Effective Methods to Tackle the Equivalent Mutant Problem when Testing Software with Mutation

Marinos Kintis

A thesis submitted in fulfilment of the

requirements for the degree of

Doctor of Philosophy

of the

Athens University of Economics and Business

Department of Informatics

Athens University of Economics and Business

June 2016

Abstract

Mutation Testing is undoubtedly one of the most effective software testing techniques that has been applied to different software artefacts at different testing levels. Apart from mutation's versatility, its most important characteristic is its ability to detect real faults. Unfortunately, mutation's adoption in practice is inhibited, primarily due to the manual effort involved in its application. This effort is attributed to the Equivalent Mutant Problem.

The Equivalent Mutant Problem is a well-known impediment to mutation's practical adoption that affects all phases of its application. To exacerbate the situation, the Equivalent Mutant Problem has been shown to be undecidable in its general form. Thus, no complete, automated solution exists. Although previous research has attempted to address this problem, its circumvention remains largely an open issue. This thesis argues that effective techniques that considerably ameliorate the problem's adverse effects can be devised. To this end, the thesis introduces and empirically evaluates several such approaches that are based on Mutant Classification, Static Analysis and Code Similarity.

First, the thesis proposes a novel mutant classification technique, named Isolating Equivalent Mutants (I-EQM) classifier, whose salient feature is the utilisation of second order mutants to automatically isolate first order equivalent ones. The empirical evaluation of the approach, based on real-world test subjects, suggests that I-EQM outperforms the existing techniques and results in a more effective testing process.

Second, the thesis formally defines nine data flow patterns that can automatically detect equivalent and partially equivalent mutants. Their empirical evaluation corroborates this statement, providing evidence of their existence in real-world software and their equivalent mutant detection capabilities.

Third, MEDIC (Mutants' Equivalence Discovery), an automated framework that implements the aforementioned patterns and manages to detect equivalent and partially equivalent mutants in different programming languages, is introduced. The experimental investigation of the tool, based on a large set of manually analysed mutants, reveals that MEDIC can detect efficiently more than half of the considered equivalent mutants and provides evidence of automated stubborn mutant detection.

Finally, the thesis proposes the concept of mirrored mutants, that is mutants affecting similar code fragments and, more precisely, analogous code locations within these fragments. It is postulated that mirrored mutants exhibit analogous behaviour with respect to their equivalence. The empirical evaluation of this concept supports this statement and suggests that the number of the equivalent mirrored mutants that have to be manually analysed can be reduced approximately by half.

To my family

Acknowledgements

First of all, I would like to thank my supervisor, Prof. Nicos Malevris, for his guidance, tireless support and for sharing his time and knowledge with me. I would also like to thank my co-supervisors, Prof. Emmanouil Giakoumakis and Prof. Yannis Kotidis, for their advice, encouragement and constructive suggestions.

I am particularly grateful to Prof. Panos Constantopoulos for his counsel and kind support and to Prof. Ion Androutsopoulos, Prof. Maria Virvou and Prof. Emmanuel Yannakoudakis for taking the time to be on my defence committee and for their insightful comments.

My sincere thanks go to Mike Papadakis for his assistance and our endless discussions and Matthew Patrick and Yue Jia for their positive advice. I would also like to thank Vassilis Zafeiris and Nikos Diamantidis for their generous help during my studies.

Many thanks go to my colleagues at the Information Systems and Databases Laboratory and the Department of Informatics for their support and fruitful discussions. I would also like to thank the anonymous reviewers of my submitted papers for their helpful comments and valuable feedback.

I particularly appreciated working with several exceptional undergraduate and postgraduate students, including Andreas Papadopoulos, Evaggelos Valvis, Maria Markaki, Ioannis Babakas, Sotiria Giannitsari, Makrina Polydorou, Foivos Anagnou-Misyris, Loukas-Pavlos Basios, Nikolaos Panagopoulos and Dimitrios Spiliotis.

I gratefully acknowledge financial support for my studies from Empirikion Foundation, AUEB's Basic Research Funding Program (BRFP) 3 and RC AUEB.

Finally, I would like to express my deepest gratitude to my fiancée and my family who continuously supported me throughout this difficult journey.

Contents

List of Figures

List of Tables

Chapter 1

Introduction

Among the various software development phases, testing typically accounts for more than 50% of total development costs, even more for safety-critical applications [1–3]. Despite this fact, testing constitutes an invaluable activity of software development: it provides a systematic way of uncovering software faults, and, thus, increases the practitioners' confidence in the software's correctness.

Software testing utilises formal *coverage criteria* to guide the testing process. These criteria require specific elements of the artefact under test, called *test requirements*, to be covered or satisfied by test cases [3]. For instance, statement coverage requires all statements of the source code of the program under test to be covered by at least one test case and branch coverage necessitates covering all branches of the program's control flow graph.

In other words, coverage criteria constitute a means of distinguishing between test cases that possess a specific property and ones that do not and, thus, guide the testing process towards those particular test cases. Additionally, they can act as stopping rules for the testing process [3].

Unfortunately, covering certain coverage criteria is quite demanding in terms of computational resources and, more importantly, human effort. There are three main reasons for this problem:

1. Various coverage criteria impose a **vast number** of test requirements.

2. The generation of appropriate test cases that cover the imposed test requirements is a difficult task that **cannot be automated** in its entirety.

3. *Infeasible test requirements*, i.e. test requirements that cannot be covered by any test case, require **human intervention** to be identified.

The present thesis introduces several techniques that attempt to address the aforementioned shortcomings in the context of mutation testing. The motivation of such a decision is presented in the next sections, along with an outline of mutation's problems and the remedies that this thesis proposes.

1.1 Context of the Thesis: Mutation Testing

Mutation testing is a very powerful technique for testing software with a rich history that began in 1971 by a class term paper of Richard Lipton [4]. Mutation has been increasingly studied since its introduction with several available literature surveys [5–9] and introductory book chapters [3, 10].

Mutation has a plethora of applications in software testing: it has been utilised in the context of many programming languages, e.g. FORTRAN [11–13], C [14–16], Java [17–22], Smalltalk [23], Python [24], Haskell [25], JavaScript [26, 27], SQL [28–32], and different testing levels, e.g. specification level [33], unit level [34], integration level [35], system level [36, 37].

Mutation is not restricted to testing program source code, it has also been applied to other software artefacts, e.g. finite state machines [38, 39], network protocols [40], security policies [41–43], software product lines [44, 45], databases [28, 46, 47]. Finally, it has been utilised to support many testing activities, e.g. test case generation [48–55], regression testing [56, 57], fault localisation [58–60], Graphical User Interface (GUI) testing [61, 62].

Mutation is a fault-based technique: it induces artificial faults to the artefact under test. These faults, which constitute the imposed test requirements, are called *mutants* and are simple syntactic changes that are based on specific rules known as *mutation operators*.

The application of mutation entails the generation of the mutants of the evaluated artefact, each one containing one artificial fault, and requires their coverage by appropriate test cases. If such a test case is found, the mutant is termed *killed*. In a different situation, it is termed *alive*. A live mutant can be either a *killable* or an *equivalent* one.

A killable mutant is one that can be killed but the available test cases are inadequate for this task, thus, new ones must be created. An equivalent mutant is one that cannot be killed by any test case, that is an equivalent mutant is semantically equivalent to the artefact under test despite being syntactically different. Examples of such mutants are presented in the next section (see Figure 1.1).

For the purposes of this introduction, this succinct description of mutation suffices. All the aforementioned concepts will be revisited and elaborated further in Chapter 2.

This thesis primarily focuses on program mutation, i.e. the application of mutation testing to the source code of a program under test. In this case, mutants correspond to different versions of this program, which is called the *original program*, and their "coverage" to the discovery of appropriate test cases that will differentiate the behaviour of the mutants from that of the original program.

1.1.1 Mutation Testing: An Example

An illustrative example of the aforementioned concepts is depicted in Figure 1.1. The figure presents the source code of the `capitalize` method[1] (Figure 1.1a), along with two of its mutants (Figure 1.1b and Figure 1.1c). Method `capitalize` capitalises all the delimiter-separated words of its first argument; for example, `capitalize("hello world", null)` returns `Hello World`.

Figure 1.1b illustrates the code fragment of a *killable* mutant, that is a mutant that can be killed. This particular mutant is generated by the Relational Operator Replacement (ROR) mutation operator (see Table 4.1 for more details) and affects the statement of line 3 of the original program. Note that the mutated statement is denoted by the Δ symbol in the figure and will replace that of the original program.

After examining the source code of the method, it becomes apparent that this mutant can be easily killed by non-empty argument values. Indeed, a test case with

[1]The method belongs to the `WordUtils` class of the Apache Commons Lang project (`https://commons.apache.org`).

```
 1: public static String capitalize (String str, char[] delimiters) {
 2:     int delimLen = delimiters == null ? -1 : delimiters.length;
 3:     if (str == null || str.length() == 0 || delimLen == 0) {
 4:         return str;
 5:     }
 6:     int strLen = str.length();
 7:     StringBuffer buffer = new StringBuffer( strLen );
 8:     boolean capitalizeNext = true;
 9:     for (int i = 0; i < strLen; i++) {
10:         char ch = str.charAt(i);
11:         if (isDelimiter(ch, delimiters)) {
12:             buffer.append(ch);
13:             capitalizeNext = true;
14:         }
15:         else if (capitalizeNext) {
16:             buffer.append(Character.toTitleCase(ch));
17:             capitalizeNext = false;
18:         }
19:         else {
20:             buffer.append(ch);
21:         }
22:     }
23:       return buffer.toString();
24: }
```

(a) Source code of method `capitalize`.

```
   ...
3: if (... || delimLen == 0) {
Δ     ... delimLen != 0 ...
4:       return str;
5: }
   ...
```

(b) Example of a *killable* mutant.

```
    ...
11: if (isDelimiter(ch, delimiters)) {
12:     buffer.append(ch);
Δ       buffer.append(ch++);
13:     capitalizeNext = true;
14: }
    ...
```

(c) Example of an *equivalent* mutant.

Figure 1.1: Examples of killable and equivalent mutants. The source code of the `capitalize` method (part a) and two of its mutants (denoted by the Δ symbol): a killable (part b) and an equivalent (part c) one.

`str="hello world"` and `delimiters={ " " }` will kill the mutant: the original program will return `Hello World`, whereas the mutant `hello world`.

Figure 1.1c presents an example of another mutant of the method. This mutant is generated by the Arithmetic Operator Insertion Short-cut (AOIS) mutation operator (see Table 4.1 for more details) and affects line 12 of the original program. By carefully executing this mutant, it can be concluded that it is an equivalent one: after the execution of the mutated statement, there is no use of variable `ch` capable of revealing the imposed change.

1.2 Motivation

From the previous sections, it is immediately apparent that mutation is an extremely versatile technique. It can be applied to different programming languages at different testing levels, to either test various software artefacts or support the testing process. Although mutation's flexibility is impressive, its most important characteristic is its *fault-detection* capabilities.

1.2.1 Mutation's Effectiveness: Fault Detection

Mutation's fundamental premise is that mutants resemble real faults. As coined by Geist et al. [63]:

> *"If the software contains a fault, it is likely that there is a mutant that can only be killed by a test case that also reveals the fault."*

Several research studies have empirically investigated whether this premise holds [64–68]. More precisely, the findings of Daran and Thévenod-Fosse [64] indicate that the erroneous program states that are caused by mutants resemble the ones caused by real faults. The studies of Andrews et al. [65, 66] suggest that mutants provide a good indication of the fault-detection ability of a test suite.

Do and Rothermel [67] evaluated the use of mutants in the empirical assessment of test case prioritisation techniques and concluded that mutants can provide practical replacements of hand-seeded faults. Finally, the findings of Just et al. [68] demonstrate that there is a correlation between a test suite's mutation score and its real-fault detection rate.

Apart from its fault-detection capabilities, researchers have empirically compared mutation with several coverage criteria, e.g. control flow [69, 70] and data flow [71–74]. Specifically, Offutt and Voas [69] formally showed that mutation testing subsumes various control flow coverage criteria. Li et al. [70] compared mutation with four unit-level coverage criteria and concluded that test suites generated to cover mutation detected more faults.

Analogous results were obtained in the case of data flow criteria. Several studies compared mutation testing with the *all-uses* data flow criterion [75–77], e.g. [71–74], and suggest that test suites that cover mutation are very close to covering all-uses and detect more faults.

The aforementioned studies provide corroborating evidence to support mutation's effectiveness. Their results suggest that test data generated to cover mutation are of high quality and are effective in detecting real faults, thus, increasing the practitioners' confidence in the software's dependability and robustness.

1.2.2 Mutation's Manual Cost: An Open Issue

Despite its effectiveness, mutation lacks widespread adoption in practice, with the main culprit being its cost. Mutation's cost can be largely attributed to:

1. The **vast number** of generated mutants.
2. The ***Equivalent Mutant Problem***, i.e. the undesirable consequences caused by the presence of equivalent mutants.

As discussed later in Chapter 2, mutation generates an enormous number of mutants by applying the employed mutation operators to all possible source code locations of the program under test. These mutants require high computational resources in order to be executed with the available test cases and considerable human effort in order to be killed. Thus, impairing mutation's ability to scale to real-world programs.

To worsen the situation, equivalent mutants cannot be killed, thus, affecting negatively all phases of the mutation's application process (see also Section 2.1.4): (1) equivalent mutants are generated without contributing to the testing process, (2) they waste computational resources when executed with test data and (3) substantial human effort is misspent when attempting to kill them.

Research studies have shown that an equivalent mutant requires approximately 15 minutes of manual analysis in order to be identified [78–80]. Additionally, several studies provide evidence that equivalent mutants are harder to detect than infeasible test requirements of other coverage criteria, e.g. all-uses [72, 74]. By considering these facts, along with the vast number of generated mutants, it becomes clear that the equivalent mutant problem constitutes a major hindrance to mutation's practical adoption.

Although researchers have proposed various approaches to manage the number of generated mutants, e.g. selective mutation [81], weak mutation [82–84], higher order mutation [85–88], automated techniques to tackle the equivalent mutant problem are scarce, mainly, due to the problem's undecidable nature [89].

1.3 Scope of the Thesis

From the previous sections, it becomes evident that there are several obstacles to be surmounted before mutation can be widely adopted in practice. This thesis attempts to tip the scales in favour of mutation by introducing several automated techniques that reduce the manual effort involved in its application.

Particularly, this thesis investigates ways of ameliorating the adverse effects of the equivalent mutant problem. To this end, the following questions are investigated:

Q1 ***Can a considerable number of equivalent mutants be automatically detected?***

The equivalent mutant problem, being undecidable in its general form, is only susceptible to partial solutions. Nevertheless, if a large number of equivalent mutants can be automatically detected, then the human effort involved in the application of mutation can be considerably reduced, boosting the technique's practical adoption.

Q2 ***Can mutant classification constitute a viable alternative to mutation?***

Various researchers have proposed approximation techniques that reduce the number of the considered equivalent mutants at the cost of the techniques' effectiveness (cf. Section 2.3.1). Mutant classification techniques are one such example. Approaches based on mutation classification classify mutants as possibly equivalent and possibly killable ones and suggest the utilisation of the resulting possibly killable mutant set for the purposes of mutation testing. If such approaches can classify most of the killable mutants correctly while maintaining the number of the misclassified equivalent ones at a reasonably low level, then their effectiveness will be significantly high and the manual cost involved in their application will be substantially reduced.

Q3 ***Can knowledge about the equivalence of the already analysed mutants be leveraged to identify new equivalent mutants in the presence of software clones?***

Research studies suggest that software systems include cloned code. Thus, if mutants belonging to software clones exhibit analogous behaviour with respect to their equivalence or killability, then considerable effort savings can be achieved by automatically classifying mutants based on the equivalence or killability of the already analysed ones.

1.4 Contributions of the Thesis

The contributions of this dissertation can be summarised in the following points:

1. The introduction of a novel mutant classification technique, termed Higher Order Mutation (HOM) classifier, that utilises higher order mutants to automatically classify first order ones (Chapter 3).

2. The proposal of a combined mutant classification scheme, named Isolating Equivalent Mutants (I-EQM), that is synthesised by two mutant classification approaches and outperforms the previously proposed ones (Chapter 3).

3. The introduction and formal definition of several data flow patterns that can automatically detect equivalent and partially equivalent mutants (Chapter 4).

4. MEDIC, an automated, static analysis tool that can efficiently detect equivalent and partially equivalent mutants in different programming languages (Chapter 5).

5. An investigation of whether or not mutants belonging to software clones, termed *mirrored mutants*, exhibit analogous behaviour with respect to their equivalence (Chapter 6).

6. An investigation of the relationship between mutants' impact and mutants' killability (Chapter 3).

7. An investigation of the relationship among equivalent, partially equivalent and stubborn mutants (Chapter 5).

8. Experimental results pertaining to the utilisation of mirrored mutants for test case generation purposes (Chapter 6).

9. A publicly available data set for comparing mutant classifiers (Chapter 3).

10. An empirical study evaluating the effectiveness and stability of various mutant classification techniques (Chapter 3).

11. An empirical study that investigates the detection power of the proposed data flow patterns and their existence in real-world software (Chapter 4).

12. An empirical study that evaluates the effectiveness, efficiency and cross-language nature of MEDIC (Chapter 5).

13. An empirical study that examines the usefulness of mirrored mutants in detecting equivalent ones and generating test cases that target other mirrored mutants (Chapter 6).

1.5 Organisation of the Thesis

The remaining of this thesis is organised as follows:

Chapter 2 furnishes a more detailed view of mutation testing. It begins by describing the two fundamental hypotheses of the approach, along with mutation's application process. Next, it presents the sources of mutation's cost and the equivalent mutant problem and continues by discussing the main causes of mutants' equivalence. Finally, the chapter concludes by describing previous work on the detection of equivalent mutants, minimum mutant sets and the reduction of mutation's computational cost.

Chapter 3 introduces a novel, dynamic mutant classification scheme, named *Isolating Equivalent Mutants* (I-EQM), that isolates first order equivalent mutants via higher order ones. The chapter begins by detailing the core concepts of the study and by presenting how mutation testing can be applied using mutant classifiers. Next, the proposed classification techniques are introduced and the conducted empirical study is presented, along with the analysis of the obtained results. Finally, the chapter concludes with a recapitulation of the most important findings.

Chapter 4 proposes a series of data flow patterns whose presence in the source code of the original program will lead to the generation of equivalent mutants. First, the chapter introduces the corresponding patterns, defining formally the conditions that need to hold in order to detect problematic code locations. Next, an empirical study, investigating their presence in real-world software and their detection power, is presented, along with a discussion of the obtained results. Finally, the chapter concludes by summarising key findings.

Chapter 5 introduces a static analysis framework for equivalent and partially equivalent mutant identification, named Mutants' Equivalence Discovery (MEDIC), which implements the aforementioned problematic data flow patterns. The chapter begins by presenting various examples of problematic situations, belonging to the studied test subjects, that were automatically detected by MEDIC. Next, the implementation details of the tool are presented and the conducted empirical study is described. The chapter continues by discussing the obtained results and possible threats to validity. Finally, the chapter concludes with a summary of the most important findings.

Chapter 6 investigates whether mutants belonging to similar code fragments, i.e. software clones, exhibit analogous behaviour with respect to their equivalence. To this end, the concept of *mirrored mutants* is introduced, that is mutants belonging to similar code fragments of the program under test and, particularly, to analogous code locations within these fragments. First, the chapter describes the conditions that need to hold for two mutants to be considered mirrored ones and, next, it details the conducted empirical study. The obtained results support the aforementioned statement, indicating that considerable effort savings can be achieved in the presence of mirrored mutants. Additionally, experimental results suggesting that mirrored mutants can be beneficial to test case generation processes are also provided. Finally, the chapter recapitulates on major findings.

Chapter 7 concludes this thesis by summarising its contributions and providing possible avenues for future research.

Chapter 2

Mutation Testing: Background and Cost-Reduction Techniques

This chapter details the core concepts of mutation testing, along with the main sources of its cost and the related work on managing it. Although this succinct description suffices for the purposes of this thesis, a more detailed introduction can be found in the work of Offutt and Untch [8] and Jia and Harman [9].

The remainder of the chapter is organised as follows. Section 2.1 presents mutation's fundamental hypotheses, along with a description of its application and the cost of its phases. Section 2.2 describes the process of manually analysing equivalent mutants and Section 2.3 discusses previous work on the reduction of mutation's cost. Finally, Section 2.4 concludes this chapter.

2.1 General Infomation

Mutation testing is a well-studied technique with a rich history that began in 1971 by a class term paper of Richard Lipton [4]. At the end of the same decade, major work on the subject was published by Hamlet [90] and DeMillo, Lipton and Sayward [34].

As mentioned in the previous chapter, mutation is a fault-based technique. It induces artificial faults to the program under test. These faults are simple syntactic changes derived from predefined sets of rules which are called *mutation operators*. Generally, a mutation operator resembles typical programmer mistakes or forces the adoption of a specific testing heuristic [3]. Mutation's efficacy is closely related to the adopted set of mutation operators. In fact, a carefully chosen set can aug-

Table 2.1: First set of mutation operators for FORTRAN 77 programs (adapted from [13]).

Mutation Operator	**Description**
AAR	array reference for array reference replacement
ABS	absolute value insertion
ACR	array reference for constant replacement
AOR	arithmetic operator replacement
ASR	array reference for scalar variable replacement
CAR	constant for array reference replacement
CNR	comparable array name replacement
CRP	constant replacement
CSR	constant for scalar variable replacement
DER	DO statement alterations
DSA	DATA statement alterations
GLR	GOTO label replacement
LCR	logical connector replacement
ROR	relational operator replacement
RSR	RETURN statement replacement
SAN	statement analysis
SAR	scalar variable for array reference replacement
SCR	scalar for constant replacement
SDL	statement deletion
SRC	source constant replacement
SVR	scalar variable replacement
UOI	unary operator insertion

ment mutation's capabilities, whereas a poorly selected one can greatly impair its effectiveness [65, 66].

