A Hybrid Genetic Algorithm and Evolutionary Strategy to Automatically Generate Test Data for Dynamic, White-Box Testing

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To Skynet. May we build it and teach it not to kill us all.

Abstract

Software testing is an important and time consuming part of the software development cycle. While automated testing frameworks do help in reducing the amount of programmer time that testing requires, the onus is still upon the programmer to provide such a framework with the inputs upon which the software must be tested. This requires static analysis of the source code, which is more effective when performed as a peer review exercise and is highly dependent on the skills of the programmers performing the analysis. It also demands the allocation of precious time for those very highly skilled programmers. An algorithm that automatically generates inputs to satisfy test coverage criteria for the software being tested would therefore be quite valuable, as it would imply that the programmer no longer needs to analyze code to generate the relevant test cases. This thesis explores a hybrid evolutionary strategy with an evolutionary algorithm to discover such test cases , in an improvement over previous methods which overly focus their search without maintaining the diversity required to cover the entire search space efficiently.

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List of Abbreviations

AST	Abstract Syntax Tree
CFG	Control Flow Graph
DbC	Design by Contract
EA	Evolutionary Algorithm
ES	Evolutionary Strategy
GA	Genetic Algorithm
OFA	One For All
OFE	One For Each
SUT	Software Under Test

Table 0.1.: List of Abbreviations

1. Introduction

1.1. Motivation

Any software, as part of the development process, needs to be tested before it is deployed. This is becoming more and more relevant in today's world, given how many critical systems are controlled by software. A bug in mission critical software could have severe and dire consequences, including the loss of equipment and possibly human life (as in the case of medical software, flight control software, mission critical rocket propulsion systems [2], etc) . As a result, it is imperative that software be thoroughly tested before it is deployed.

The testing process consumes approximately 50% of the software development timeline [3]. Considering how expensive it is to develop software, it is clear that reducing the amount of time spent on testing the SUT (**S**oftware **U**nder **T**est) would lead to an optimization of the time spent in the development process and therefore an optimization in the cost of producing software. This reduction in time may possibly come from any of the following avenues:

1. Producing software that is less complex
2. Producing software that is initially bug free, thus eliminating the need for testing
3. Automating the process of testing

1.2. Software Complexity

It is clear that software has been increasing in complexity with time. This is easily observable from the evolution of computer programs from punch cards to modern software with applications in auto-pilot systems, security (both electronically and physically, as in building security systems) and even health care systems.

Further, with advances in computational intelligence and in methodologies employed in producing hardware and the capabilities of hardware itself, it is clear that the complexity of modern software will only increase over time. Therefore, it is irrational to expect reductions in the required time to test software from a decrease in the complexity of modern software.

1.3. Eliminating the Need for Testing

Since software is architected and developed by human beings, it is almost impossible to expect a programmer to code a full specification correctly on the first attempt, without any debugging. This problem is only exasperated when one considers that most modern software is written by teams of programmers, communicating amongst themselves. Owing to errors in communication, it is even less rational to expect software collaboratively authored by such teams to be bug-free in the first release without proper testing. Even with theoretic proofs of code, there is no guarantee that there are no bugs in the software. Indeed, there is no guarantee that the developed software even accurately implements the specification that it was supposed to. This is one of the motivations behind black-box testing, or specification based testing (discussed further in sec. 2.4) [4]. Thus, it is unlikely that any optimization in SUT testing time can be achieved from eliminating the need for testing.

1.4. Automating the Process of Testing

From the discussion in sec. 1.2 and sec. 1.3, it is clear that the only remaining method of optimizing the time spent on the testing process is to automate the software testing process itself. Testing the SUT requires that the agent performing the tests (whether that agent is human or a computer program) provides the software with some inputs and compares them against the expected behavior. If the SUT behaves as expected, it passes the test, else it fails the test. While the running of the tests themselves can be executed by automated testing frameworks[5], it is the generation of input data, that is included in the test cases, that seems to require human input and resources. It is the generation of such test case data that is of most interest in this thesis.

1.5. Thesis Contribution

This thesis uses evolutionary algorithms to generate inputs with which to test software. Further, it explores problems faced by genetic algorithms arising from unfavorable initial conditions and attempts to mitigate the effects of these problems with a hybrid evolutionary algorithm (composed of an Evolutionary Strategy and a Genetic Algorithm) to find better initialization conditions for the Genetic Algorithm. Thus, the Genetic Algorithm is able to better generate inputs with which to test the software at hand. It is important to note that the work presented in this thesis is only applicable to software that compiles cleanly and does not contain syntax errors; only the semantics of the software are tested to determine if the implementation of the software is faithful to the specification of which it claims to be an implementation.

Thus, the contributions of this thesis can be summarized as:

1. Generate inputs with which to test the given software
    - Perform this generation of inputs faster than the current state of the art
    - Search the space of test-input more thoroughly than the current state of the art

2. Find more appropriate initialization conditions for the Genetic Algorithms used to solve the above objective

    - Provide a mechanism for the Genetic Algorithm to learn better initialization conditions over time, so that it may discover the inputs with which to test the software, faster than the current state of the art

1.6. Thesis Organization

The remainder of this thesis is organized as follows. chapter 2 introduces the different types of software testing and highlights the paradigm that will be studied in this thesis. Further, it contains a brief introduction to the two classes of evolutionary algorithms used in this thesis. Next, chapter 3 contains a survey of the use of genetic algorithms in software testing, classifying them into the two main paradigms against which the hybrid algorithm presented in this thesis will be compared. Finally, chapter 4 discusses the implementation of the hybrid algorithm in detail, including all parametric settings and software packages used. The analysis on the effects of these parameters is shown in chapter 5 and chapter 6 discusses the limitations and future directions of this thesis.

2. Software Testing Methodology Overview

2.1. Overview

Software testing can be broadly categorized into static and dynamic testing, explained in the following subsections.

2.2. Static Software Testing

Under the static testing paradigm, a code reviewer (e.g. a human) performs code reviews and walkthroughs of the SUT with hypothetical inputs, visually following the logical program flow. This is highly dependent on the skill of the reviewer and requires a lot of the reviewer's time [6, 7].

Further improvements in static testing allowed code to be symbolically analyzed, collecting predicates for the various paths of execution of the code. From these predicates, it is determined which paths may be infeasible or erroneous [8]. Others have used such an approach and combined these predicates with a constraint solver to determine which paths may be infeasible in a SUT [9].

2.3. Dynamic Software Testing

On the other hand, under the dynamic testing paradigm, the code for the SUT is actually run with the given test inputs. The behavior of the SUT is observed and compared against its expected behavior and the test passes or fails depending on whether the observed behavior matches the expected behavior.

As outlined in [10], Dynamic testing can be split into two categories:

Black Box Testing also known as functional testing; tests the SUT to ensure that it is faithful to the specifications from which it was authored;

White Box Testing also known as structural testing; tests the SUT to attain some level of code coverage and to test it on boundary conditions, etc (to be discussed further in sec. 2.5).

2.4. Black Box Testing

The purpose of black box testing is to ensure that the classes and functions in the SUT are indeed correct implementations of the specification, based on which they were developed [10]. As such, test cases for Black Box Testing are generally composed of input/output pairs; a SUT passes a test case if it produces the expected output, when run on the given input. Thus, this testing paradigm provides a testing methodology to ensure that the implemented functions and classes are indeed a correct implementation of the specification of the SUT (i.e. functional testing).

Note that in this paradigm, the source code is not necessarily available to the tester, as a result of which, it can not be tested for the presence of code bloat, inexecutable code, etc.

2.5. White Box Testing

White box testing, also known as structural testing, aims to test code coverage and edge cases. It is generally accepted for this purpose that "code coverage" means "covering sufficiently many paths of execution". Using path coverage as a heuristic, it is possible to determine the existence of paths in source-code that may not be executable. Further, once sufficient path coverage has been achieved, the SUT is declared to be adequately tested and any test cases not covered by the automated testing process are done so by a human agent.

This is still an improvement, as the test cases automated by the test case generator would have otherwise been generated by a human agent as well.

2.5.1. Overview

White box testing is a software testing paradigm that uses the source code of the SUT to test it. It is used to ensure that all parts of the code's structure are executable - to ensure code coverage[1]. As such, there are several forms of white-box testing[2]. In each form, the SUT is converted into a control flow graph (CFG) - a mathematical representation of the logical program flow of the SUT. In a CFG, each statement is a node and sequential statements are connected by edges. Branching statements (`if-then-else` statements, `for-loops` and `while-loops`) are characterized by multiple outgoing edges from a node, with conditions on each edge.

2.6. Path Coverage

Path coverage is one of the stronger testing criteria[3], and is widely accepted as a natural criterion of program testing completeness [8]. It requires that every path in the CFG be executed at least once by the test suite. This is true despite the fact

[1]seee sec. 2.6 for mo
[2]see B for more
[3]See for background information on the different forms of coverage in white-box testing

that the presented test suite satisfies this criterion . As a result, this thesis focuses on generating input vectors that satisfy path coverage. It is left to the tester of the software to determine what percentage of all paths in the CFG need to be induced by the inputs generated by the work presented in this thesis.

2.7. Summary

It is clear that Path Coverage is the strongest criterion with which to perform software testing. It requires the generation of a CFG from the source code of the SUT, and a threshold (set by the tester) for the minimum percentage of paths to be covered by the test suite. This thesis focusses on generating input vectors that satisfy the path coverage criterion to test SUTs.

3. Related Work

3.1. Overview

Jones et. al. [1] use a GA to structurally test software. They use single-chromosome individuals that encode test values for all input variables. For example, a population of S individuals represents S test cases for the SUT; each individual encodes a test value for each of the input variables in a segment of the chromosome. Thus, for a program with N input variables, there are $\sum_{i=0}^{N} n_i$ bits in a chromosome encoding test values for it, where n_i is the number of bits required to encode a test value for the ith input variable. An example representation of the input vector `<3,1>` is shown in Figure Fig. 3.1.

Such a GA is analogous to one that uses S individuals with N chromosomes each [1].

Input Variable 1			**Input Variable 2**	
1	0	1	0	1

Figure 3.1.: An Example of the Chromosome Representation Used in [1]

Jones et. al. use the reciprocal of the minimum absolute difference between the generated and required values for variables in path predicates as the fitness function of an individual. For example, if a path predicate requires that variables `A` and `B` are equal (i.e. `A == B`), then the fitness function would calculate $\frac{1}{|A-B|}$[2], using appropriate guards to ensure that division-by-zero cases are appropriately handled. If this GA

[1]of course, in such a GA, crossover and mutation operators will need to be modified slightly to accommodate the difference in representation. These are explained further, when analyzing the presented reproduction operations

[2]Similarly, if a path predicate requires `A>B`, then the fitness function would calculate $\frac{1}{|A-B|+1}$

were modeled with multi-chromosome individuals, then two chromosomes would be required - one each for the variables `A` and `B`. Such semantic analysis is beyond the scope of the work presented in this thesis, as a result of which the fitness function used therein does not perform such semantic analysis[3].

In addition, Jones et. al. define a uniform crossover function (as described in sec. C.1.9.1). This is analogous to performing two uniform crossovers with each of the two corresponding pairs of chromosomes in a GA using two-chromosome individuals. However, such a crossover function may move the GA to a completely new point in the solution space, and not create an individual that resides part way between the parents as is typically expected of GAs. Still, this has the advantage of escaping local optima with higher probability, especially towards the end of evolution (where one-point crossovers are unable to make a meaningful contribution due to the low probability of a one-point crossover producing an offspring that can escape a particular local optimum).

It is interesting to note that Jones et. al. use a mutation function that flips each bit in a chromosome with probability $\frac{1}{\sum_{i=0}^{N} n_i}$. This implies that it is likely that exactly one bit per chromosome will be flipped as a result of this mutation operator. This can be viewed as the alteration of one random bit in the encoding of the value of one of the input variables. While it is reasonable to use this mutation operation, using a mutation operation that flips a random bit in the encoding of each variable should also be explored. Such a mutation operation would allow the GA to escape local optima more quickly by generating mutants that are not constrained to any values along any axes in the search space (as would be the case if only one bit was mutated). Jones et. al. were able to overcome this limitation by mutating the most and least significant bits with higher probability than the rest of the bits in the chromosome. Also, the GA that they used extremely favored diversity, so that each individual in each generation of the population was unique. This is to say that in any generation of the population, there were no two individuals that encoded the same test inputs.

[3]The actual fitness function used is defined in sec. 4.5.3

While this is one way to force the GA to discover inputs that satisfied more paths in the CFG, it is also likely to generate illegal inputs. Indeed, this is one of the problems that Jones et. al. acknowledge and explicitly do not solve. As a result of ignoring this problem, it is likely that a larger than desirable fraction of the population would traverse the same path on the CFG. Since this is undesirable, a GA that is used to generate test input data should address this problem by not generating too many individuals that traverse the same path on the CFG.

Further, biasing the GA to this degree, towards diversity has the additional consequence of slowing down the runtime, as each individual (either generated randomly for the initial population or as a result of reproduction operations) must be checked for pre-existing doppelgangers (i.e. individuals in the population that are identical to and were generation prior to the currently generated individual) in the population.

On the other hand, Pei et. al. note that generating inputs to cover all possible paths in the CFG of a SUT is sometimes intractable and as a result, paths need to be selected for adequate coverage [8]. This can be achieved in one of two ways:

1. a human agent provides a list of paths that need to be covered for adequate test coverage; or
2. paths are classified into several bins and a human-selected path from each bin needs to be covered in order to satisfy coverage

(item 1) is counter intuitive to the purpose of automation. Since there are automated methods of generating CFGs [11] and computing the similarity between pairs of paths within a CFG [12], it seems that selecting appropriate paths for adequate test coverage should be automated, as part of automating the testing of the SUT. However, since this technology was not available at the time, Pei et. al. employ user-provided paths to test the individuals of their GA.

Similarly, (item 2) is also counter intuitive to the idea of automation, since it is possible to task a GA with generating inputs to cover all paths in a group [6, 12].

Pei et. al. use the same encoding scheme as in [1], but use a single point crossover function with the same mutation function. This combats the issue of generating an individual that resides in a completely new point in the solution space (high discovery). However, it fails to allow for discovery towards the end of evolution as described in [6].

Pei et. al. use a biased roulette wheel as a selection mechanism (as explained in sec. C.1.7) but use an interesting fitness function. Their fitness function computes the degree of match between the executed path and the target path, but computing the sum of distances in branch predicates described in Table Tab. 3.1[4].

Table 3.1.: Degree of Match Between Two Paths Based on Path Predicates

Branch Predicate[5]	Branch Function	When
$E1 > E2$	$E1 - E2$	$E1 - E2 > 0$
$E1 \geq E2$	0	$E1 - E2 \leq 0$
$E1 < E2$	$E2 - E1$	$E2 - E1 > 0$
$E1 \leq E2$	0	$E2 - E1 \leq 0$
$E1 = E2$	$\|E1 - E2\|$	$\|E1 - E2\| > 0$
$E1 \neq E2$	0	$\|E1 - E2\| \leq 0$

[8]

The disadvantage of using this fitness function is that it must be computed for all required paths for each individual. This makes the fitness computation for a generation of the population very expensive: ($O(P \times N)$ time complexity, where P is the size of the population and N is the number of target paths). This is one possible reason as to why their experiments were performed with smaller population sizes.

Ahmed et. al [6] devise a system that first attaches tags to the beginning and end of various functions and classes in a SUT so that the path induced by test inputs can be tracked. They use a complex fitness function that incorporates both unmatched branches (as in [8]) and unmatched nodes between candidate solutions and the target paths. However, this fitness function calculates the fitness of each individual against every target path. This has the same performance bottle-neck, previously described while discussing [8]. While they offer very little explanation as to the setup

[4]Note that in this case, the optimizing the fitness function entails minimizing the fitness value of an individual

of their GA, they do mention that computing normalized deviation[6] and violation[7] scores functions as a more effective fitness function. The fitness function they use is computed as a function of the intermediate fitness function shown in equation (3.1).

$$IF_{ij} = D_{ij} + V_{ij} \tag{3.1}$$

where

$$D_{ij} = \sum_{k=1}^{n} D_{ij,k}$$

$$V_{ij} = \sum_{k=1}^{n} V_{ij,k}$$

i the index of the target path

j the index of the individual

k the index of the node in the target path and the index of the node in the path induced by the jth individual

Here, D_{ij} is the sum of the distances between the values of variables that are composed from unmatched predicate nodes in the induced and target paths. For example, given the induced and target paths shown in Tab. 3.2, for the code shown in Algorithm 3.1 on the individual in the GA representing the inputs `<A=3,B=4>`:

$D = 1$, since the required inputs for the target path require that $A \geq B$ and the minimum value of A that satisfies this condition for the given value of B is 4 and the

[6]a measure of how many target node-branches were not traversed by the path induced by the test input

[7]a measure of how many target nodes were not traversed by the path induced by the test input

difference between 4 and the given value is $|4 - A| = 1$. Similarly, $V = 1$ since there is exactly one unmatched node between the induced and target paths. Thus, the IF for this (target path, induced path) pair is 2.

Algorithm 3.1 Algorithm to Demonstrate Deviation and Violation

```
1: function FOO(A,B)
2:     print "starting function"
3:     if A < B then
4:         print "A is smaller"
5:     else
6:         print "A is at least as large as B"
7:     end if
8:     print "ending function"
9: end function
```

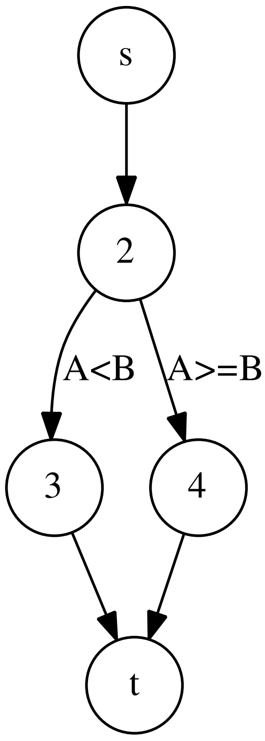


Figure 3.2.: CFG for Algorithm 3.1

Part of their methodology is to attempt to create individuals to induce all target paths. In order to do this, the GA is initialized with all target paths involved in the fitness function. As each target path comes to be induced by some individual in the GA's population, the path, as well as the individual that induced that path, are noted and evolution proceeds without the involvement of that particular path in the fitness function any further [6].

