes the keys, we see two possibilities: **naturalness** and **power laws**.

**Naturalness:** Hindle and Devanbu wrote at ICSE’12 that “Programming languages, in theory, are complex, flexible and powerful, but the programs that real people actually write are mostly simple and rather repetitive, and thus they have... statistical properties that can be captured in... models and leveraged for SE tasks.” [28] To say that another way, computer programs...
are written using a programming language and “language” is a technology that humans have been using for millennia to enable succinct communication. Repeated structures simplify communication since they let the observer learn expected properties of a “typical” systems. This means, in turn, they can recognize when some part of a system is anomalous (because it lacks the usually repeated structures) [39]. Consequently, when we write things in a language (human or programming) then the frequency counts of those things usually correspond to Zipf’s law; i.e. our words and our code repeats a small number of things very often and a large number of other things very rarely [40].

Power-laws: Code is written by people. The social interactions between people mean that those humans focus their work on tiny parts of the code (see Lin and Whitehead at MSR’15 [41]). To see this, consider a large system with modules A,B,C,D.... Developer1 may only understand a small part of the code; e.g. module A. If Developer2 asks for help, then Developer1 will teach more about A than B,C,D. When this cycle is repeated for Developer3, Developer4, etc then we will observe these programmers know more and more about only a small part of the code. Hence it is hardly surprising that 20% of the code contains 80% of the errors since developers mostly work in small corners of a code base. Again, just to state the obvious, power laws explain keys; i.e. keys are created when core effects are localized to a few regions in the code.

In summary, for many reasons, it should be expected that software often contains numerous repeated structures. Hence, it makes sense to adjust (e.g.) SAT solver technology to exploit that repetition.

2.3. Theorem Prover For Large Problems

This section discusses prior work on SAT solving for software engineering applications. From this review, we will argue that the QuickSampler tool from ICSE’18 [12] is an appropriate comparison algorithm for our Snap study.

As shown in Table 1 much prior research has explored scaling theorem proving for software engineering. One way to tame the theorem proving problem is to simplify or decompose the CNF formulas. A recent example in this arena was GreenTire, proposed by Jia et al. [42]. GreenTire supports constraint reuse based on the logical implication relation among constraints. One advantage of this approach is its efficiency guarantees. Similar to the analytical methods in linear programming, they are always applied to a specific class of problem. However, even with the improved theorem prover, such methods may be difficult to be adopted in large models. GreenTire was tested in 7 case studies. Each case study was corresponding to a small code script with ten lines of code, e.g. the BinTree in [43]. For the larger models, such as those explored in this paper, the following methods might do better.

Another approach, which we will call sampling, is to combine theorem provers Z3 with stochastic sampling heuristics. For example, given random selections for b, c, Eq. [1] might be used to generate a new test suite, without calling a theorem prover. Theorem proving might then be applied to some (small) subset of the newly generated tests, just to assess how well the heuristics are working.

The earliest sampling tools were based on binary decision diagrams (BDDs) [44]. Yuan et al. [25, 27] build a BDD from the input constraint model and then weighted the branches of the vertices in the tree such that a stochastic walk from root to the leaf was able to generate samples with the desired distribution. In other work, Iyer proposed a technique named RACE which has been applied in multiple industrial solutions [26]. RACE (a) builds a high-level model to represent the constraints; then (b) implements a branch-and-bound algorithm for sampling diverse solutions. The advantage of RACE is its implementation simplicity. However, RACE, as well as the BDD-based approach introduced above, return highly biased samples, that is, highly non-uniform samples. For testing, this is not recommended since it means small parts of the code get

### Table 1: Snap and its related work for solving theorem proving constraints via sampling.

| Reference | Year | Citation | Sampling methodology | Case study size (max|variables|) | Verifying samples | Distribution/diversity reported |
|-----------|------|----------|----------------------|---------------------|-------------------|-------------------|--------------------------------|
| [25]      | 1999 | 105      | Binary Decision Diagram | ≈1.3K               | ○                 | ○                 |
| [26]      | 2003 | 50       | Interval-propagation-based | 200               | ○                 | ○                 |
| [27]      | 2004 | 54       | Binary Decision Diagram | < 1K                | ○                 | ○                 |
| [28]      | 2004 | 141      | Random Walk + WalkSat   | No experiment conducted | ○                 | ○                 |
| [29]      | 2011 | 88       | Sampling via determinism | 6k                 | ○                 | ○                 |
| [30]      | 2012 | 25       | MaxSat + Search Tree    | Experiment details not reported | ○                 | ○                 |
| [31]      | 2014 | 29       | Hashing based           | 400K                | ○                 | ○                 |
| [32]      | 2015 | 28       | Hashing based (parallelizing) | 400K            | ○                 | ○                 |
| [33]      | 2016 | 29       | Universal hashing       | 400K                | ○                 | ○                 |
| [34]      | 2018 | 5        | Z3 + Eq. [1] flipping   | 400K                | ○                 | ○                 |
| Snap      | 2020 | this paper | Z3 + Eq. [1] + local sampling | 400K            | ○                 | ○                 |

○/●: the absence / presence of corresponding item; ○: only partial case studies (the small case studies) were reported.
explored at a much higher frequency than others.