Table 2.1 depicts the first set of such operators that were included in MOTHRA, a mutation testing system for FORTRAN 77 programs [13, 91]. The first column of the table presents the name of the operators and the second one, a brief description of the imposed changes. For instance, the Relational Operator Replacement (ROR) mutation operator replaces each relational operator of the original program with others. An example of a mutant produced by such an operator was depicted in Figure 1.1b.

2.1.1 Underlying Principles

Mutation attempts to simulate real faults by inducing artificial faults to the program under test. These faults are restricted to simple syntactic changes based on two hypotheses: the *Competent Programmer Hypothesis* (CPH) [12, 34] and the *Coupling*

Effect (CE) [34].

The Competent Programmer Hypothesis, which was introduced by DeMillo et al. [34], states that programs written by competent programmers are close to being correct. Based on this assumption, if such a program is incorrect, it will contain only a few simple faults that can be corrected by a small number of simple syntactic changes. Thus, mutation attempts to mimic the faults that competent programmers make by introducing simple syntactic changes to the program under test. In the work of Budd et al. [92], a theoretical discussion on CPH is presented.

Based on the above observation, DeMillo et al. [34] introduced the Coupling Effect:

> *"Test data that distinguishes all programs differing from a correct one by only simple errors is so sensitive that it also implicitly distinguishes more complex errors."*

Or, equally:

> *"A test suite that detects all simple faults in a program is so sensitive that it will also detect more complex faults."*

Thus, complex faults are coupled to simple ones. This definition was extended by Offutt [93, 94] who introduced the *Mutation Coupling Effect* (MCE):

> *"Complex mutants are coupled to simple mutants in such a way that a test data set that detects all simple mutants in a program will detect a large percentage of the complex mutants."*

There is an analogy between the aforementioned definitions: a simple fault is represented by a simple mutant and a complex fault by a complex mutant. Simple mutants are the ones that induce one syntactic change and complex mutants, the ones that induce more. The former mutants are termed first order mutants and the latter ones, higher order mutants.

Higher order mutants introduce more than one syntactic changes to the program under test. According to the number of the induced changes, higher order

```
public static String capitalize (String str, char[] delimiters) {
    int delimLen = delimiters == null ? -1 : delimiters.length;
    if (str == null || str.length() == 0 || delimLen != 0) {
        return str;
    }
    int strLen = str.length();
    StringBuffer buffer = new StringBuffer( strLen );
    boolean capitalizeNext = true;
    for (int i = 0; i < strLen; i++) {
        char ch = str.charAt(i);
        if (isDelimiter(ch, delimiters)) {
            buffer.append( ch++ );
            capitalizeNext = true;
        }
        else if (capitalizeNext) {
            buffer.append(Character.toTitleCase(ch));
            capitalizeNext = false;
        }
        else {
            buffer.append(ch);
        }
    }
     return buffer.toString();
}
```

Figure 2.1: Example of a second order mutant. The mutant introduces both changes of the first order mutants presented in Figure 1.1 to the examined method (these changes are highlighted in the figure).

mutants are termed second order mutants (if they introduce two changes), third order mutants (in the case of three changes), etc. Figure 2.1 depicts an example of a second order mutant that introduces both changes of the first order mutants presented in Figure 1.1.

Based on the aforementioned principle, mutation testing focuses on simple syntactic changes, i.e. first order mutants. CE and MCE have been empirically investigated by several research studies which provide evidence supporting their validity [93–99].

2.1.2 The Mutation Analysis Process

Figure 2.2 illustrates the traditional mutation analysis process [8]. In summary, mutation involves the following phases:

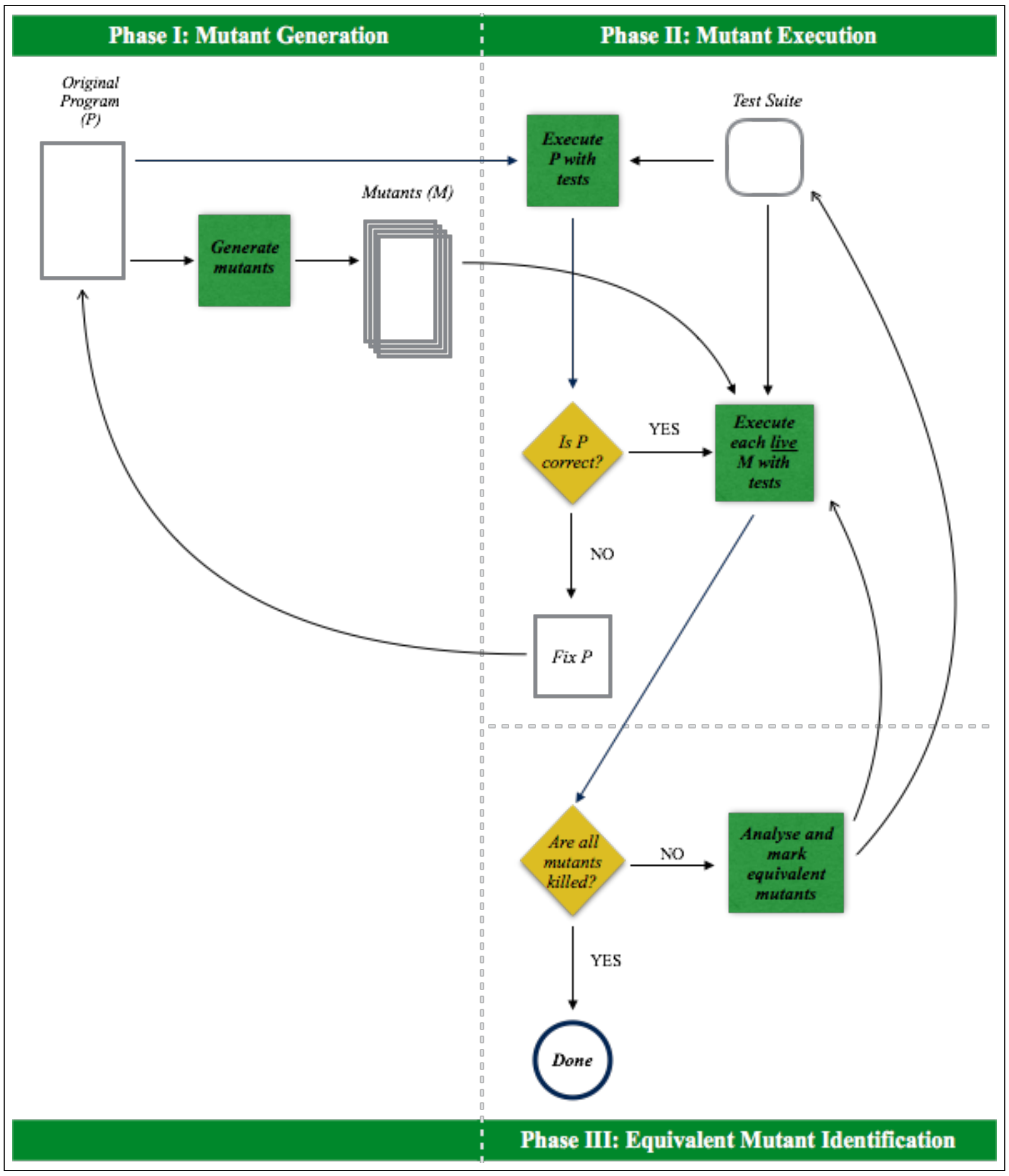

Phase I: Mutant Generation
Phase II: Mutant Execution
Original Program (P)
Test Suite
Execute P with tests
Mutants (M)
Generate mutants
Is P correct?
YES
Execute each live M with tests
NO
Fix P
Are all mutants killed?
NO
Analyse and mark equivalent mutants
YES
Done
Phase III: Equivalent Mutant Identification

Figure 2.2: Mutation Analysis Process (adapted from [8]). The mutants of the original program are generated (Mutant Generation Phase) and executed against the available test cases (Mutant Execution Phase). The live mutants are then manually analysed to determine their equivalence or to produce new test cases (Equivalent Mutant Identification Phase). The process repeats from Mutant Execution phase.

- **Phase I Mutant Generation.** The first step of the process is the generation of the mutants of the program under test. This step is fully automated by tools that apply specific mutation operators to the program under test. Examples of such tools are the MUJAVA testing framework [19] for the Java programming language and the MILU framework [16] for C.

- **Phase II Mutant Execution.** The next step entails the execution of the original program and its mutants with test data[1]. First, the original program is executed in order to verify whether its output is correct. If the output is incorrect, then a bug has been discovered and the program must be fixed before continuing. In the opposite situation, the mutants are executed with the available test data and their output is compared with the original's one in order to discover which mutants are killed. Killed mutants are no longer considered in the process.

- **Phase III Equivalent Mutant Identification.** After the execution of the mutants, the *mutation score* is calculated. As can be seen from Equation 2.1, the mutation score is the ratio of the killed mutants to the total number of killable ones. If all killable mutants have been killed or the mutation score is deemed adequate, the process stops; in a different case, the process continues as follows: the mutants that have not been killed must be manually inspected to determine whether they are equivalent ones or the available test cases are inadequate for killing them. In the former case, the detected mutants are marked as equivalent ones and are removed from the process. In the latter, new test data must be created and the process repeats from the previous phase. It should be mentioned that a test suite that manages to kill all killable mutants is called *mutation adequate test suite*.

$$Mutation\ Score = \frac{Killed\ Mutants}{All\ Mutants - Equivalent\ Mutants} \tag{2.1}$$

2.1.3 Mutation's Cost

As mentioned in Chapter 1, the coverage of a test criterion is a laborious task; covering mutation is no exception. Mutation requires significant computational re-

[1] In this thesis, the terms *test data* and *test cases* are used interchangeably.

sources and, more importantly, substantial human effort in order to be covered. In the following, this cost is outlined per considered phase:

- **Phase I Mutant Generation.** At this stage, mutation generates a vast number of mutants, i.e. a vast number of test requirements. Research studies suggest that this number is proportional to the product of the number of data references and the number of data objects ($O(Refs * Vars)$), for a software unit [81, 100]; a number that can be large even for simple programs. This large number of generated mutants influences the remaining phases negatively.

- **Phase II Mutant Execution.** This phase includes two activities that contribute to mutation's cost: the manual verification of the correctness of the original program's output and the execution of the original program and its mutants with the available test cases. The former activity, which is generally known as the human oracle problem [101], necessitates human intervention and, thus, increases the effort involved. It should be mentioned that this problem is not unique to mutation testing, on the contrary, it pertains to almost every testing scenario [101]. The latter activity requires the execution of the original program and all of its mutants with at least one test case, and, potentially many. This activity is the main source of mutation's high computational cost.

- **Phase III Equivalent Mutant Identification.** This phase is responsible for mutation's manual cost: it includes two challenging tasks that cannot be automated in their entirety. The first task is the generation of additional test cases to kill the live mutants and the second one, the identification of the equivalent mutants of the original program. Both of these tasks are complicated and involved and require an excellent understanding of the internal mechanics of the program under test.

From the aforementioned, it becomes clear that mutation testing involves considerable human effort and computational resources. Although many solutions to mutation's computational cost have been proposed, its manual cost remains a major hindrance to its adoption in practice. This cost can be primary attributed to the *Equivalent Mutant Problem*, which is detailed below.

2.1.4 The Equivalent Mutant Problem

The Equivalent Mutant Problem is a well-known impediment to the practical adoption of mutation. In consequence of its undecidable nature, a complete automated solution is unattainable [89]. To worsen the situation, detecting equivalent mutants is an error-prone and time-consuming task.

The manual identification of equivalent mutants is often prohibitive due to the large number of mutants that have to be considered and the complexity of the underlying process. This manual effort has been estimated to require approximately 15 minutes per equivalent mutant [78, 79]. Taking this fact into consideration, along with the estimated number of equivalent mutants per program which ranges between 10% and 40% of the generated ones [9], it can be easily concluded that the required human effort can become unbearable even for small projects.

Additionally, owing to the human judgement involved, human errors cannot be precluded. In the study of Acree [102], 20% of the studied mutants were erroneously classified, i.e. a killable mutant mistakenly classified as equivalent or vice versa.

Every step of the mutation analysis process is influenced by the presence of equivalent mutants. At the *Mutant Generation* phase, equivalent mutants are created without increasing the quality of the testing process; at the *Mutant Execution* phase, equivalent mutants waste computational resources by being executed with all the available test data without the possibility of being killed; and, finally, at the *Equivalent Mutant Identification* phase, manual effort is misspent by attempting to kill live mutants that are equivalent ones and by trying to identify equivalent mutants.

Considering the above-mentioned facts, the need to develop heuristics to tackle mutation's cost, and particularly the equivalent mutant problem, becomes apparent. Before introducing the techniques suggested by the present thesis, the procedure of manually analysing a mutant is detailed and previous work on reducing mutation's cost is discussed.

2.2 Manual Analysis of Equivalent Mutants

Three conditions must be satisfied by test data in order to kill a mutant. These conditions are known as the *RIP model* [3, 48, 96, 103–105]:

- **Reachability (R):** A test case must cause the execution of the mutated statement, i.e. the mutant must be reached by test data.
- **Infection (I):** The execution of the mutated statement must result in an erroneous program state, i.e. immediately after the execution of the mutated statement, the internal state of the mutated program and the corresponding state of the original program must differ.
- **Propagation (P):** The infected state must propagate to the ”exit” of the program and result in an incorrect output.

Due to the fact that all the above conditions must hold in order for a mutant to be killed, the RIP model implicitly defines three broad categories of mutants' equivalence, i.e. the cases where one of these conditions cannot be satisfied. Table 2.2 outlines the corresponding categories:

- **$\neg$R:** The first category refers to mutants that cannot be reached by any test case. Such mutants can never infect the program state and, as a consequence, no difference between their output and the one of the original program can be observed. The primary cause of mutants' equivalence for this category is the existence of dead code. In the case of boolean expressions another possible explanation can be given based on the short-circuit evaluation of complex sub-expressions [106]. Many programming languages include operators that exhibit such behaviour. For instance, the conditional operators `&&` and `||` of the Java programming language do not guarantee the evaluation of all parts of a boolean expression: if the value of the expression can be determined by the evaluation of only the first operand, then the second one will not be evaluated.

Table 2.2: Causes of Mutants' Equivalence (based on the *RIP Model*).

Category	Description
¬R	The mutant cannot be *reached*
R¬I	The mutant cannot *infect*
RI¬P	The infected state cannot *propagate*

Thus, if a mutant affects an operand that will never be evaluated, the mutant cannot be reached and, thus, can be identified as an equivalent one.

- **R¬I:** The second category pertains to mutants that can be reached but cannot infect the original program's state. The output of such mutants is always the same as the one of the original program. This situation can be attributed solely to the change of the mutant or the change of the mutant and the state of the program at that particular location [106]: for example, if a mutant changes the statement `int i = a` to `int i = -a` and the value of `a` is always zero at this program location, then the mutant cannot infect the program state.

- **RI¬P:** The last category corresponds to mutants that can be reached and can infect the original program's state but this infected state cannot propagate to the "exit" of the program. Thus, the imposed change can never be discerned. Two specific cases belong to this particular category [106]: first, the case where no parts of the infected state can be observed, e.g. an infected variable that is not used at any `return` statement; and, second, the case where the state of the program is infected but, at a later point, this infected state is coincidentally "corrected", e.g. an infected variable that can be returned by the program but is re-defined before the `return` statement.

2.3 Cost-Reduction Techniques

As discussed in the previous sections, mutation is a demanding testing technique. It requires high computational resources for mutant execution and significant human effort for equivalent mutant identification.

Researchers have proposed several techniques to manage mutation's cost. A synopsis can be found in the work of Jia and Harman [9] and Madeyski et al. [80]. The former focuses on mutation testing in general, whereas the latter on the equivalent mutant problem in particular. This section describes several of mutation's cost-reduction techniques, starting with the ones introduced to tackle the equivalent mutant problem.

2.3.1 Tackling the Equivalent Mutant Problem

At the core of the equivalent mutant problem is its undecidable nature [89], which prohibits the creation of fully automated solutions. As a consequence, the problem is solely amenable to partial, semi-automated ones. Despite this fact, researchers have proposed several techniques to ameliorate its adverse effects. These approaches can be divided into three general categories[2]: Equivalent Mutant Reduction techniques, Equivalent Mutant Detection techniques and Equivalent Mutant Classification techniques.

2.3.1.1 Equivalent Mutant Reduction Techniques

The approaches that belong to this category attempt to reduce the number of the considered equivalent mutants. A promising direction is the utilisation of higher order mutants [86], i.e. mutants that introduce more than one syntactic changes to the program under test. According to Higher Order Mutation's terminology, a mutant that induces one change is termed first order mutant, one that induces two is called second order mutant and so on.

Polo et al. [85] were the first to propose the creation of a set of second order mutants via the combination of the generated first order ones and the utilisation of this particular set for the purposes of mutation testing. They introduced and empirically investigated three mutant combination strategies. The obtained results suggest that the utilisation of these strategies could reduce the number of the considered mutants approximately by half and the number of equivalent mutants by more than 80%.

[2]Analogous, but not identical, terms have been utilised in the work of Madeyski et al. [80].

Papadakis and Malevris [88] evaluated several first and second order mutation testing strategies. The corresponding findings corroborated the equivalent mutant reduction but reported evidence of test effectiveness loss. More precisely, the test suites that covered the second order strategies were 10% less effective compared to the ones that covered mutation. Another finding was that the size of these test suites was 30% smaller, indicating a less expensive testing technique.

Analogous results were obtained by Madeyski et al. [80]. In their study, they evaluated further the strategies proposed by Polo et al. [85] and introduced an additional one. Their findings indicate that second order strategies are more efficient than mutation testing, but are less effective.

Kintis [107] introduced various second order strategies based on the dominator analysis [108] of the original program's control flow graph in an attempt to increase the interaction between the combined first order mutants. The experimental evaluation of these strategies indicated that they are superior to the previously-proposed ones [107, 109].

Kintis et al. [87] extended the previously introduced, dominator-based second order strategies by introducing several *hybrid* strategies. The main characteristic of these strategies is that the resulting mutant set contained both first and second order mutants. The conducted empirical study concluded that hybrid strategies are more effective than the previously introduced ones.

Apart from utilising higher order mutation for equivalent mutant reduction, other approaches suggest the use of co-evolutionary search techniques to avoid the creation of equivalent mutants. Particularly, in the work of Adamopoulos et al. [110], test cases and mutants are evolved in parallel with the aim of producing both high quality test cases and hard-to-kill mutants. By adopting a fitness function that penalises the mutants that are not killed by any test case (among the available ones), equivalent mutants are weeded out during the co-evolution process.

2.3.1.2 Equivalent Mutant Detection Techniques

The techniques that belong to this category manage to correctly identify a portion of the total equivalent mutants of the program under test. It should be noted that these techniques reduce mutation's cost without affecting its effectiveness.

One of the earliest studies is the one of Baldwin and Sayward [111] who suggested the utilisation of compiler optimisation techniques to identify equivalent mutants. The key intuition behind this approach is that mutants are, in a sense, optimised or de-optimised versions of the program under test. In their work, Baldwin and Sayward proposed six types of compiler optimisation strategies that could identify equivalent mutants produced by specific mutation operators.

Offutt and Craft [112] implemented the aforementioned strategies in MOTHRA [91], a mutation testing framework for FORTRAN 77 programs. Their implementation was based on the data flow analysis of the program under test and utilised an intermediate representation of this program. The empirical evaluation of these strategies revealed that they can detect 10% of the equivalent mutants, on average.

The idea of utilising compiler optimisation techniques to identify equivalent mutants was revisited by Papadakis et al. [113], who investigated whether the available compiler optimisation strategies of the GCC compiler[3] could be leveraged to identify equivalent mutants. The obtained results suggest that 30% of the equivalent mutants could be automatically detected, for the studied C programs.

Offutt and Pan [114, 115] proposed another approach to tackle the equivalent mutant problem that is based on mathematical constraints. Specifically, they formally introduced a heuristic-based set of strategies in order to determine the infeasibility of constraint systems that modelled the conditions under which a mutant can be killed (see also the RIP model in Section 2.2). If such an infeasible constraint system is detected, then the corresponding mutant can be safely identified as equivalent. The experimental evaluation of this approach revealed that it could detect approximately 50% of the examined equivalent mutants.

Nica and Wotawa [116, 117] proposed a similar technique for equivalent mutant detection. Their approach creates a constraint representation of the program under test and its mutants and attempts to generate test cases that kill them based on this representation. If such test cases cannot be generated, then the examined

[3]`https://gcc.gnu.org/`

mutant could be an equivalent one.

Bardin et al. [118] focused on the identification of infeasible test requirements of several coverage criteria[4], including weak mutation (see also Section 2.3.2.4). The proposed approach combined two static analysis techniques, a forward data flow analysis (*Value Analysis*) and a technique to prove program properties (*Weakest Precondition calculus*), to identify weak equivalent mutants, i.e. equivalent mutants generated by the weak mutation technique[5]. The obtained results suggest that a considerable number of the weak equivalent mutants generated by the studied mutation operators can be automatically detected.

Finally, another direction in equivalent mutant identification is the utilisation of program slicing [122]. Voas and McGraw [123] were the first to propose that program slicing can identify code locations that are unaffected by some statement and, thus, should not be mutated because the resulting mutants would be equivalent ones. Hierons et al. [124] developed this proposal and suggested that amorphous slicing [125, 126] can be used to support the manual analysis of particularly hard-to-kill mutants. Finally, Harman et al. [127] showed how dependence-based analysis can be leveraged to assist in the detection of equivalent mutants.

2.3.1.3 Equivalent Mutant Classification Techniques

Mutant classification has been proposed as another possible direction for equivalent mutant isolation. The approaches that belong to this category do not detect equivalent mutants, but rather classify mutants as possibly killable or possibly equivalent ones based on specific characteristics of the program under test. It is postulated that mutants exhibiting these characteristics are more likely to be killable.

Ellims et al. [128] reported that mutants having the same output as the original program for a given test suite can have different running profiles in terms of execution time and CPU and memory usage. Thus, they suggested that such differences could be used as a means of detecting killable mutants.

[4]Several studies have also considered ways to circumvent infeasible test requirements, e.g. [119–121].

[5]Note that if a mutant is equivalent under weak mutation is also equivalent under strong mutation.