Table 3.2.: Target and Induced Paths for Algorithm 3.1

Target Path	(s,2,3,t)
Induced Path	(s,2,4,t)

Doing so poses an optimization problem for the GA. The GA starts by attempting to create individuals that induce all target paths, an impossibility in itself. However, as target paths are induced, the population of a GA is in a state wherein the removal of the induced path causes the fitness of the individuals in the population to plunge. This is to say that the existence of the path that was just induced as a member of the fitness function caused a thrust in the fitness values of the individuals in the population. The result is that individuals who may have been considered as unfit in the past (and therefore became extinct in the process of evolution), could have been considered fit once the induced path is removed; these individuals will need to be rediscovered by the GA - a redundant task, which is a significant source of inefficiency.

This problem is addressed minimally by Berndt et. al. in [10]. They maintain a fossil record - a record of all individuals that have ever been generated by the GA. With that information, the fitness function computes two values:

Novelty a measure of how unexplored the area in the search space where this individual is

Proximity a measure of how likely it is that this individual would induce a path in the CFG leading to the discovery of an error

Novelty is computed as $k_n \times \sum \sqrt{\sum (c_{ij} - f_{ij})^2}$. In this expression, c_{ij} denotes the jth parameter of the ith individual in the current generation of the population, while f_{ij} is the jth parameter of the ith fossil; and k_n is a constant used to penalize or reward such novelty.

Similarly, proximity is computed as $k_p \times \sum \sqrt{\sum (c_{ij} - e_{ij})^2}$, where e_{ij} is the jth parameter of the ith fossil record that induced a path in the CFG that caused an error; and k_p is a constant used to penalize or reward such proximity.

In order to force the discovery of new inputs, k_n is kept high and k_p is kept low.

It is important to note at this point, that because of the definition of the fitness function, the computation of the fitness function becomes progressively more expensive over time. This is because the fitness function has a time complexity of $O(F \times E)$, where F is the size of the fossil record and E is the size of the subset of the fossil record containing individuals that induced a path in the CFG that caused an error. Since the fossil record stores each generation cumulatively, $F = P \times G$ where P is the population size and G is the number of generations that have passed so far. Thus it is not difficult to see that the runtime complexity of the fitness function could easily surpass $O(P^4)$, which is catastrophically expensive. Further, downplaying the proximity measure may not be a good idea, as there may be a neighborhood of test inputs in the search space that cause errors, and downplaying proximity would not allow for thorough exploration of such neighborhoods. However, since Brendt et. al. found a good balance between k_p and k_n, they are able to force the exploration of exactly such neighborhoods. Still, such searching is very expensive and possibly dependent on the SUT.

Further, there is no method proposed to detect whether inputs in a neighborhood repeatedly induce the same path. This means that although multiple error-causing inputs may be found, it is possible that all inputs may induce the same path in the CFG. This results in a run of evolution that appears to be more successful than it really is. Though this method has been successfully used in [10] to generate inputs that induce multiple paths in the triangle classification problem, it is still unclear that it may reliably find such paths in other SUTs.

This problem can be somewhat mitigated by reducing the number of paths that need to be induced by all test inputs in a run of the GA. Such a reduction in the set of paths can be accomplished by grouping similar paths together and executing one run of the GA per group of paths, as outlined in [12]. However, in performing such grouping, the following conditions need to be met:

1. Only those paths that have adequate subpaths in common with each other

should be grouped. If this is not the case, the grouping ceases to be meaningful as it is reduced to a smaller scale version of the work presented in [10].

2. The groups need to be disjoint. If this is not the case, then the fitness function across some runs of the GA will be redundant, and thus inefficient.

3. In order for the grouping to afford a runtime optimization from a reduction in the size of the search space, the runs of the GA on each individual group must be capable of being executed independently of all other runs on other groups.

4. The group sizes should be as even as possible. Suppose this is not the case, and as a result, one of the groups contains more target paths than the others. Then a run of the GA with a fitness function using this group would take longer to finish than a run of the GA with a fitness function using a different group (with fewer target paths). As a result, even if all GAs were run in parallel, the extra time required to run a GA with this larger group of target paths will slow down the time required to complete the run of the overall set of GAs. However, this will not be the case if all groups contained an equal number of target paths; in which case, if the overall set of GAs were run in parallel, they would all finish in approximately equal amounts of time. With this in mind, Dong et. al. divide P target paths into M groups such that each group contains approximately $\frac{P}{M}$ paths, and the difference in size between any two groups is at most 1.

Dong et. al. suggest that the measure expressed in equation (3.2) should be used to compute similarity between two target paths; and that the paths can be grouped together if the similarity is higher than a threshold that they determined experimentally [12].

$$s(p_i, p_j) = \frac{|p_i \cap p_j|}{max(|p_i|, |p_j|)} \tag{3.2}$$

where p_i, p_j are target paths

and $|p_i|$ is the number of nodes in path p_i

and $|p_i \cap p_j|$ are the number of consecutive identical nodes in paths p_i and p_j.

Note that $s(p, p) = 1$ for all paths p.

It seems logical that the formation of these groups should be dictated by the similarity index computed by equation (3.2). However, Dong et. al. choose to partition target paths among groups by selecting the $\frac{P}{M}$ most similar remaining target paths. While this method of partitioning target paths into groups would work for the first few groups, it is trivial to see that in the worst case, the last group will be composed of paths that are very dissimilar to each other. As a result, a run of the GA on such a last group would indeed be a scaled down version of a run of the GA described in [6] and would suffer from the same evolutionary bottleneck discussed above.

Still, each run of the GA within a group still functions as does the GA presented in [6]. The only advantage is that the search space is much narrower and the search is therefore restricted to a smaller neighborhood of the original search space. Furthermore, since the GA starts with a random population initialization as it normally would, this information about the narrowed search space is lost. Though it is true that this information would be discovered quite quickly, it is still a learning that is not strictly necessary for the GA to undergo. A GA might indeed perform better if the initial population covered the narrow neighborhood of the search space more thoroughly, than the the entire search space evenly.

Given today's advances in computational power, focusing more on forming prudent groups rather equal sized groups might lead to a better evolutionary run-time. For instance, if in the worst case, a group contains several very dissimilar paths, then it becomes analogous to running the GA described in [6] for a smaller number of paths. Hence, a run of the GA on that group might itself be a bottleneck, almost as severe as executing one run of the GA for all target paths. Thus, it would likely be wiser to create groups of variable size which contain paths that share a similarity higher than an experimentally determined threshold. Intuitively, this provides more of a guarantee that all machines executing a run of the GA on some input would complete execution in minimal maximum running time.

This is exactly the notion explored by Gong et. al. in a follow up paper [13] in which target paths are grouped together only if they have a high similarity[8] between them. Once such groups are formed (note that the number of groups has an upper bound of the number of paths), a run of the GA is executed for each group. While in this case, the groups are formed well (to contain only paths that are very similar), the problem still remains that the initial population is created without using the knowledge that all the target paths in a group are in a narrow neighborhood of the search space. The GA is forced to learn this with the imposed penalty in the fitness function that penalizes individuals for not inducing the required target paths. Still, there are two problems with this approach:

1. The GA is required to learn that all the target paths (and therefore the fittest individuals to be evolved) are located in a relatively small neighborhood in the search space.
2. The fitness function still compares all individuals in a population to all target paths in a group.

The effects of (item 1) are somewhat mitigated by the introduction of the penalty; but that is still an ad-hoc reactionary solution and does not preempt the problem. Rather, it foresees the problem, and does nothing to prevent it from happening. A GA with an initial population that explored this neighborhood more thoroughly is more likely to produce results in a more efficient manner

On the other hand, (item 2) is an improvement on past technology. Still, it can be improved further. Clearly, the most accurate and directed evolution can be designed for exactly one path. Yet, it does not make sense to make several singleton groups (for that would negate the purpose of grouping target paths). An improvement over this will be suggested and discussed in the methodology.

[8]Similarity is computed as $s(p_i, p_j) = \frac{k-1}{max(|p_i|,|p_j|)}$, where p_i and p_j share the first k nodes

The literature holds examples of other representations of the problem space as well. For example, Zhang et. al. use a Petri Net representation to generate inputs with which to test multimedia applications [14]. They use petri nets as an alternative representation of the SUT (as compared with the CFG representation used in this thesis). Further, they rely on constraint solvers to facilitate input generation and only test for reachability. This is loosely related to the notion of detecting infeasible paths (and thus identifying code bloat) in static white box testing[9]. While Petri Nets are a helpful representation tool, they are inappropriate for use in this thesis as they cause an additional layer of abstraction and transformation between the source code of the SUT and the input generation mechanism.

Finally, Labiche et. al. use GAs to test real-time systems but are more focussed on reducing the amount of compute time required by these systems at run-time, so as not to delay the returning of results, even when under heavy load [15]; or to determine the order in which software should be tested in order to minimize the amount of time required for testing bootstrap activities such as method stubbing [16]. These focus less on generating the inputs with which to test software itself, and are therefore considered out of the scope of this thesis.

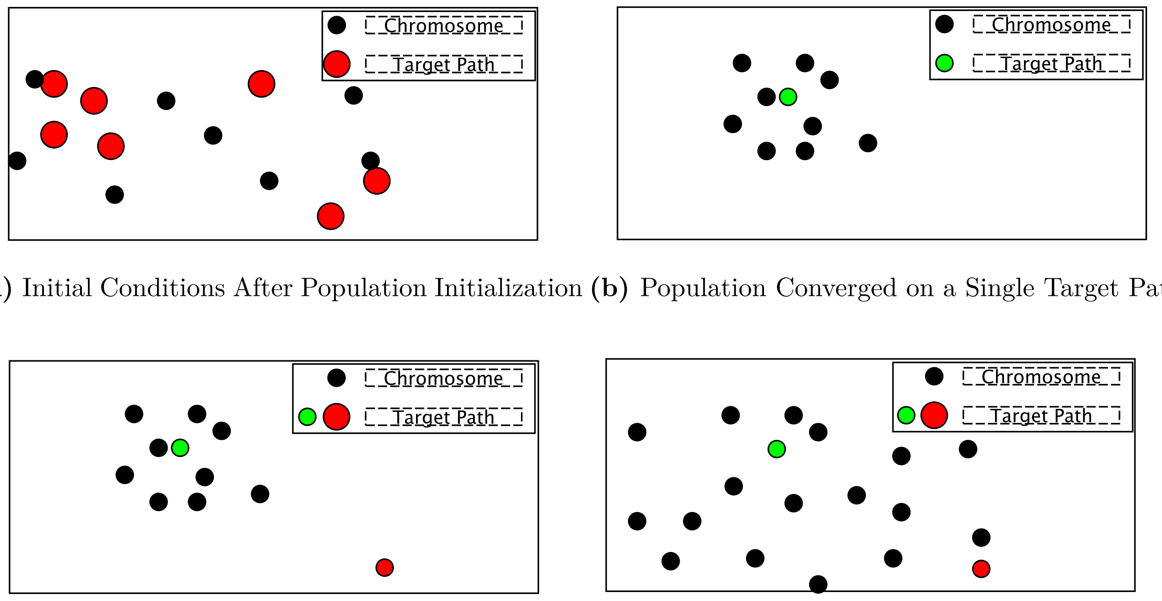
It is clear from the reviewed publications that the current methodologies can be broadly classified into the following two approaches.

3.2. One For All (OFA)

Under this paradigm, one run of a GA is used to generate test inputs that induce all target paths. The fitness measure used to compute the fitness of an individual, under this paradigm, measures a defined distance between the path induced by the individual (or the inputs that it represents) and each of the target paths. These distances then become the inputs to the fitness function which applies some form of normalization to these values.

[9]see sec. 2.5 for more

Suppose that most of the target paths fall into one small cluster of the search space and that there are a few target paths that occupy some other neighborhoods of the search space that are remote from this cluster. By sheer density of this cluster, the fitness function will favor individuals that induce paths similar to the target paths in the cluster, more than it will favor those in the remote neighborhoods. As a result, individuals that encode inputs that induce paths similar to target paths in those neighborhoods become extinct. Thus, they must be rediscovered by the GA after individuals encoding the inputs for all the target paths in the primary cluster have been discovered. The disadvantage of using this paradigm therefore, is that any GA under this paradigm has to undergo some inefficient un-learning and relearning phases, as seen in Fig. 3.3. This disadvantage is improved upon in the paradigm discussed in sec. 3.3.



(a) Initial Conditions After Population Initialization **(b)** Population Converged on a Single Target Path

(c) Converged Population and Dissimilar Target Path **(d)** Unlearning Leads to Chromosomes Similar to Initial Conditions

Figure 3.3.: Progression of a GA Demonstrating Inefficient Convergence in the OFA Paradigm

3.3. One For Each (OFE)

Under this paradigm, one run of a GA is tasked with discovering an individual that encodes the inputs for a specific target path. However, if there exists a cluster of very similar target paths, then each run of a GA, tasked with discovering one of those target paths, will have to independently converge on that cluster in the search space. This implies multiple instances of independent and redundant learning on the part of several GAs. This redundant learning is inefficient and is improved upon by the paradigm discussed in sec. 3.2.

3.4. Summary

Both the OFA and the OFE methods combat each other's shortcomings without addressing their own. Clearly, a hybrid solution encompassing both their strengths would be beneficial. Such a hybrid would also mitigate the problems that GAs face, given the uncertain nature of the randomness of their initialization conditions.

4. Implementation

4.1. Overview

As discussed in chapter 3, there are several problems concerning the use of one run of a GA per collection of target paths in order to discover test input data for a SUT. At the same time, executing one run of the GA per target path seems inefficient. Therefore, a balance needs to be struck with a hybrid system. This thesis proposes to develop such a more appropriate hybrid method to use GAs and ESs to discover test input data for a SUT.

Consider the merge sort algorithm. It functions by recursively splitting a list of numbers in half, sorting each half and merging corresponding halves together [17]. The first version of the algorithm, indeed the one still taught in introductory computer science courses today, uses a linear insertion technique to merge corresponding halves of lists; i.e. to merge two lists containing n elements each, a total of n comparisons are made. Of importance is the notion that the input list is first recursively divided into sublists until at least one and at most two singleton lists remain.

With a little analysis, it is not difficult to see that merging techniques other than linear insertion may be used to merge two sorted halves of lists, as explored in [17]. Further, note that this is only one implementation to recursively use merge sort on each half of the divided list. Indeed it is a logical choice in the interest of runtime efficiency, though it is also possible to use any other sorting technique to sort the sublists and any merging technique to merge sorted sublists.

With that in mind, this thesis explores a hybrid evolutionary strategy and genetic algorithm to discover test input data for a SUT. Many works in the literature have been reviewed that use a GA to either discover one target path [1], several target paths iteratively[2], or several target paths iteratively within a grouped set of similar target paths (without giving the GA any knowledge about such a similarity)[3].

In the spirit of the work presented in [13], this thesis will generate groupings (i.e. bins) of similar target paths. However, a run of the GA for each group will not start with a normal random population generation function. Rather, the initial population will be primed in some sense to reflect the context of the grouping of similar target paths. Thus, the algorithm begins with an ES with a random initial population, recursively classifying target paths into bins of similar target paths. This is done by computing a similarity index between every pair of target paths[4] and assigning multiple target paths to a specific bin only if their mutual similarity indices surpass an experimentally determined threshold. At each level of the recursion, an individual from the current population is computed to be the seed (explained in sec. 4.5) for each bin and mutated several times to spawn the next generation of the population of individuals for that particular bin. This continues until there is only one target path left in a bin; at which point, the GA is used with the spawned population, to find the test inputs that induce the only target path in the bin.

All algorithms presented in this thesis were implemented using the Python programming language, with the `trace` and `Pyvolution`[5] packages, and their dependencies with Python version `2.7.3`.

[1]see chapter 3 for more
[2]see chapter 3 for more
[3]see chapter 3 for more
[4]see Algorithm 4.5
[5]See sec. 4.7

4.2. Workflow

As mentioned in sec. 4.4, the target paths are known *a priori* to the hybrid evolutionary algorithm. However, that is an ambiguous assumption as it allows for the necessity that the target paths must be extracted before invoking the algorithm, most likely by a human agent. Since involving a human agent at this stage would be against to the notion of automation (especially since the set of target paths is likely to change, following each iteration of code debug, refactor, etc), the paths are automatically extracted from the SUT's source-code. The algorithms used to extract these paths are demonstrated in Algorithm 4.1 to Algorithm 4.4. Note that Algorithm 4.1 requires a list of execution scopes of the SUT, which is provided by the `cfg` package[6].

As expected, once the target paths have been extracted, the hybrid algorithm is invoked. While the workflow of the algorithm itself is presented in Fig. 4.2 and Fig. 4.3, the entire workflow, starting with the extraction of target paths from the SUT is illustrated in Fig. 4.1.

Algorithm 4.1 Finding the Parent Scope of a Scope in the SUT

```
 1: function FINDPARENTSCOPE(scope, scopes)
 2:     lowerBound ← $-\infty$
 3:     upperBound ← $\infty$
 4:     for key ∈ keys of scopes do
 5:         start ← $key_0$
 6:         end ← $key_1$
 7:         if lowerBound $\leq$ start $\leq$ $scope_0$ & upperBound $\geq$ end $\geq$ $scope_1$ then
 8:             lowerBound ← start
 9:             upperBound ← end
10:         end if
11:     end for
12:     if lowerBound==$-\infty$ & upperBound==$\infty$ then
13:         lowerBound ← 0
14:         upperBound ← max($\{key_0 \in$ keys of scopes$\} \bigcup \{key_1 \in$ keys of scopes$\}$)
15:     end if
16: end function
```

[6]See A

Algorithm 4.2 Computing the Nested Scopes of a List of all Scopes in the SUT

```
function getNestedScopes(scopes)
    answer ← new HashMap
    for scope ∈ scopes do
        if scope ∉ keys of scopes then
            $answer_{scope} \leftarrow answer_{scope} \bigcup \{scope\}$
        end if
        parent ← findParentScope(scope, scopes)
        $answer_{scope} \leftarrow answer_{scope} \bigcup scope$
    end for
    return answer
end function
```

4.3. Algorithm Overview

1. We begin with the SUT by generating its CFG using an appropriate library[7]. As a preprocessing step to the evolutionary algorithm to follow, we compute the similarity between every pair of target paths extracted from the CFG, using the similarity measure described in [13], repeated here for convenience:
   $s(p_i, p_j) = \frac{k-1}{max(|p_i|,|p_j|)}$
   where $1 \leq k \leq max(|p_i|, |p_j|)$ is maximal
   and for all $a \leq i \leq k$, the ith node in p_i is exactly the ith node of p_j (for some $1 \leq a \leq max(|p_i|, |p_j|)$).
   Further, we define a relative similarity $s_R(p_i, p_j) = \frac{s(p_i,p_j)}{\sum_{k=0}^{|PATHS|} s(p_i,p_k)+s(p_j,p_k)}$.
   This measure effectively views the two paths p_i and p_j as strings, whose characters are node numbers, and computes the ratio of the longest common substring to the length of the longer path. This is computed using a Dynamic Programming technique, as shown in Algorithm 4.7 using Algorithm 4.8, an implementation of what is discussed as the traditional method in [18] using the python programming language.