Using a SAT solver WalkSat [45], Wei et al. [28] proposed SampleSAT. SampleSAT combines random walk steps with greedy steps from WalkSat—a method that works well for small models. However, due to the greedy nature of WalkSat, the performance of SampleSAT is highly skewed as the size of the constraint model increases.

For seeking diverse samples, some use universal hashing [46] which offers strong guarantees of uniformity. Meel et al. [33] list key ingredients of integration of universal hashing and SAT solvers; e.g. guarantee uniform solutions to a constraint model. These hashing algorithms can be applied to the extreme large models (with near 0.5M variables). More recently, several improved hashing-based techniques have been proposed to balance the scalability of the algorithm as well as diversity (i.e. uniform distribution) requirements. For example, Chakraborty et al. proposed an algorithm named UniGen [31], following by the Unigen2 [32]. UniGen provides strong theoretical guarantees on the uniformity of generated solutions and has applied to constraint models with hundreds of thousands of variables. However, UniGen suffered from a large computation resource requirement. Later work explored a parallel version of this approach. Unigen2 achieved near linear speedup on the number of CPU cores.

To the best of our knowledge, the state-of-the-art technique for generating test cases using theorem provers is QuickSampler [12] which run faster than prior work [30] [32] for larger programs (and found test suites with more valid tests [12]). QuickSampler used the heuristic that “valid tests can be built by combining other valid tests”; e.g. a new test can be built from valid tests a, b, c using ⊕ (“exclusive or”):

\[ d = c \oplus (a \oplus b) \]  

This heuristic is useful since “exclusive or” is faster than, say, running a theorem prover. QuickSampler was evaluated on large real-world case studies, some of which have more than 400K variables. At ICSE'18, it was shown that QuickSampler outperforms aforementioned Unigen2 as well as another similar technique named SearchTreeSampler [30]. QuickSampler starts from a set of valid solutions generated by Z3. Next, it computes the differences between the solutions using Eq. 1. New test cases generated in this manner are not guaranteed to be valid. QuickSampler defines three terms, we use later in this paper:

- A test suite is a set of valid tests.
- A test is valid if it uses input settings that satisfy the CNF.
- One test suite is more diverse than another if it uses more variable within the CNF disjunctions. Diverse test suites are preferred since they cover more parts of the code.

According to Dutra et al.’s experiments, the percent of valid tests found by QuickSampler can be higher than 70%. The percent of valid tests found by SNAP, on the other hand, is 100%. Further, as shown below, SNAP builds those tests with enough diversity much faster than QuickSampler.

3. About SNAP

The SNAP algorithm is shown in Fig. 2. In summary, SNAP cluster some candidate tests, then search for valid tests by proposing small mutations to the cluster centroids. Mutations are generated via the deltas described below (and deltas are applied according to their frequency of occurrence). This technique effectively removes repeated structures in the tests since many repeated structures are replaced with one centroid. Another way SNAP exploits repeated structures is that the algorithm tend to mutate across the repeated structures; i.e. the higher frequency deltas.

As to the details, within SNAP, each test is a set of zeros or ones (false, true) assigned to all the variables in a CNF formula. As shown in initial samples (steps 1a,1b), instead of computing some deltas between many tests, SNAP restricts mutation to the deltas between a few valid tests (generated from Z3). SNAP builds a pool of 10,000 deltas from N = 100 valid tests (which mean calling a theorem prover only N = 100 times). SNAP uses this pool as a set of candidate “mutators” for existing tests (and by “mutator”, we mean an operation that converts an existing test into a new one).

After that, in delta preparation (steps 2a,2b), SNAP applies Eq. 1. Step 2b sorts the deltas on occurrence frequency. This sort is used in step 3b.

In sample (steps 3a,3b), SNAP samples around the average values seen in a few randomly selected valid tests. Here, “averaging” is inferred by using the median values seen in k clusters.

0) Set up
- (a) Let N = 100; i.e. initial sample size;
- (b) Let k = 5; i.e. number of clusters;
- (c) Let suite = \emptyset; i.e. the output test suite;
- (d) Let sample = \emptyset; i.e. a temporary work space.

1) Initial samples generation:
- (a) Add N solutions (from Z3) to samples
- (b) Put all samples into suite (since they are valid)

2) Delta preparation:
- (a) Find delta \( \delta = (a \oplus b) \) for all \( a, b \in \text{samples} \)
- (b) Weight each delta by how often it repeats

3) Sampling
- (a) Find k centroids in samples using k-means;
- (b) For each centroid c, repeat N times:
  i. stochastically pick deltas \( \delta_i, \delta_j \) at prob. equal to their weight.
  ii. compute a new candidate using \( c \oplus (\delta_i \lor \delta_j) \)
  iii. verify new candidate using Z3;
  iv. if invalid, repair using Z3 (see §3.1). Add to sample;
  v. add the repaired candidate to suite;

4) Loop or terminate:
- (a) If improving (see §3.2), go to step 2. Else return suite.