Grün et al. [129] made a similar suggestion: they proposed that changes in the program behaviour between the original program and one of its mutants could indicate that the mutant is killable. They investigated whether mutants that impact the control flow of the original program's execution are more likely to be killable ones, and whether the ones that do not are more likely to be equivalent ones. The obtained results provided evidence supporting this statement.

Schuler et al. [130] examined whether the impact on dynamic invariants is a good indicator of mutants' killability. More precisely, their approach deduced pre- and post-conditions for every function of the program under test from its execution with test data and examined whether mutants violating such invariants are more likely to be killable. Its experimental evaluation supported this hypothesis.

Schuler and Zeller [78, 79] investigated further the classification power of the mutants' impact on control flow coverage and on methods' return values. The obtained empirical evidence suggested that impact on coverage is a better indicator of mutants' killability than the previously-proposed ones.

Finally, Papadakis and Le Traon [131] and Papadakis et al. [132] investigated the effectiveness of two mutant classification strategies based on the impact on control flow coverage. The conducted empirical study revealed that the examined mutant classification strategies managed to reduce the number of the considered equivalent mutants but were less effective than mutation testing.

2.3.2 Reducing Mutation's Computational Cost

Apart from mutation's manual effort, mutation requires considerably high computational resources. As discussed in Section 2.1.3, this computational cost springs from the fact that a large number of mutants have to be executed, at least once and potentially many times, against the available test cases. Researchers have proposed various techniques to deal with this problem. A brief description of several key approaches follows.

2.3.2.1 Mutant Sampling

One of the simplest approaches to reduce the number of the considered mutants is *Mutant Sampling* [100, 102]. Mutant Sampling selects a small subset of the generated mutants and performs mutation based on this subset.

Wong [133] investigated different sampling percentages ranging from 10% to 40% in steps of 5%. The experimental results revealed that a sampling percentage of 10% is only 16% less effective than the full set of generated mutants, implying that mutation testing strategies with a sample percentage greater than 10% form viable alternatives to mutation. This finding is in accordance to the studies of DeMillo et al. [91] and King and Offutt [13].

Papadakis and Malevris [88] empirically examined the test effectiveness of various mutant sampling strategies, ranging from 10% to 60% in steps of 10%. They found that the recorded test effectiveness loss, ranges between 26% and 6%.

2.3.2.2 Selective Mutation

Selective Mutation [81, 134] is another approximation technique that reduces the number of the considered mutants. It seeks to find a small set of mutation operators whose mutants can simulate the mutants generated by all the available operators. Selective Mutation was first introduced by Mathur [135] and was termed *Constrained Mutation*.

Mathur [135] proposed the application of mutation without the mutation operators that generated the most mutants. Offutt et al. [81, 134] developed further this idea and examined the effectiveness of different, reduced mutation operator sets. The corresponding findings revealed that from the 22 mutation operators of the MOTHRA system [91], 5 are sufficient to perform mutation effectively. It should be mentioned that the number of mutants generated by Selective Mutation is proportional to the number of data references in the program under test ($O(Refs)$), which is considerably smaller than the one of standard mutation (cf. Section 2.1.3).

Barbosa et al. [136] proposed 6 guidelines to determine sufficient mutation operators. The application of these guidelines resulted in a set of 10 operators which achieved a mutant reduction of 65% with approximately no loss in test effectiveness.

Namin and Andrews [137, 138] and Namin et al. [139] utilised statistical methods for the same purpose. Their studies identified a sufficient set of 28 mutation operators out of the 108 operators of the PROTEUM mutation testing framework for C [15], which achieved a mutant reduction of more than 92%.

Other research studies have examined the effectiveness of applying mutation with only one or two mutation operators. Wong [133] examined the effectiveness of utilising the Absolute Value Insertion (ABS) mutation operator in conjunction with the Relational Operator Replacement (ROR) mutation operator. The empirical evaluation of this approach indicated that it could reduce the number of the considered mutants by 80% with only a 5% loss in test effectiveness [133, 140].

Untch [141] examined the idea of utilising only the Statement Deletion mutation operator (SDL), an operator that deletes entire statements, presenting promising results. Deng et al. [142] investigated further the application of this particular operator to programs written in the Java programming language. The experimental results suggest that it could reduce the number of the considered mutants by 80% with an 8% loss in test effectiveness. Analogous results were obtained in the study of Delamaro et al. [143] for the C programming language.

Zhang et al. [144] compared Selective Mutation with Mutant Sampling. They evaluated the effectiveness of three selective mutation approaches (Offutt et al. [81], Barbosa et al. [136] and Namin et al. [139]) against two mutant sampling techniques. The empirical findings of this study suggest that Mutant Sampling is as effective as Selective Mutation. Finally, Zhang et al. [145] proposed that Selective Mutation and Mutant Sampling can be used in tandem and investigated the effectiveness of eight such strategies, obtaining promising results.

2.3.2.3 Minimum Mutant Sets

The results presented in the previous section suggest that a large number of mutants can be killed *collaterally* (see also [146]), i.e. by targeting other mutants. Thus, researchers have attempted to provide an estimation of the minimum number of mutants that are sufficient to cover the whole set of generated ones, i.e. to estimate the cardinality of a *minimum mutant set*.

Kintis et al. [87] were the first to empirically approximate this number in the context of the Java programming language. They introduced the concept of *disjoint mutants*, that is, mutants whose killing test cases are as disjoint as possible. The conducted empirical study considered minimal mutant disjointness in the context of two mutant sets: the set of all generated mutants and the set of hard-to-kill, stubborn[6] ones. The obtained results revealed that only a small portion of the generated mutants (9%) is required to cover the whole set even in the case of the hard-to-kill ones (35%).

Ammann et al. [147] investigated further this problem, both theoretically and empirically. They utilised *dynamic subsumption* to minimise the number of mutants. Given a test suite, mutant x dynamically subsumes mutant y *iff* the test cases that kill x also kill y. The experimental evaluation of dynamic subsumption, in the context of the C programming language, revealed that only 1.2% of the generated mutants is required to cover the whole set.

Finally, Kurtz et al. [148, 149] provided additional insights regarding mutant subsumption and investigated whether dynamic and static analysis techniques can be used to approximate this relationship. Their findings suggest that static analysis techniques should be used in tandem with dynamic ones in order to achieve the best results.

2.3.2.4 Strong, Weak and Firm Mutation

Apart from restricting the number of the considered mutants to manage mutation's cost, researchers have introduced various techniques to reduce the execution cost of running all mutants against the available test suite. The most prominent of these techniques is *Weak Mutation*, proposed by Howden [82, 83].

Weak Mutation attempts to reduce the computational resources required to perform mutation by avoiding the complete execution of the original program and its mutants. To achieve this, Weak Mutation redefines the condition that needs to hold for a mutant to be considered killed (see also the RIP model in Section 2.2): instead of comparing the final output of the original program and the mutant, the internal

[6]A stubborn mutant is a killable mutant that is difficult to be killed [106, 124].

states of these programs are compared immediately after the execution of the mutant or the mutated component. It should be mentioned that standard mutation is referred to as *Strong Mutation* when compared with Weak Mutation.

Woodward and Halewood [84] introduced the concept of *Firm Mutation*, a mutation approach that occupies the middle ground between Strong and Weak Mutation. They argue that the comparison between the states of the original program and its mutants can be performed at any point between the first execution of the mutated statement and the end of the program.

Various research studies corroborate Weak Mutation's cost-effectiveness. Girgis and Woodward [150] developed a Weak Mutation framework for FORTRAN 77 programs and empirically evaluated its performance. The obtained results suggest that Weak Mutation requires less computational resources than Strong Mutation.

Horgan and Mathur [151] showed that test suites that satisfy Weak Mutation can satisfy Strong Mutation with a high probability. Marick [152] presented results indicating that Weak Mutation is nearly as effective as Strong Mutation. The study of Kintis et al. [87] revealed that Weak Mutation also reduces mutation's manual effort by considering fewer equivalent mutants.

Offutt and Lee [153, 154] evaluated the effectiveness and efficiency of Weak Mutation, along with different implementations of the technique. Their results suggest that it forms a cost-effective alternative to Strong Mutation. Regarding the examined implementations, the authors suggest that the internal states of the original program and its mutants should be compared after the first execution of the mutated statement or the basic block that contains it.

2.4 Summary

This chapter presented the core concepts of mutation testing. First, mutation's fundamental hypotheses were described, along with the phases of the traditional mutation analysis process. Next, the cost of mutation per phase was outlined, with an emphasis on the equivalent mutant problem and its negative effects. Finally, the conditions that need to hold for a mutant to be equivalent or killable were detailed and previous work on equivalent mutant elimination, minimum mutant sets and mutant reduction techniques was introduced.

This chapter presented the necessary background of this thesis. The subsequent chapters will discuss the techniques that the thesis proposes to tackle the equivalent mutant problem.

Chapter 3

Equivalent Mutant Isolation via Higher Order Mutation

As stated in Chapter 2, equivalent mutants constitute a major obstacle to the practical adoption of mutation. This chapter introduces and empirically evaluates a novel, mutant classification technique, named *Isolating Equivalent Mutants* (I-EQM), that is able to automatically isolate first order equivalent mutants via higher order ones.

In an attempt to ameliorate the adverse effects of the equivalent mutant problem, Schuler and Zeller [78, 79] suggested a technique, hereafter referred to as the coverage impact method, that is able to isolate equivalent mutants. This method is based on the observation that mutants affecting the program execution are more likely to be killable than those that do not do so [128, 129]. According to this, mutants can be classified as possibly killable and possibly equivalent ones.

The empirical results of the study of Schuler and Zeller [78, 79] revealed that 75% of the mutants of the resulting possibly killable mutant set were indeed killable ones. Thus, they suggested that practitioners should target this mutant set in order to minimise the consequences of equivalent mutants. Although such a practice reduces the possibility of encountering equivalent mutants, this set was found to include only the 56% of the total killable ones, thus, missing a large number of them. The approach described in the present chapter expands the coverage impact method by aiming at overcoming the aforementioned limitation.

The proposed technique uses second order mutants to isolate possible first order equivalent ones and is the first one to utilise higher order mutants in this context.

As mentioned in Chapter 2, a second order mutant is a mutant that induces two syntactic changes to the program under test (see Figure 2.1 for an example).

The approach is based on the intuition that since equivalent mutants have a small effect on the state of the program, they should not have an apparent impact on the state of another mutant. Thus, it is argued that a killable mutant is likely to impact the output of another first order mutant when these mutants are combined, i.e. forming a second order one. Although such a technique is not clearly competitive to the coverage impact method, it enables the correct classification of different mutants. This fact motivated the design of a combined classification scheme that utilises both aforementioned techniques with promising results.

This chapter describes three variations of the proposed technique and investigates their ability to classify killable mutants. Additionally, it empirically validates the coverage impact method and compares it with the proposed ones. Experimental evaluation, conducted on two independently selected sets of manually classified mutants, confirms the coverage impact method's published results and reveals that its combination with the proposed approaches is capable of retrieving approximately 20% more killable mutants. In general, the contributions of this chapter are the following:

1. A novel, dynamic method to effectively and automatically classify first order mutants using second order ones.

2. An empirical study validating the coverage impact method and the proposed approaches. In particular, the coverage impact method achieves a classification precision of 73% and a classification recall of 65%, whereas the proposed technique realises a precision score of 71% and a recall value of 81%.

3. A manually identified set of killable and equivalent mutants which amplifies an existing benchmark set [78, 79] and is made publicly available[1] with the aim of enabling replication and comparative studies.

[1]This set and the results of the present study are publicly available at `http://pages.cs.aueb.gr/~kintism/#stvr2014`.

The rest of the chapter is organised as follows. Section 3.1 introduces background information and briefly describes the coverage impact method. Section 3.2 details the proposed mutant classification schemes and Section 3.3 the conducted empirical study. Next, Section 3.4 analyses and discusses the obtained results, along with possible threats to the validity of this study. Finally, Section 3.5 concludes this chapter, summarising key findings.

3.1 Background

The work presented in this chapter suggests the use of a mutant classification approach in order to isolate equivalent mutants. The proposed classification scheme utilises second order mutants and the mutants' impact in order to highlight the majority of the killable mutants. This section details these techniques and concepts.

3.1.1 Mutants' Impact

The approaches studied in this chapter were founded on an assertion, known as the *mutants' impact*, which pertains to killable mutants. The intuition behind mutants' impact is that mutants altering certain aspects of the original program's execution are more likely to be killable. In other words, given a test case, if some aspect of the execution of the original program and a mutant differs, then the mutant can be classified as possibly killable. These differences are referred to as the mutants' impact. Various research studies have investigated how to measure mutants' impact, e.g. violated dynamic program invariants [130], different execution program traces [78, 79, 129] and different methods' return values [78, 79].

Mutants' impact represents a variation in the behaviour of the original program and its mutants. Such differences appear during program executions and, in particular, after executing the mutated location up to the exit of the program [129]. Along these lines, impact on coverage measures the differences in the control flow coverage between the original program and its mutants [78, 79]. Impact on return values measures the differences in the values returned by the public methods encountered during program execution [78, 79]. Impact on dynamic program invariants measures the number of invariants that were violated by the introduction of mutants

[130].

Generally, it has been empirically found that mutants with impact are more likely to be killable than those with no impact, regardless of the impact measure [78, 79]. However, different impact metrics, or their combinations, result in different mutant classifiers with variations in their effectiveness. Constructing a more effective classifier forms the objective of the present work, which proposes the use of higher order mutants as impact measures. Based on this novel measure, different mutants from the previously introduced approaches can be classified appropriately.

3.1.2 Mutation Analysis using Mutant Classifiers

As described in Section 2.1.2, applying mutation testing entails the generation of a mutant set. Next, the mutants of this set are executed with the available test cases to determine the killed ones. Finally, the live mutants are analysed by the tester to produce new test cases or to determine their equivalence. This process iteratively continues until all killable mutants have been killed.

It can be easily seen that the ratio of the equivalent to killable mutants increases as more test cases are added to the test suite. This is attributed to the fact that the number of equivalent mutants remains constant, whereas the number of killable ones decreases (because they are killed). Thus, if the live mutants could be automatically classified as possibly killable and possibly equivalent ones, considerable effort savings could be achieved by analysing only the possibly killable mutants [78, 79, 130, 155].

Based on the aforementioned argument, automated mutant classification approaches have been proposed in the literature. A typical mutant classification process is depicted in Figure 3.1. Steps (a)-(c) divide up the set of live mutants into two disjoint sets, the possibly killable mutant set and the possibly equivalent one. Before applying the classification scheme, the set of live mutants must be found, i.e. the first order mutants of the original program must be generated (Figure 3.1 (a)) and executed with the available test data (Figure 3.1 (b)).

At this point, a set of killed and a set of live mutants have been created. Killed mutants do not add any value to the testing process and are discarded. In contrast,

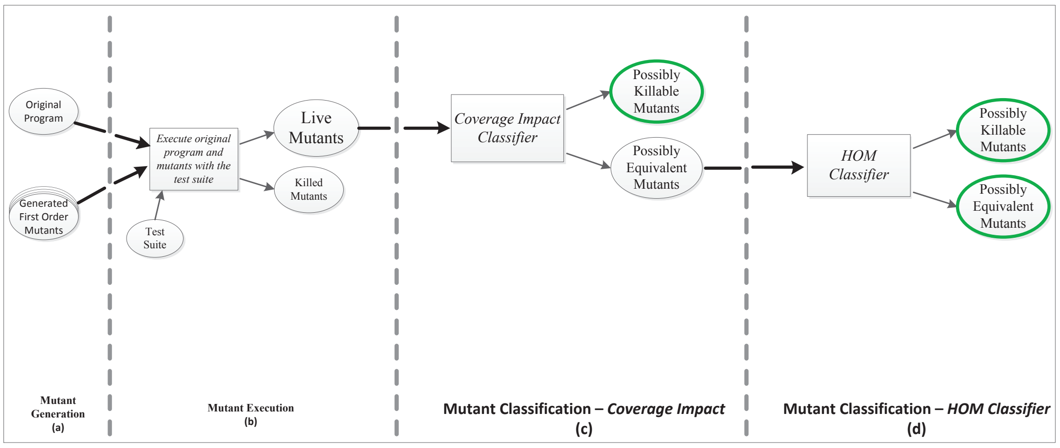

Original Program
Generated First Order Mutants
Execute original program and mutants with the test suite
Test Suite
Live Mutants
Killed Mutants
Coverage Impact Classifier
Possibly Killable Mutants
Possibly Equivalent Mutants
HOM Classifier
Possibly Killable Mutants
Possibly Equivalent Mutants
Mutant Generation (a)
Mutant Execution (b)
Mutant Classification – Coverage Impact (c)
Mutant Classification – HOM Classifier (d)

Figure 3.1: Mutation Analysis using Mutant Classifiers. The live mutants are classified as possibly killable and possibly equivalent. The Isolating Equivalent Mutants (I-EQM) process works in two phases. First, the live mutants are classified via the Coverage Impact classifier and subsequently the produced possibly equivalent mutant set is classified by the High Order Mutation (HOM) classifier. The highlighted first order mutant sets are the outcome of the I-EQM classification process.

the set of live mutants improves the quality of the process by guiding the generation of new test data. However, this set is most likely composed of both equivalent and killable mutants. Therefore, the live mutant set is provided as input to the classification system. The live mutants are then categorised as possibly killable or possibly equivalent ones. (Figure 3.1 (c)). Finally, the testing process continues by considering only the mutants of the possibly killable mutant set.

3.1.2.1 Mutant Classification: Effectiveness Measures

Mutant classification categorises mutants as possibly killable or possibly equivalent. Being a heuristic method, it may correctly classify some mutants and fail on others. For example, a killable mutant may be correctly classified as possibly killable, whereas an equivalent one may be incorrectly classified as possibly killable.

To distinguish between the correctly and incorrectly classified mutants, the following definitions are given, which are in accordance to the respective ones used in the Information Retrieval literature [156]:

Definition 3.1 ***True killable.*** *Killable mutants correctly classified as possibly killable.*

Definition 3.2 ***False killable.*** *Equivalent mutants incorrectly classified as possibly killable.*

Definition 3.3 ***True equivalent.*** *Equivalent mutants correctly classified as possibly equivalent.*

Definition 3.4 ***False equivalent.*** *Killable mutants incorrectly classified as possibly equivalent.*

To quantify the classification ability and provide a basis for comparison between the examined approaches, the following measures were utilised. Note that these metrics are usually employed to compare classifiers in Information Retrieval experiments [156].

$$Precision = \frac{True\ killable}{True\ killable + False\ killable} \tag{3.1}$$

$$Recall = \frac{True\ killable}{True\ killable + False\ equivalent} \tag{3.2}$$

$$Accuracy = \frac{True\ killable + True\ equivalent}{True\ killable + False\ killable + True\ equivalent + False\ equivalent} \tag{3.3}$$

$$F_\beta = (1+\beta^2) \times \frac{Precision \times Recall}{\beta^2 \times Precision + Recall} \tag{3.4}$$

Equation 3.1 and Equation 3.2 quantify the ability of the classifier to correctly classify killable mutants. Specifically, the *precision* metric quantifies the ability of the classifier to categorise correctly killable mutants, whereas the *recall* value measures the capability of the classifier in retrieving killable mutants. Thus, a high precision value indicates that the classifier can sufficiently distinguish between killable and equivalent mutants, whereas a high recall value shows that the classification scheme is able to recover the majority of the live killable mutants.

Equation 3.3 and Equation 3.4 are utilised to better compare the examined classifiers. The *accuracy* metric depicts the percentage of the correctly classified mutants. The F_β score[2] constitutes a general metric that combines the precision and recall values into a single measure of overall performance and enables different weighting between the two measures. Thus, by changing the value of β, different performance scenarios could be investigated. For instance, a scenario where the classification precision and recall are equally balanced corresponds to a β value of 1. In this chapter, three such scenarios are explored, which are described in Section 3.3.4.

Mutation testing requires the employed test cases to be capable of killing all killable mutants. Mutant classification changes this requirement to killing all possibly killable mutants. Thus, mutant classification can be seen as an approximation method to mutation. The effectiveness of this approximation can be measured as the number of killable mutants that are correctly classified as such, i.e. by the recall metric, because the testing process will be based only on these mutants. The efficiency of the method can be measured by the number of equivalent mutants that are incorrectly classified as possibly killable, because these mutants will be manually analysed by the tester. Thus, the methods' efficiency can be expressed by the precision value[3] of the classifier.

In general, high precision is difficult to be achieved, but is extremely desirable for efficiency reasons. However, if high precision is not accompanied by a relatively high recall, the process might lose some valuable mutants. Because low recall indicates that many killable mutants are ignored, such processes will experience losses of their strength. On the contrary, high recall is easily achieved by classifying most or all undetected mutants as possibly killable. In such a case, higher testing quality is achieved at a considerable cost.

It is obvious that a combination of high precision and high recall is more suitable for a mutant classification scheme. In this manner, most of the killable mutants would be correctly classified as such and, at the same time, testing based on the retrieved killable mutants can be deemed adequate. In a different situation, the clas-

[2]For non-negative real values of β.

[3]The percentage of the equivalent mutants that are incorrectly classified as possibly killable is actually $(1 - \textit{precision})$. Thus, higher precision indicates that fewer equivalent mutants are to be considered and, hence a higher efficiency.

sifier would be deficient as it would categorise many equivalent mutants as possibly killable ones (a case of a classifier with low precision) or it would classify many killable mutants as possibly equivalent ones (a classifier with low recall). Consequently, it is the reconciliation of a classifier's precision and recall scores that stipulates its success.

3.1.2.2 Mutant Classification using Code Coverage

Classifying mutants using code coverage has been empirically found to be superior to previously proposed classifiers, such as those using dynamic program invariants and methods' return values [78, 79]. Following the suggestions of Schuler and Zeller [78], a coverage measure is determined by counting how many times each program statement is executed during a test case run. The comparison of the coverage measures of both the original program's and a mutant's execution results in the impact measure (coverage difference) of the examined mutant.