2. A random population of test input data is generated with a chromosomal structure encoding the correct number of inputs within their legal domain values (discussed in detail in sec. 4.5.1.2).

[7]SUTs in this thesis were written in the python programming language. The CFG was generated using the `cfg` package in python

3. The target paths are divided into bins based on target paths whose similarity is greater than an experimentally determined threshold. This binning algorithm is shown in Algorithm 4.5 which, in turn, uses Algorithm 4.6, Algorithm 4.7 and Algorithm 4.8.
4. The chromosome in the population that has the highest fitness among each group is then considered to be the seed for the next generation of test input data for that group of target paths. The algorithm used to determine the seed for each group is shown in Algorithm 4.9.
5. This chromosome is mutated several times in various ways to form the new population for the group of similar target paths.
6. Repeat steps item 3 - item 5 until the resulting groups of similar target paths are all singletons.
7. Execute a run of the GA algorithm per target path (i.e. per singleton group of target paths) until a test input is discovered that induces the target path.
8. Record the discovered test input and the target path and terminate the evolutionary process for that group.

This algorithm is visualized in Figure Fig. 4.2 on page 51 and Figure Fig. 4.3 on page 52.

Despite the drawbacks to executing separate runs of the evolutionary process per group or target path, the following justifications can be made:

1. This method is highly parallelizable.
2. Due to the small size of each group, the evolutionary process to execute a run of the GA would not take as long.
3. Since the initial population for the GA has already undergone several generations of evolution, the initial population is already composed of multiple very

fit chromosomes[8]. This would only expedite the process of evolution.

4. Since the GAs themselves can be executed fairly quickly (as explained above), the maximum delay of the last machine to finish such a run of the GA in a parallel environment can be reduced.

4.4. Binning, Seed Finding and Similarity Computation Algorithms

Since the target paths are known before starting the hybrid evolutionary algorithm, the core algorithm classifies the target paths into bins, finds a seed per bin and spawns a new population of individuals per bin, by mutating the seed. The algorithm then recursively repeats this process until only one target path remains in any bin; at which time, a GA is used on the bin(s) containing only one target path, while the recursion continues on all other bins. This process is illustrated in Fig. 4.4 (in the interest of brevity, the process flow of only one bin is expanded). The algorithms associated with this process flow are described in this section.

4.5. Detailed Algorithm Design

4.5.1. An Individual

An individual represents a vector of inputs to be used to test the SUT, given the domain of values each input may reside in.

4.5.1.1. Representation

The individuals used in this thesis were single-chromosome individuals, representing the values of the input variables as binary bit-strings. Thus, each gene is a disjoint

[8]These chromosomes are at least much more fit than the chromosomes in the initial, randomly generated population

section of the chromosome that encodes the value for a particular input variable. For example, Fig. C.1 (repeated in sec. 4.5.1.2 for convenience) illustrates the structure of a chromosome encoding the three inputs that form the input vector `<3,4,5>`.

4.5.1.2. Creation

In this example, each gene is created by concatenating the results of four calls to a random number generator to generate a number in the appropriate domain[9]. This number is then converted into a binary bit-string representation using a function call provided in the Python standard library. Once converted, this binary bit string is padded with `0`s on the left to ensure that it is represented by a full four bits. This algorithm is visualized in Fig. 4.6.

Input 1			**Input 2**			**Input 3**		
0	1	1	1	0	0	1	0	1

Figure 4.5.: Example Chromosome for Input Vector `<3,4,5>`

4.5.2. Population Initialization

4.5.2.1. Initialization for the Hybrid Algorithm

Given

1. the number of input variables (N)
2. the data types and the ranges of domain for the input variables
3. the number of individuals in the population (*popSize*)

the initial population is created by creating *popSize* many unique individuals. The creation of each individual is visualized in Fig. 4.6, while the generation of the initial population is visualized in Fig. 4.7.

[9]Part of Python's standard library

4.5.2.2. Initialization in the Seeded Evolutionary Strategy and the Seeded Genetic Algorithm

After the target paths have been binned (by the binning algorithm described in sec. 4.4), a seed individual is computed for each bin. This done by Algorithm 4.9 by computing the relative similarities between the path induced by each individual and the bin or target paths. The individual that induces the path with the highest relative similarity is considered to be the seed for that bin

4.5.3. Computing the Fitness of an Individual

The fitness of an individual is computed against a target path.

First, the chromosome of the individual is decoded into the test input values. The SUT is then run on these variables, using a software harness[10] and the path of execution (the induced path) is tracedfootnote 10. Next, the similarity between the induced path and the target path is computed (as discussed in sec. 4.3. This computed similarity is the fitness of the individual. This process is visualized in Fig. 4.8.

4.5.4. Selecting Individuals for Mating

Individuals in the population are selected in a fitness-proportional manner by using a roulette-wheel selection scheme as described in sec. C.1.7.

4.5.5. Crossover

A one-point crossover mechanism was used to perform crossover operations between pairs of individuals. This was used over a uniform crossover scheme, as is it possible that changing one input variable to a SUT may significantly alter the induced path. A one-point crossover ensures that only one variable's value is changed. On the other hand, the likelihood of only one input parameter to the SUT changing as the result

[10]This is accomplished by using the `tracer` module in Python's standard library

of a a uniform crossover is very low. It is for similar reasons that n-point crossovers were also not considered (for $n > 1$).

4.5.6. Mutation

A point mutation (as discussed in sec. C.1.10) was implemented. This mutation mechanism flips one random bit in the encoding of one of the input variables.

4.5.7. Spawning

A spawning function is used in the seeded GA and seeded ES algorithms to produce a full population of individuals from a seed. The spawn function used was exactly the mutation function. This allows the algorithm to generate a full population of individuals that are very similar to the seed. This allows for the creation of a population that is highly localized to the neighborhood in the search space occupied by the target paths in the bin. This process is visualized in Fig. 4.4.

4.5.8. Termination

The Seeded GA algorithm terminates either when an individual that encodes inputs that induce the desired target path is found; or when the maximum number of allowed fitness evaluations has been reached.

4.6. Implementation Parameters

The implemented algorithmic parameters for each SUT are listed in Tab. 4.1. The effects of these values are discussed in chapter 5.

Table 4.1.: Experimental Parameters

Parameter Name	Description	Experimental Range	Implemented Value
initThreshold	the hybrid's threshold to classify paths into bins based on similarity	$\{0.1, 0.2, 0.3\}$	0.1
midThreshold	the seededES's threshold to classify paths into bins based on similarity	$\{0.6, 0.7, 0.8\}$	0.7

4.7. The Pyvolution Software Package

Note: this section is an extract from a published paper in the IEEE conference Congress of Evolutionary Computation [19].

4.7.1. Previous Work

There are several frameworks geared toward the development of evolutionary algorithms, written for the Python programming language. However, many of these frameworks suffer from net being very extensible, i.e. it is not always easy to solve a new class of problem with an evolutionary algorithm using these framework. Further, all of these frameworks suffer from the problem that the framework provides no easy methodology to debug an evolutionary algorithm developed using it. Design by Contract is one way of supplementing python's native error reporting to assist with the debugging process.

4.7.2. An Example: A Genetic Algorithm to solve the Traveling Salesman Problem

The Traveling Salesman Problem on the well known Berlin-52 map, which contains 52 cities is used to demonstrate parts of the developed software package.

A genetic algorithm (GA) begins by generating an initial population of random tours for the traveling salesman. Once this initial population is created, it selects individuals to probabilistically crossover and mutate, thereby making child individuals, which comprise the next generation of this population. Repeating this process of selection, crossover and mutation over several generations allows the GA to converge on an optimal solution.

An Individual Individuals in a GA to solve this problem are made up of one chromosome. This chromosome is a `list` of 52 integers, each one representing a city on the map. In order for an individual to represent a legal solution in the solution space, the chromosome is a permutation of $\{0, 1, 2, ..., 51\}$, thus making it a valid tour for the traveling salesman problem.

Fitness of an Individual Since the optimal solution for this problem is an individual whose tour length is minimal, the fitness of each individual could be the length of the tour it represents. However, since the goal is to maximize the fitness, a better fitness measure of an individual would be the negative of the length of the tour it represents. This can be easily computed under the following assumptions:

1. Each of the 52 cities on the map is represented as a point on the xy plane
2. There is a straight line (road) connecting every pair of the 52 cities on the map

Thus, the fitness of an individual can be computed as shown in eq. 4.1

$$fitness = -dist(city_{51}, city_0) - \sum_{c=0}^{50} dist(city_c, city_{c+1}) \tag{4.1}$$

where

$dist(c_i, c_j) = \sqrt{(city_i.x - city_j.x)^2 + (city_i.y - city_j.y)^2}$

Selecting Individuals In order to create new individuals out of existing individuals, two are selected for crossover and mutation operations. The selection mechanism is fitness proportional, meaning that individuals with higher fitness are selected more often than individuals with lower fitness.

Crossover A crossover is an operation that takes two parent individuals and creates a new child individual, whose chromosomes are comprised of parts of the corresponding chromosomes from both parents (as explained in sec. C.1.9). In the case of this traveling salesman problem, one possible crossover function is defined as follows:

1. Select points A and B such that $0 < A < B < 51$
2. Make an empty child chromosome which is intended to hold 52 cities (a new tour for the traveling salesman)
3. Copy over all the cities between points A and B in the tour represented by $parent_1$ into the child chromosome
4. Copy over all the cities before point A and after point B in the tour represented by $parent_2$ into the corresponding location in the child chromosome, as long as the city does not already exist between points A and B in the child chromosome.
5. Fill in the remaining cities in the child chromosome based on the order in which they appear in $parent_1$.
6. Insert this child chromosome into a new individual - the child individual of the crossover.

Note that it is imperative that the child individual of a crossover represent a legal solution so as to ensure that the GA does not create individuals that are outside the solution space.

Mutation As explained in sec. C.1.10, a mutation is an operation that slightly changes an individual. One possible mutation is to swap the positions of two cities in the tour. Another possible mutation is to reverse the order of the cities in one contiguous part of the tour.

Note that it is imperative that a mutated individual must still represent a legal solution so as to ensure that the GA does not create individuals that are outside the solution space.

4.7.3. Introducing Design by Contract

The Design by Contract Principle Design by contract (DbC) is the principle that interfaces between modules of a software system should be governed by precise specifications. The contracts will cover mutual obligations (preconditions), benefits (postconditions), and consistency constraints (invariants) [20]. This principle is especially applicable in large modular systems with multiple levels of abstraction, such as a framework for implementing GAs.

The Advantage of Using DbC in this Framework Two of the core design principles of the python programming language are

1. Almost all expressions that a programmer tries to compute must be computed in some meaningful way.
2. All error reporting and tracebacks should be meaningful in order to help a programmer better debug their program. In particular, core-dumps and crashes should be avoided.

In most cases, these are very desirable principles in a programming language. However, when working with Genetic Algorithms (GAs), where even simple off-by-one errors can cause individual solutions in a population to leave the solution space and where mutation and crossover operations are probabilistic, bugs become difficult to reproduce and traditional step-through debugging becomes infeasible (except in a small subset of the program's functional body). While this error reporting explains why the GA may crash, it does very little to reveal the real source of the error (for example, it may be clear that two variables of very different data types may not be added together, but the bug that causes either variable to be of that different datatype is not identified). Thus, whereas the error messages may be well written for most other algorithms, they are rendered far too cryptic to help debug a GA.

Further, due to the amount of data that a GA works with on the stack, traditional print-debugging (or logging) would also be infeasible as the signal-to-noise ratio in the debug logs would be too low to be useful to a programmer.

One particularly difficult bug was found to be caused by mistyping `if a>b: a,b = b,a` as `if a<b: a,b = b,a` in the crossover function for the GA solving the traveling salesman problem [21]. This had the effect of causing this error, mid evolution: `IndexError: pop from empty list`. This is because the correctly implemented crossover function, despite implementing its specification accurately, made certain assumptions that were incorrect. These assumptions were incorrect due to the aforementioned mistyping. However, the raised `IndexError` does not provide any information as to the source of this error.

Further, assuming that the GA runs without any errors, if the end result of a run of the GA is unfavorable or unexpected, it is unclear as to whether this divergence in expectations was caused by the stochastic nature of evolution (and incorrectly programmed parameters thereof) or by faulty programming logic. As a result, implementing contracts for each of the functions in this framework allows programmers to catch errors in programming logic early, trace the error to the buggy function in the program, and eliminate programming errors as the reason for unexpected results at the end of a run of the GA (assuming that the correct contracts have been implemented).

4.7.4. A DbC Framework for Python

In order to implement DbC to this GA framework, two packages were evaluated. These packages are reviewed in this section

PyContract PyContract is a DbC package that allows a programmer to annotate functions with contract expressions. The fact that its syntax allows for the development of richer contract expressions makes up for the shortcomings of other DbC frameworks, making it the preferred framework with which to implement DbC expressions for this package.

For example, the contract expressions in algorithm Algorithm 4.10 for a function that multiplies two matrices denotes that:

1. The input parameter `a` is a `nested list` of positive row and column dimensions.
2. The input parameter `b` is an `array` of positive row and column dimensions.
3. The number of rows in `b` is equal to the number of columns in `a`.
    a) This ensures that `a` and `b` are of compatible dimensionalities.
4. The function returns an array of `M` rows and `P` columns.
5. The inputs are unchanged

In addition, PyContract also allows for the expression of class invariants. These are expressible with the `inv` declaration in the contract expressions along with referencing `self`. However, there is a limitation to PyContract's ability to express invariants in functions. For example, it is not possible to express contracts about loop invariants whose expressions contain variables that are not class variables, but are instead local to the scope of the function itself. In order to express such invariants in this GA framework, a hybrid approach using both PyContract and assert statements native to Python were used.

As previously stated, the DbC implementation for this GA framework is a hybrid of PyContract and `assert` statements native to the python programming language. For example, the crossover function described in section sec. 4.7.2 has the contracts shown in algorithm Algorithm 4.11 (explained in table 4.7.4).

Table 4.2.: Explanations of Contracts in Algorithm 4.11

Contract Expression	**Explanation**
`pre:`	The next block of indented expressions are pre-conditions of this function
`isinstance(p1, list)`	`p1` is a list
`isinstance(p2, list)`	`p2` is a list
`len(p1) == len(p2)`	`p1` and `p2` have equal number of elements
`sorted(p1) == range(len(p1))`	`p1` is a permutation of $\{0, 1, 2, ..., L-1\}$ where `L` is the number in elements in `p1`
`sorted(p2) == range(len(p2))`	`p2` is a permutation of $\{0, 1, 2, ..., L-1\}$ where `L` is the number in elements in `p2`
`post[p1, p2]:`	The next block of indented expressions are post-conditions of this function on the variables `p1` and `p2`
`p1 == __old__.p1`	`p1` remains unchanged as a result of executing this function
`p2 == __old__.p2`	`p2` remains unchanged as a result of executing this function
`post:`	The next block of indented expressions are general post-conditions of this function
`isinstance(__return__, list)`	A `list` is returned

`len(__return__) == len(p1)`	The number of elements in the returned list is equal to the number of elements in `p1`
`id(__return__) not in [id(p1), id(p2)]`	The returned list does not reside in the same memory location as either `p1` or `p2`
`forall(__return__, lambda city: city in p1 and city in p2)`	Every element in the returned list exists in `both p1` and `p2`
`len(set(__return__))== len(__return__)`	Every element in the returned list occurs exactly once

Notice that there are no contracts that express invariants in the PyContract syntax. This is because contractual invariant clauses may express invariants that refer to only class variables. This does not include variables that are not bound to a defined class but are still within the local scope of the function for which the contract is written. Therefore, loop invariants that refer to loop counters cannot be checked using PyContract. As a result, the second part of the hybrid implementation of contract checking uses `assert` statements native to python to enforce invariants which express properties of non-class-variables within the local scope of the function. For example, contractual loop invariants are expressed in Algorithm 4.12.

These loop invariant contract expressions check to ensure that the invariant is True and the hyp. guard is False in every iteration of the while-loop.

It is important to note that GAs themselves usually have a long runtime. Furthermore, contract checking implies that every time a function is called, the pre-conditions, post-conditions and invariants of that function are verified. In addition, checking post-conditions in this framework, especially against values of variables before the execution of the function requires making a copy of the stack before each execution. The result is a drastic increase in the runtime of these functions, explicitly because of contract checking. In order to alleviate such effects of DbC on the GA framework, a new configuration parameter was introduced into the framework. This parameter (named `testmode`) is a boolean flag, which when set `True` forces contract checking on all functions for which a contract has been written. When this flag is set `False`, the contracts are not checked, allowing the GA framework to operate at its maximal efficiency without being interrupted by contract checking [22]. Therefore, the ideal usage of a simulation using this framework (now augmented with DbC) would be to run the simulation once for a very short period of time (evolutionary time, not realtime) to ensure that all contracts are being followed. Once it is clear that all contracts are being followed, then the simulation may be run for the required (presumably longer) period of time without contract checking, so that it may run at an efficiency that is not hindered by contract checking.

A list of all contracts implemented in this framework is available in the official documentation of the Pyvolution package [22].

4.8. Summary

The hybrid algorithm uses an ES to recursively classify target paths into bins, based on similarity between target paths. Each bin is assigned a seed member from the population, based on the generalizability of the seed to each member of the bin. This seed is then mutated several times to form the next generation of the population, and the ES continues. This continues until there is exactly one tartget path in a bin, at which time a GA is run with the then current population for that bin. This form of recursive clustering and seed selection based on generalizability combats the inefficiencies due to unlearning, faced by the OFA method; and the inefficiencies due to redundant relearning, faced by the OFE method.

This hybrid evolutionary algorithm is implemented using the Pyvolution evolutionary algorithms framework; the CFG of the SUT is obtained using the CFG software package.