Figure 2: SNAP
Note that, in step 3b, we use deltas that are more likely to be valid (i.e. we use the deltas that occur more frequently).

Step 3b.iii is where we verify the new candidate using Z3. SNAP explores far fewer candidates than QuickSampler (10 to 750 times less, see §5.2). Since we are exploring less, we can take the time to verify them all. Hence, 100% of SNAP’s tests are valid (and the same is not true for QuickSampler—see Fig. 6).

Note that in 3b.iv, we only add our new tests to the clusters if it fails verification (taking care to first repair it). We do this since test cases that pass verification do not add new information. But when an instance fails verification and is repaired, that offers new settings.

3.1. Implementing “Repair”

SNAP’s repair function deletes “dubious” parts of a test case, then uses Z3 to fill in the the gaps. In this way, when we repair a test, most bits are set and Z3 only has to search a small space.

To find the “dubious” section, we reflect on how step 3b.ii operates. Recall that the new test uses \( \delta = a \oplus b \) and \( a, b \) are valid tests taken from samples. Since \( a, b \) were valid, then the “dubious” parts of the test is anything that was not seen in both \( a \) and \( b \). Hence, we preserve the bits in \( c \oplus \delta \) bits (where the corresponding \( \delta \) bit was 1), while removing all other bits (where \( \delta \) bit was 0). For example:

- To mutating \( c = (1,0,1,1,0,0,0) \) use \( \delta = (1,0,0,0,1,0,1,0) \).
- If \( c \oplus \delta = (0,1,1,1,0,0,1,1) \) is invalid, then SNAP deletes the “dubious” sections as follows.
- SNAP preserves any “1” bits that were seen in \( \delta \).
- SNAP deletes the others; e.g. bits 2, 4, 6, 8 (0,0,1,1,0,1,0,1,0).
- Z3 is then called to figure out the missing bits of \( (0?!?!?!) \).

3.2. Implementing “Termination”

To implement SNAP’s termination criteria (step 4a), we need a working measure of diversity. Recall from the introduction that one test suite is more diverse than another if it uses more of the variable settings with disjunctions inside the CNF. Diverse test suites are better since they cover more parts of the code.

To measure diversity, we used Feldt et al.'s normalized compression distance (NCD). A test suite with high NCD implies higher code coverage during the testing. NCD uses gzip to the estimate Kolmogorov complexity of the tests. If \( C(x) \) is the length of compression of \( x \) and \( C(X) \) is the compression length of binary string set \( X \)'s concatenation, then:

\[
\text{NCD}(X) = \frac{C(X) - \min_{x \in X} C(x)}{\max_{x \in X} [C(X \setminus \{x\})]} \tag{2}
\]

To understand how the NCD is revealing the diversity of a test suite, consider the following test suite where each row in the matrix represents one test case:

\[
\begin{bmatrix}
T1 & = & \begin{bmatrix}
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 \\
0 & 0 & 0 & 1 & 0
\end{bmatrix}
\end{bmatrix}
\]

Here, \( \text{NCD}_1 = 0.142 \). Now, assuming that we have obtained the following test suite after several iterations

\[
\begin{bmatrix}
T2 & = & \begin{bmatrix}
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 \\
0 & 0 & 0 & 1 & 0 \\
1 & 0 & 0 & 0 & 0 + \\
0 & 1 & 0 & 1 & 1 + 
\end{bmatrix}
\end{bmatrix}
\]

then \( \text{NCD}_2 \) is now 0.272. Note that \( + \) marks the new test cases obtained since \( T1 \). and (b) \( \text{NCD}_2 \) is larger since the new cases cover various options in first two bits.

On the other hand, if we further consider the following test suite:

\[
\begin{bmatrix}
T3 & = & \begin{bmatrix}
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 1 & 1 + \\
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 1 & 1 + \\
0 & 1 & 0 & 1 & 0 + 
\end{bmatrix}
\end{bmatrix}
\]

then \( \text{NCD}_3 = 0.305 \). Here, due to new test cases (marked as \( + \)), we do see NCD improvements in \( T3 \), as compared to \( T2 \). Such scale of improvements, however, is not significant: from \( T1 \) to \( T2 \), we got \( 0.272 \rightarrow 0.142 = 91\% \) NCD improvements, while in the \( T3 \), we got \( 0.305 \rightarrow 0.272 = 12.1\% \) increases. This is because the new cases in \( T3 \) does not explore the diversity of new bits, such as the third bit.\footnote{In this example, we examine the diversity via single bit. However, the NCD also examines the bits-group, such as the combinations of bit pair \((x,y)\), or bit tuple \((x,y,z)\) etc.}

Another point to note is that NCD is presenting the diversity of a string-block (i.e. every substring matters). One substring \( x \) where \( C(x) \rightarrow 0 \) does not imply NCD \( \rightarrow 0 \). This is because the \( x \) itself can attribute a lot to NCD of the whole string-block. Take the aforementioned \( T1 \) as an example: among all three cases \( x_1, x_2 \) and \( x_3, C(x_1) \rightarrow 1 \), NCD \((x_1 \cup x_2 \cup x_3) \ll 1 \).