Mutants' impact is defined based on the coverage impact as "the number of methods that have at least one statement that is executed at a different frequency in the mutated run than in the normal run, while leaving out the method that contains the mutated statement" [78]. This approach is also adopted in the present study and referred to as the Coverage Impact classifier.

3.2 First Order Mutant Classification via Second Order Mutation

The primary purpose of this chapter is the introduction of a new mutant classification scheme, hereafter referred to as Higher Order Mutation (HOM) classifier, which would further attenuate the negative effects of the equivalent mutant problem. The salient feature of the suggested approach is the employment of higher order mutation in the classification process.

The HOM classifier categorises mutants based on the impact they have on each other. In view of this, it produces pairs of mutants by combining each examined (first order) mutant with others. The classifier works based on the intuition that since equivalent mutants have a small effect on the state of the original program, in a similar fashion, they should also have no apparent impact on the state of another mutant when combined as a second order mutant. Hence, a possibly equivalent mutant will have a minor impact on the execution and no observable impact on the output of another mutant. Any departure from this situation implies that the mutant is possibly killable, leading to the HOM Classifier Hypothesis.

HOM Classifier's Hypothesis. Let *fom* be a first order mutant, *umut* an unclassified mutant, *umut.fom* the second order mutant created by the combination of the two corresponding mutants and *Killable* the set of killable mutants of the considered program under test. The HOM classifier hypothesis states that if the results of the executions of the first order mutant *fom* and the second order mutant *umut.fom* differ, then the first order mutant *umut* is killable. More formally:

$$outputOf(fom, test) \neq outputOf(umut.fom, test) \Rightarrow umut \in Killable$$

The aforementioned hypothesis forms the basis of the proposed classification scheme. Thus, if the condition of the aforementioned formula holds, then *umut* is classified as possibly killable. Otherwise, *umut* is classified as possibly equivalent. This practice is presented in Figure 3.2. Although this condition may not always hold, the conducted experimental study suggests that it can provide substantial guidance on identifying killable and equivalent mutants.

3.2.1 HOM Classifier: Mutant Classification Process

The mutant classification process of the HOM Classifier requires three main inputs. These inputs are requisites for the evaluation of the HOM Classifier Hypothesis:

- The first input is the set of the live-unclassified mutants that need to be classified. The mutants of this set will be categorised as possibly killable or possibly equivalent based on the truth or the falsehood of the classification's predicate.

- The second required input is the set of mutants, referred to as the *classification mutant set* (CM), that will be used for constructing the sought mutant

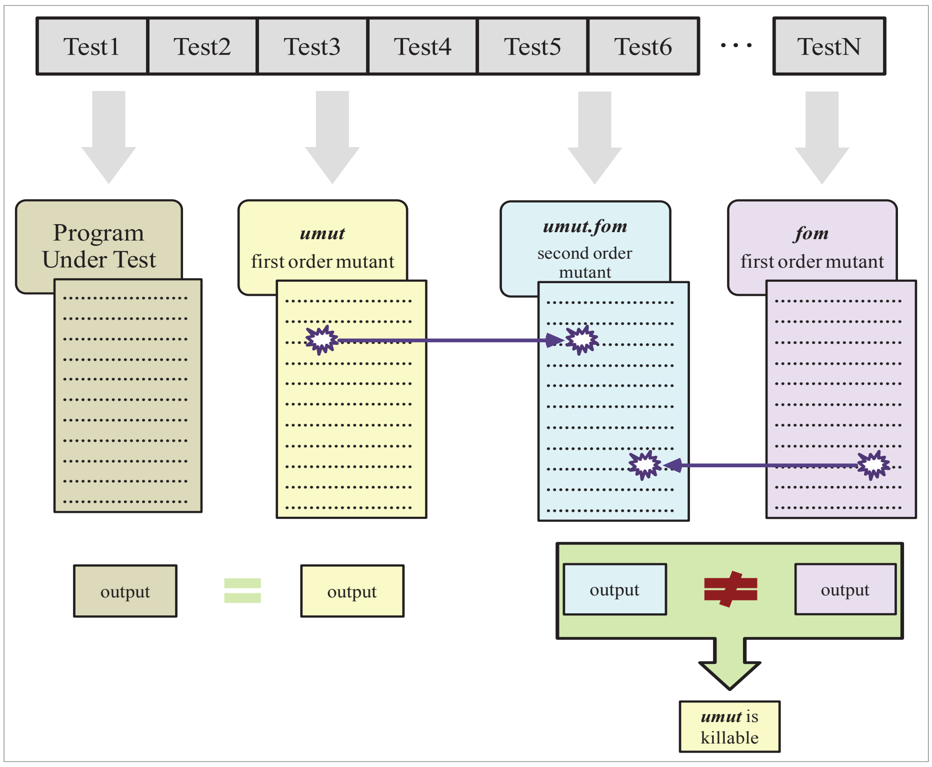


Figure 3.2: HOM Classifier's Hypothesis. The unclassified first order mutant *umut* is classified as possibly killable based on its impact on other *fom* mutants.

pairs. The mutant pairs are constructed by combining these mutants with the unclassified ones.

- The final input of the classification process is the test suite, with which the second order mutants and their corresponding first order ones will be executed.

Algorithm 3.1 presents the underlying classification process. The algorithm takes as inputs: (a) the set of the live-unclassified first order mutants; (b) the first order mutants of the CM set that will be used for the generation of the second order ones; and, (c) the available test suite. The mutants' impact is defined as the number of first order mutants in the CM set whose output is changed after being combined with the live-unclassified mutant.

Algorithm 3.1 HOM Classifier's Classification Process.

```
Let $Live$ represent the live-unclassified mutant set
Let $CM$ represent the *classification mutant set*
Let $T$ represent the available test suite
Let $PK$ represent the resulting set of possibly killable mutants
Let $PE$ represent the resulting set of possibly equivalent mutants

1:  $PK = \emptyset$
2:  $PE = \emptyset$
3:  foreach $umut \in Live$ do
4:      foreach $fom \in CM$ do
5:          foreach $test \in T$ do
6:              fom_output = EXECUTEORRETRIEVEOUTPUT($fom$, $test$)
7:              $umut.fom$ = COMBINE($umut$, $fom$)
8:              som_output = EXECUTEORRETRIEVEOUTPUT($umut.fom$, $test$)
9:              if fom_output $\neq$ som_output then
10:                 $PK$.ADD($umut$)
11:                 continue with the next $umut$
12:             end if
13:         end for
14:     end for
15:     $PE$.ADD($umut$)
16: end for
17: return $PK$, $PE$
```

3.2.1.1 Classification Mutant (CM) Set

As already stated, the proposed classification technique determines the impact of mutants using other mutants which are referred to as the CM set. For example, in Figure 3.2, the CM set is the set of the *fom* mutants to be employed in order to perform an effective classification process. The question that is raised here is which mutants are suitable to support the mutant classification process. Specifically, it has been found that not all mutants are of the same value in assessing the mutants' impact. Perhaps, by utilising all the available mutants, one could obtain the best results. However, such an approach is prohibitive because it requires executing all mutants with all test cases for each mutant to be classified.

Considering the aforementioned issue, a necessary restriction was imposed on the utilised CM mutant set; only mutants appearing in the same class as the aimed unclassified mutant were considered. Thus, for each mutant to be classified, a different CM set was used. This choice was based on the intuition that mutants belonging to the same class are more likely to interact and be exercised by the same test cases. It is noted that since there is no available test case able to kill *umut*, if there is no interaction between the mutants composing the second order one (*umut* and *fom*), then the outputs of *fom* and *umut.fom* will be the same for all the employed test cases.

3.2.1.2 HOM Classifier Variations

Three variations of the HOM classifier have been considered in the present study: “HOM classifier (all foms)”, “HOM classifier (killed foms)” and “HOM classifier (same method foms)”. These approaches differ in the sets of mutants that will be used for the creation of the second order ones. Recall that the employed CM set is the one composed of the mutants that belong to the same class as the aimed unclassified mutant.

The “HOM classifier (all foms)” variation considers the whole CM set, whereas the other approaches utilise only a specific subset. “HOM classifier (killed foms)” uses only those mutants that have been killed by the employed test cases, whereas “HOM classifier (same method foms)” employs only those that appear in the same method as the aimed unclassified mutant.

The reason for using only the already killed mutants is that these mutants are more sensitive to the utilised test cases (easy-to-kill) than the live ones and, thus, they will be more sensitive to the impact of the examined ones. Similarly, using mutants belonging to the same method as the examined mutant increases the chances of these mutants to be coupled. Besides these reasons, their application was empirically found to be sound. Furthermore, constructing the sought second order mutants based on the killed mutant set or the mutants of the same method results in the reduction of the overall computational cost of the technique due to the reduced number of mutant combinations and their respective executions.

3.2.2 Isolating Equivalent Mutants (I-EQM) Classifier

In addition to the techniques described in the previous section, the possibility of employing a combined strategy is also investigated. To this end, the Isolating Equivalent Mutants (I-EQM) classification scheme is proposed.

The I-EQM classifier constitutes a combination of the coverage impact classifier [78, 79] and the variations of the HOM classifier. The utilisation of the coverage impact classifier is based on its evaluation, which presented the best results among those examined in previous studies [78, 79]. Specifically, it resulted in a classification precision of 75% and a recall value of 56%.

In addition, the coverage impact classifier manages to successfully classify most of the mutants that are correctly classified by the rest of the examined approaches [78, 79]. Due to the fact that the precision measure of the coverage impact classifier can be considered as an accurate one, i.e. it does not misclassify many equivalent mutants; effort should be put into improving the recall measure. Achieving higher recall results in considering a larger number of killable mutants, thus, strengthening the testing process.

In order to effectively combine different classifiers, they must satisfy the following two requirements: first, the precision of both classification schemes must be reasonably high; and, second, they should classify different killable mutants as possibly killable. In other words, both produced sets must be accurate and their intersection must be of small size. As a result, the precision of the combined classifiers will not be greatly affected, whereas their recall will be significantly improved. Combining classifiers has been attempted by Schuler and Zeller [78, 79] but without success.

The I-EQM classification process is summarised in Figure 3.1. After obtaining the set of live mutants (Figure 3.1 (a), (b)), the coverage impact classifier is employed in order to perform the first step of the I-EQM's classification procedure (Figure 3.1 (c)). This step will produce the set of the possibly killable and the possibly equivalent mutants of the coverage impact classifier.

Next, the HOM classifier is applied to the possibly equivalent mutant set that was previously generated (Figure 3.1 (d)). This phase will create the set of the possibly killable mutants and the set of the possibly equivalent ones of the HOM classifier. The I-EQM classifier's resulting set of possibly killable mutants is the union of the possibly killable mutant set of the coverage impact classifier and the corresponding killable set of the HOM classifier. The possibly equivalent mutant set of the I-EQM classifier is the one generated by the HOM classifier. The aforementioned sets appear highlighted in Figure 3.1.

It should be noted that the order in which the coverage impact and HOM classifiers are applied to the set of live mutants is indifferent, that is, the resulting sets of the possibly killable and the possibly equivalent mutants would be the same regardless of the application order of the two classifiers. This is due to the fact that the resulting set of the possibly killable mutants will be composed of the mutants that are categorised as such by at least one of the combined classifiers. The possibly equivalent mutant set will contain the mutants that are categorised as such by all the combined classifiers. This can also be generalised to a classification process that includes more than two classifiers.

3.3 Empirical Study

The present study investigates a new aspect of higher order mutants, their ability to classify first order ones. This characteristic constitutes the basis of the HOM and I-EQM classifiers, detailed in the previous section.

The present section describes the empirical evaluation of these approaches, which is based on two independently selected sets of manually classified mutants and directly compares them to the coverage impact classifier [78, 79]. Additionally, a revalidation of the coverage impact classifier is performed.

3.3.1 Research Questions

The following research points summarise the primary purpose of the presented empirical evaluation:

- **RQ 3.1** *Can second order mutation provide adequate guidance in equivalent mutant isolation, or equally, how effective are the HOM and I-EQM classi-*

Table 3.1: Subject Program Details.

Program	**Description**	**Version**	**LOC**	**Test Cases**
`AspectJ`	AOP extension to Java	cvs: 2007-09-15	25,913	336
`Barbecue`	Bar code creator	svn: 2007-11-26	4,837	153
`Commons`	Helper utilities	svn: 2009-08-24	19,583	1,608
`Jaxen`	XPath engine	svn: 2008-12-03	12,438	689
`Joda-Time`	Date and time library	svn: 2009-08-17	25,909	3,497
`JTopas`	Parser tools	1.0 (SIR)	2,031	128
`XStream`	XML object serialisation	svn: 2009-09-02	16,791	1,122

fiers in terms of their recall and precision metrics?

- **RQ 3.2** *Do the HOM and I-EQM classifiers perform better than the coverage impact classifier?*

- **RQ 3.3** *How stable is the categorisation ability of the HOM, I-EQM and coverage impact classifiers across the two different mutant sets? Are there any important differences between the two sets?*

3.3.2 Subject Programs and Supporting Tool

The evaluation of the examined classification schemes is based on a set of seven open source projects. The motivation behind the selection of these test subjects is twofold. First, they were also used in the empirical evaluation of the coverage impact classifier [78, 79], hence they facilitate a direct comparison. Second, these programs constitute real-world examples and therefore would provide valuable insights into the practical applicability and the efficacy of the examined mutant classification techniques.

Table 3.1 presents the corresponding details. Specifically, the table reports the subjects' name, a brief description of their usage, their versions, the lines of code and the number of accompanying test cases. It should be noted that in the case of `AspectJ`, only the `org.aspectj.ajdt.core` package was considered.

For mutant generation and execution, the JAVALANCHE mutation testing framework (version 0.3.6) [20] for the Java programming language was utilised.

Table 3.2: JAVALANCHE's Mutation Operators.

Mutation Operator	Description
Replace Numerical Constant (RNC)	Replaces a numerical constant instance by $+1$, -1 or 0
Negate Jump Condition (NJC)	Inserts the negation operator to logical conditional instances
Replace Arithmetic Operator (RAO)	Replaces an arithmetic operator instance by another one
Omit Method Calls (OMC)	Omits a method call and replaces it with a default value (the default value replaces the returned one)

The main reason for selecting this framework is because it implements the coverage impact classification method and it was utilised in its empirical evaluation. JAVALANCHE enables the efficient application of mutation by implementing a large number of optimisations and has been used in many previous studies [78, 79, 129, 130, 157], providing evidence of its usefulness. Table 3.2 records details about the mutation operators supported by the tool.

3.3.3 Benchmark Mutant Sets

In order to investigate the effectiveness of the proposed approaches, the mutant set of the studies of Schuler and Zeller [78, 79] was utilised, hereafter referred to as "control mutant set 1". "Control mutant set 1" is composed of 140 manually classified mutants, each one belonging to a different class of the subject programs, with a total number of 20 mutants per test subject.

To avoid overfitting or coincidental results, a second set of mutants was also considered. The second set, referred to as "control mutant set 2", was constructed for the purposes of the present study, in a similar fashion to "control mutant set 1". Specifically, for each test subject, 10 live mutants were randomly selected for manual classification, each one belonging to a different class. Thus, "control mutant set 2" is comprised of 70 manually classified mutants, with a total number of 10 mutants per test subject.

Details about the considered control mutant sets with respect to the examined programs and utilised mutation operators are recorded in Table 3.3 and Table 3.4.

Table 3.3: Control Mutant Sets' Profile w.r.t. Subject Programs.

	Considered Mutants		**Manually Classified Mutants**					
Subject	Number of	Reached	Killable			Equivalent		
Program	Mutants	Mutants	Set_1	Set_2	Sets_{1+2}	Set_1	Set_2	Sets_{1+2}
`AspectJ`	6,613	2,878	15	6	21	5	4	9
`Barbecue`	3,283	1,603	14	9	23	6	1	7
`Commons`	8,693	8,305	6	6	12	14	4	18
`Jaxen`	6,619	3,944	10	7	17	10	3	13
`Joda-Time`	5,322	4,197	14	7	21	6	3	9
`JTopas`	1,676	1,402	10	4	14	10	6	16
`XStream`	2,156	1,730	8	5	13	12	5	17
Total	34,362	24,059	77	44	121	63	26	89

The former presents the number of killable and equivalent mutants per control mutant set and subject program and the latter, the same information per mutation operator. *manually identified set*. It must be noted that these sets are among the largest manually analysed sets of mutants utilised in the literature (cf. Table 4 in the study of Yao et al. [106]).

More precisely, the "Considered Mutants" column of Table 3.3 refers to the number of the considered mutants, among those generated by the JAVALANCHE framework. It should be mentioned that the considered mutants are the ones that belong to the same classes as the manually classified ones. Column "Number of Mutants" presents the total number of the corresponding mutants and column "Reached Mutants", the ones reached by the available test cases. Finally, the "Manually Classified Mutants" column reports the number of the equivalent and killable mutants among the manually classified ones.

Table 3.4 records the contribution of each mutation operator to the employed control mutant sets. Specifically, the number of mutants per operator and the number of killable and equivalent ones are reported. From the table, it can be observed that the Replace Numerical Constant (RNC) and Replace Arithmetic Operator (RAO) operators contribute 20% more equivalent mutants than the Negate Jump Condition (NJC) and Omit Method Calls (OMC) operators.

By examining the two control mutant sets, it can be seen that they have dif-

Table 3.4: Control Mutant Sets' Profile w.r.t. Mutation Operators.

Mutation	**Mutants**			**Killable**			**Equivalent**		
Operator	Set_1	Set_2	Sets_{1+2}	Set_1	Set_2	Sets_{1+2}	Set_1	Set_2	Sets_{1+2}
RNC	78	48	126	34	27	61	44	21	65
NJC	12	8	20	10	7	17	2	1	3
RAO	7	2	9	3	1	4	4	1	5
OMC	43	12	55	30	9	39	13	3	16

ferent distributions of killable and equivalent mutants. For instance, 55% of the mutants of "control mutant set 1" are killable ones, whereas the same percentage in the case of "control mutant set 2" is 63%. Thus, "control mutant set 2" contains more killable mutants (as a ratio). The difference between the two sets can be attributed to various factors, such as the random selection process, the sample sizes or the researchers performing the classification. Because both sets were selected from the same programs, the population distribution can be estimated based on both samples (Sets_{1+2}). Therefore, the examined population is estimated to contain 58% killable mutants and 42% equivalent ones. Recall that the examined population is the mutants that remained alive after their execution with the employed test cases.

3.3.4 Experimental Setup

In order to answer the posed research questions, the recall and precision values of the examined classification techniques were determined. To this end, the HOM, I-EQM and coverage impact classifiers are applied to the mutants of both control mutant sets with the aim of classifying them as possibly killable or possibly equivalent ones.

The conducted experiment[4] utilised the JAVALANCHE mutation testing framework to generate the first order mutants of the classes that the mutants of the control mutant sets belong to. Next, these mutants were executed with the available test cases[5] and their coverage impact was determined. For the application of the coverage impact technique, the tool's default execution settings were used. For the rest

[4]The experiment was conducted on a single machine (CPU: i3 - 2.53GHz (2 processor cores), RAM: 3GB), running Windows 7 x64 and Oracle Java 6 with default jvm configuration (JAVALANCHE by default sets the -Xmx option to 2048 megabytes).

[5]The same test cases as in the studies of Schuler and Zeller [78, 79] were used.

Algorithm 3.2 Generation Process of Second Order Mutants.

```
Let $umut$ represent a first order mutant of the control mutant sets
Let $SOMS$ represent the resulting set of second order mutants

1: $SOMS = \emptyset$
2: $SOMS$ = GENERATESOMSOF($umut$, FINDCLASSOF($umut$))
3: foreach $umut.fom \in SOMS$ do
4:     if COMBINEDFOMSAFFECTSAMELINE($umut.fom$) then
5:         if ARECOMBINEDFOMSOFSAMEMUTOP($umut.fom$) then
6:             $SOMS$.REMOVE($umut.fom$)
7:         end if
8:     end if
9: end for
10: return $SOMS$
```

of the examined approaches, mutant execution options were set as follows: (a) 100 seconds for timeout limit[6], and (b) execution of all test cases with all mutants.

Due to the fact that JAVALANCHE does not support second order mutation, a process for generating second order mutants was derived. Algorithm 3.2 illustrates the details of this process. Initially, the source code of each first order mutant of the control mutant sets was created manually. This resulted in a total of 210 different class versions. Next, JAVALANCHE was employed to produce mutants for each of these 210 classes. Note that this process yields second order mutants. Mutants belonging to the same position[7] as the examined one and produced by the same mutation operator were discarded from the considered second order mutant set. Should such an action not be performed, the impact of the examined mutant would be impossible to be assessed.

Based on the aforementioned process, all the required mutant pairs, i.e. second order mutants, were generated. Each pair is composed of the examined mutant and another one belonging to the same class. Finally, the HOM classification process, as presented by Algorithm 3.1, was applied.

In summary, for each mutant of the control mutant sets, the following proce-

[6]If mutant execution time exceeded this limit, the mutant is treated as killed, provided that the original program has successfully terminated.

[7]Position refers to the exact part of the original program's source code that differs from the mutants.

dure was employed:

- The first order mutants of the appropriate class were generated and executed with the available test cases.

- The appropriate second order mutants were generated and executed with the available test cases.

- The outputs of the first order mutants and the second order ones were compared in order to classify the examined mutants.

This process was performed for the HOM and I-EQM classifiers for all their respective variants, i.e. all foms, killed foms and same method foms. Recall that the basic difference of these approaches is the set of second order mutants they rely on. In the case of the I-EQM classifier, first the coverage impact method classified the examined mutants as possibly killable and possibly equivalent ones and those classified as possibly equivalent were subsequently categorised based on the HOM classifier (cf. Figure 3.1).

A comparison between mutant classifiers was attempted based on the accuracy and the F_β measure scores, metrics usually used in comparing classifiers in Information Retrieval experiments [156]. These measures were utilised to validate in a more typical manner the differences between the classifiers. Note that in order to avoid the influence of outliers, the median values were used.

Regarding the F_β measure, three possible scenarios are examined. Recall that high recall values indicate that more killable mutants are to be considered, leading to a more thorough testing process. High precision indicates that fewer equivalent mutants are to be examined, leading to a more efficient process.