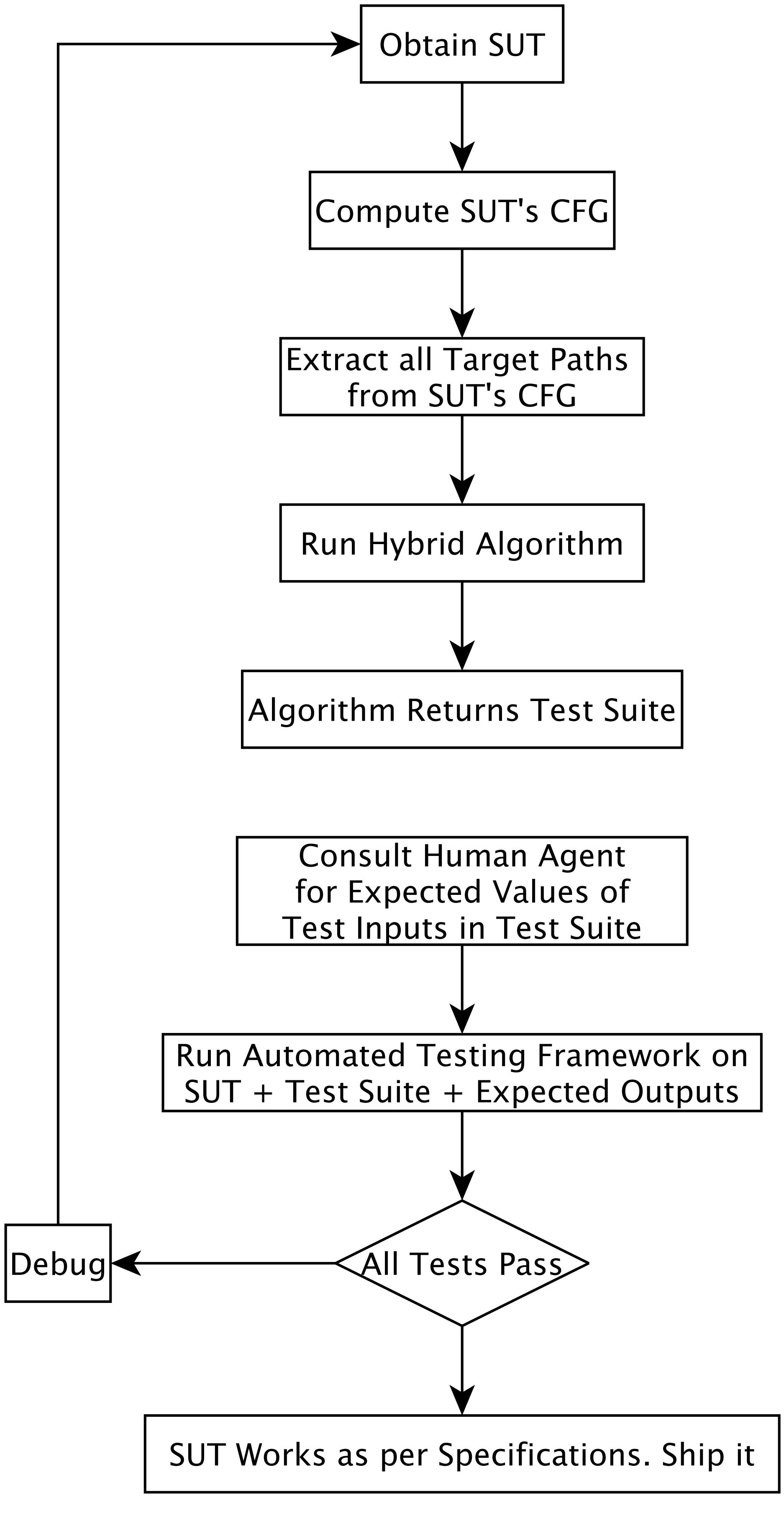

Obtain SUT
Compute SUT's CFG
Extract all Target Paths from SUT's CFG
Run Hybrid Algorithm
Algorithm Returns Test Suite
Consult Human Agent for Expected Values of Test Inputs in Test Suite
Run Automated Testing Framework on SUT + Test Suite + Expected Outputs
All Tests Pass
Debug
SUT Works as per Specifications. Ship it

Figure 4.1.: Full Process Workflow

Algorithm 4.3 Path Generator's Helper Function

```
1: function PATHGENHELPER(G=(V,E), scopes, paths, start, end, curr)
2:     answer ← new empty array
3:     if curr belongs to the current scope (indicated by start and end) then
4:         if $|\{p \in paths | p_0 = 0\}| = 0$ then
5:             currPath ← new singleton array containing curr
6:             if {(u,v) ∈ E|u} = ∅ or {(u,v) ∈ E|u} = {$NULL$} then
7:                 return new singleton array containing currPath
8:             end if
9:             for v ∈ {$v$|(u,v) ∈ E & u=curr} do
10:                if $v \leq curr$ then
11:                    if $v = NULL$ then
12:                        Add -v to currPath
13:                        Add currPath to answer
14:                    elseadd currPath to answer
15:                    end if
16:                else
17:                    for path ∈ PATHGENHELPER(G, scopes, paths, start, end, v) do
18:                        Concatenate currPath with path
19:                        Add currPath to answer
20:                    end for
21:                end if
22:            end for
23:            return answer
24:        else
25:            for path ∈ $\{p \in paths | p_0 = curr\}$ do
26:                currPath ← MEMCPY(currPath) for path in pathGenHelper(G, scopes, paths, start, end, currPath[-1])
27:                for path ∈ PATHGENHELPER(G, scopes, paths, start, end, $\text{currPath}_{|\text{currPath}|-1}$) do
28:                    Concatenate the array comprised of all but the first element of currPath to currPath
29:                    Add currPath to answer
30:                end for
31:            end for
32:            return answer
33:        end if
34:    else
35:        if $curr = NULL$ then
36:            return new vector containing an empty vector
37:        else
38:            return new vector containing a singleton vector containing $-|curr|$
39:        end if
40:    end if
41: end function
```

Algorithm 4.4 The Path Generator Algorithm

```
1: function PATHGENERATOR(G=(V,E), scopes, root)    ▷ the "root" parameter defaults to NULL, if it is not specified
2:     answer ← new empty vector
3:     paths ← new empty vector
4:     rootWasNull ← FALSE
5:     for scope ∈ $\text{scopes}_{\text{scope}}$ do
6:         if scope does not contain any scopes within itself then
7:             if $\text{scope}_0$ is a terminal node in the CFG of the SUT or a function definition node then
8:                 toor $leftarrow$ first element of $\{s \in scopes_{\text{scope}} | s \neq NULL\}$
9:                 if toor contains any scopes within itself then
10:                    callWithScopes ← new HashMap
11:                    for $scope$ ∈ keys of scopes$|k = toor \textbf{or} k = toor$ do
12:                        if scope ∉ keys of callWithScopes then $\text{callWithScopes}_{\text{scope}}$ ← ∅
13:                        end if
14:                        $\text{callWithScopes}_{\text{scope}}$ ← $\text{callWithScopes}_{\text{scope}} \bigcup \text{scopes}_{\text{scope}}$
15:                        pgpaths ← PATHGENERATOR(G, callWithScopes, toor)
16:                    end for
17:                else
18:                    tStart ← $\text{toor}_0$
19:                    tEnd ← $\text{toor}_1$
20:                end if
21:                Add pgpaths to answer
22:            end if
23:        else
24:            concatenate PATHGENERATOR(G, scopes, scope) to paths
25:        end if
26:    end for
27:    Add PATHGENERATOR(G, scopes, scope) to answer
28:    if $rootWasNULL = NULL$ then
29:        funcalls ← $\{path \in answer | path_0 \neq 0\}$
30:        answer ← $answer \ \setminus funcalls$
31:        loopingPaths ← $\{path \in answer | path_{|path|-1} < 0\}$
32:        tempAnswer ← new empty array
33:        answer ← $answer \setminus loopingPaths$
34:        while $|loopingPaths| \neq 0 \ \& \ \exists(p \in loopingPaths| \ \nexists(n \in p | n = |p_{|p|-1}|))$ do
35:            for loopingPath ∈ loopingPaths do
36:                extensions ← $\{f \in funcalls || f_0| = |loopingPath_{|loopingPath|-1}|\}$
37:                if $|extensions| > 0$ then
38:                    append a new empty vector to extensions
39:                end if
40:                for extension ∈ extensions do
41:                    loopingPath ← MEMCPY(loopingPath)
42:                    concatenate all but the first element of extension to loopingPath
43:                    breakMe ← false
44:                    while breakMe ≠ false and $\text{tempLoopingPath}_{|tempLoopingPath|-1} < 0 \textbf{and} \ / \ \exists(n \in tempLoopingPath_{0...|tempLoopingPath-1|} | n = tempLoopingPath_{|tempLoopingPath-1|})$ do
45:                        X ← $|tempLoopingPath_{-1}|$
```

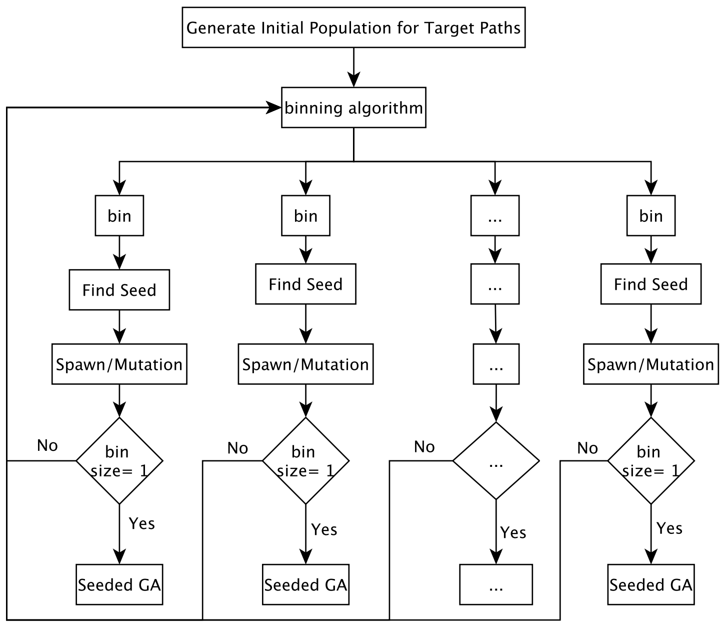


Figure 4.2.: Initialization and Seeded ES Algorithm

Algorithm 4.5 Classifying Target Paths into Bins

```
1: function binningAlgorithm(paths, threshold)
2:     bins ← {}
3:     similarities ← computeRelativeSimilarities(paths)
4:     for $p_1$ ∈ keys of similiarities do
5:         bin ← $\{p_1\}$
6:         for $p_2$ ∈ similarities[$p_1$] do
7:             if similarities[$p_1$][$p_2$] $\geq$ threshold then
8:                 bin ← bin $\bigcup$ $\{p_2\}$
9:                 for $p \in$ {keys of similarities|$p \neq p_1$} do
10:                    if $p_2$ ∈ similarities[$p$] then
11:                        similarities[$p$] ← $\{path \in$ similarities[$p$]$|path \neq p_1\}$
12:                    end if
13:                end for
14:            end if
15:        end for
16:        bins ← bins $\bigcup$ {bin}
17:        Remove $p_1$ from similarities
18:    end for
19: end function
20: return bins
```

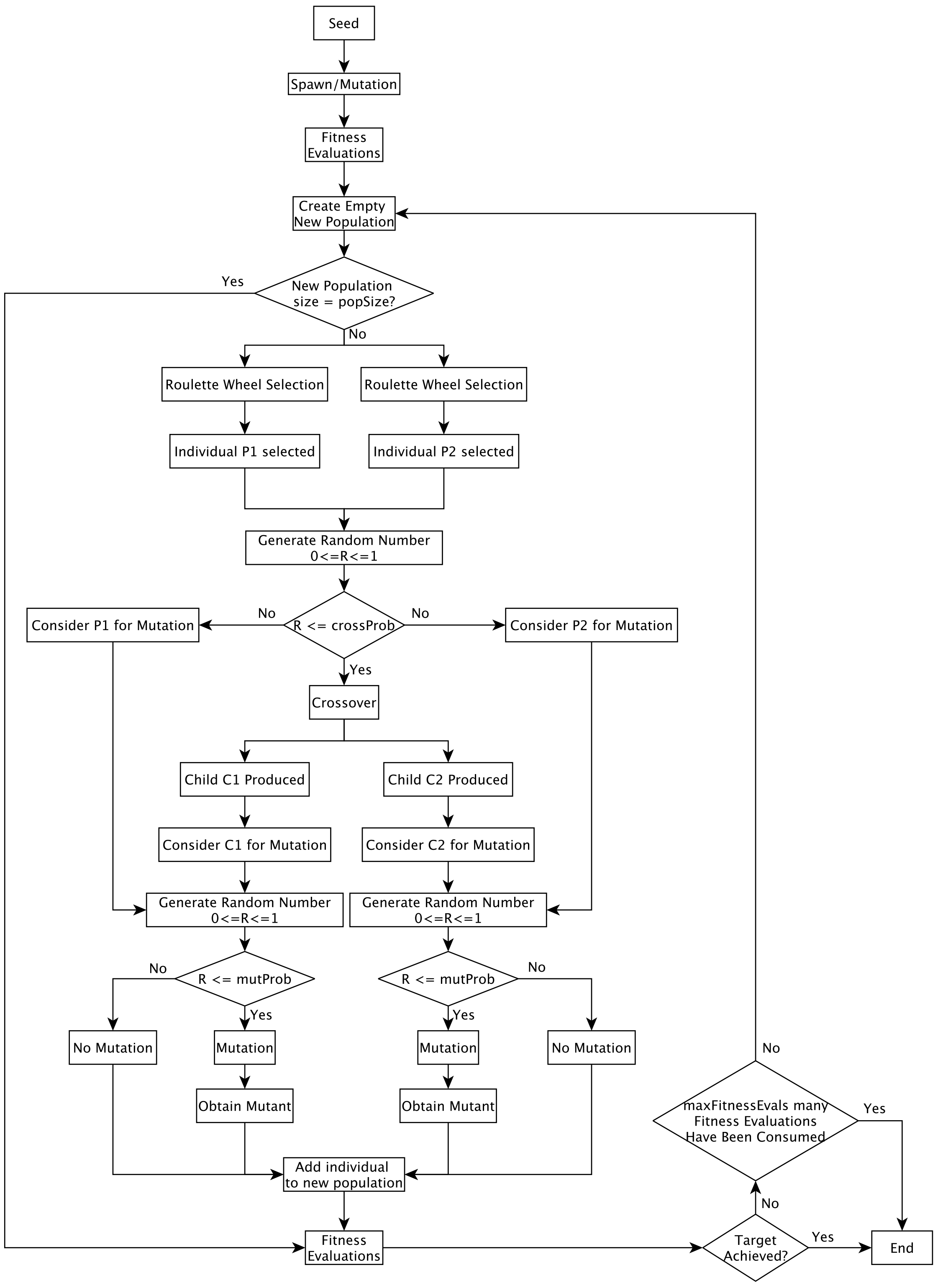


Figure 4.3.: The SeededGA Algorithm

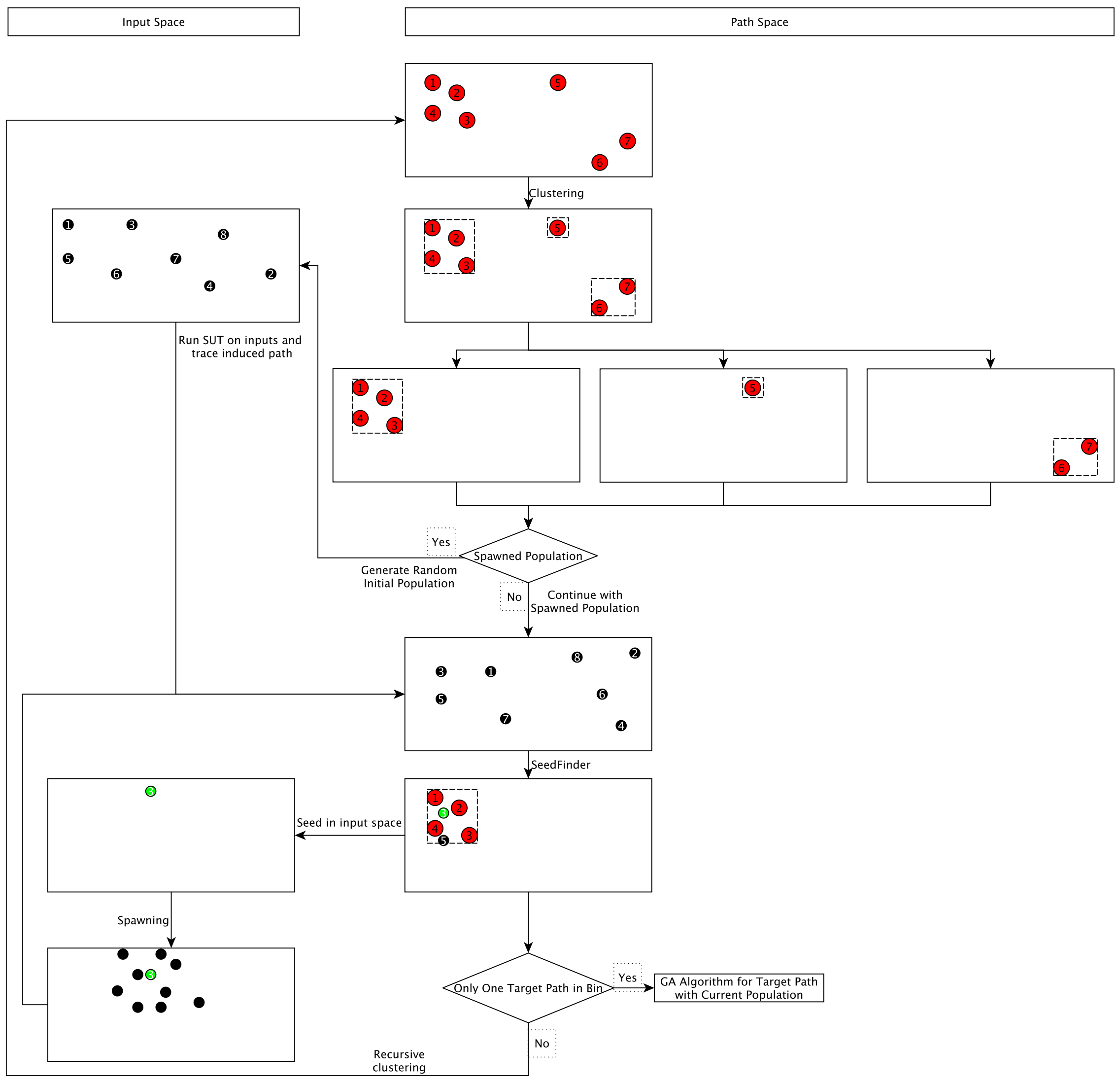

Input Space
Path Space
Clustering
Run SUT on inputs and trace induced path
Yes
Spawned Population
Generate Random Initial Population
No
Continue with Spawned Population
SeedFinder
Seed in input space
Spawning
Yes
Only One Target Path in Bin
GA Algorithm for Target Path with Current Population
No
Recursive clustering