3.3. Other Engineering Choices

SNAP takes great care in how it calls a theorem prover. Theorem provers are much slower for generating new tests than repairing invalid tests than for verifying that a test is valid (since there are more options for generation than for repairing than for verification). Hence, SNAP needs to verify more than it repairs (and also do repairs more than generating new tests). More specifically:

- The call to Z3 in step 1a is a generating call. This can be slowest since this must navigate all the constraints of our CNF. Therefore, we only do this \( N = 100 \) times.
4. Experimental Set-up

4.1. Code

To explore the research questions shown in the introduction, the SNAP system shown in Fig. 2 was implemented in C++ using Z3 v4.8.4 (the latest release when the experiment was conducted). A k-means cluster was added using the free edition of ALGLIB [49], a numerical analysis and data processing library delivered for free under GPL or Personal/Academic license. QuickSampler does not integrate the samples verification into the workflow. Hence, in the experiment, we adjusted the workflow of QuickSampler so that all samples are verified before termination, which is the same as SNAP as in §3.2. Also, the outputs of QuickSampler were the assignments of independent support. The independent support is a subset of variables which completely determines all the assignments to a formula. In practice, engineers need the complete test case input; consequently, for valid samples, we extended the QuickSampler to get full assignments of all variables from independent support’s assignment via propagation.

4.2. Case Studies

Table 2 lists the case studies used in this work. We can see that the number of variables ranges from hundreds to more than 486K. The large examples have more than 50K clauses, which is very huge. For exposition purposes, we divided the case studies into three groups: the small case studies with vars < 6K; the medium case studies with 6K < vars < 12K and the large case studies with vars > 12K.

For the following reasons, our case studies are the same as those used in the QuickSampler paper:
- We wanted to compare our method to QuickSampler;
- Their case studies were online available;
- Their studies are used in many papers [31, 32, 33, 12].

These case studies are representative of scenarios engineers met in software testing or circuit testing in embedded system design. They include bit-/blasted versions of SMTLib case studies, 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 theorem proving. For more introduction of the case studies, please see [32, 12].

For pragmatic reasons, certain case studies were omitted from our study. For example, we do not report on diagStencilClean.sk_41_36 in the experiment since the purpose of this paper is to sample a set of valid solutions to meet the diversity requirement; while there are only 13 valid solutions from this model. The QuickSampler spent 20 minutes (on average) to search for one solution.

Also, we do report on the case studies marked with a star (*) in Table 2. Based on the experiment, we found that even though the QuickSampler generates tens of millions of samples for these examples, all samples were the assignment to the independent support (defined in §4.1). The omission of these case studies is not a critical issue. Solving or sampling these examples is
Figure 3: RQ1 results: Time to terminated (seconds). The y-axis is in log scale. The SNAP sampling time for s1238a_3_2 and parity.sk_11,11 is not reported since their achieved NCD were much worse than QuickSampler’s (see Fig. 6). Fig. 4 illustrates the corresponding speedups.

not difficult; since they are all very small, as compared to other larger case studies.

4.3. Experimental Rig

We compared SNAP to the state-of-the-art QuickSampler, technique. To ensure a repeatability, we update the Z3 solver in QuickSampler to the latest version.

To reduce the observation error and test the performance robustness, we repeated all experiment 30 times with 30 different random seeds. To simulate real practice, such random seeds were used in Z3 solver (for initial solution generation), ALGLIB (for the k-means) and other components. Due to space limitation, we cannot report results for all 30 repeats. Instead, we report the medium or the IQR (75-25th variations) results.

All experiments were conducted on Xeon-E5@2GHz machines with 4GB memory, running CentOS. We only used one core per machine.

5. Results

The rest of this paper use the machinery defined above to answer the four research questions posed in the introduction.

5.1. RQ1: How Much Faster is the SNAP Tactic?

Fig. 3 shows the execution time required for SNAP and QuickSampler. The y-axis of this plot is a log-scale and shows time in seconds. These results are shown in the same order as Table 2. That is, from left to right, these case studies grow from around 300 to around 3,000,000 clauses.

For the smaller case studies, shown on the left, SNAP is sometimes slower than QuickSampler. Moving left to right, from smaller to larger case studies, it can be seen that SNAP often terminates much faster than QuickSampler. On the very right-hand side of Fig. 3 there are some results where it seems SNAP is not particularly fastest. This is due to the log-scale applied to the y-axis. Even in these cases, SNAP is terminating in less than an hour while other approaches need more than two hours.