The first scenario refers to the case where a balanced importance between the recall and precision metrics is desirable. This case is realised by evaluating the F_β measure with $\beta = 1$. The second scenario emphasises on the recall value and is achieved by assigning a value of $\beta = 2$. The last scenario, which is accomplished by using $\beta = 0.5$, weights precision higher than recall.

In the present experiment, special care was taken to handle certain cases because of some inconsistencies of the utilised tool. Specifically, it was observed that in the case of execution timeouts, the tool gave different results when some mutants were executed in isolation than together with others. To circumvent this problem, in the case of the HOM and I-EQM classifiers, when mutants were categorised as possibly killable owing to timeout conditions (if either the first order mutant or the second order one resulted in a timeout), the corresponding mutants of the considered mutant pairs were isolated and re-executed individually with an increased timeout limit.

Similarly, in the case of the coverage impact, the mutants that were classified differently with respect to the previous study [78], were re-executed in isolation with a greater timeout limit. Although the previous study's results [78] could be used, this would constitute a potential threat to the validity of the comparison because of the different execution environments and the use of "control mutant set 2".

Other special considerations include issues concerning the comparison of the programs' output. Note that such a comparison is performed between every first order mutant and its respective second order one. Many programs had outputs dependent on each specific execution. Execution outputs containing time information, e.g. the `Joda-Time` and `AspectJ` test subjects, or directory locations, e.g. `JTopas`, are examples of such cases. To effectively handle these situations, the execution dependent portions of the considered outputs were replaced with predefined values via the employment of appropriate regular expressions.

3.4 Empirical Findings

3.4.1 RQ 3.1 and RQ 3.2: Precision and Recall

The evaluation results of the coverage impact classifier are recorded in Table 3.5, which presents the classification precision and recall for the examined control mutant sets and test subjects. On average, the coverage impact method achieves a precision of 72% and a recall of 66% for "control mutant set 1". In the case of "control mutant set 2", the obtained precision score is 76% and the corresponding

Table 3.5: Mutant Classification using the Coverage Impact Classifier.

Subject Program	**Possibly Killable Set 1**		**Possibly Killable Set 2**	
	Precision	Recall	Precision	Recall
`AspectJ`	72%	87%	60%	100%
`Barbecue`	77%	71%	100%	89%
`Commons`	0%	0%	100%	17%
`Jaxen`	57%	40%	100%	43%
`Joda-Time`	79%	79%	57%	57%
`JTopas`	100%	80%	100%	50%
`XStream`	56%	63%	67%	80%
Total	72%	66%	76%	64%

Table 3.6: Mutant Classification using the HOM Classifier: Control Mutant Set 1 (w.r.t. all foms, killed foms and same method foms variations).

Subject Program	**Possibly killable Set 1**					
	Precision			**Recall**		
	All	Killed	Method	All	Killed	Method
`AspectJ`	73%	73%	80%	53%	53%	27%
`Barbecue`	90%	88%	88%	64%	50%	50%
`Commons`	50%	50%	67%	67%	67%	67%
`Jaxen`	67%	63%	60%	60%	60%	30%
`Joda-Time`	82%	90%	90%	64%	64%	64%
`JTopas`	100%	100%	100%	30%	30%	30%
`XStream`	42%	45%	42%	63%	63%	63%
Total	69%	70%	71%	57%	55%	45%

recall value is 64%.

It is noted that these results were obtained by executing JAVALANCHE with the settings described in the previous section. Thus, the difference between the aforementioned results and the ones reported in the respective studies of Schuler and Zeller [78, 79] is attributed to the execution environment used for performing the present study.

The respective results of the HOM classifier are recorded in Table 3.6 and Table 3.7, for the corresponding control mutant sets. Both tables have similar structure to Table 3.5, except that each figure of each cell refers to a different variation of the method. Thus, the first figure corresponds to the "HOM classifier (all foms)" varia-

Table 3.7: Mutant Classification using the HOM Classifier: Control Mutant Set 2 (w.r.t. all foms, killed foms and same method foms variations).

Subject Program	**Possibly killable Set 2**					
	Precision			**Recall**		
	All	Killed	Method	All	Killed	Method
`AspectJ`	83%	83%	80%	83%	83%	67%
`Barbecue`	100%	100%	100%	22%	22%	22%
`Commons`	75%	75%	67%	50%	50%	33%
`Jaxen`	100%	100%	100%	57%	57%	43%
`Joda-Time`	100%	100%	100%	57%	57%	43%
`JTopas`	100%	0%	0%	25%	0%	0%
`XStream`	75%	75%	67%	60%	60%	40%
Total	88%	88%	84%	50%	48%	36%

tion, the second one to "HOM classifier (killed foms)" and the third one to "HOM classifier (same method foms)".

By examining Table 3.6, it can be seen that "HOM classifier (all foms)" achieves a precision value of 69% and a recall value of 57%, the "HOM classifier (killed foms)" variation realises a precision of 70% and a recall of 55% and the "HOM classifier (same method foms)" variation, a precision of 71% and a recall of 45%, respectively. Considering "control mutant set 2", i.e. the results presented in Table 3.7, the precision of the "HOM classifier (all foms)" technique is 88% and its recall is 50%, the corresponding values of the "HOM classifier (killed foms)" variation are 88% and 48%, and the ones obtained for the "HOM classifier (same method foms)", 84% and 36%, respectively.

The I-EQM classifier's experimental findings are depicted in Table 3.8 and Table 3.9, which present details about the precision and recall metrics of I-EQM's variations for the examined control mutant sets. Note that the same structure as Table 3.6 and Table 3.7 is used.

From the results of Table 3.8 with regard to "control mutant set 1", it can be seen that the average precision of the I-EQM's variation that employs the "HOM classifier (all foms)" method is 67% and its recall is 83%, the corresponding values of using the "HOM classifier (killed foms)" variation are 68% and 83% and the

Table 3.8: Mutant Classification using the I-EQM Classifier: Control Mutant Set 1. (w.r.t. all foms, killed foms and same method foms variations).

Subject Program	**Possibly killable Set 1**					
	Precision			**Recall**		
	All	Killed	Method	All	Killed	Method
`AspectJ`	74%	74%	72%	93%	93%	87%
`Barbecue`	75%	75%	75%	86%	86%	86%
`Commons`	40%	40%	50%	67%	67%	67%
`Jaxen`	60%	60%	63%	60%	60%	50%
`Joda-Time`	76%	81%	81%	93%	93%	93%
`JTopas`	100%	100%	100%	90%	90%	90%
`XStream`	40%	43%	40%	75%	75%	75%
Total	67%	68%	69%	83%	83%	81%

Table 3.9: Mutant Classification using the I-EQM Classifier: Control Mutant Set 2. (w.r.t. all foms, killed foms and same method foms variations).

Subject Program	**Possibly killable Set 2**					
	Precision			**Recall**		
	All	Killed	Method	All	Killed	Method
`AspectJ`	60%	60%	60%	100%	100%	100%
`Barbecue`	100%	100%	100%	89%	89%	89%
`Commons`	75%	75%	67%	50%	50%	33%
`Jaxen`	100%	100%	100%	71%	71%	71%
`Joda-Time`	63%	63%	63%	71%	71%	71%
`JTopas`	100%	100%	100%	75%	50%	50%
`XStream`	63%	63%	63%	100%	100%	100%
Total	76%	76%	75%	80%	77%	75%

ones obtained by utilising "HOM classifier (same method foms)" are 69% and 81%, respectively[8].

With respect to "control mutant set 2", i.e. the results of Table 3.9, the I-EQM classifier's variation that utilises the "HOM classifier (all foms)" technique realises a precision score of 76% and a recall value of 80%, the one that employs the "HOM classifier (killed foms)" variation achieves a precision of 76% and a recall of 77%, whereas the variation that uses "HOM classifier (same method foms)" achieves a

[8]The difference between these results and the previously published ones [155] is due to the coverage impact method's re-evaluation; the previous results were based on the reported results of Schuler and Zeller [78], whereas the new ones on the method's re-evaluation

precision and recall value of 75%.

These results provide evidence that the HOM Classifier Hypothesis is an appropriate mutant classification property. Therefore, the employment of second order mutation can be beneficial to equivalent mutant isolation. Additionally, the results of the HOM classifier's variations indicate that the utilisation of only the killed, first order mutants as the CM set achieves approximately the same classification effectiveness as the employment of all the generated first order mutants. Regarding the "HOM classifier (same method foms)" technique, it is less effective than the other two variations, but in most cases is more efficient because of the reduced size of the considered CM set.

By considering the above-mentioned facts, the utilisation of the "HOM classifier (killed foms)" technique is advised, mainly because it is more efficient than "HOM classifier (all foms)". Compared with the coverage impact classifier, the HOM classifier attains lower precision and recall values, indicating that the coverage impact classifier is a better one.

Regarding the I-EQM classifier's results, it is evident that it forms an effective classification scheme. It achieves to retrieve more than 80% of the killable mutants with a reasonably high precision of approximately 70% for each control mutant set. This high retrieval capability is attributed to the ability of the HOM classifier to classify different killable mutants than the coverage impact one. As a consequence, their combination enhances the corresponding recall value by nearly 20%, meaning that approximately 20% more killable mutants are to be considered.

To better compare these two classifiers, Table 3.10 presents the classification precision and recall values of the coverage impact technique when applied to the union of the control mutant sets and Table 3.11 the same results for I-EQM's variations. Note that the tables are structured in a similar manner to the previously described ones.

On average, the coverage impact method achieves a classification precision of 73% and a recall value of 65%. The I-EQM classifier's variation that uses the "HOM classifier (all foms)" approach realises a precision score of 70% and a recall value of

Table 3.10: Mutant Classification using the Coverage Impact Classifier: Control Mutant Sets 1+2.

Subject Program	**Possibly Killable Sets 1+2**	
	Precision	Recall
`AspectJ`	68%	90%
`Barbecue`	86%	78%
`Commons`	33%	8%
`Jaxen`	70%	41%
`Joda-Time`	71%	71%
`JTopas`	100%	71%
`XStream`	60%	69%
Total	73%	65%

Table 3.11: Mutant Classification using the I-EQM Classifier: Control Mutant Sets 1+2. (w.r.t. all foms, killed foms and same method foms variations).

Subject Program	**Possibly killable Sets 1+2**					
	Precision			**Recall**		
	All	Killed	Method	All	Killed	Method
`AspectJ`	69%	69%	68%	95%	95%	90%
`Barbecue`	83%	83%	83%	87%	87%	87%
`Commons`	50%	50%	55%	58%	58%	50%
`Jaxen`	73%	73%	77%	65%	65%	59%
`Joda-Time`	72%	75%	75%	86%	86%	86%
`JTopas`	100%	100%	100%	86%	79%	79%
`XStream`	48%	50%	48%	85%	85%	85%
Total	70%	71%	71%	82%	81%	79%

82%, the one that employs the "HOM classifier (killed foms)" variation achieves a precision of 71% and a recall of 81%, and the variation that utilises "HOM classifier (same method foms)" achieves a precision of 71% and a recall value of 79%.

These results indicate that the coverage impact technique, by realising a recall score of 65%, misses 35% of the killable mutants, thus, leading to a potential ineffective testing process. In contrast, all three variations of I-EQM realise a high recall value, with a maximum recall of 82%, thus, improving the effectiveness of the testing process by considering 17% more killable mutants and by achieving a reasonably high precision score.

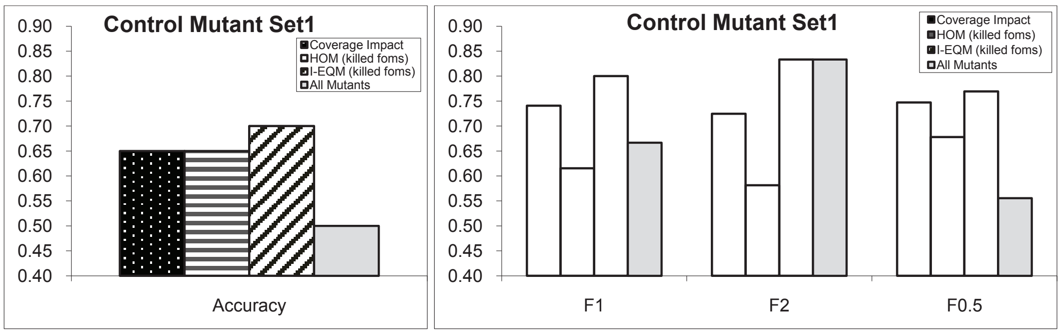


Figure 3.3: Mutant Classifiers' Comparison: Control Mutant Set 1.

3.4.2 RQ 3.1 and RQ 3.2: Accuracy and F_β scores

The accuracy and the F_β measure scores of the examined approaches with respect to "control mutant set 1" and "control mutant sets 2" are given in Figure 3.3 and Figure 3.4. The left part of the figures presents the accuracy metric and the right one the examined F_β measure scores. Note that the reported results correspond to median values.

In these figures, the "All Mutants" series refers to a naive classifier that categorises all mutants as possibly killable. In such a case, it achieves a precision of 55% and 63% for "control mutant set 1" and "control mutant sets 2", respectively. In both sets, the recall value is equal to 100%. The I-EQM and HOM methods refer to their respective killed foms variation. It is noted that the all foms and killed foms variations were found to have similar effectiveness.

From the findings of Figure 3.3 referring to the accuracy measure, it can be observed that the I-EQM classification technique is the most accurate one, followed by the coverage impact and HOM classifiers which have similar performance, and, lastly, the "All Mutants" approach. Similar results are obtained for "control mutant sets 2", as shown in the left part of Figure 3.4.

As mentioned in Section 3.3.4, by evaluating the F_β measure with different values of β, three possible scenarios are examined. Note that high recall values indicate a more thorough testing process, whereas high precision a more efficient one.

The first scenario, which considers recall and precision of equal importance,

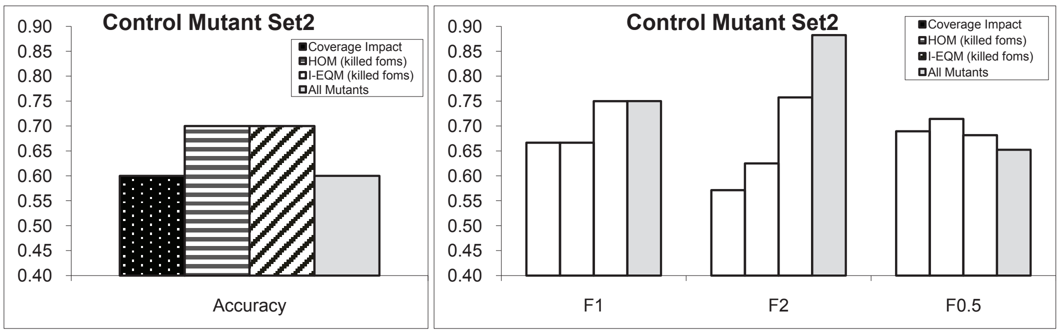


Figure 3.4: Mutant Classifiers' Comparison: Control Mutant Set 2.

is represented by the F1 measure ($\beta = 1$). The corresponding results, depicted in the right part of Figure 3.3 and Figure 3.4, suggest that the I-EQM approach outperforms the rest.

The second scenario, described by the F2 measure ($\beta = 2$), emphasises on the recall value. It can be seen that the I-EQM classification approach achieves far better results than the coverage impact and HOM techniques for both examined control mutant sets, but worse than the "All Mutants" classifier for "control mutant set 2". This is expected, because the "All Mutants" categorises all examined mutants as possibly killable.

The last scenario, which limits the selection of equivalent mutants, favours the precision metric over the recall one. For this case, described by the F0.5 measure ($\beta = 0.5$), the I-EQM classifier achieves better results than the rest of the examined approaches for "control mutant set 1". Regarding "control mutant set 2", the I-EQM classifier achieves approximately the same (slightly worse) results as the coverage impact one. However, in this case, the HOM classifier scores better than the rest.

Generally, the I-EQM classification method provides better results than the coverage impact one with respect to accuracy and all the considered scenarios. Despite the variation of HOM classifier's classification ability between the two control mutant sets, I-EQM achieves a higher accuracy for both examined sets. This fact indicates that the coverage impact and HOM classifiers detect-classify different mutants, hence their combination is effective.

Figure 3.5 presents the overall, i.e. with respect to the union of the control mu-

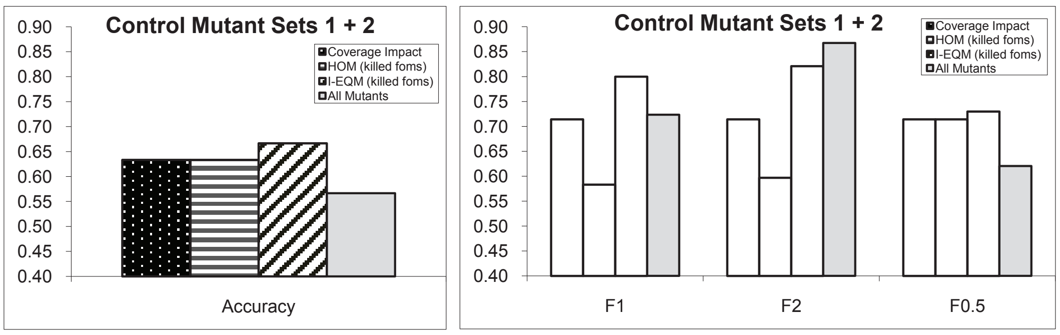


Figure 3.5: Mutant Classifiers' Comparison: Control Mutant Sets 1+2.

tant sets, accuracy and F_β measure scores of the classification approaches. Again, the results refer to the killed foms variations of the I-EQM and HOM classifiers using median values. From the presented findings, it can be argued that I-EQM constitutes a better mutant classifier than the rest of the examined approaches.

3.4.3 RQ 3.3: Classifiers' Stability

In order to examine the stability of the considered classifiers across the test subjects, the standard deviation of the precision and recall metrics with respect to the union of the control mutant sets was calculated per examined technique. Figure 3.6 displays these findings. The columns of the charts depict the mean precision and recall values per utilised program for each of the examined approaches, and, the vertical bars, the corresponding values that lie within one standard deviation of the mean. Again, the presented results for the HOM and I-EQM techniques refer to the killed foms variation.

Regarding precision, the coverage impact technique presents the greatest variation among the examined methods with a standard deviation of 21%. The HOM and I-EQM classifiers demonstrate similar variation levels of approximately 18%. With respect to the recall metric, the coverage impact approach experiences a variation level of 28%, whereas the HOM and I-EQM classifiers 16% and 13%, respectively.

From the presented data, it can be concluded that the I-EQM approach tends to be more stable than the rest of the examined techniques. To visualise the variation among the precision and recall values of the classifiers, Figure 3.7 presents two groups of boxplots for the corresponding measures. It can be seen that the coverage

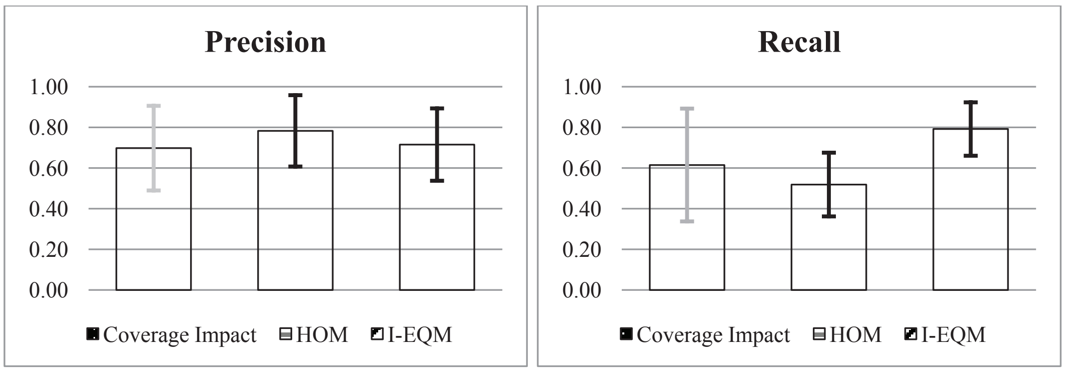


Figure 3.6: Classifiers' Stability. Mean and standard deviation of the precision and recall metrics for control mutant sets 1+2.

impact (CI) and I-EQM techniques have a similar spread regarding their precision values, with coverage impact having a slight advantage. However, regarding the recall values, the I-EQM is clearly better.

By comparing the three classification approaches based on the results presented both here and in the previous subsections, it becomes evident that the I-EQM technique manages to provide better recall values with only a minor loss on its precision and with the highest level of stability, for the examined test subjects.

3.4.4 Statistical Analysis

In order to investigate whether the previously described differences among the examined classifiers are statistically significant, the Wilcoxon Signed Rank Test was employed per compared technique. The Wilcoxon Signed Rank Test is a non-parametric test for two paired samples that tests whether or not the two populations from which the corresponding samples are drawn are identical. A non-parametric test was utilised, instead of a parametric one, because it is based on no distributional assumptions for the considered data observations.