Figure 4.4.: Process flow of Recursive Binning and Seed Finding

Algorithm 4.6 Computing Relative Similarities among Paths

```
1: function COMPUTERELATIVESIMILARITIES(paths)
2:     answer ← new HashMap
3:     for $(p_1, p_2) \in \{(p, q) \in paths \times paths | p \neq q\}$ do
4:         rawSimilarity ← COMPUTEABSOLUTESIMILARITY($p_1, p_2$)
5:         totalSimilarity ← $\sum_{p \in \text{paths}}$ COMPUTEABSOLUTESIMILARITY($p_1$,$p$) + $\sum_{p \in \text{paths}}$ COMPUTEABSOLUTESIMILARITY($p_2$,$p$)
6:         answer[$p_1$][$p_2$] ← $\frac{\text{rawSimilarity}}{\text{totalSimilarity}}$
7:         answer[$p_2$][$p_1$] ← $\frac{\text{rawSimilarity}}{\text{totalSimilarity}}$
8:     end for
9:     return answer
10: end function
```

Algorithm 4.7 Computing Absolute Similarities among Paths

```
1: function computeAbsoluteSimilarity($p_1$, $p_2$)
2:     matrix ← computeSimilarityMatrix($p_1$, $p_2$)
3:     return $\frac{\max(\text{matrix})}{max_{length}(p_1,p_2)}$
4: end function
```

Algorithm 4.8 Computing Similarity Matrix

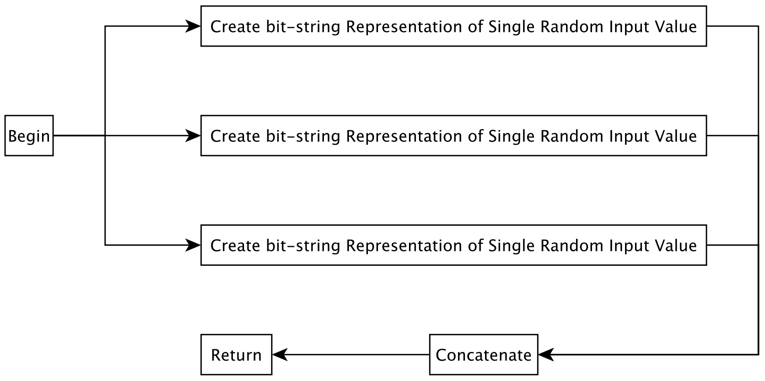
```
1: function computeSimilarityMatrix($p_1$, $p_2$)
2:     for i ← 1 ... max($|p_2| - |p_1|$, 0) do
3:         $p_1 \leftarrow p_1 \bigcup$ NULL
4:     end for
5:     for i ← 1 ... max($|p_2| - |p_1|$, 0) do
6:         $p_2 \leftarrow p_2 \bigcup$ NULL
7:     end for
8:     answer ← $\underbrace{\left.\begin{array}{|c|c|c|}\hline 0.0 & \dots & 0.0 \\ \hline \vdots & \ddots & \vdots \\ \hline 0.0 & \dots & 0.0 \\ \hline \end{array}\right\}|p_1|}_{|p_1|}$
9:     for r ← 1 ... $|p_1| - 1$ do
10:        for c ← 1 ... $|p_1| - 1$ do
11:            if $p_1[r-1] == p_2[c-1]$ then
12:                answer[r][c] ← answer[r-1][c-1] +1
13:            else
14:                answer[r][c] ← 0.0
15:            end if
16:        end for
17:    end for
18:    return answer
19: end function
```

Algorithm 4.9 Computing the Seed Individual of a Bin of Target Paths

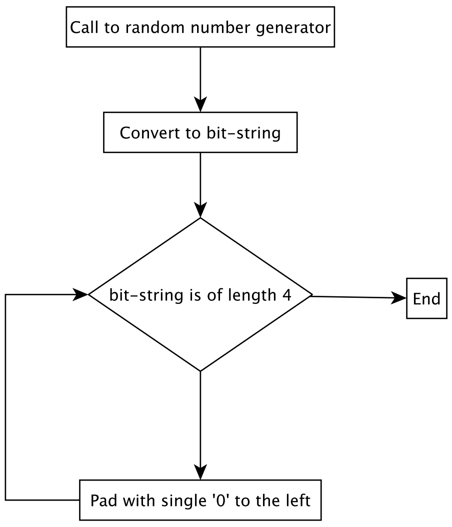
```
1: function seedFinder(individuals, targetPaths, tracer, tracerParams)
2:     bestSeed ← NULL
3:     seedSimilarity ← 0
4:     for individual ∈ individuals do
5:         inputVector ← individual[0]
6:         inputVector ← Decode binary representation into input parameters
7:         inducedPath ← trace(SUT, inputVector)
8:         inTarget ← inducedPath ∈ targetPaths
9:         Add inducedPath to targetPaths
10:        relativeSimilarities ← values of computeRelativeSimilarities(targetPath)[inducedPath]
11:        averageRelativeSimilarity ← $\frac{\sum \text{relativeSimilarities}}{|\text{relativeSimilarities}|}$
12:        if inTarget == FALSE then
13:            Remove inducedPath from targetPaths
14:        end if
15:        if averageRelativeSimilarity ≥ seedSimilarity then
16:            bestSeed ← individual
17:            seedSimilarity ← averageRelativeSimilarity
18:        end if
19:    end for
20:    return encoded version of bestSeed
21: end function
```

Algorithm 4.10 Contracts for a Matrix Multiplication Function in PyContract

```python
def matrix_multiply(a, b):
    ''' Multiplies two matrices together.
        pre:
            isinstance(a, array)
            isinstance(b, array)
            len(a) > 0
            len(a[0]) > 0
            len(b) == len(a[0])
        post:
            __old__.a == a
            __old__.b == b
            isinstance(__return__, array)
            len(__return__) == len(a)
            len(__return__[0]) == len(b[0])
    '''
```


Create bit-string Representation of Single Random Input Value
Begin
Create bit-string Representation of Single Random Input Value
Create bit-string Representation of Single Random Input Value
Return
Concatenate

(a) Concatenating Three Genes into One Chromosome


Call to random number generator
Convert to bit-string
bit-string is of length 4
End
Pad with single '0' to the left

(b) Creating a Single Gene in a Chromosome

Figure 4.6.: Creating a Single Individual Encoding 3 Input Variables

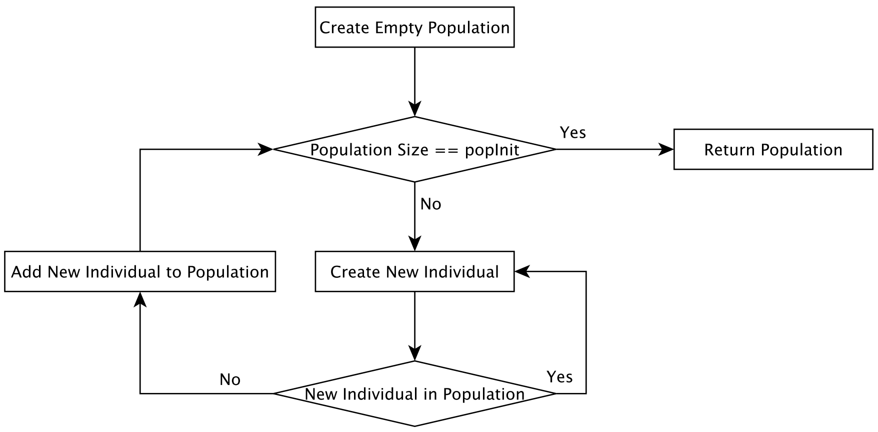

Create Empty Population
Yes
Population Size == popInit
Return Population
No
Add New Individual to Population
Create New Individual
No
Yes
New Individual in Population

Figure 4.7.: Generating the Initial Population

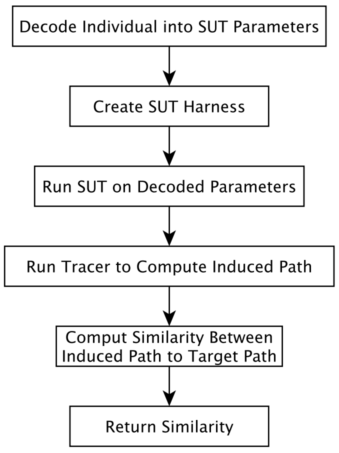

Decode Individual into SUT Parameters
Create SUT Harness
Run SUT on Decoded Parameters
Run Tracer to Compute Induced Path
Comput Similarity Between Induced Path to Target Path
Return Similarity

Figure 4.8.: Computing the Fitness of an Individual Against a Specific Target Path

Algorithm 4.11 Contracts for the Crossover function for the Traveling Salesman Problem

```
def injectionco(p1, p2):
    """
        pre:
            isinstance(p1, list)
            isinstance(p2, list)
            len(p1) == len(p2)
            sorted(p1) == range(len(p1))
            sorted(p2) == range(len(p2))
        post[p1, p2]:
            p1 == __old__.p1
            p2 == __old__.p2
        post:
            isinstance(__return__, list)
            len(__return__) == len(p1)
            id(__return__) not in [id(p1), id(p2)]
            forall(__return__, lambda city: city in p1 and city in p2)
            len(set(__return__)) == len(__return__)
    """
```

Algorithm 4.12 Contracts for the Crossover function for the Traveling Salesman Problem

```
def runTSPGA(kwargs):
    ...
    while g < maxGens:
        if testmode:
            assert g < maxGens
            assert best[1] < targetscore
    ...
```

5. Parametric Analysis and Discussion

5.1. The Benchmark SUTs

In order to test the parameters of the hybrid algorithm proposed in this thesis, three benchmark problems were used as SUTs. These SUTs and their respective CFGs are listed in this section. The triangle classification algorithm (Algorithm 5.1) is a commonly used benchmark algorithm in software testing, while the bubble-sort algorithm (Algorithm 5.2) is a more complex example of software likely to be encountered in the real world. On the other hand the simplex algorithm (Algorithm 5.3) is a SUT used to demonstrate one property of the hybrid algorithm to be discussed in further sections of this chapter.

Algorithm 5.1 The Triangle Classification Algorithm

```
function CLASSIFY(x,y,z)
    if x<y+z & y<z+x & z<x+y then
        if x≠y & y≠z & z≠x then
            return SCALENE
        else
            if x=y=z then
                return EQUILLATERAL
            else
                return ISOSCELES
            end if
        end if
    else
        return NOTATRIANGLE
    end if
end function
```

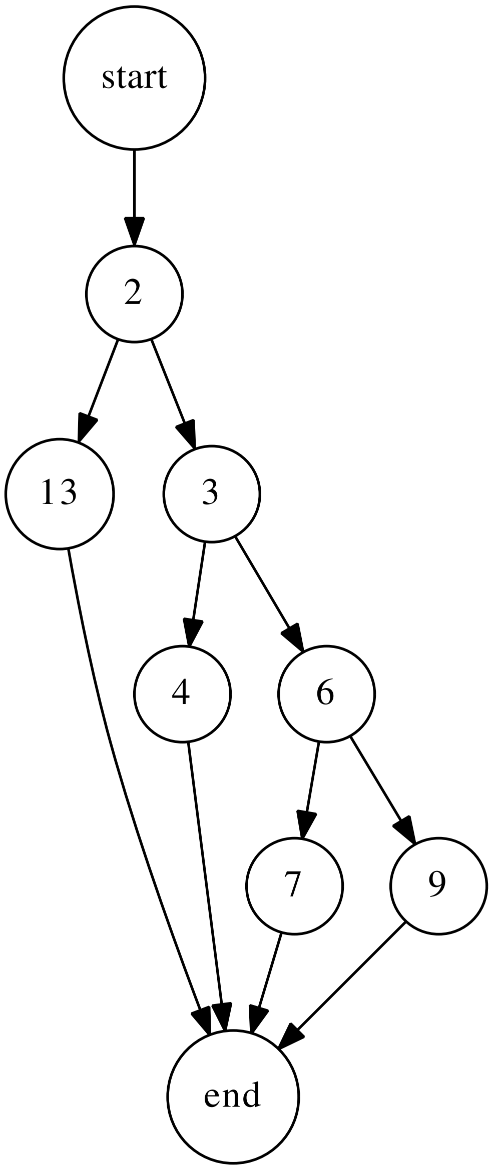


Figure 5.1.: The CFG of Algorithm 5.1

5.2. Experimental Data

The two current state of the art algorithms, namely the OFA and the OFE were run on each benchmark SUT 30 times in order to acquire statistically significant data (for these are stochastic algorithms and therefore, it is unlikely that any two distinct runs are exactly alike). Similarly, the hybrid algorithm proposed in this thesis was also run on each benchmark SUT 30 times. Performance metrics from these runs were gathered and are presented in the graphs and tables of this section. The SUTs and parameter sets in these graphs are numbered. The numbered SUTs and parameter

Algorithm 5.2 The Bubble-Sort Algorithm

```
function BUBBLESORT(L)
    for i=1 → $|L|$ do
        for j=$i + 1$ → $|L|$ do
            if $L_j > L_{j+1}$ then
                $L_i \leftarrow L_{i+1}$
                $L_{i+1} \leftarrow L_i$
            end if
        end for
    end for
end function
```

sets and their corresponding values are listed in Table Tab. 5.1 on page 60. In order to determine the best similarity threshold for the binning aspect of the hybrid algorithm, various values within a subrange of $[0, 1]$ were experimented with. These values were used in parameter sets as shows in Table Tab. 5.1 on page 60.

Table 5.1.: Identifying Parameter Sets, SUTs, and Algorithms

(a) Identifying Parameter Sets

Parameter Set	initThreshold	midThreshold
1	0.1	0.6
2	0.1	0.7
3	0.1	0.8
4	0.2	0.6
5	0.2	0.7
6	0.2	0.8
7	0.3	0.6
8	0.3	0.7
9	0.3	0.8

(b) Identifying SUTs

SUT ID	SUT Name
1	Triangle Classification
2	Bubble-sort
3	Simplex

(c) Identifying Algorithms

Algorithm ID	Algorithm
1	Hybrid
2	OFA
3	OFE

5.2.1. Selecting the Best Parameters for the Hybrid Algorithm

Statistics on some performance metrics of the hybrid algorithm are shown in Figure Fig. 5.4 on page 70.

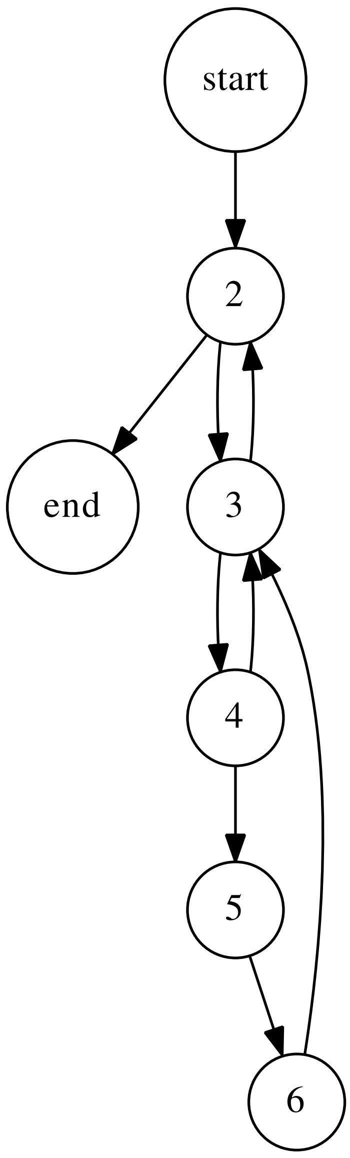


Figure 5.2.: The CFG of Algorithm 5.2

Figure 5.4b on page 70 shows that parameter sets 1,2,3,5,7,9 cover approximately the same percentage of target paths in each SUT, while Figure 5.4a on page 70 shows that parameter set 2 has the lowest variance (or close enough to the lowest variance) and tightest (95%) confidence interval for the number of fitness evaluations consumed. Thus, it is considered the best parameter set of the 9 that were experimented with. The fact that all parameter sets are approximately equi-functional (as demonstrated by Figure Fig. 5.5 on page 71) demonstrates the robustness of the hybrid algorithm in its ability to generalize to a neighborhood of parameters for any SUT.

Having thusly identified the best parameter set for the hybrid algorithm, it must now

Algorithm 5.3 The Simplex Algorithm

```
function SIMPLEX(a,b,c)
    if $a + b \leq c \vee b + c \leq a \vee c + b \leq a$ then
        return CONDITION1
    else if $x = y = z$ then
        return CONDITION2
    else if $x \neq y \neq z \neq x$ then
        return CONDITION3
    else if $a = b \neq c \vee b = c \neq a \vee c = a \neq b$ then
        return CONDITION4
    else if $a + b > 10$ then
        return CONDITION5
    else if $a + b > 5$ then
        return CONDITION6
    else if $a + c > 10$ then
        return CONDITION7
    else if $a + c > 5$ then
        return CONDITION8
    else if $b + c > 10$ then
        return CONDITION9
    else if $b + c > 5$ then
        return CONDITION10
    end if
end function
```

be benchmarked against the OFA and OFE algorithms. The performance metrics of the Hybrid compared with the OFA and OFE are shown in Figure Fig. 5.6 on page 72. From Figure Fig. 5.6 on page 72, it is clear that the hybrid algorithm discovers at least as many paths as the OFA or OFE algorithms and performs more fitness evaluations in less time when run on the more complex SUTs. The increased number of fitness evaluations is potentially an artifact of the binning algorithm using the same comparison methodology as the fitness function. However, even with this other source of fitness evaluations, the hybrid performs fewer total fitness evaluations as the recursive binning functionality forces it to consider progressively fewer target paths in the fitness evaluation.