Fig. 4 is a summary of Fig. 3 that divides the execution time for both systems. From this figure it can be seen:

**Conclusion #1:** SNAP terminated 10 to 3000 times faster than QuickSampler (median to max).

There are some exceptions to this conclusion, where QuickSampler was faster than SNAP (see the right-hand-side of Fig. 5). Those cases are usually for small models (17,000 clauses or less). For medium to larger models, with 20,000 to 2.5 million clauses, SNAP is often orders of magnitude faster.
5.2. RQ2: Does the Snap tactic find fewer test cases?

Table 3 compares the number of tests from QuickSampler and Snap. As shown by the last column in that table:

**Conclusion #2:** Test cases from Snap were 10 to 750 times smaller than from QuickSampler (median to max).

Hence we say that using Snap is easier than other methods, where “easier” is defined as per our Introduction. That is, when test suites are 10 to 750 times smaller, then they are faster to run, consumes less cloud-compute resources, and means developers have to spend less time processing failed tests.

5.3. RQ3: How “good” are the tests found via the Snap tactic?

Generating small test suites, and doing so very quickly, is not interesting unless those test suites are also “good”. This section applies two definitions of “good” to the Snap output:

- **Credibility:** Recalling Fig. 1, test suites need to satisfy the CNF clauses generated from source code. As defined in the introduction, we say that the “more credible” a test suite, the larger the percentage of valid tests.

- **Diversity:** A CNF clause is conjunction of disjunctions. Diversity measures how many of disjunctions are explored by the tests. This is important since a high diversity means that most code branches are covered.

### 5.3.1. Credibility

Regarding credibility, we note that Snap only prints valid tests. That is, 100% of Snap’s tests are valid. The same cannot be said for QuickSampler. That algorithm ran so quickly since it assumed that tests generated using Eq. 1 did not need verification. To check that assumption, for each case study, we randomly generated 100 valid solutions, \( S = \{s_1, s_2, \ldots, s_{100}\} \) using Z3. Next, we selected three \( \{a, b, c\} \in S \) and built a new test case using Eq. 1, i.e. new = c ⊕ (a ⊕ b).

Table 3 lists the number of identical deltas seen in 100\(^2\) of those deltas. We rarely found large sets of unique deltas; i.e. among the 100 valid solutions given by Z3, many \( \delta_i \)s were shared within pairwise solutions. This is important since if otherwise, the Eq. 1 heuristic would be dubious.

The percentage of these deltas that proved to be valid in step 3b.iii of Algorithm 1 are shown in Fig. 6. Dutra et al.’s estimate was that the percentage of valid tests generated by Eq. 1
was usually 70% or more. As shown by the median values of Fig. 6 this was indeed the case. However, we also see that in the lower third of those results, the percent of valid tests generated by Eq. 1 is very low: 25% to 50% (median to max). This result makes us cautious about using QuickSampler since, when the Eq. 1 heuristics fails, it seems to be inefficient.

By way of comparisons, it is relevant to remark here that Snap verifies every test case it generates. This is practical for Snap, but impractical for QuickSampler since these two systems typically process $10^2$ to $10^8$ test cases, respectively. In any case, another reason to recommend Snap is that this tool delivers tests suites where 100% of all tests are valid.

In summary, in terms of credibility, Snap’s tests are 100% “good” while other methods may find fewer “good” tests.

5.3.2. Diversity

Regarding diversity, Fig. 7 shows test diversity of our two systems (expressed as NCD ratios). Results less than one indicate that Snap’s test suites are less diverse than QuickSampler. In the median case, the ratio is one; i.e. in terms of central tendency, there is no difference between the two algorithms. A bootstrap test at 95% confidence (to test for statistically significant results), and a Cohen’s effect size test (to rule out trivially small differences) showed that in $\frac{27}{30} = 93\%$ cases, there is no significant difference (of non-trivial size).

That said, in there two cases with a statistical significant difference that are markedly less than Snap (see s1238a_3_2 and parity.sk_11_11) (Fig. 7). In terms of scoring different algorithms, it could be argued that these examples might mean that QuickSampler is the preferred algorithm but only (a) if numerous invalid tests are not an issue; (b) if testing resources are fast and cheap (so saving time and money on cloud-compute test facilities is not worthwhile); and (c) if developer time is cheap (so the time required to specify expected test output, or processing large numbers of failed tests, is not an issue).

Hence we recommend Snap since,

| Figure 6: RQ3 results for “credibility”: percentage of valid mutations found in step3b.iii (computed separately for each case study). |

| Figure 7: RQ3 results for “diversity”: Normalized compression distance (NCD) when QuickSampler and Snap terminated on the same case studies. Median results over 30 runs (and small black lines show the 75th-25th variations). Same color scheme as Table 2. |

6. Threats to Validity

6.1. Baseline Bias

One threat to the validity of this work is the baseline bias. Indeed, there are many other sampling techniques, or solvers, that Snap might be compared to. However, our goal here was to compare Snap to a recent state-of-the-art result from ICSE’18. In further work, we will compare Snap to other methods.

6.2. Internal Bias

A second threat to validity is internal bias that raises from the stochastic nature of sampling techniques. Snap requires many random operations. To mitigate the threats, we repeated the experiments for 30 times.