A series of two-tailed hypothesis tests were performed to investigate whether the HOM and I-EQM classifiers have similar effectiveness to the coverage impact technique, regarding the precision and recall metrics. For example, the hypotheses that were tested in the case of the HOM classifier, regarding its precision metric, are the following:

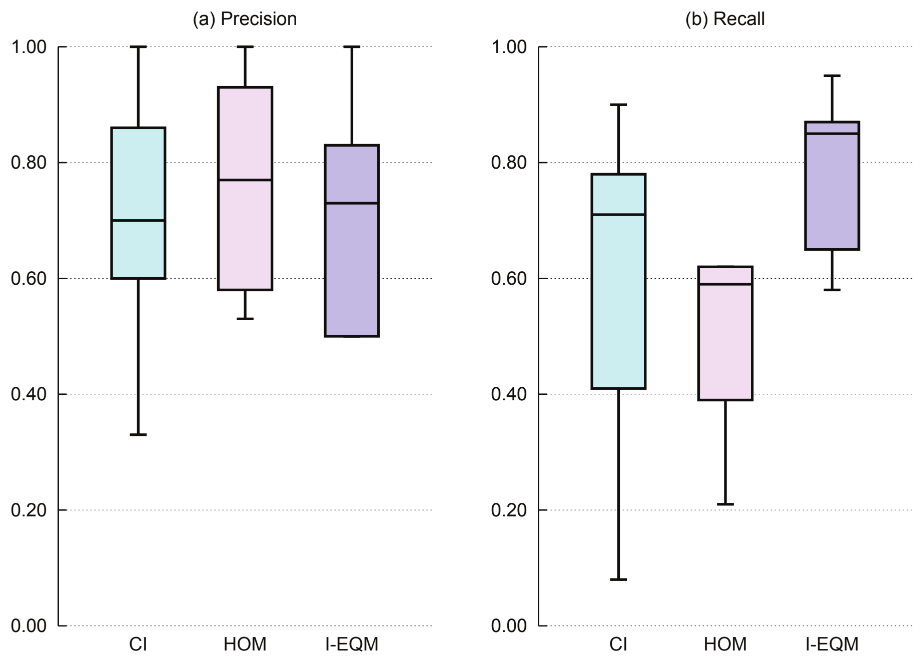


Figure 3.7: Variation of the Classifiers' Precision and Recall Metrics: Control Mutant Sets 1+2.

H_0: *The HOM and Coverage Impact classifiers perform the same with regard to the precision metric.*

H_1: *The HOM and Coverage Impact classifiers perform differently with regard to the precision metric.*

Similar hypotheses were tested with respect to the I-EQM classifier and the recall metric. A significance level of $\alpha = 0.05$ was employed for all conducted tests. Thus, the tests reject the null hypothesis H_0 if a p-value smaller than α is obtained; otherwise the null hypothesis is accepted. Table 3.12 presents the corresponding findings.

The first column of the table refers to the considered effectiveness measures, the second one to the classification methods being compared and the last one presents the obtained p-values (two-tailed). Regarding the precision metric, the null hypothesis is rejected only in the case of "HOM versus I-EQM", i.e. there is a statistically significant difference in the effectiveness of the two classifiers. For the remaining cases, i.e. "CI versus HOM" and "CI versus I-EQM", the null hypothesis

Table 3.12: Statistical Significance based on the Wilcoxon Signed Rank Test.

	Compared Techniques	***p*-value** (two-tailed)
Precision	CI versus HOM	0.094
	CI versus I-EQM	0.563
	HOM versus I-EQM	**0.031**
Recall	CI versus HOM	0.469
	CI versus I-EQM	**0.016**
	HOM versus I-EQM	**0.031**

is accepted.

With respect to the recall measure, the null hypothesis is rejected in the cases of “CI versus I-EQM” and “HOM versus I-EQM”, thus, it can be concluded that there is strong evidence to establish a difference in the effectiveness of the I-EQM classifier with respect to the HOM and coverage impact methods. Finally, in the case of “CI versus HOM”, the null hypothesis is accepted.

These findings suggest that there is statistically insufficient evidence to establish a difference in the performance of the coverage impact and I-EQM classifiers, concerning precision. On the contrary, there is a strong, statistically significant difference in their performance regarding recall, with a *p*-value of 0.016.

3.4.5 Discussion

Comparing the coverage impact method’s results between the two sets, a slight increase in the precision metric for “control mutant set 2” and a minor decrease in the corresponding recall value can be observed. These variations indicate that the coverage impact’s classification ability is not greatly affected by different mutants.

Considering the classification results of the HOM classifier, the aforementioned trend is also present, i.e. the precision for “control mutant set 2” is increased while its recall is decreased. It must be mentioned that in this case, the deviation is higher, indicating that HOM’s classification ability is more affected by different mutants than the one of the coverage impact technique.

Finally, the trend observed for the previous classifiers is consistent with the differences between the results of the I-EQM technique. Concerning its results, it is obvious that I-EQM manages to enhance the recall of the coverage impact technique for both examined control mutant sets (Table 3.8 and Table 3.9) while maintaining its precision at a reasonably high level.

Another aspect of the presented results that should be noted relates to the "HOM classifier (same method foms)" approach. By examining the entries of Table 3.6 and Table 3.7, it is apparent that this approach experiences a decrease of nearly 10% on its recall value compared with the other variations of the HOM classifier (i.e., killed foms and all foms) and approximately 20% compared with the one of the coverage impact method. Interestingly, the I-EQM (same method foms) classification scheme, according to Table 3.11, suffers only a loss of 3% compared with the rest of the approaches of the I-EQM classifier and has an enhanced recall of nearly 15% compared with the coverage impact classifier. These findings suggest that the majority of the misclassified killable mutants of the coverage impact classifier can be correctly classified by the "HOM classifier (same method foms)" variation.

Generally, the application of the I-EQM classifier on the studied subjects results in the identification of 81% of the live killable mutants and 46% of the total equivalent mutant instances. The coverage impact classifier identifies 65% of the live killable mutants and 33% of the equivalent ones. These values suggest that by killing the identified killable mutants, a mutation score[9] such as 95.2% will be achieved for the coverage impact technique and one of 97.4% for I-EQM. Therefore, it becomes obvious that a more thorough testing process is established by the I-EQM method. However, this is borne with the overhead of analysing 1.17% more equivalent mutants[10].

3.4.6 Mutants with Higher Impact

The behaviour of the considered approaches with respect to higher impact values is also investigated. To this end, the impact values of the examined mutants based on

[9]These scores were evaluated by counting the mutants killed by the employed tests plus the identified killable mutants of the totally estimated killable ones.

[10]This number was evaluated by counting the identified equivalent mutants of the totally estimated number of equivalent ones.

the coverage impact and HOM classifiers are determined for both examined control mutant sets.

Note that the impact value of a mutant based on the coverage impact technique is defined as "the number of methods that have at least one statement that is executed at a different frequency in the mutated run than in the normal run, while leaving out the method that contains the mutated statement" [78]. The corresponding impact value of the HOM classifier is defined as the number of first order mutants in the CM set whose output has changed after being combined with the live-unclassified mutant (see also Section 3.2.)

Figure 3.8 presents the results of the coverage impact technique for both examined control mutant sets. The left part of the figure provides information about the precision metric (y-axis) and how it changes according to different impact value thresholds (x-axis). Based on different thresholds, different mutants are classified as possibly killable or possibly equivalent. For instance, by employing a threshold value of 50, mutants with higher impact values will be classified as possibly killable, otherwise they will be classified as possibly equivalent.

From the left part of the figure, it can be seen that for impact values lower than 20, the precision metric increases, whereas for impact values between 20 and 100, the opposite holds. Note that the highest precision scores are obtained when the impact value thresholds are between 10 and 20. The right part of the figure describes a plot between precision (y-axis) and the percentage of mutants with the highest impact (x-axis); for example, an x_1 value of 0.2 indicates that 20% of these mutants are examined. Thus, lower values of the x-axis represent mutants with higher impact values.

It can be observed that, in general, the precision metric decreases as the percentage of the examined mutants with the highest impact decreases. Consider the top 10% of the mutants with the highest impact (i.e. $\mathrm{x}_1 = 0.1$), by examining only these mutants a precision value of approximately 70% is obtained. In contrast, by examining the top 30%, a precision score of 80% is realised. These findings suggest that an analogy between mutants with the highest impact and high killability ratios

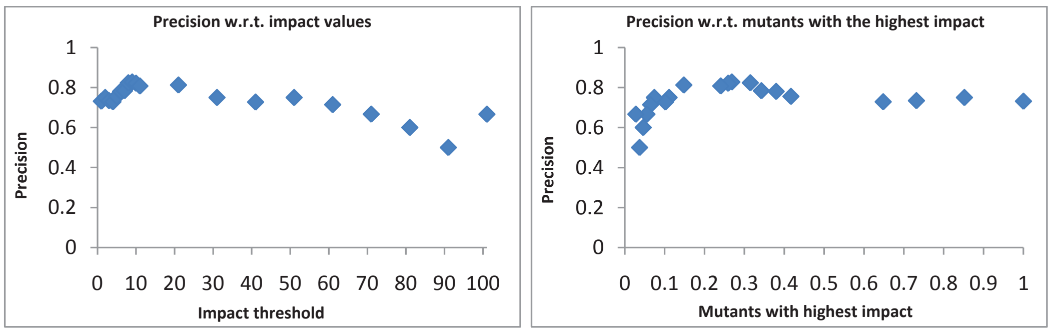


Figure 3.8: Coverage Impact Classifier: Higher Impact Values. The left part of the figure presents the precision metric w.r.t. impact values and the right one, precision w.r.t. mutants with the highest impact.

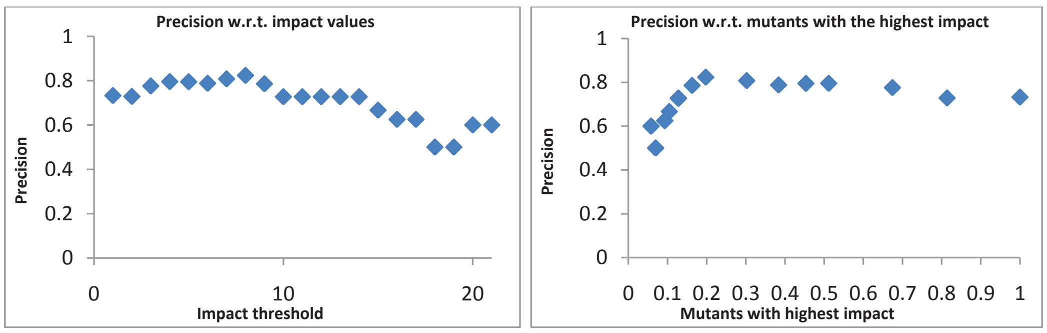


Figure 3.9: HOM Classifier: Higher Impact Values. The left part of the figure presents the precision metric w.r.t. impact values and the right one, precision w.r.t. mutants with the highest impact.

cannot be drawn.

Figure 3.9 depicts the same results as Figure 3.8 in the case of the HOM classifier. By examining the two figures, it is apparent that the same trends exist.

In conclusion, it can be argued that mutants with the highest impact do not necessarily guarantee the highest killability ratios. On the contrary, the results suggest that the precision metric for higher impact values decreases. This trend is in accordance with the findings of Schuler and Zeller [78, 79], where the precision of the top 25% of the mutants with the highest impact was found higher than the one obtained by examining only the top 15% (cf. Table IX [78]). The presented results indicate that the relationship between impact and killability needs further investigation.

To investigate the differences between "control mutant set 1" and "control mutant set 2", Figure 3.10 illustrates the coverage impact's classification precision (*y*-

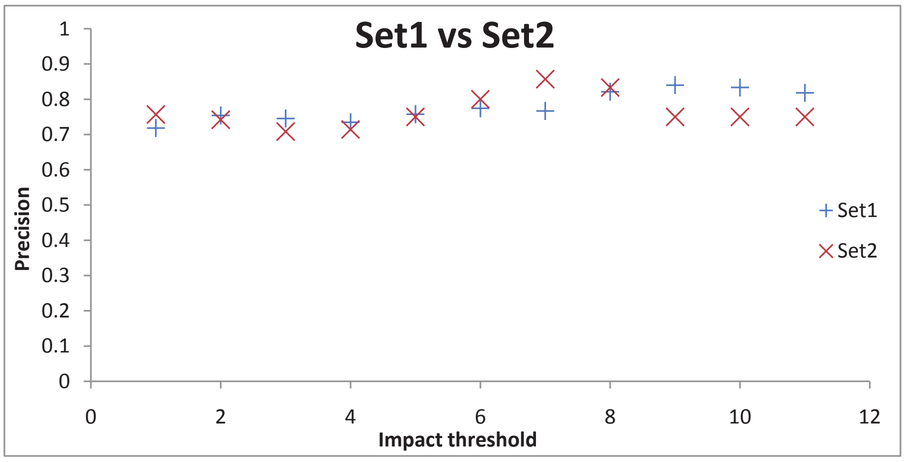


Figure 3.10: Differences between Studied Control Mutant Sets. Coverage Impact Classifier's precision w.r.t. impact values for "control mutant set 1" and "control mutant set 2".

axis) with respect to the different impact value thresholds (*x*-axis). It must be noted that the maximum impact value considered for this diagram is 12 because it is the maximum impact value of "control mutant set 2".

From this graph, it can be observed that for impact values lower than 8, both sets demonstrate a similar behaviour. For impact values greater than 8, the precision of "control mutant set 1" remains approximately the same, whereas the one of "control mutant set 2" decreases. Overall, due to the fact that the differences between the two sets are small, it is believed that the above-mentioned conclusions hold for both studied sets.

3.4.7 Threats to Validity

This section discusses potential threats to the validity of the present study. Threats to the *internal*, *external* and *construct* validity are presented, along with the actions taken to mitigate their consequences.

- **Internal Validity.** The internal validity concerns the degree of confidence in the causal relationship of the studied factors and the observed results. One such factor is the utilisation of the specified test subjects and the use of the JAVALANCHE framework. As mentioned in Section 3.3.2, their choice was mainly based on enabling a direct comparison between the proposed classification techniques and the coverage impact classifier. Owing to the fact that the employed subjects are large in size and of different application domains, they are considered as appropriate. Furthermore, various empirical studies, e.g. [78, 79, 130, 157], utilised the same tool, thus, increasing the confidence in its results. The employed mutation operators constitute another possible issue. Different operator sets, as those suggested by Offutt et al. [81], might give different classification results. However, the present study focuses on mutants' impact, which is believed to be an attribute independent of the nature of the studied mutants [79]. Additionally, the present study replicates the findings of the coverage impact technique [78, 79], thus it is natural to use the same mutants. Another potential threat that falls into this category concerns the employed test suites. It is possible that different test suites could produce different classification results. However, the utilised test suites were independently created by the developers of the considered programs without using mutation testing. Furthermore, the manually classified mutants were randomly selected among those that were executed and not killed by the employed test cases. These two facts give confidence in that the studied methods can provide useful guidance in increasing the quality of the testing process and that the mutants' impact constitutes an effective mutant classification property that can lead to a better testing process.

- **External Validity.** The external validity of an experiment refers to the potential threats that inhibit the generalisation of its results. The generalisation of a study's results is difficult to be achieved because of the range of different aspects that the experimental study must consider. The results presented in this chapter are no exception. Despite this, actions have been taken to attenuate the effects of these threats. First, the empirical evaluation of this study was based on a benchmark set of real-world programs which has been used in similar research studies, e.g. [78, 79, 130, 157]. Second, the examined programs vary in size and complexity. Finally, the evaluation of the proposed classification techniques was based on two independently created sets of manually classified mutants; one created for the evaluation of the coverage impact classifier [78, 79] and the other, for the purposes of the present experimental study.

- **Construct Validity.** The construct validity refers to the means of defining the employed measurement of an experiment and the extent to which it measures the intended properties. A possible threat pertains to the manual classification of the mutants of the examined control mutant sets. The mutants classified as killable pose no threat as the basis of their classification is a test case that is able to "kill" them, whereas the mutants classified as equivalent could do so due to the complexity of the involved manual analysis. To ameliorate the effects of this threat, the studied programs and control mutant sets were made publicly available.

3.5 Summary

This chapter introduced a novel mutant classification technique, named Higher Order Mutation (HOM) classifier. The originality of the proposed technique stems from the fact that it leverages higher order mutation to automatically isolate first order equivalent mutants. Specifically, the HOM classifier utilises second order mutation to classify a given set of first order mutants as possibly killable or possibly equivalent ones.

This chapter also investigated the possibility of introducing a combined mutant classification scheme. To this end, the Isolating Equivalent Mutants (I-EQM) classifier was proposed. I-EQM combines the HOM classifier with the state-of-the-art Coverage Impact classifier.

The conducted empirical study, based on two independently developed sets of manually analysed mutants, revealed that I-EQM managed to correctly classify more killable mutants than the other studied approaches with approximately no loss on its precision, indicating that I-EQM is a better mutant classifier. This finding was also supported by the performed statistical analysis.

Additionally, the relationship between mutant' impact and killability was investigated. The obtained results indicate that mutants with the highest impact do not necessarily guarantee the highest killability ratios. On the contrary, for higher impact values the precision metric decreased. These results suggest that the relationship between impact and killability warrants further investigation.

The introduced mutant classification technique, albeit more powerful than the previously proposed ones, cannot overcome the inherent characteristics of mutant classification, i.e. the possibility of misclassifying mutants. The next chapter introduces and formally describes a series of data flow patterns that can be leveraged to automatically identify equivalent mutants.

Chapter 4

Equivalent Mutant Detection via Data Flow Patterns

Detecting equivalent mutants is an arduous task, primarily due to the undecidable nature of the underlying problem. Chapter 3 introduced a mutant classification technique that managed to automatically isolate possibly equivalent mutants, thus, ameliorating their adverse effects. This chapter also targets the equivalent mutant problem by focusing on specific source code locations that can generate equivalent mutants.

Harman et al. [127] proposed the use of dependence analysis [158] as a means of avoiding the generation of equivalent mutants. This chapter augments their work by formalising a set of data flow patterns that can reveal source code locations able to generate equivalent mutants. For each pattern, a formal definition is given, based on the *Static Single Assignment* (*SSA*) [159, 160] intermediate representation of the program under test, and the necessary conditions implying the pattern's existence in the program's source code are described. By identifying such problematic situations, the introduced patterns can provide advice on code locations that should not be mutated and can automatically detect equivalent mutants that belong to these locations.

Apart from dealing with equivalent mutants, the proposed patterns are able to identify specific paths for which a mutant is functionally equivalent to the original program; such a mutant is termed *partially equivalent*. Thus, if one of these paths is to be executed with test data, the output of the mutant and the original program would be the same. This knowledge can be leveraged by test case generation techniques in order to avoid targeting these paths when attempting to kill partially equivalent mutants.

The contributions of this chapter can be summarised in the following points:

1. The introduction and formal definition of nine problematic data flow patterns that are able to automatically detect equivalent and partially equivalent mutants.

2. An empirical study, based on a set of approximately 800 manually identified mutants from several open source projects, which indicates that the introduced patterns exist in real-world software and provides evidence regarding their detection power.

It should be mentioned that Chapter 5 examines further the proposed data flow patterns. More precisely, it introduces an automated framework, named Mutants' Equivalence Discovery (MEDIC), which implements the corresponding patterns and empirically assesses the tools' effectiveness and efficiency.

The rest of the chapter is organised as follows: Section 4.1 introduces the necessary background information and Section 4.2 details the proposed data flow patterns along with illustrative examples. In Section 4.3, the empirical study and the obtained results are presented. Finally, Section 4.4 summarises this chapter.

4.1 Background

4.1.1 Employed Mutation Operators

As mentioned in Section 2.1, mutation's effectiveness depends largely on the employed set of mutation operators. The present study considers the mutation operators utilised by the MUJAVA mutation testing framework [19]. MUJAVA is a mutation testing tool for the Java programming language that has been widely used in the literature of mutation testing. Note that the utilisation of this particular set does not reduce the applicability of the proposed data flow patterns since analogous mutation operators have been developed for other programming languages and have been in-

Table 4.1: Mutation operators of MUJAVA.

Mutation Operator	**Description**
Arithmetic Operator Replacement Binary (AORB)	$\{(op_1,op_2) \mid op_1,op_2 \in \{+,-,*,/,\%\} \wedge op_1 \neq op_2\}$
Arithmetic Operator Replacement Short-Cut (AORS)	$\{(op_1,op_2) \mid op_1,op_2 \in \{++,--\} \wedge op_1 \neq op_2\}$
Arithmetic Operator Insertion Unary (AOIU)	$\{(v,-v)\}$
Arithmetic Operator Insertion Short-cut (AOIS)	$\{(v,--v),(v,v--),(v,++v),(v,v++)\}$
Arithmetic Operator Deletion Unary (AODU)	$\{(+v,v),(-v,v)\}$
Arithmetic Operator Deletion Short-cut (AODS)	$\{(--v,v),(v--,v),(++v,v),(v++,v)\}$
Relational Operator Replacement (ROR)	$\{((\mathrm{a}\ op\ \mathrm{b}),\ \texttt{false}),((\mathrm{a}\ op\ \mathrm{b}),\ \texttt{true}),(op_1,\ op_2) \mid op_1,op_2 \in \{>,>=,<,<=,==,!=\} \wedge op_1 \neq op_2\}$
Conditional Operator Replacement (COR)	$\{(op_1,op_2) \mid op_1,op_2 \in \{\&\&,\|\|,\wedge\} \wedge op_1 \neq op_2\}$
Conditional Operator Deletion (COD)	$\{(!cond,cond)\}$
Conditional Operator Insertion (COI)	$\{(cond,!cond)\}$
Shift Operator Replacement (SOR)	$\{(op_1,op_2) \mid op_1,op_2 \in \{>>,>>>,<<\} \wedge op_1 \neq op_2\}$
Logical Operator Replacement (LOR)	$\{(op_1,op_2) \mid op_1,op_2 \in \{\&,\|,\wedge\} \wedge op_1 \neq op_2\}$
Logical Operator Insertion (LOI)	$\{(v,\sim v)\}$
Logical Operator Deletion (LOD)	$\{(\sim v,v)\}$
Short-Cut Assignment Operator Replacement (ASRS)	$\{(op_1,op_2) \mid op_1,op_2 \in \{+=,-=,*=,/=,\%=,\&=,\|=,\wedge=,>>=,>>>=,<<=\} \wedge op_1 \neq op_2\}$

corporated into appropriate tools, e.g. the Unary Operator Insertion (UOI) of the MILU mutation testing tool [16] for C.

MUJAVA is based on the selective mutation approach, i.e. it utilises a subset of mutation operators that are considered particularly effective (see also Section 2.3.2.2). Table 4.1 presents the employed mutation operators, along with a brief description of the imposed changes. In total, the tool implements 15 mutation operators, which fall into 6 general categories: arithmetic operators, relational operators, conditional operators, shift operators, logical operators, and assignment operators.

The Arithmetic Operator Insertion Short-cut (AOIS) mutation operator inserts the *pre-* and *post*-increment and decrement arithmetic operators to valid variables of the original program. The inserted post-increment or decrement operators are of particular interest. The basic characteristic of such operators is that they do not change the value of the affected variable at the evaluation of the affected expression. The variable is used unchanged and the next time it is referenced, it will be incremented or decremented by one. As discussed in Section 4.2.2, the application of these operators can result in the generation of equivalent mutants.