It can be argued at this point that the OFE algorithm starts with a population for each target path and must therefore perform fewer fitness evaluations than the hybrid algorithm. Such an argument would suggest that the data presented here is incorrect. This argument is invalid as it is incomplete; while it is true that the OFE algorithm does start with each path being in its own bin (in the vernacular used while describing the hybrid), each bin (containing a single target path) has its own initial random population. This population occupies a large neighborhood, nor does it converge quickly. On the other hand, the initial population of a seededGA algorithm in the hybrid (the part of the hybrid algorithm invoked on singleton bins of target paths) densely occupies a small neighborhood. Further, it contains many duplicated individuals, which leads to fewer distinct fitness function evaluations. Thus, the observed behavior of the hybrid performing fewer fitness evalutions than the OFE algorithm is not erroneous, but is a property of the hybrid algorithm itself.

5.3. Properties of the Hybrid Algorithm

5.3.1. Fewer Fitness Evaluations

As discussed in sec. 5.2.1, it is an expected property of the hybrid algorithm to perform fewer fitness evaluations than the OFA and OFE algorithms. This is a desirable property as it implies a faster turn around time in getting back results.

5.3.2. Local Optima

One of the problems faced by most stochastic algorithms is the difficulty of escaping a local optimum. Indeed, this is a problem faced by the herein presented hybrid algorithm as well. However, the effects of this problem on this algorithm are somewhat mitigated by the nature of the similarity measures used to compute the fitness function. The fitness function computes the similarity of the path induced by an individual to the target path of that GA. Since there may be many input vectors (and therefore many individuls) that could induce the target path, the GA is considered to be working in a multi-modal fitness landscape. However, since all individuals that induce the target path have the same fitness, discovering any of them would suffice as a termination condition.

The only remaining issue concerning local optima pertains to individuals, whose encodings represent a maximal (not maximum) fitness value (individuals that cannot be made to induce paths that are more similar to the target path with only simple changes made to their encodings). However, due to the ESs ability to search the neighborhood around the seed individual thoroughly, the GA is arguably primed with a sufficiently diverse population that would allow for crossover and mutation operations to facilitate the escape from local optima in the fitness landscape.

5.3.3. Parallelizability

In the recursive binning behavior of this hybrid algorithm, the recursive seededES and seededGA steps are computed on each bin independently of the others. Therefore, this hybrid algorithm is highly parallelizable. It is worth noting that this property is a significant improvement over the OFA algorithm, which is no more parallelizable than a classical GA. On the other hand, the OFE algorithm is also highly parallelizable, but the hybrid requires demonstrably lower CPU time (as seen in Figure 5.6b on page 72), which means that in a highly parallel system, it will still outperform the OFE.

Further, due to the definition of the binning algorithm and its dependence on the similarity threshold thereof, it is possible for the hybrid algorithm to generate singleton bins of target paths while simultaneously recursively classifying target paths in other bins. In such situations, one CPU may compute the seededGA algorithm on a singleton set of target paths, while another continues to recursively classify the remaining target paths into bins. Thus, it is possible in few cases for the first CPU to complete the computation of the seededGA algorithm before the second computes the next singleton bin of target paths. This afford the hybrid algorithm the property that even though it is approximately as parallel as the OFE algorithm, it does not always require as many CPUs as the OFE in order to finish its computations. Indeed the number of CPUs required by the OFE to be fully parallel is a tight upper bound on the number of CPUs required by the hybrid algorithm to be fully parallel.

5.3.4. Inability to Stop Early

One of the observations from Figure 5.6c on page 72 and Figure 5.6b on page 72 is that the hybrid algorithm performs poorly on the triangle classification SUT on the elapsed runtime and number of fitness evaluations metrics. This is because, for very simple SUTs, the inputs that induce the required target paths may exist in the initial population. The OFA and OFE algorithms notice this and stop immediately. The hybrid on the other hand, goes on to classify the target paths into bins, find a seed for each bin and proceed with the rest of the algorithm until it does eventually find the required individual that induces the target path. This is a shortcoming of the hybrid algorithm. However, as seen in the various benchmarks in this section, this shortcoming only applies to very small (almost trivial) SUTs, while the hybrid does outperform both the OFA and the OFE in the more complex SUTs, to be expected in the real world.

5.3.5. SUT Structure

The third benchmark SUT, namely the simplex algorithm is used to demonstrate one of the properties of the hybrid algorithm. Indeed, this is a property of all evolutionary algorithms that search for inputs that induce specific target paths. Recall from Figure Fig. 4.4 on page 53 (repeated here for convenience in Figure Fig. 5.7 on page 73), that the input vectors generated by the evolutionary algorithm are points in the input space and the target paths that they are intended to induce are points in the path space. It is therefore clear that the success of an evolutionary algorithm in discovering inputs for target paths is a function of the semantic similarity between the two spaces. Thus, an evolutionary algorithm will be more successful if a change of certain magnitude and direction in the input space induces a change of similar magnitude and direction in the path space. This is confirmed by the observation that all three algorithms (the hydrid, OFA and OFE) perform consistently worse on the simplex SUT than they do on the triangle classificaiton SUT. This is because small variations in the inputs to each SUT cause varying changes in each SUT.

The triangle classification SUT is composed of highly nested `if-then-else` statements, wherein the nested conditions are subsets of (or stronger conditions upon) the parent condition. This implies that crossover and mutation operations have a high probability of generating individuals that induce paths, nested one level higher or lower than the the ones that the current individuals induce. This is particularly useful when analysing locality and theoretically discussing and analyzing the progression of the evolutionary algorithm over time.

However, the simplex SUT is specifically not structured this way. As a result, small variations in an individual's encoding can have very profound effects on the induced path. This is to say that there is likely a larger distance between induced paths (in the path space) of two individuals that are much closer in the input space. As a result, the crossover and mutation operations do not have the desired localized exploration properties for the simplex SUT that they do for the triangle classification SUT. This is confirmed by the fact that all three evolutionary algorithms discovered more target paths in the triangle classification SUT than in the simplex SUT[1].

5.4. A Real World SUT

Having surpassed the other algorithms on classical benchmarking SUTs, the hybrid was benchmarked against the OFA and OFE algorithms using a Huffman encoder as a SUT. The code and the CFG (of the implementation) for this SUT are shown in Algorithm 5.4, Algorithm 5.5, Algorithm 5.6, Algorithm 5.7 and Figure Fig. 5.8 on page 74.

Clearly, this is a more complex SUT and can well be expected to be found in the real world. It was found that the hybrid algorithm outperformed both the OFA and the OFE algorithms on the following metrics:

- percentage of target paths discovered

[1]see Section sec. 6.3 for how to deal with this problem

Algorithm 5.4 The Huffman Tree Maker

```
1: function MAKETREE(text)
2:     characters ← LETTERFREQUENCIES(text)
3:     characters ← $\{(key, value) \in characters\}$
4:     characters ← $\text{characters}_1$
5:     while |characters| > 1 do
6:         $c_2 \leftarrow min_{n[1][2]}$characters
7:         $c_1 \leftarrow min_{n[1][2]}\{n \in \text{characters}|n \neq c_2\}$
8:         characters ← characters $\setminus\{c_1\}$
9:         characters ← characters $\setminus\{c_2\}$
10:        parent ← $\{(c_1[1][1] + c_2[1][1], c_1[1][2] + c_1[1][2])\}$
11:        parent ← parent $\bigcup\{c_1\}$
12:        parent ← parent $\bigcup\{c_2\}$
13:        characters ← characters $\bigcup$ parent
14:    end while
15:    return parent
16: end function
```

Algorithm 5.5 The Helper Function to `encode`

```
1: function __ENCODE(char, tree)
2:     root ← tree.root
3:     if $root_{1_1}$ = char then
4:         return ""
5:     end if
6:     if $\text{root}_1 \neq \emptyset$ & char $\in \text{root}_{2_{1_1}}$ then
7:         return "0" + __ENCODE(char, $\text{root}_2$)
8:     else
9:         return "1"+ __ENCODE(char, $\text{root}_3$)
10:    end if
11: end function
```

- elapsed runtime
- number of fitness function evaluations

This is proven by the graphs in Figure Fig. 5.9 on page 75. Note that even though the hybrid algorithm performs fewer fitness evaluations, it discovers more target paths, still outperforming the OFA and OFE algorithms.

5.5. Summary

It is clear that the hybrid algorithm proposed in this thesis outperforms the two existing paradigms (OFA and OFE) in some ways. It is, however, not without its own

Algorithm 5.6 The Encoding Function

```
1: function ENCODE(text, tree)
2:     answer ← {}
3:     for char $d \in$ text do
4:         cipher ← _ENCODE(char, tree)
5:         answer ← answer $\bigcup$ {cipher}
6:     end for
7:     return STRING(answer)
8: end function
```

Algorithm 5.7 Main

```
1: function MAIN(text)
2:     tree ← MAKETREE(text)
3:     return ENCODE(text, tree)
4: end function
```

shortcommings, such as its inability to stop early, etc (outlined in sec. 5.3), which are promising areas for future work.

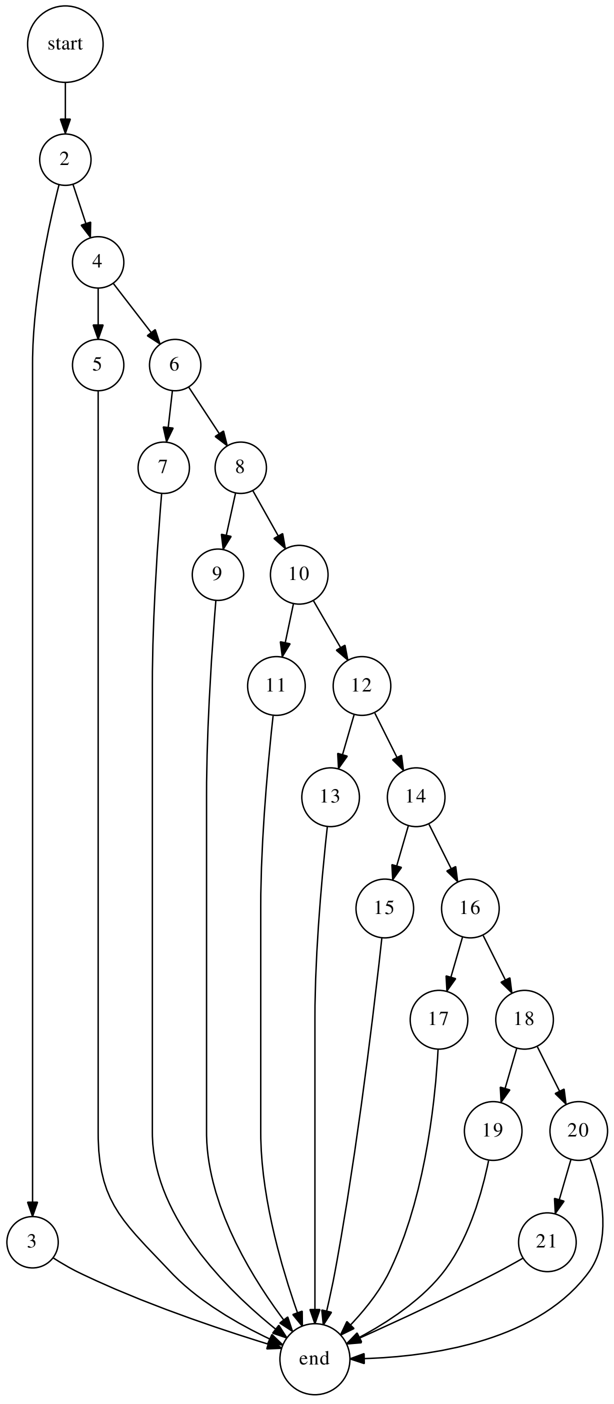
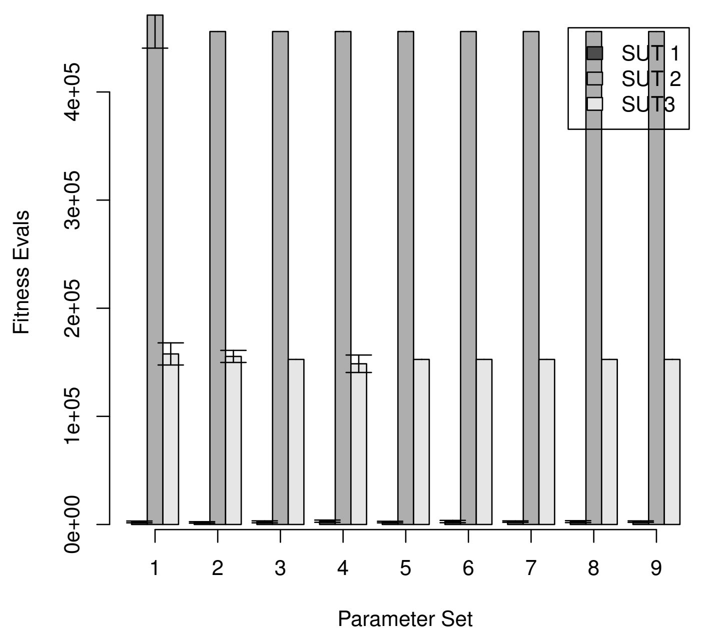
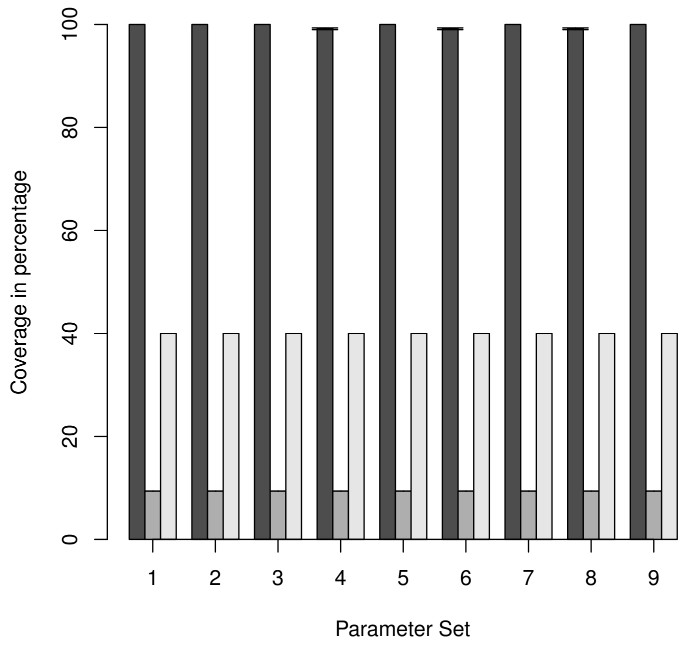


Figure 5.3.: The CFG of Algorithm 5.3



(a) The Effects of Parameters on the Number of Fitness Evaluations



(b) The Effects of Parameters on the Path Coverage

Figure 5.4.: The Effects of Threshold Parameters on the Hybrid

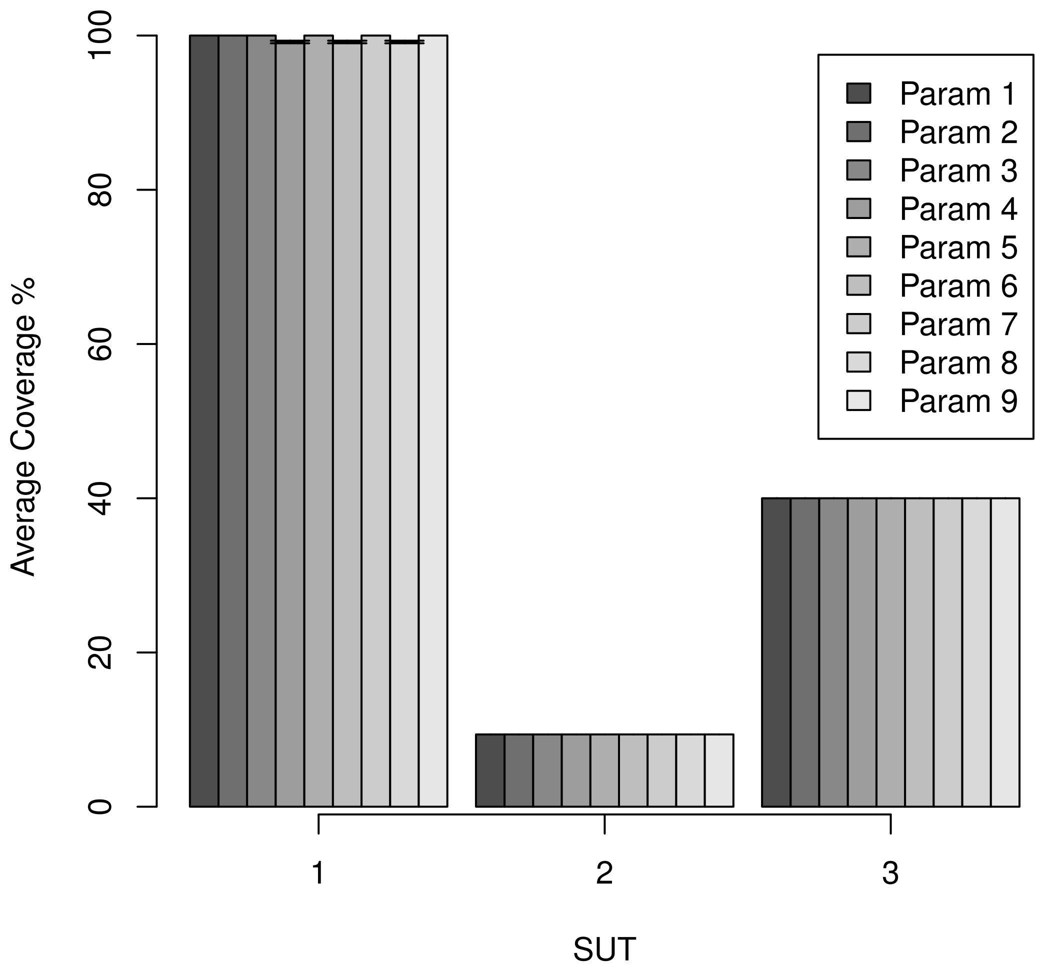
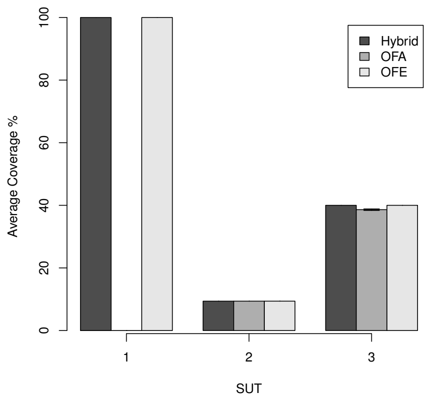
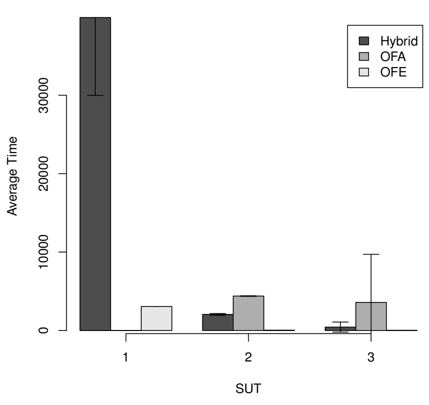