6.3. Hyperparameter Bias

Another threat is hyperparameter bias. The hyperparameter is the set of configurations for the algorithm. The hyperparameter used in these experiments were shown in §3.3. Learning how to automatically adjust these settings would be a useful direction for future work.

**Conclusion #3:**

Usually, Snap’s tests are far more credible and very nearly as diverse as those from QuickSampler.
How long would it take to learn better parameters? As shown in Fig. 4 it can take $10^5$ (approx) seconds to complete one run of our test generation systems. Standard advice for hyperparameter optimization with (say) a genetic algorithm is to mutate a population of 100 candidates over 100 generations [50]. Allowing for 20 repeats (for statistical validity), then the runtimes for hyperparameter optimization experiments could require:

$$10^5 \times 100 \times 100 \times 20/3600/168/52 \approx 650 \text{ years}$$

This is clearly an upper bound. If we applied experimental hyperparameter optimizers that tried less than 50 configurations (selected via Bayesian parameter optimization [51 52]), then that runtimes could be three years of CPU:

$$10^5 \times 50 \times 20/3600/168/52 \approx 3 \text{ years}$$

Yet another method, that might be more promising, is incremental transfer learning where optimizers transfer lessons learned between hyperparameter optimizations running in parallel [53]. In this approach, we might not need to wait $10^5$ seconds before we can find better parameters.

In summary, it would be an exciting and challenging task to perform hyperparameter optimization in this domain.

6.4. Construct Validity

There are cases where the above test scheme would be incomplete. All the above assumes that the the constraints of the program can be expressed in terms of the literals seen within the conditionals that define each branch of a program. This may not always be true. For example, consider constraints between fields of buried deep within a nested data structure being passed around the program. To address constraints of that type, we would need access to (e.g.) invariants that many be defined within those structs, but which are invisible to the tests in the path conditionals. Strongly typed languages like Haskell or OCaml which can reason about nested types might be of some assistance here. This would be a promising area for future work.

6.5. External Validity

Apart for issues of nested type constraints, this section lists two other areas that would require an extension to the current SNAP framework. Specifically, SNAP is not designed for testing non-deterministic or nonfunctional requirements.

Functional requirements define systems functions; e.g. “update credit card record”. On the other hand, a non-functional requirements specify how the system should do it. For example, nonfunctional requirements related to software “ilities” such as usability, maintainability, scalability, etc. When designing tests for nonfunctional requirements, it may be required to access variables that are not defined in the conditionals that define program branches; (e.g. is the user happy with the interaction?). SNAP does not do that since it draws its tests only from the variables in the branch tests.

As to testing non-deterministic systems, a deterministic function is one where the output is fully determined by their inputs; i.e. if the function is called $N$ times with the same inputs then in a deterministic environment, we would expect the same output. On the other hand, a non-deterministic function is one where identical inputs can lead to different outputs. When designing tests for non-deterministic systems, it would be useful to make multiple tests fall down each program branch since that better samples the space of possible non-deterministic behaviours within that branch. SNAP may not be the best tool for non-deterministic systems since, often, it only produces one test for each of the branches it visits.

In future work, it would be insightful to consider how SNAP might be extended for non-functional and/or non-deterministic systems.

6.6. Algorithm Bias

Our results used a termination criteria based on NCD, which is different from some prior work. So is NCD a fair diversity comparison metric?.

To explore this, we need some way to compare the results of text case generation algorithms, given the same CPU allocation, i.e. getting rid of NCD. Fig. 8 shows one way to make that comparison (this figure comes from the QuickSampler paper):

- Three different test case generation algorithms [12, 30, 32] (and a uniform random generator) are executed.
- Each algorithm was given 10 hours of CPU.
- Fig. 8 counts the repeated solutions within each run. That figure shows that (e.g.) 25,000 solutions are found 15 times (approximately) within all four methods.

The authors of the QuickSampler paper used Fig. 8 to argue that, assuming a large CPU allocation, then at the end of the run, all these algorithms achieve similar solution diversity. Aside: just to defend QuickSampler here– merely because the same solutions are found in Fig. 8 by different methods does not mean that there is no benefit to QuickSampler. As discussed in [12], QuickSampler wins over the other algorithms of Fig. 8 since (a) it scales to larger problems and (b) it produces test suites with more valid tests, faster than previous methods.

To illustrate SNAP’s diversity in a similar manner to Fig. 8 we have the following observations:
• Recalling the Table 3 results: SNAP found far fewer test cases than other algorithms. Hence, we cannot use the y-axis of Fig. 8 to compare our method to previous methods.

• We need another non-NCD measure of diversity that does not favor either QuickSampler or SNAP. For that purpose, we used Shannon Entropy $[5, 4]$, i.e.

$$H(p) = -p \log_2 p - (1 - p) \log_2 (1 - p)$$

where $p$ is the probability of one(1)s in the solution.