Note that the AOIS operator is not specific to Java: other programming languages, e.g. C, support such arithmetic operators and other mutation tools have implemented it as well, e.g. the PROTEUM mutation testing tool [15] for C. The data flow patterns of the *Use-Def* and *Use-Ret* categories, described in Section 4.2.2, detect problematic situations where the application of this operator results in the creation of equivalent mutants.

4.1.2 Static Single Assignment (SSA) Form

The definition of the proposed data flow patterns is based on an intermediate representation of the program under test, which is known as the *Static Single Assignment* (*SSA*) form [159, 160]. Many modern compilers use the SSA form to represent internally the input program and perform various optimisations. Furthermore, several research studies have utilised the SSA form as a means of program analysis, e.g. [161].

The basic characteristic of the SSA representation is that each variable of the program under test is assigned exactly once. More precisely, for each assignment

$$\begin{aligned} v &= 4 \\ x &= v + 5 \\ v &= 6 \\ y &= v + 7 \end{aligned}$$

(a) Source Code Fragment.

$$\begin{aligned} v_1 &= 4 \\ x_1 &= v_1 + 5 \\ v_2 &= 6 \\ y_1 &= v_2 + 7 \end{aligned}$$

(b) Its SSA representation.

Figure 4.1: Static Single Assignment Form Example. (adapted from [162]).

to a variable, that variable is given a unique name and all its uses reached by that assignment are appropriately renamed [162]. Figure 4.1 depicts an example of a code fragment and its SSA form (adapted from the work of Cytron et al. [162]): the left part of the figure illustrates the source code fragment and the right one, its SSA representation.

Cytron et al. [162] presented the first algorithm to efficiently translate a program to its SSA form. Note that this translation restricts the definition points of a variable: after the translation, each variable is bound to have only one definition point, instead of multiple in the original program (cf. variables v_1, v_2 and v of Figure 4.1). This fact enables a more compact representation of the underlying data flow information and facilitates powerful code analysis and optimisation techniques. This simple example suffices for the purposes of this chapter, a more detailed one is presented in Section 5.1 of Chapter 5.

4.2 Equivalent Mutants and Data Flow Analysis

This work focuses on detecting equivalent mutants by leveraging the data flow information of the program under test. To this end, the SSA representation of the program is utilised. This is believed to lead to a more powerful analysis and a clearer definition of the conditions that need to hold for a particular situation to be pathogenic.

Four groups of problematic patterns are introduced: the *Use-Def* (*UD*), the *Use-Ret* (*UR*), the *Def-Def* (*DD*) and the *Def-Ret* (*DR*) categories of patterns. The first two categories target equivalent mutants that are due to mutation operators that insert the post-increment (e.g. `var++`) or decrement (e.g. `var−−`) arithmetic operators or other similar operators. The remaining categories target problematic situations that are caused by mutation operators that affect variable definitions, e.g. the Arithmetic Operator Replacement Binary (AORB) mutation operator.

The search for these patterns is performed on the source code of the original program. Therefore, these patterns can be used in two ways: (a) they can be incorporated into mutation testing frameworks to avoid the generation of equivalent mutants, or (b) in the case where the mutants have already been generated, they can be used to detect equivalent or partially equivalent mutants. Before elaborating on these categories, the necessary functions, used in the patterns' definitions, are described.

4.2.1 Function Definitions

This subsection introduces a set of functions that will be used in the definition of the problematic data flow cases. First, functions related to the *control* and *data flow* of the program under test are described and, subsequently, the concept of a partially equivalent mutant is formally introduced.

4.2.1.1 Control Flow Functions

$reach(p,s,t)$	Denotes that path p traverses nodes s and t, starting at node s and ending at node t. Note that s and t need not be the starting and ending nodes of the corresponding control flow graph.
$frstIns(i)$	A function that returns the first instruction of the node that contains instruction i.
$bb(i)$	A function that returns the node which contains instruction i.
$isExit(n)$	Denotes that node n contains a statement that forces the program to exit.

The aforementioned functions utilise the control flow analysis of the program under test. Note that the terms *node* and *basic block* are used interchangeably; the nodes of a Control Flow Graph (CFG) are the basic blocks of the respective program. For the purposes of this study: a *path* is a sequence of two or more nodes, where each pair of adjacent nodes represents an edge of the corresponding CFG and an *instruction* is considered to be a simple statement that belongs to a single line and one basic block.

4.2.1.2 Data Flow Functions

$def(v_x)$	A function that returns the instruction that defines variable v_x.
$use(n, v_x)$	A function that returns the instruction that contains the *n*th use of variable v_x.
$defAftr(i, v_x)$	A function that returns the instruction of the first definition of the variable of the original program denoted by v_x, *after* instruction i. The scope of this function is limited to the basic block that contains instruction i.
$useBfr(i, v_x)$	A function that returns the instruction of the first use of the variable of the original program denoted by v_x, *before* instruction i. The scope of this function is limited to the basic block that contains instruction i.
$useAfr(i, v_x)$	A function that returns the instruction of the first use of the variable of the original program denoted by v_x, *after* instruction i. The scope of this function is limited to the basic block that contains instruction i.
$defClr(p, v_x)$	Denotes that except from the starting and ending nodes of path p, no other node can include a definition of the variable of the original program denoted by v_x, i.e. no *intermediate* node of p defines that particular variable.
$useClr(p, v_x)$	Denotes that except from the starting and ending nodes of path p, no other node can include a use of the variable of the original program denoted by v_x, i.e., no *intermediate* node of p uses that particular variable.

As mentioned at the beginning of this subsection, the data flow analysis is based on the SSA representation of the program under test. Although the definitions of the last five functions refer to the original program, the desired behaviour is achieved by utilising information from the corresponding SSA form.

4.2.1.3 Equivalent and Partially Equivalent Mutants

This work introduces the concept of a *partially equivalent* mutant, a mutant that is equivalent to the original program for a specific subset of paths. Recall that this study refers to strong mutation testing, thus, the following definitions will be tailored to that particular approach.

Definition 4.1 ***Partially Equivalent Mutant.***

$\exists\, m \in Muts,\ \exists\, p \in Paths,\ \forall\, t \in T_p$

$$(output(orig,t) = output(m,t))$$

where p refers to a path of the CFG of the program under test that contains the basic block of the mutated statement. *Muts* refers to the mutants of the examined program, T_p to the set of test cases that cause the execution of p and *output(prog,t)* to a function that returns the output of program *prog* with input t.

This definition states that there is at least one path of the program under test whose execution will not reveal the induced change of mutant *m*, i.e. mutant *m* is equivalent to the original program with respect to path *p*.

Given the definition of a partially equivalent mutant, an *equivalent mutant* can be defined as follows:

Definition 4.2 ***Equivalent Mutant.***

$\exists\, m \in Muts,\ \forall\, p \in Paths,\ \forall\, t \in T_p$

$$(output(orig,t) = output(m,t))$$

that is, the execution of each path p with all available test data will result in the same output for the original program and mutant *m*.

It follows from the definitions that:

"A partially equivalent mutant is a mutant that is equivalent to the original program only for a specific set of paths, while an equivalent one is equivalent to the original program for all paths."

It should be mentioned that the partial equivalence of a mutant does not indicate that a mutant is equivalent. It indicates that the path for which the mutant is partially equivalent should not be used to kill that mutant.

4.2.2 Use-Def (UD) and Use-Ret (UR) Categories of Patterns

The Use-Def (UD) and Use-Ret (UR) categories of patterns target equivalent mutants that are created by mutation operators that insert the post-increment or decrement arithmetic operators, e.g. the AOIS mutation operator, or similar mutation operators. These operators do not change the value of the affected variable at the evaluation of the affected expression. Therefore, if such a mutant affects a use of a variable that cannot reach another use, the induced change is bound to be indiscernible, leading to the generation of equivalent mutants.

An instance of the application of AOIS is depicted in Figure 4.2, which presents the source code of the `Bisect` program[1], along with its corresponding basic blocks. The application of AOIS at line 10 results in 8 mutants that affect variables x and M; the two subsequent lines of the figure depict two of these mutants. By examining them, it becomes apparent that they are equivalent ones.

This example reveals a data flow pattern that is able to detect equivalent mutants generated by the application of AOIS: a code location where a variable is used and defined at the same statement. The data flow patterns of the UD category can detect equivalent mutants generated by such problematic situations.

The UD category is comprised of three problematic patterns: the *SameLine-UD*, the *SameBB-UD* and the *DifferentBB-UD* patterns. All three attempt to reveal equivalent or partially equivalent mutants by searching the source code of the original program for uses of variables that reach a definition and can be mutated by AOIS or a similar mutation operator.

[1]This program was also used in various previous studies, e.g. [85].

```
sqrt (double N) {
    double x = N;                                   // BB:1
    double M = N;
    double m = 1;
    double r = x;
    double diff = x * x - N;
    while ($ABS(diff) > mEpsilon$) {                // BB:2
        if ($diff < 0$) {                           // BB:3
            m = x;                                  // BB:4
            x = (M + x) / 2;
          Δ x = (M + x++) / 2
          Δ x = (M + x−−) / 2
        }
        else if ($diff > 0$) {                      // BB:5
            M = x;                                  // BB:6
            x = (m + x) / 2;
        }
        diff = x * x - N;                           // BB:7
    }
    r = x;                                          // BB:8
    mResult = r;
    return r;
}
```

Figure 4.2: Source Code of the `Bisect` test subject. The depicted mutants (denoted by the Δ symbol) are equivalent and can be automatically detected by the SameLine-UD problematic pattern.

As a special case of the UD category of patterns, the UR category is also introduced. The patterns of this category search the source code of the examined program for uses of variables that do not reach another use. It can be easily seen that the application of AOIS to that particular code locations would result in the creation of equivalent mutants. The UR category consists of the *SameLine-UR*, the *SameBB-UR* and the *DifferentBB-UR* problematic patterns.

4.2.2.1 SameLine-UD Problematic Pattern

The SameLine-UD problematic pattern detects equivalent mutants that affect a variable that is being used and defined at the same statement. More formally:

Definition 4.3 ***SameLine-UD Pattern.***

$\exists\, v_k, v_j \in SVars,\ i \in \mathbb{N}^+$

$$(use(i,v_k) = def(v_j) \wedge$$

$$\nexists\, m \in \mathbb{N}^+ \; ((m > i) \;\wedge\; (use(m,v_k) = use(i,v_k))))$$

where *SVars* is the set of variables of the SSA representation of the program under test that refers to the same variable of the original program (cf. variables v, v_1, v_2 of Figure 4.1).

The first condition states that an instruction must exist that uses and defines the same variable with respect to the original program and the second one necessitates that the ith use of variable v_k is the last one in the corresponding instruction. It must be mentioned that variable v_k should be a valid target for AOIS, otherwise the discovered source code locations do not constitute a problem. Examples of this problematic situation are depicted in Figure 4.2 and Figure 5.2a of Chapter 5.

4.2.2.2 SameLine-UR Problematic Pattern

SameLine-UR is a special case of the SameLine-UD problematic pattern. It detects problematic situations which involve uses of variables at `return` statements, or statements that cause the program to exit, in general. The conditions that must be satisfied for the manifestation of a problematic situation are the following:

Definition 4.4 ***SameLine-UR Pattern.***

$$\exists\, v_k \in SVars,\; i_\varepsilon \in ExitIns,\; i \in \mathbb{N}^+$$

$$(use(i,v_k) = i_\varepsilon \wedge$$

$$\nexists\, m \in \mathbb{N}^+ \; ((m > i) \;\wedge\; (use(m,v_k) = i_\varepsilon)))$$

where $ExitIns$ is the set of instructions that cause the program to exit.

The first condition states that the instruction of the ith use of variable v_k must be an instruction that can exit the program. The next one requires the ith use to be the last one in the corresponding instruction.

An example of this problematic situation is present in Figure 4.2 at line 20, where variable r is used at a `return` statement. The application of AOIS will result in two equivalent mutants[2], which can be detected automatically by the present pattern. Another example of equivalent mutant detection based on the SameLine-UR pattern is depicted in Figure 5.3a.

4.2.2.3 SameBB-UD Problematic Pattern

The SameBB-UD pattern resembles SameLine-UD, but in this case the search focuses on the same basic block. In order for this pattern to be present in the source code of the original program the following conditions must hold:

Definition 4.5 ***SameBB-UD Pattern.***

$\exists\, v_k, v_j \in SVars,\ i \in \mathbb{N}^+$

$$(bb(use(i,v_k)) = bb(def(v_j)) \wedge$$

$$\nexists\, m \in \mathbb{N}^+\ ((m > i)\ \wedge\ (bb(use(m,v_k)) = bb(use(i,v_k)))) \wedge$$

$$defAftr(use(i,v_k),v_k) = def(v_j))$$

The first condition states that the definition of v_j and the use of v_k must belong to the same basic block. Recall that v_j and v_k are variables of the SSA representation of the program under test and refer to variable v of the corresponding program. The second condition denotes that the ith use of v_k is the last one before the definition of v_j, in the respective basic block. The last condition requires instruction $def(v_j)$ to be the first definition of variable v of the original program after instruction $use(i,v_k)$.

An example of a problematic code location detected by this pattern is presented in part a of Figure 4.1: variable v is used in the second line of the code fragment and in the third, it is defined. Thus, mutating v with the AOIS operator will result in two equivalent mutants[3]. Examining the SSA representation of this code fragment (part b of the figure), it is evident that the aforementioned conditions do hold, thus, the corresponding equivalent mutants can be detected by the SameBB-UD problematic pattern. Another instance of a problematic situation detected by this pattern is presented in Figure 5.2b.

[2] Equivalent mutants (line 20, Figure 4.2): return r++ and return r−−.

[3] Equivalent mutants (line 2, Figure 4.1): $x = v{+}{+} + 5$ and $x = v{-}{-} + 5$.

4.2.2.4 SameBB-UR Problematic Pattern

As a special case of SameBB-UD, consider line 18 of Figure 4.2: it can be seen that the application of AOIS will result in two equivalent mutants[4]. This is due to the fact that variable x is never used between lines 18 and 20.

This problematic situation leads to the SameBB-UR problematic pattern, which searches the source code of the original program for uses of variables that belong to a basic block that can exit the program. More formally:

Definition 4.6 ***SameBB-UR Pattern.***

$\exists\ v_k \in SVars,\ i \in \mathbb{N}^+$

$$(isExit(bb(use(i, v_k))) \wedge$$

$$\nexists\ m \in \mathbb{N}^+\ ((m > i)\ \wedge\ (bb(use(m, v_k)) = bb(use(i, v_k)))) \wedge$$

$$\nexists\ v_j \in SVars\ (defAftr(use(i, v_k), v_k) = def(v_j)))$$

The first condition necessitates the existence of a use inside a basic block that can exit the program and the second one is the same as in the case of the SameBB-UD pattern. The last condition requires the absence of any definitions of the used variable after the using instruction.

Although the last condition is not required, its exclusion would cause instances of the SameBB-UD pattern to be treated as instances of this particular one. For the same reason, it is added in analogous cases of the Def-Def (DD) and Def-Ret (DR) categories of patterns. An example of a problematic situation detected by this pattern is illustrated in Figure 5.3b.

4.2.2.5 DifferentBB-UD Problematic Pattern

The DifferentBB-UD problematic pattern manages to detect partially equivalent mutants and in specific cases, equivalent ones. This pattern searches for uses of variables that can reach definitions by different paths, i.e. a variable is used in one basic block and the same variable is defined in another one and these basic blocks are connected via one or more paths.

[4]Equivalent mutants (line 18, Figure 4.2): r = x++ and r = x−−.

In order for this pattern to detect a problematic situation, the intermediate nodes of at least one of the connecting paths must not include any uses or definitions of the respective variable. Such being the case, the change imposed on the used variable (due to AOIS) cannot be revealed by targeting that path because the variable is redefined prior to being used. More formally:

Definition 4.7 ***DifferentBB-UD Pattern.***

$\exists\, p \in Paths,\ v_k, v_j \in SVars,\ i \in \mathbb{N}^+$

$$(reach(p, bb(use(i,v_k)), bb(def(v_j))) \wedge$$

$$\nexists\, m \in \mathbb{N}^+\ ((m > i)\ \wedge\ (bb(use(m,v_k)) = bb(use(i,v_k)))) \wedge$$

$$\nexists\, v_q \in SVars\ (def(v_q) = defAftr(use(i,v_k),v_k)) \wedge$$

$$defAftr(frstIns(def(v_j)),v_j) = def(v_j) \wedge$$

$$\nexists\, v_q \in SVars,\ n \in \mathbb{N}^+\ (useBfr(def(v_j),v_j) = use(n,v_q)) \wedge$$

$$useClr(p,v_k) \wedge$$

$$defClr(p,v_k))$$

where *Paths* is the set of paths of the CFG of the program under test.

Elaborating on these conditions, the first one requires the existence of a path traversing the node that uses variable v_k and the one that defines variable v_j, i.e. the nodes that use and define variable v of the original program. The next two conditions refer to the basic block that contains the instruction of the ith use of variable v_k (as returned by $use(i,v_k)$), hereafter referred to as the *using* basic block. The first one states that the ith use of v_k must be the last use of that variable in the *using* basic block, i.e. there are no other uses of v_k after instruction $use(i,v_k)$. The other one prohibits the existence of a definition of variable v of the original program after the ith use of v_j (belonging to the *using* basic block).

The fourth and fifth conditions refer to the basic block that contains the instruction that defines variable v_j (as returned by $def(v_j)$), hereafter referred to as the *defining* basic block. The first of them states that $def(v_j)$ is the first instruction of the *defining* basic block that defines variable v of the original program, i.e. there is no prior definition of variable v in the *defining* basic block. The next one necessitates that there are no uses of variable v of the original program before the $def(v_j)$ instruction in the *defining* basic block.

Finally, the last two conditions require the intermediate nodes of path p to not include a use or definition of variable v of the original program. Recall that path p traverses the *using* and the *defining* basic blocks.

As mentioned earlier, this pattern identifies partially equivalent or equivalent mutants. In the case of partially equivalent mutants, the aforementioned conditions hold for at least one path. Although such mutants cannot be killed by targeting the corresponding path, there are other paths for which these conditions do not hold. Thus, by targeting those paths, a killing test case might be produced. Note that this study does not consider the feasibility of these paths, i.e. whether or not it is possible to execute them with test data; it is solely concerned with the existence of such paths, i.e. with the possibility of a mutant to be killable.

In the case of equivalent mutants, the aforementioned conditions hold for all paths connecting the respective basic blocks. Thus, there is no path to consider for killing the examined mutants. Chapter 5's empirical evaluation of this pattern provides further insights into the conditions that need to hold for this pattern to detect equivalent mutants (see Section 5.1.1).

An example of a problematic situation that falls into the described category is presented in Figure 4.2 and more precisely at lines 12 and 16, where variable *diff* is used and defined, accordingly. The application of AOIS at line 12 would result in two equivalent mutants[5] due to the fact that *diff* is not used between lines 12 and 16, thus, the mutants' change cannot be detected. This situation is managed by DifferentBB-UD, which successfully identifies these mutants as equivalent. Figure 5.2c and Figure 5.2d depict two additional examples of problematic situations detected by this pattern; Figure 5.2c presents an instance of partially equivalent mutant detection and Figure 5.2d an instance of equivalent mutant identification.

[5]Equivalent mutants (line 12, Figure 4.2): else if (diff$++>$ 0) and else if (diff$-->$ 0).

4.2.2.6 DifferentBB-UR Problematic Pattern

A special case of DifferentBB-UD is the DifferentBB-UR problematic pattern, which investigates pathogenic situations that arise when a use of a variable does not reach another use, either because there is none or due to a statement that can cause the program to exit, e.g. a `return` statement. In this case, the following conditions need to hold for a code location to constitute a problematic situation:

Definition 4.8 ***DifferentBB-UR Pattern.***

$$\exists\, p \in Paths,\ v_k \in SVars,\ i_\varepsilon \in ExitIns,\ i \in \mathbb{N}^+$$

$$\begin{aligned}
&(reach(p, bb(use(i,v_k)), bb(i_\varepsilon)) \wedge \\
&\nexists\, m \in \mathbb{N}^+\ ((m > i) \wedge (bb(use(m,v_k)) = bb(use(i,v_k)))) \wedge \\
&\nexists\, v_q \in SVars\ (defAftr(use(i,v_k),v_k) = def(v_q)) \wedge \\
&\nexists\, v_q \in SVars\ (bb(def(v_q)) = bb(i_\varepsilon)) \wedge \\
&\nexists\, v_q \in SVars,\ n \in \mathbb{N}^+\ (bb(use(n,v_q)) = bb(i_\varepsilon)) \wedge \\
&useClr(p,v_k) \wedge \\
&defClr(p,v_k))
\end{aligned}$$

where *ExitIns* is the set of instructions that cause the program to exit.

These conditions are in accordance to the ones of the DifferentBB-UD problematic pattern. The first one requires the existence of a path connecting the basic blocks that contain the use of variable v_k and an instruction that forces the program to exit. The next two state that at the basic block containing the $use(i,v_k)$ instruction, the ith use of v_k is the last one and that there is no definition of variable v of the original program after the corresponding use.

The following two conditions require that there are no definitions or uses of variable v of the original program at the basic block containing instruction i_ε, respectively. Finally, due to the last two conditions the intermediate nodes of path p must not contain definitions or uses of variable v. Examples of partially equivalent and equivalent mutant detection, based on this pattern, are presented in Figure 5.3c and Figure 5.3d, respectively.

4.2.3 Def-Def (DD) and Def-Ret (DR) Categories of Patterns

As already mentioned, the Def-Def (DD) and Def-Ret (DR) categories of patterns target equivalent mutants that are generated by mutation operators that affect variable definitions. These categories are composed of the DD problematic pattern and the SameBB-DR and DifferentBB-DR patterns, respectively.