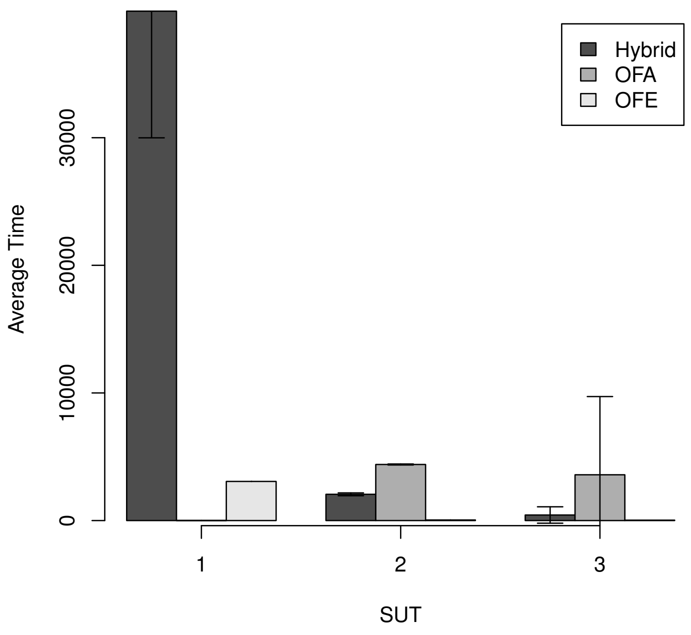
Figure 5.5.: Performance of Each Parameter Set on Each SUT



(a) Comparing Path Coverage



(b) Comparing Elapsed Run Time



(c) Comparing Fitness Evaluations Consumption

Figure 5.6.: Comparing Hybrid with OFA and OFE

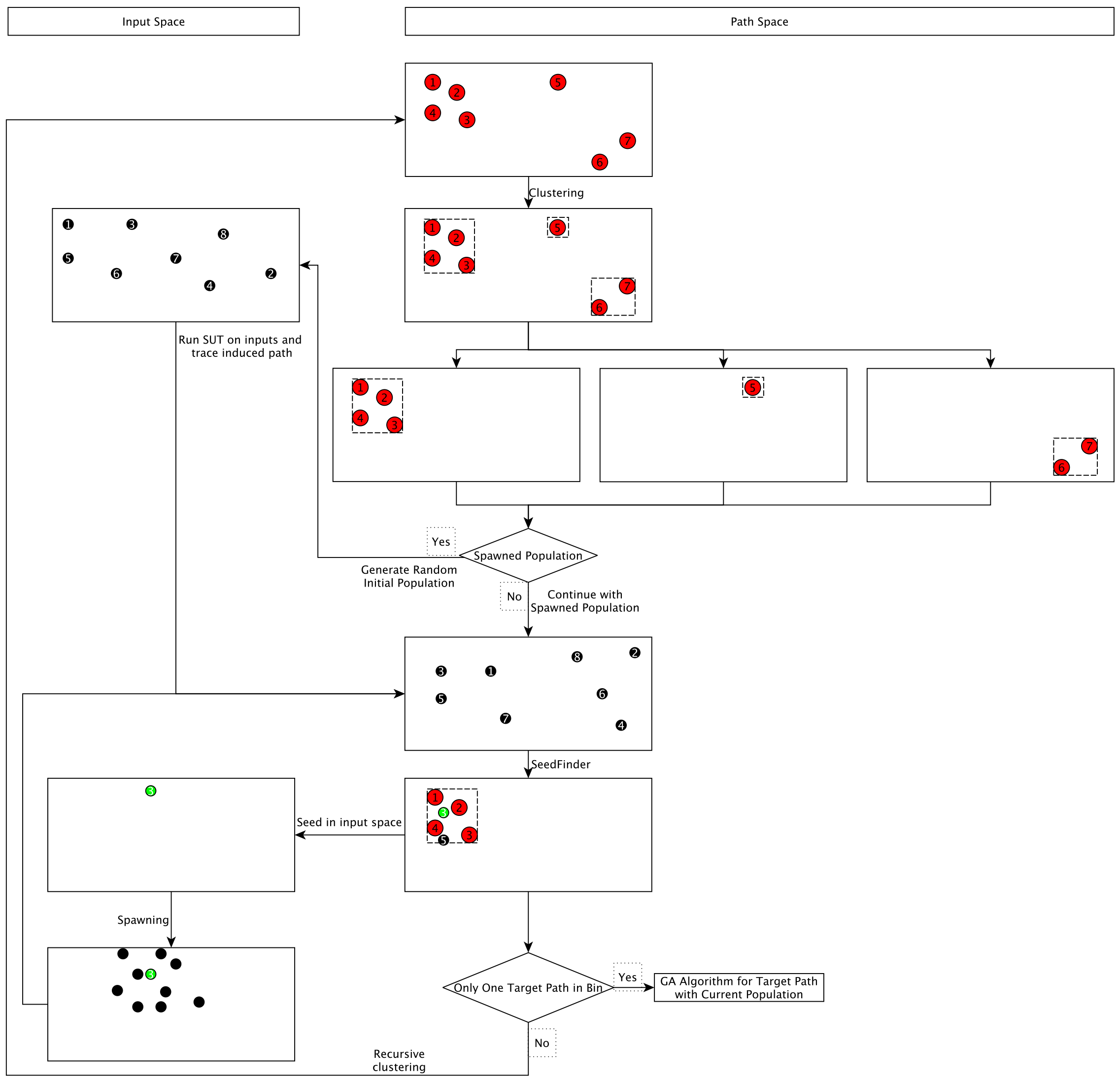

Input Space
Path Space
Clustering
Run SUT on inputs and trace induced path
Yes
Spawned Population
Generate Random Initial Population
No
Continue with Spawned Population
SeedFinder
Seed in input space
Spawning
Only One Target Path in Bin
Yes
GA Algorithm for Target Path with Current Population
No
Recursive clustering

Figure 5.7.: Process flow of Recursive Binning and Seed Finding

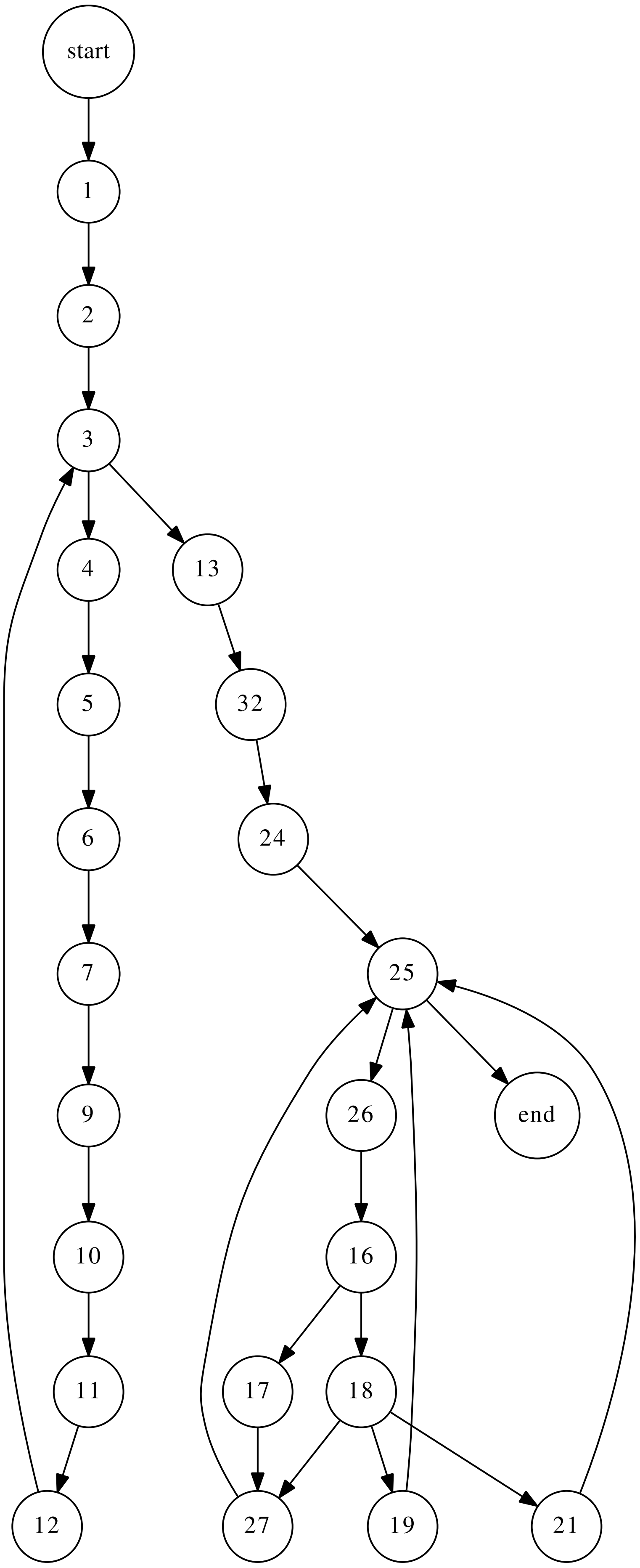
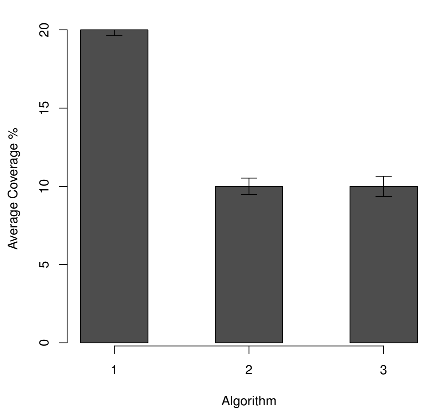
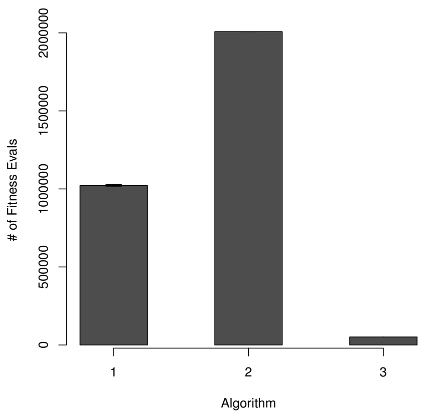


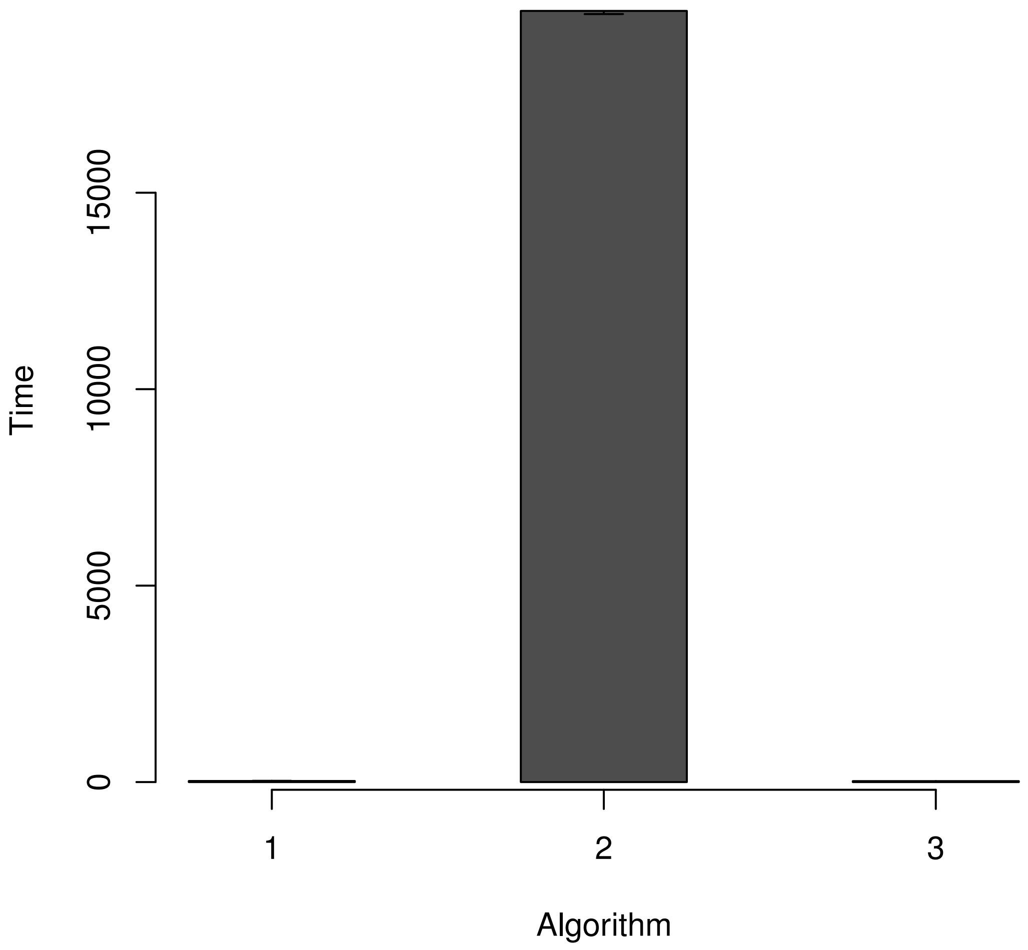
Figure 5.8.: CFG of Algorithm 5.7



(a) Total Elapsed Time



(b) Number of Fitness Function Evaluations



(c) Target Path Coverage

Figure 5.9.: Performance Metrics on the Huffman Encoder

6. Conclusions and Future Work

6.1. Overview

As discussed in chapter 5, the hybrid algorithm proposed in this thesis is indeed an improvement over the OFA and OFE algorithms. Further, since the preliminary results of this thesis have been peer reviewed [23], it is accurate to claim that this thesis presents a new solution to the studied problem, which outperforms the current state of the art.

Further, chapter 5 shows that this algorithm works well for classification algorithms (the triangle classification algorithm), sorting algorithm (the bubble-sort algorithm), comparison algorithms (the simplex algorithm) and transformation algorithms (the Huffman encoding algorithm). These algorithms together form somewhat a spanning set of the operations found in most modern deterministic software. Thus, it is logical to conclude that good performance on these SUTs will yield similarly good performance on real world SUTs composed of similar SUTs. Thus, it is expected that the hybrid algorithm presented in this thesis will generalize well to most software in the real world.

6.2. Summary of Contributions

This thesis presents a hybrid evolutionary algorithm, comprised of a Genetic Algorithm (GA) and an Evolutionary Strategy (ES). It is the purpose of the ES to shape the evolutionary population in such a way as to aid the GA by providing an adequately diverse population in a neigborhood suspected of harboring a sufficiently fit individual. When applied to a problem such as path coverage in software testing (which is represented in a multi-modal fitness landscape), this hybrid algorithm outperforms the current state of the art.

6.3. Future Work

It is worth noting that only deterministic software was used at SUTs in the results presented in this thesis. It is therefore not guaranteed to perform comparably on non-deterministic SUTs such as evolutionary algorithms, neural networks, etc. However, it is acceptable to expect it to perform comparably on non-deterministic software that uses a random seed for testing purposes. This is a useful avenue to pursue for future work, as it would bring with it, the ability to test the software written for this thesis itself.

Further, the hybrid algorithm could be improved upon by including the ability to remove target paths from consideration if individuals that induce them have already been generated; even before singleton bins of target paths are computed. This would increase the efficiency of the algorithm, especially in the cases of simpler SUTs such as the triangle classification SUT.

Another possible improvement combines principles from static software testing and compiler optimization technology that reorders lines of code [24]. Since the structure of the conditional statements does have an impact on the performance of the algorithm, a system that performs static analysis to compute the predicates on each line of code and subsequently reorder the lines of code in order to nest the predicates themselves, would yield an improvement in the performance of the hybrid algorithm as a whole. As mentioned in Chapter chapter 5, this is one of the reasons for the poor performance of the hybrid algorithm on the simplex SUT.

The final improvement takes advantage of automated bug reporting systems such as those used by modern web browsers [25] to automatically determine what target paths need to be tested with high priority. Thus, the hybrid algorithm can automatically be tasked with discovering inputs for that particular target path to generate a more detailed bug report for the developers of the SUT.

Appendix A.

The CFG Package

A.1. Motivation

The CFG (Control Flow Graph) package is designed to extract a CFG out of the source code for a given SUT. Given that the SUT in this thesis is written in Python, this is accomplished with the `cfg` package [26], presented in this appendix.

A.2. Overview

There are existing packages for the python programming language that compute a call graph for the given source-code [27]. However, these packages do not allow for extracting a CFG out of the source-code, despite the fact that they likely use such a CFG internally. Further, the python interpreter itself (written in C) [28] converts the source-code into a CFG, as an intermediary step in converting source-code into machine code. However, this is done "on the fly" and therefore is not accessible either. Thus, the `cfg` package was created and used in this thesis.

Since python is an interpreted language, it is possible to use built-in methods [29] to obtain its AST (Abstract Syntax Tree). It is from this AST that the CFG is built. Since the AST is tree data structure that contains pointers from parent nodes to child nodes, but not from child nodes to parent nodes, the AST is first converted into an XML structure affords this functionality, which is then converted into a CFG. This process is illustrated in Fig. A.1.

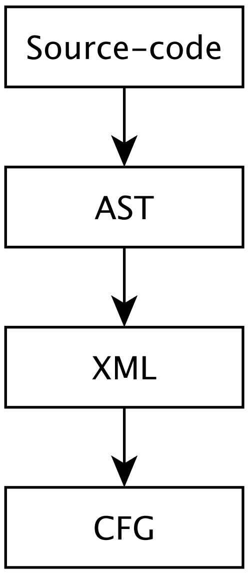


Figure A.1.: Converting Source-code to CFG

A.3. Source-code to XML

Given the source-code of the SUT, it is compiled using built-in methods of the python programming language, and an AST is obtained. This AST is then converted into XML with minimal modifications to aid the generation of the CFG. For example, the SUT in Algorithm A.1 is characterized by the AST illustrated in Fig. A.2, which is then converted into the XML document shown in Fig. A.3.