In combination, our comparison proceeds as follows. QuickSampler and SNAP were run on each case study, terminating after the same number of minutes. Since our goal was to see “what is lost by SNAP”, we terminated in times similar to the termination times seen in the RQ1 study. Specifically, those termination times were assigned to the case studies, basing on their number of clauses, from the set $\{1, 5, 10\}$ minutes. As shown above in the RQ2 study, the number of solutions generated by SNAP and QuickSampler are not in the same scale. Accordingly, we only recorded the unique solutions found in this study. At termination, we collected all unique valid test cases when the execution terminated at the given time and compared the diversities among them.

As seen in Fig. 9, we output the distribution of entropies, expressed as the percentage of tests that have that entropy (and not as Fig. 8's absolute number of test with that entropy).

Fig. 9 shows the distributions of the diversity of SNAP and QuickSampler results seen in blasted_case47, blasted_case10, s820a_7_4, s820a_15_7 and LoginService2.sk_23_36. These data sets were selected for presentation here since, in the QuickSampler paper, they were singled out for special analysis (according to that paper, these algorithm yield a large and count-

![Figure 9: Diversity distributions (from Shannon entropy). Both QuickSampler and SNAP were terminated at the same time – Blasted cases = 1min, s820a cases = 5mins, LoginService2 = 10mins. Y-axis shows valid solutions (those with same Shannon Entropy were clustered together) Y-axis shows occurrences in results.](image-url)
able range of diverse results). In that figure, we see that

- Among all these test cases, SNAP and QuickSampler yielded solutions within same entropy range.
- In fact, usually we see a very narrow range of entropy on the x-axis: In 4/5 cases, the range was less than 3%. This means that these case studies yield solutions with similar entropy.

In summary, from Fig. 9, we say that if solutions were generated by QuickSampler with a particular entropy, then it is likely that the SNAP was generating that kind of solutions as well. Hence, we do not see a threat to validity introduced by how SNAP selects its termination criteria.

6.7. Evaluation Bias

This paper has evaluated the SNAP test case generator using the five goals described in the introduction: i.e. runtime, scalability, redundancy, credibility and minimality. But as the following examples show, these are not the only criteria for assessing test suites. For future work it could be useful and insightful to apply other evaluation criteria.

Firstly, Yu et al. [19] discuss the information needs for test case prioritization. They argue that in modern complex cloud-based test environment, it can be advantageous not to run all tests all the time. Rather, there are engineering benefits to first running the tests that are most likely to fail. His results show that different kinds of systems need different kinds of prioritization schemes, but not all projects collect the kinds of data needed for different prioritization schemes. Hence it is an open issue if tools like SNAP and QuickSampler can contribute to test case prioritization.

Secondly, once tests are run, then faults have to be localized and fixed. Spectrum-based Reasoning (SR) is a research hot-spot on this. Given a system of M components, a test suite T as well as the obtained errors after executing T on the system, SR approaches utilize similarity-like coefficient to find a correlation between component and the errors location. Perez et al. [55] warn that though high-coverage test suites can detect errors in the system, it is not guaranteed that inspecting tests will yield a straightforward explanation, i.e. root cause, for the error. It will be of insightful to test how effective are QuickSampler or SNAP in localizing faults in real-world executions.

Thirdly, Ostrand et al. [56] argues that the value of quality assurance methods is that they focus the analysis on what parts of the code base deserve most attention. By this criteria, we should assess test suites by how well they find the most bugs in the fewest lines of code.

Fourthly, a common way to assess test suite generators is via the uniformity of the generated tests [57]. Theorem provers report their solutions in some implementation-specific order. Hence, it is possible that after running a theorem prover for some finite time, then the solutions found in that time may only come from a small “corner” of the space of possible solution [51]. When test for uniformity for a theorem prover sampling the space of N possible tests, then the frequency of occurrence of some test Ti should be approximately 1/N.

We argue that issues of uniformity are less important than branch coverage (which is measured above as diversity, see §6.6). To make that argument, we draw a parallel from the field of data mining. Consider a rule learner that is building a rule from the set of all possible literals in a data sets. In theory, this space of literals is very large (all attributes combined with all their ranges combined any number of logical operators and combined to any length of rule). Nevertheless, a repeated result is that such learners can terminate very quickly [58] since, rather that searching all literals, these learners need only explore the small set of literals commonly seen in the data.

We draw this parallel since the success of SNAP is consistent with the conjecture that the programs we explore are using just a small subset of the space of all settings. In that situation, uniformity is less of an issue than diversity since the latter reports how well the tests match the “shape” of the data.

We note that other researchers endorse our position here that effective testing need only explore a small portion of the total state space. Miryung Kim and colleagues [59] were testing scripts that processed up to 10^10 rows of data. In theory, the test suite required here is very large indeed (the cross-produce of all the possible values in 10^10 rows). However, a static analysis showed that those scripts could be approximated by less than 3 dozens pathways. Hence in that application, less than three dozen tests were enough to test those scripts. Note the parallels of the Kim et al. results to the SNAP work and the data mining example offered above:

- Kim et al. did not cover all possible data combinations.
- Rather, they constrained their tests to just cover the standard “shape” of the code they were testing.

Accordingly, when seeking the smallest number of tests that cover the branches, it may be a secondary concern whether or not those test cases “bunch up” and do not cover the cross product of all possible solutions.

7. Related Work

In essence, the algorithms of this paper are samplers that explore some subset of seemingly large and complex problems. Sampling is not only useful for finding test suites in theorem proving. It also has applications for other SE problems such as requirement engineering, resource planning optimization, etc [60, 61, 62, 63]. A repeated problem with all these applications was the time required to initialize the reasoning. In that initialization step, some large number of samples had to be collected. In practice, that step took a significant percentage of the total runtime of those systems. We conjecture that SNAP can solve that initialization problem. Using the techniques of this paper, it might be time now to repeat all the above work. This time, however, instead of wasting much time on a tedious generation process, we could use something like SNAP to quick start the reasoning.

As to other related work, like SNAP, the DODGE system of Agrawal et al. [64] made an assumption that given a set of solutions to some SE problem, there is much redundancy and repetition within those different solutions. A tool for software analytics, DODGE needed just a few dozen evaluations to explore billions of configuration options for (a) choice of learner,
for (b) choice of pre-processor, and for (c) control parameters for the learner and pre-processor. DODGE executed by:
1. Assign random weights to configuration options.
2. Randomly pick options, favoring those with most weight;
3. Configuring and executing data pre-processors and learners using those options;
4. Dividing output scores into regions of size $\epsilon = 0.2$;
5. When some new configuration has scores with $\epsilon$ of prior configurations then...
6. ...reduce the weight of those configuration options;
7. Go Step2
Note that after Step5, then the choices made in subsequent Step1s will avoid options that arrive within $\epsilon$ of other observed scores. Experiments with DODGE found that best learner performance plateau after just a few dozen repeats of Steps12345. To explain this result, Agrawal et al. [64] note that for a range of software analytics tasks, the outputs of a learner divide into only a handful of equivalent regions. For example, when an software analytics task is repeated 10 times, each time with 90% of the data, then the observed performance scores (e.g., recall, false alarm) can vary by 5 percent, or more. Assuming normality, then scores less than $\epsilon = 1.96 \times 2 \times 0.05 = 0.196$ are statistically indistinguishable. Hence, for learners evaluated on (say) $N = 2$ scores, those scores effectively divide into just $C = \left(\frac{1}{\epsilon \times 100}\right)^{N^2} = 26$ different regions. Hence, it is hardly surprising that a few dozen repeats of Step1,2,3,4,5 were enough to explore a seemingly very large space of options.

It has not escaped our notice that some analogy of the DODGE result could explain the curious success of the QuickSampler heuristic. Consider: one way to summarize Eq. 1 is that the space around existing valid test cases contains many other valid test cases– which is an analogous idea to Agrawal’s $\epsilon$ regions. That said, we would be hard pressed to defend that analogy. Agrawal’s $\epsilon$ regions are a statistical concept based on continuous variables while Eq. 1 is defined over discrete values.

Also, there are many other ways in which DODGE is fundamentally different to SNAP. DODGE was a support tool for inductive data mining applications while SNAP is most accurately described as a support tool for a deductive system (Z3). Further, DODGE assumes very little structure in its inputs (just tables of data with no more than a few dozen attributes) while SNAP’s inputs are far larger and far more structured (recall from Table 2 that SNAP processes CNF formula with up to hundreds of thousands of variables). Lastly, recalling Step6 (listed above), DODGE incrementally re-weights the space from which new options are generated. SNAP, on the other hand, treats the option generator as a black box algorithm since it does not reach inside Z3 to alter the order in which it generates solutions.

8. Conclusion
Exploring propositional formula is a core computational process with many areas of application. Here, we explore the use of such formula for test suite generation. SAT solvers are a promising technology for finding settings that satisfy propositional formula. The current generation of SAT solvers is challenged by the size of the formula seen in the recent SE testing literature.

Using the criteria listed in the introduction (runtime, scalability, redundancy, credibility and minimalism), we recommend the following “Snap tactic” to tame the computational complexity of SAT solving for test suite generation:

Cluster candidate tests, then search for valid tests by via small mutations to the cluster centroids.

When this tactic was applied to 27 real-world test case studies, test suite generation can run 10 to 3000 times faster (median to max) than a prior report. While that prior work found tests that were 70% valid, our SNAP tool generated 100% valid tests.

Another important result was the size of the test set generated in this manner. There is an economic imperative to run fewer tests when companies have to pay money to run each test, and when developers have to spend time studying the failed test. In that context, it is interesting to note that SNAP’s tests are 10 to 750 times smaller (median to max) than those from prior work.

We conjecture that:
• SNAP’s success is due to widespread repeated structures in software. Without such repeated structures, we are at a loss to explain our results.
• Given the presence of such repeated structures, the SNAP tactic might be useful for many other SE tasks.

Acknowledgements
This work was partially funded by an NSF award #1703487.

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