Algorithm A.1 A Simple Python SUT

```
def f(x):
    if x > 0:
        return "positive"
    else:
        return "non-positive"
```

This XML is converted into a CFG. Since the general algorithm is too large to be shown here, only the sections necessary to handle this XML is shown in Algorithm A.2.

Ultimately, once the `parse` function has finished execution, a CFG is created. This CFG holds a representation of the graph shown in Fig. A.4.

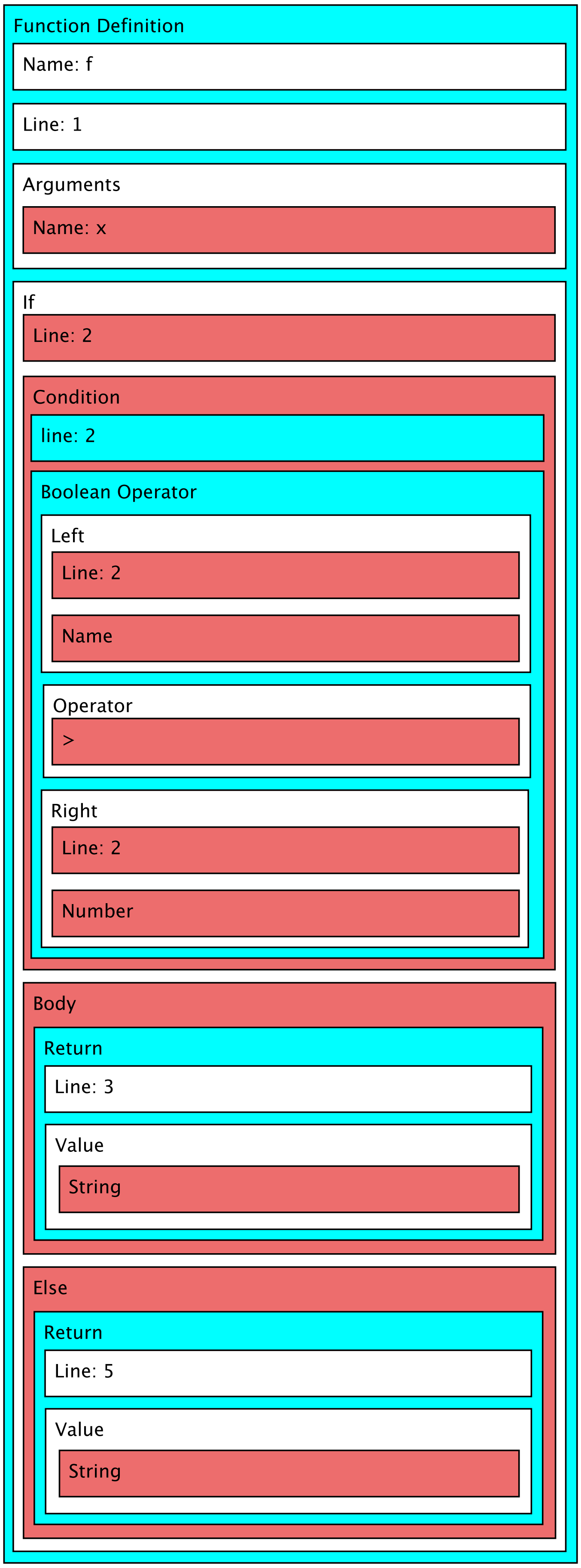


Figure A.2.: The AST of Algorithm A.1

```
<?xml version="1.0" ?>
<functiondef>
    1
    <name>1</name>
    <if>
        2
        <compare>
            2
            <name>2</name>
            <gt>gt</gt>
            <num>2</num>
        </compare>
        <return>3</return>
        <else>
            4
            <return>5</return>
        </else>
    </if>
</functiondef>
```

Figure A.3.: The XML Derived from Fig. A.2

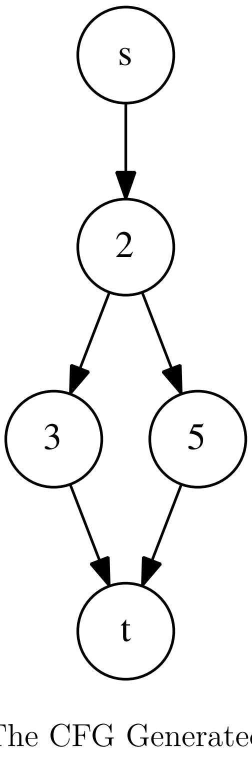


Figure A.4.: The CFG Generated from Fig. A.3

Algorithm A.2 Converting Fig. A.3 to a CFG

```
class xmlToCFG
function initialize(xmlFilePath)
                                   ▷ ‘self‘ describes the object itself, similar to ‘this‘ in Java
    self.xml ← root of the XML document
    self.edges ← new HashMap
    self.last ← line number of root
    self.currScope ← new array
    self.funcstarts ← $\emptyset$
end function
function parse
    self.scopes ← self.scopes $\bigcup\{(0, \text{largest line number in the XML})\}$
    self.handleNode(self.xml)
end function
function handleNode(node)
    curr ← line number of node
    if curr $\notin$ self.last then
        for last in self.last do
            add curr as an outgoing edge from last
            remove last from self.last
        end for
    end if
    add curr to self.last
    self.HANDLERS[node.tag](node)
end function
function handleIf(node)
    elseblock ← last child of node
    add the line number of the first child of elseblock as an outgoing node from
elseblock
    for child $\in$ { children of node | child $\neq$ elseblock } do
        self.handleNode(child)
    end for
    cache ← memcpy(self.last)
    add the line number of node to self.last
    remove line numbers of all child nodes from self.last
    for child $\in$ children of elseblock do
        self.handleNode(child)
    end for
    add the line number of the last line of node to self.last
    self.last ← self.last $\bigcup$ cache
end function
function handleCondition(node)
    for child $\in$ children of node do
        self.handleNode(child)
    end for
end function
function handleReturn(node)
    for child $\in$ children of node do
        self.handleNode(child)
    end for
end function
end class
```

Appendix B.

Dynamic White Box Testing

B.1. Overview

White box testing is a software testing paradigm that uses the source code of the SUT to test it. It is used to ensure that all parts of the code's structure are executable - to ensure code coverage. As such, there are several forms of white-box testing. In each form, the SUT is converted into a control flow graph (CFG) - a mathematical representation of the logical program flow of the SUT. In a CFG, each statement is a node and sequential statements are connected by edges. Branching statements (`if-then-else` statements, `for-loops` and `while-loops`) are characterized by multiple outgoing edges from a node, with conditions on each edge.

B.2. Node or Statement Coverage

This form of white box testing requires that each statement in the SUT's code be executed by at least one input vector from the set of test input vectors. While this seems acceptable, it is trivial to show that this testing method is incomplete. Consider the following example of a program that is said to implement the following specifications:

Table B.1.: Specification for AlgorithmAlgorithm B.1

Parameter	Value
Number of Inputs	2
Name of Input 1	`A`
Name of Input 2	`B`
Type of `A`	`int`
Type of `B`	`int`
Type of Output	`int`
Output Value	`A/B` if neither `A` nor `B` is `0`. Else `0`.

Suppose this specification is implemented in the SUT in Algorithm B.1.

Algorithm B.1 A Simple Program

```
1: function F(A,B)
2:     if A==0 & B==0 then
3:         return 0
4:     else
5:         return $\frac{A}{B}$
6:     end if
7: end function
```

The CFG for this SUT is presented in Fig. B.1

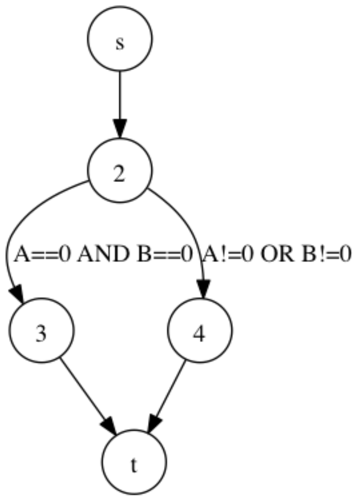


Figure B.1.: CFG for the SUT Presented in Algorithm B.1

where the statements represented by the nodes are presented in Tab. B.2

From the above description, it is clear that all nodes of the CFG will be covered by the inputs presented in Tab. B.3.

Table B.2.: Node-Statement Representation

Node	Statement
s	Start function
2	`if (A == 0) AND (B == 0)`
3	`return 0`
4	`return A/B`
t	End function

Table B.3.: Inputs for Node Coverage

A	B	Path
0	0	(s,2,3,t)
0	1	(s,2,4,t)

Having covered all nodes of the SUT, the test suite comprised of the input vectors presented in Tab. B.3 would declare the SUT bug-free. However, note that the input vector (`A=1, B=0`) was not tested and would cause an error due to division-by-zero. This is an error case, that is not caught by the test suite which declared this code to be bug-free.

Thus, node coverage is not an adequate code coverage criterion for testing

B.3. Edge Coverage

Edge coverage is a stronger testing criterion than node coverage [6]. Similar to node coverage, edge coverage attempts to execute all edges in the SUT's code. This is to say that a test suite T satisfies edge coverage if and only if for every edge e in the CFG of the SUT, there exists a test case (i.e. a vector of inputs) $t \in T$ such that the path induced by executing the SUT on t contains e.

Using the same example as in sec. B.2, we can see that edge coverage is also incomplete. The two input vectors in the test suite, together cover all edges. Still, they miss the fact that the input vector (`A=1, B=0`) would cause an error due to division-by-zero.

B.4. Condition Coverage

Condition coverage is a stronger testing criterion than edge coverage [6]. This criterion requires that every condition that can induce a path of execution in the SUT be executed at least once by the test suite [6]. This is to say that a test suite T satisfies condition coverage if and only if for each set of path predicates P in the paths of the CFG of the SUT, there exists a test case (i.e. a vector of inputs) $t \in T$ such that the path induced by executing the SUT on t contains P.

However, in the above SUT, it is clear that this criterion is incomplete, just as the edge coverage criterion is also incomplete. Since condition coverage is satisfied by the test suite presented in sec. B.2, and that test suite has been shown to be incomplete, condition coverage is also incomplete.

B.5. Path Coverage

Path coverage is one of the stronger testing criteria[1], and is widely accepted as a natural criterion of program testing completeness [8]. It requires that every path in the CFG be executed at least once by the test suite. This is true despite the fact that the presented test suite satisfies this criterion . As a result, this thesis focuses on generating input vectors that satisfy path coverage. It is left to the tester of the software to determine what percentage of all paths in the CFG need to be induced by the inputs generated by the work presented in this thesis.

[1]See for background information on the different forms of coverage in white-box testing

Appendix C.

Evolutionary Algorithms

C.1. Genetic Algorithms

C.1.1. Overview

As outlined by Juang [30], a Genetic Algorithm (GA) encodes a candidate solution to a problem in an *individual* of a *population* of such individuals. These indivuals are composed of *chromosomes*, which encode parts of the candidate solution. After initializing a random population of such individuals, these are evaluated for fitness (i.e. a measure determining the optimality of the candidate solution in its ability to solve the problem). Fit individuals are reproduced to the next generation of the population. Further, all members of the current generation of the population undergo probabilistic crossover and mutation operations so that parts of candidate solutions may be combined with each other in the hope of creating a better individual (i.e. a candidate solution) for the next generation. This process of reproduction, crossover and mutation operations are repeated for several generations over a run of the GA.

The various components of a GA are explained in the following subsections.

C.1.2. Chromosome

A chromosome is an encoding of a part (or the whole) of a candidate solution to the given problem. It is typically implemented as an array, each segment of which is considered a gene. In the context of discovering useful test input data, a chromosome may encode an input vector (a vector of values - one per input variable in the SUT), while each gene encodes a value for the corresponding input variable, as was done in [31].

For example, Fig. C.1 shows a chromosome, using binary encoding, for the values of the three inputs that form the input vector `<3,4,5>`.

Input 1			**Input 2**			**Input 3**		
0	1	1	1	0	0	1	0	1

Figure C.1.: Example Chromosome for Input Vector `<3,4,5>`

C.1.3. Individual

An individual is a full representation of a candidate solution to the problem. Therefore, an individual may be a single chromosome (in the event that a single chromosome encodes a candidate solution entirely), or a collection of chromosomes.

The example in sec. C.1.2 can be equivalently implemented as a three-chromosome individual as show in Fig. C.2.

Chromosome	**Value**		
1	0	1	1
2	1	0	0
3	1	0	1

Figure C.2.: Tri-Chromosome Individual for Input Vector `<3,4,5>`

C.1.4. Population Generation

In order to begin the process of evolution, the first generation of the population needs to be synthesized. It is important that the first generation of the population cover as much of the search space as possible (be as diverse as possible), so that the subsequent genetic operations (crossover and mutation operations) do not get stuck in local optima; i.e. in order to ensure that there is still adequate diversity in the encoding of the chromosomes that some genetic operations would allow the GA to escape local optima situations. This is typically done by creating a random initial population. For example, if the population were made up of single-chromosome individuals and each chromosome was a bit string, n bits long, then each chromosome for each individual is generated by concatenating the results of n calls to a random single-bit generator[1] [31].

C.1.5. Fitness

In order for a GA to evolve better individuals over time (i.e. individuals that represent better candidate solutions to the problem), there needs to be a measure of the quality of each candidate solution. Such a measure is provided by an objective fitness function. In the context of evolving test case data for path coverage (as mentioned in sec. B.5), one possible fitness function for an individual encoding a full test suite might be the percentage of all paths covered by the test suite. The actual fitness function used in this thesis is explained in sec. 4.5.3.

C.1.6. Selection

In order to improve individuals over time, appropriate individuals must be selected from the current population. Typically, a selection mechanism favors fit over unfit individuals. Two such selection mechanisms are discussed in sec. C.1.7 and sec. C.1.8.

[1]Single bit generators are commonly found as part of programming languages or their associated libraries

C.1.7. Biased Roulette Wheel Selection

A biased roulette wheel selection models a situation where individuals bet on a roulette wheel, and the winner will be chosen for reproduction (crossover and mutation) operations. In order to bias the bets that the individuals place, each individual is to bet on an entire section of the roulette wheel. The size of the section is directly proportional to the fitness of the individual, relative to the population [8]. For example, if a population consists of three individuals whose fitness scores are as shown in Tab. C.1, the biased roulette wheel could be modeled along the continuous interval $[0, 1]$, for the individuals to place bets as shown in Tab. C.2.

Table C.1.: Relative Fitness of Individuals in a Population

Individual	Raw Fitness	Relative Fitness[2]
1	5	0.5
2	1	0.1
3	4	0.4

Table C.2.: A Biased Roulette-Wheel for the Individuals in Table Tab. C.1

Individual	**Section of the Roulette Wheel**
1	0.0 - 0.5
2	0.5 - 0.6
3	0.6 - 1.0

After creating the biased roulette wheel and assigning sections for each individual to place bets on, a selection operation is performed by picking a random number in the interval. The individual that placed a bet on a section of the roulette wheel containing this random number is determined to be the winner. Thus if the random number was 0.506934, then *Individual 2* is selected for mating operations.

C.1.8. Tournament Selection

A tournament selection is based on of the following parameters:

Tournament size (T) The size of the tournament to be conducted

Number of winners (W) The number of winners of a tournament. Typically, this is either 1 or 2; this number has a lower bound of 1 and an upper bound of T

This selection mechanism functions by sampling T individuals from the population and selecting the best (fittest) W of them for mating operations [32]. The idea is that fitter individuals have a higher probability of mating to produce children, which will populate the next generation of the population of chromosomes. Note that this selection mechanism guarantees that the $T - W$ least fit individuals in any generation of the population will never be selected for reproduction operations.

Thus, while this method is another way to implement fitness-proportional selection, it is less forgiving that the biased roulette wheel selection mechanism, as a biased roulette wheel does not make it impossible for the least fit $T - W$ individuals to be selected for reproduction operations (even though this probability will be very low in a biased roulette-wheel selection).

C.1.9. Crossover

In order to combine components of known candidate solutions to form new candidate solutions, a process named crossover is employed. During crossover, corresponding parts of corresponding pairs of chromosomes from two parent individuals are recombined to form the chromosomes of the child individual. While several methods for crossover do exist and are used, two are examined in sec. C.1.9.1 and sec. C.1.9.2.

C.1.9.1. Uniform Crossover

Uniform crossover generates a child chromosome in which each gene is a copy of the corresponding gene in one of the parents. Which parent a particular gene comes from is decided probabilistically. For example, suppose:

1. the two parents (p_1 and p_2) were as shown in Figure C.3a on page 94
2. the probability of selecting a gene from p_2 is 0.5

Then, the probability of the first gene in the child from crossover being A_2 is 0.5. Thus, the probability of generating the child shown in C.3b as a result of crossover is 0.0625.

p_1	A_1	B_1	C_1	D_1
p_2	A_2	B_2	C_2	D_2

(a) Hypothetical Parents of Crossover

Child	A_1	B_2	C_1	D_2

(b) Possible Child of Crossover

Figure C.3.: Uniform Crossover Example

Indeed, the probability of generating one of the parents as a result of crossover is also 0.0625. This crossover technique was used in generating test inputs for testing a vehicular cruise control system [31].

C.1.9.2. One Point Crossover

One point crossover generates a child chromosome by concatenating complement segments of corresponding chromosomes of the parent individuals. The point of segmentation (called the crossover point) is selected at random. For example, suppose the two parents (p_1 and p_2) were as shown in Figure C.3a on page 94, it is possible that a child chromosome would be (if the crossover point were between the third and fourth gene) as shown in Fig. C.4.

Child	A_1	B_1	C_1	D_2

Figure C.4.: Possible Child of One-Point Crossover

C.1.10. Mutation

Mutation is a process by which a chromosome is altered slightly in order to create a variant of itself. This is done in order to allow the GA to escape local optima by allowing the chromosome, hence the individual, to move to a different point in the solution space. For example, if a chromosome is represented as a binary bit-string, a mutation operation would flip the value of a random bit in this bit-string. This can be observed in the fourth gene in Fig. C.5.

Before Mutation	0	1	0	0
After Mutation	0	1	0	1

Figure C.5.: Possible Mutation

C.2. Evolutionary Strategy

An Evolutionary Strategy (ES) is an evolutionary algorithm similar to a GA. The main difference is that ESs do not use crossover operators. Instead, once the initial random population has been generated, it then advances from one generation to the next by selecting the fittest individual of that generation and mutating it several times in order to form the individuals of the next generation of that population. This is performed over several generations, to execute one run of the ES.

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