4.2.3.1 DD Problematic Pattern

Th DD problematic pattern identifies problematic code locations based on subsequent definitions of a variable. Expanding on this, if a definition can reach another definition of the same variable and there is no intermediate use of that variable, then any change affecting the first definition cannot be revealed due to the fact that the variable is redefined prior to being used.

Thus, mutants affecting that definition are bound to be partially equivalent, or in specific cases, equivalent ones. It should be clarified that this category is not restricted to a particular type of mutation operator; any mutation operator that can affect the right part of an assignment statement (or a variable definition in general) constitutes a possible target for the respective patterns.

An instance of a problematic situation that is detected by the present pattern involves lines 3 and 13 of Figure 4.2, where variable M is defined. The only use of the variable is at line 10 of basic block 4. Thus, mutants affecting the definition of line 3 are bound to be partially equivalent for all paths from node 1 that include node 6 and do not include node 4. Additional examples of partially equivalent and equivalent mutant detection, based on this pattern, are presented in Figure 5.4a and Figure 5.4b, respectively.

Recall that the equivalent mutant problem, in this study, is addressed for the case of strong mutation, i.e. a mutant is considered equivalent if its output is the same as the one of the original program for every possible input. Furthermore, it should be mentioned that the partial equivalence of a mutant does not imply that the mutant is equivalent; this knowledge should be utilised in order to avoid targeting those paths that will not yield a killing test case for the examined mutant.

Unlike the UD and UR categories of patterns, DD is solely concerned with problematic situations involving code locations that belong to different basic blocks. Although, two definitions of the same variable can belong to the same basic block, if these definitions are not accompanied with intermediate uses, they constitute a problematic situation on their own. A more obscure problematic situation arises when one definition of a variable can reach another one (of the same variable) along a path that does not contain a node that uses that variable.

Mutants affecting such definitions would be partially equivalent and the corresponding paths would never result in a test case that is able to kill the respective mutants. Furthermore, if all paths traversing the basic blocks of the two definitions do not include a node that uses the defined variable, then the above mentioned mutants can be safely classified as equivalent. Thus, the identification of such problematic cases will result in saving valuable resources, human and machine alike.

More formally, the necessary conditions that need to hold in order to detect the described problematic situations are the following:

Definition 4.9 ***DD Pattern.***

$$\exists\, p \in Paths,\ v_k, v_j \in SVars$$

$$\begin{aligned}
&(reach(p, bb(def(v_k)), bb(def(v_j))) \wedge \\
&\nexists\, v_q \in SVars\ (defAftr(def(v_k), v_k) = def(v_q)) \wedge \\
&\nexists\, v_q \in SVars,\ n \in \mathbb{N}^+\ (useAfr(def(v_k), v_k) = use(n, v_q)) \wedge \\
&defAftr(frstIns(def(v_j)), v_j) = def(v_j) \wedge \\
&\nexists\, v_q \in SVars,\ n \in \mathbb{N}^+\ (useBfr(def(v_j), v_j) = use(n, v_q)) \wedge \\
&useClr(p, v_k) \wedge \\
&defClr(p, v_k))
\end{aligned}$$

These conditions are analogous to the ones of DifferentBB-UD, except that in this case two definitions of a variable are considered and not a use and a definition. The first condition requires the existence of a path traversing the node that defines variable v_k and the one that defines variable v_j. The next two conditions state that the $def(v_k)$ instruction is the last definition of variable v of the original program in the corresponding basic block and that there are no uses of v between the defining instruction and the end of the basic block.

The remaining conditions are the same as in the case of the DifferentBB-UD pattern and are restated here for completeness: they state that the $def(v_j)$ instruction is the first definition of variable v of the original program in the corresponding basic block and that there are no uses of v between the first instruction of the basic block and the defining instruction. Finally, the last two conditions require path p not to contain any intermediate nodes that use or define variable v of the original program.

4.2.3.2 SameBB-DR Problematic Pattern

The patterns of the DR category resemble the previously described one, but instead of searching for two definitions without an intermediate use, they search for a definition that cannot reach a use, either because there is none or due to a statement that forces the program to exit.

This situation can manifest in the same or different basic blocks of a program under test. In the former case, the SameBB-DR problematic pattern, the defining statement belongs to a basic block that can exit the program. It should be mentioned that in both cases the variable whose definition is affected must be local, i.e. it should not be possible to access that variable after the exit of the corresponding method (see also Section 5.1.4). In order for this pattern to become problematic the following conditions must hold:

Definition 4.10 ***SameBB-DR Pattern.***

$\exists\ v_k \in SVars$

$$(isExit(bb(def(v_k))) \wedge$$

$$\nexists\ v_q \in SVars,\ n \in \mathbb{N}^+\ (useAfr(def(v_k), v_k) = use(n, v_q)) \wedge$$

$$\nexists\, v_j \in SVars\ (defAftr(def(v_k), v_k) = def(v_j)))$$

The first condition states that the instruction that defines variable v_k belongs to a basic block that can exit the program. The next one requires that there are no uses of variable v of the original program after the corresponding defining instruction and the last one prohibits the existence of another defining instruction of the considered variable after instruction $def(v_k)$.

4.2.3.3 DifferentBB-DR Problematic Pattern

The remaining pattern of the DR category, the DifferentBB-DR problematic pattern, searches for problematic situations that manifest in different basic blocks, i.e. one basic block which defines a variable is connected by at least one path (that does not contain any intermediate nodes that use the corresponding variable) to a basic block that can exit the program. More formally:

Definition 4.11 ***DifferentBB-DR Pattern.***

$$\exists\, p \in Paths,\ v_k \in SVars,\ i_\varepsilon \in ExitIns$$

$$(reach(p, bb(def(v_k)), bb(i_\varepsilon)) \wedge$$

$$\nexists\, v_q \in SVars\ (defAftr(def(v_k), v_k) = def(v_q)) \wedge$$

$$\nexists\, v_q \in SVars,\ n \in \mathbb{N}^+\ (useAfr(def(v_k), v_k) = use(n, v_q)) \wedge$$

$$\nexists\, v_q \in SVars\ (bb(def(v_q)) = bb(i_\varepsilon)) \wedge$$

$$\nexists\, v_q \in SVars,\ n \in \mathbb{N}^+\ (bb(use(n, v_q)) = bb(i_\varepsilon)) \wedge$$

$$useClr(p, v_k) \wedge$$

$$defClr(p, v_k))$$

where *ExitIns* is the set of instructions that cause the program to exit.

These conditions are analogous to the ones of the DD problematic pattern. The first one requires the existence of a path that traverses the basic block that contains the definition of variable v_k and one that can exit the program. The next two state that, at the defining basic block, the $def(v_k)$ instruction is the last one that defines variable v of the original program and that there is no use of the variable in the corresponding basic block after the definition.

The following two conditions require that there are no definitions or uses of variable v of the original program at the node containing instruction i_ε, respectively. Finally, the last two conditions require path p not to contain any intermediate nodes that use or define variable v of the original program.

4.3 Empirical Study and Results

This study tackles the equivalent mutant problem by identifying problematic situations in the data flow information of the program under test that can lead to the generation of equivalent or partially equivalent mutants. In order to investigate the detection power of the introduced patterns as well as their presence in real-world software, an empirical study was conducted based on a set of manually classified mutants, hereafter referred to as the *control mutant set*. In the next subsections, details about the experimental setup, the considered test subjects and the obtained results are given.

4.3.1 Experimental Setup

4.3.1.1 Control Mutant Set and Subject Programs

This study is based on six Java test subjects[6] which vary in size and application domain. Table 4.2 presents the corresponding details. The first two columns of the table depict the name of the studied test subjects and a short description of their usage. The remaining columns introduce the corresponding lines of code and the number of killable and equivalent mutants that were manually analysed for the purposes of this study and comprise the control mutant set.

As can be seen from the table, the control mutant set is comprised of 747 manually classified mutants, 663 of which are killable and 84 are equivalent ones. These mutants were generated by the application of all method-level mutation operators of the MUJAVA (version 3) mutation testing framework [19, 163].

[6]Note that the same test subjects and manually analysed mutants were utilised in the study presented in Chapter 6.

Table 4.2: Subject Program Details.

Program	Description	LOC	Killable	Equivalent
`Bisect`	Square root calculation	36	40	4
`Commons`	Various utilities	19,583	110	28
`Joda-time`	Date and time utilities	25,909	42	4
`Pamvotis`	WLAN simulator	5,149	142	10
`Triangle`	Returns triangle type	32	183	30
`Xstream`	XML object serialisation	16,791	146	8
Total		67,500	663	84

Since this study targets the equivalent mutant problem and the introduced patterns do not yield false positive results, only the equivalent mutants of the control mutant set are utilised. Studying the respective killable ones would be valuable in the case of partially equivalent mutants. Note that Chapter 5 presents more information about this kind of mutants.

4.3.1.2 Experimental Procedure

In order to investigate the detection power of the introduced problematic patterns, the mutated location of each equivalent mutant was manually investigated in order to determine whether or not this particular location can be identified as problematic by the proposed patterns, i.e. if the conditions of at least one of the introduced patterns are satisfied.

Note that the manual investigation is performed solely for the purposes of this experiment. The proposed data flow patterns can be incorporated into an automated framework and, thus, can facilitate the automated detection of equivalent mutants. Chapter 5 presents such a framework.

4.3.2 Empirical Findings

The empirical results of the conducted study are presented in Table 4.3. The second and third columns of the table present the number of the manually detected equivalent mutants and the number of these mutants that can be automatically detected by the application of the proposed data flow patterns per test subject, respectively. The last column presents the achieved reduction in the number of mutants that have to

Table 4.3: Data Flow Patterns' Detection Power.

Program	Manually Detected Equiv. Mutants	Automatically Detected Equiv. Mutants	Cost Reduction
`Bisect`	4	4	100%
`Commons`	28	16	57%
`Joda-time`	4	4	100%
`Pamvotis`	10	8	80%
`Triangle`	30	26	87%
`Xstream`	8	0	0%
Total	84	58	69%

be manually analysed.

It can be seen that the introduced patterns are able to automatically detect 58 out of 84 equivalent mutants and can decrease the number of equivalent mutants that have to be manually analysed by approximately 70%. In other words, only 30% of the examined equivalent mutants have to be manually investigated. A clear outlier is the `XStream` test subject, whose equivalent mutants could not be detected by the presented patterns. Upon inspection, this particular program did not contain any of the problematic situations that can be addressed by the introduced data flow patterns.

The obtained findings are very promising, indicating that a considerable portion of the equivalent mutants can be automatically detected, relieving the practitioners from the burden of manually analysing all equivalent mutants. These results become even stronger if the required time of the manual equivalent detection is considered, which is estimated at 15 minutes per equivalent mutant [78–80].

It should be mentioned that AOIS accounted for 58 equivalent mutants out of 84 of the control mutant set and these mutants were the ones that were automatically detected. This finding justifies the introduction of the UD and UR categories of problematic patterns and provides evidence of the extent to which AOIS is responsible for the generation of equivalent mutants. Finally, it is noted that most of the undetected equivalent mutants are caused by the Relational Operator Replacement (ROR) mutation operator, a mutation operator that cannot be handled solely by data flow information.

4.4 Summary

This chapter introduced and described formally nine data flow patterns that are able to automatically detect equivalent and partially equivalent mutants. For each pattern, the specific conditions, between variable definitions and uses, that need to hold for the existence of the respective problematic situations in the source code of the program under test are defined.

The Static Single Assignment (SSA) intermediate representation of the examined program was utilised for the purposes of the patterns' definition. The salient feature of this representation is that each variable is assigned exactly once, thus, it facilitates powerful code analysis and a clearer definition of the aforementioned conditions.

An empirical study, conducted on approximately 800 manually analysed mutants from several open source projects, investigated the detection power of the proposed data flow patterns and their existence in real-world software. The obtained results revealed that the introduced patterns were indeed present in such software and were able to detect approximately 70% of the examined equivalent mutants, thus, considerably reducing mutation's manual effort.

The next chapter investigates further the proposed data flow patterns. An automated tool, named Mutants' Equivalence Discovery (MEDIC), that incorporates these patterns is implemented and its effectiveness and efficiency are empirically evaluated.

Chapter 5

A Static Analysis Framework for Equivalent Mutant Identification

It is generally known that the equivalent mutant problem impedes the adoption of mutation testing in practice. This situation is exacerbated further by its undecidable nature. Thus, the need to introduce automated solutions, albeit partial, to tackle this problem becomes apparent. In view of this, this chapter introduces a static analysis framework for equivalent mutant identification, named Mutants' Equivalence Discovery (MEDIC).

MEDIC implements the data flow patterns introduced in Chapter 4. The presence of these patterns in the source code of the program under test was found to lead to the generation of equivalent and partially equivalent mutants. Recall that a partially equivalent mutant is equivalent to the original program for specific paths and, as a consequence, these paths cannot produce killing test cases for the corresponding mutant. Despite this fact, partially equivalent mutants can be killable.

A salient characteristic of the utilised patterns is that they are determined statically, i.e. they can be incorporated into mutation testing frameworks to weed out a portion of the total equivalent mutants *before* their generation, without the need to *execute* the considered mutants. Thus, their utilisation would greatly boost the frameworks' efficiency. The empirical assessment of MEDIC evaluates this statement and investigates further the detection power of the implemented patterns.

Apart from examining MEDIC's effectiveness and efficiency, this chapter also explores the cross-language nature of the aforementioned patterns, i.e. whether or not they can detect equivalent and partially equivalent mutants in programs written in different programming languages. Finally, the killability of the detected partially equivalent mutants and the difficulty in performing such a task were also investigated.

In summary, the present chapter makes the following contributions:

1. An automated framework, named Mutants' Equivalence Discovery (MEDIC) which implements the data flow patterns introduced in Chapter 4 and is able to detect equivalent and partially equivalent mutants in different programming languages.

2. An empirical study, based on 1,287 manually analysed mutants from real-world projects, which investigates MEDIC's detection power, performance and cross-language nature.

3. Insights into the nature of partially equivalent mutants and the difficulty in killing them.

The rest of this chapter is organised as follows. Section 5.1 succinctly describes the implemented data flow patterns in conjunction with examples belonging to the examined test subjects, in order for this chapter to be self-contained. Section 5.2 presents the implementation details of MEDIC and Section 5.3 the conducted empirical study. Next, Section 5.4 describes the obtained experimental results and discusses possible threats to validity. Finally, Section 5.5 concludes this chapter, summarising key findings.

5.1 Background: Problematic Data Flow Patterns

Chapter 4 introduced several data flow patterns that detect source code locations capable of generating equivalent mutants. These patterns examine the data flow information of the program under test. The underlying analysis is based on the Static Single Assignment (SSA) intermediate representation [159, 160]; a form utilised by modern compilers for the internal representation of the input program.

The basic characteristic of the SSA representation is that each variable of the program under test is assigned exactly once. Essentially, for each assignment to a variable, that variable is uniquely named and all its uses, reached by that assignment, are appropriately renamed [162]. An example of this representation is illustrated in Figure 5.1.

The first part of the figure presents a portion of the source code of the `uncapitalize` method of the `Commons` test subject[1] and the second part its SSA representation, as obtained by the T. J. Watson Libraries for Analysis (WALA) framework [164], a program analysis tool utilised by MEDIC. The lines of each part of the figure are numbered in such a way that directly relates the source code with its SSA representation: the SSA representation of line 1 of the source code (part a) is line 1 of part b, for line 5 of part a, the corresponding line is part b's line 5 and so on.

By examining this figure, it becomes clear that each variable is uniquely named in the SSA representation based on its assignments in the source code and that its uses are also renamed appropriately. Section 5.2 elaborates on this example and describes the WALA and MEDIC frameworks in more detail.

The considered data flow patterns can lead to the detection of equivalent and partially equivalent mutants. A partially equivalent mutant is a mutant that is equivalent to the original program only for a specific set of paths, whereas an equivalent one is equivalent to the original program for all paths.

The identification of partially equivalent mutants is considered valuable due to the discovery of the subset of paths that will not yield a killing test case for the corresponding mutant. The present work empirically studies the concept of partially equivalent mutants and discusses the corresponding findings in Section 5.4.

5.1.1 Use-Def (UD) Category of Patterns

As mentioned in Section 4.2.2, the Use-Def (UD) category of patterns targets equivalent mutants that are due to mutation operators that insert the post-increment or decrement arithmetic operators or other similar operators. The patterns belonging

[1] Apache Commons Lang project (`https://commons.apache.org`).

```
    ...
 1: int strLen = str.length();
 2: StringBuffer buffer = new StringBuffer(strLen);
 3: boolean uncapitalizeNext = true;
 4: for (int i = 0; i < strLen; i++) {
 5:     char ch = str.charAt(i);
 6:     if (isDelimiter(ch, delimiters)) {
 7:         buffer.append(ch);
 8:         uncapitalizeNext = true;
 9:     }
10:     else if (uncapitalizeNext) {
11:         buffer.append(Character.toLowerCase(ch));
12:         uncapitalizeNext = false;
13:     }
14:     ...
15: }
    ...
```

(a) Example Code fragment.

```
    ...
 1: v12 = v1.length()                    → defines: strLen, uses: str
 2: v13 = new StringBuffer(v12)          → defines: buffer, uses: strLen
 4: v30 = phi v15:#1, v28                → defines: uncapitalizeNext
    v31 = phi v10:#0, v29                → defines: i
    conditional branch(lt) v31,v12       → uses: i and strLen
 5: v17 = v1.charAt(v31)                 → defines: ch, uses: i and str
 6: v19 = isDelimiter(v17, v2)           → uses: ch and delimiters
    conditional branch(eq) v19,v10:#0    → uses: v19 (internal) and v10
 7: v21 = v13.append(v17)                → uses: ch and buffer
10: conditional branch(eq) v30,v10:#0    → uses: uncapitalizeNext and v10
11: v23 = Character.toLowerCase(v17)     → uses: ch
    v25 = v13.append(v23)                → uses: buffer and v23 (internal)
14: v28 = phi v15:#1, v10:#0, v30        → defines: uncapitalizeNext
    v29 = v31 + v15:#1                   → defines: i
    ...
```

(b) Its SSA representation.

Figure 5.1: SSA Representation Example. Code fragment of the `Commons` test subject and its SSA representation (generated by the WALA program analysis framework [164]).

to this category search for uses of variables that do not reach another use. More precisely, they search for uses of variables that (1) reach definitions before reaching other uses and/or (2) they reach no other use.

These problematic situations are bound to generate two equivalent mutants.

Consider, for instance, the use of variable *ch* at line 11 of Figure 5.1. This variable constitutes a valid target for the Arithmetic Operator Insertion Short-cut (AOIS) mutation operator of the MUJAVA framework. Furthermore, note that the use of line 11 will either reach another use only *after* a definition of the same variable or will not reach another use (in the case the `for` block exits).

Taking these facts into account, it becomes clear that the application of the post-increment and decrement operators to this variable, i.e. the application of AOIS, will result in two equivalent mutants. Analogous cases are handled by the patterns of this category, which are briefly described subsequently:

- **SameLine-UD Problematic Pattern.** The SameLine-UD problematic pattern detects solely equivalent mutants that affect a variable that is being used and defined at the same statement. In this particular case, the changes induced by the post-increment and decrement operators can never be distinguished. Figure 5.2a presents an example from the `classify` method of the `Triangle` test subject: the application of AOIS at line 29 will generate two equivalent mutants, denoted by the symbol Δ, affecting variable *trian*. The SameLine-UD pattern discovers this problematic source code location by identifying the use and the definition of *trian* at the corresponding line, as highlighted in the figure.

- **SameBB-UD Problematic Pattern.** This pattern also detects solely equivalent mutants, but in this case the use of the variable and its definition belong to the same basic block. Thus, SameBB-UD searches for basic blocks that contain uses and definitions of the same variable and the use precedes the definition with no intermediate uses. The application of AOIS to such a case will inevitably lead to the generation of equivalent mutants. An example of this problematic situation belonging to the `wrap` method of the `Commons` test subject, is depicted in Figure 5.2b, where variable *offset*, which constitutes a valid target for AOIS, is used at line 56 and is later defined at line 57. This situation is detected by SameBB-UD, leading to the discovery of the two equivalent mutants depicted in the figure.

```
...
if (a == c) {
    trian = trian + 2;
Δ       ... trian++ ...
Δ       ... trian−− ...
}
...
```

(a) `Triangle`: SameLine-UD – Equiv.

```
...
else {
    ...(str.substring( offset ));
Δ               ...(offset++));
Δ               ...(offset−−));
    offset = inputLineLength;
}
...
```

(b) `Commons`: SameBB-UD – Equiv.

```
...
while (ABS(diff) > mEpsilon) {
    if (diff < 0) {
        m = x;      // BB:4
        x = ( M + x) / 2;
Δ         ... M++ ...
Δ         ... M−− ...
    }
    else if (diff > 0) {
        M = x;    // BB:6
        x = (m + x) / 2;
    }
    diff = x * x - N;
}
...
```

(c) `Bisect`: DifferentBB-UD – Partially Eq.

```
for (; i < length; i++) {
    char c = name.charAt(i);
    if (...) {
        ...
    }
    else if (...) {
        ...
    }
    else {
        result.append( c );
Δ               ...(c++);
Δ               ...(c−−);
    }
}
...
```

(d) `XStream`: DifferentBB-UD – Equiv.

Figure 5.2: Problematic Situations Detected by the Use-Def (UD) Category of Patterns. Each part presents a code fragment of a studied test subject, the name of the discovering pattern and the type of the detected mutants (denoted by the Δ symbol).

- **DifferentBB-UD Problematic Pattern.** The DifferentBB-UD pattern detects partially equivalent mutants and in specific cases equivalent ones. This pattern searches for uses and definitions of variables between different basic blocks. More precisely, it searches for uses of variables at one basic block (the using basic block) that can reach a definition of that variable at another basic block (the defining basic block), without other intermediate uses or definitions. Such being the case, a path connecting the using and defining basic blocks cannot yield a killing test case for the considered mutants (ones generated by the AOIS mutation operator). Thus, these mutants can be identified as partially equivalent for this specific path. An instance of this case is illustrated in Figure 5.2c. This figure presents a code fragment of the `sqrt` method of the `Bisect` test subject. It can been seen that variable *M* is used at basic block 4 and is defined at basic block 6. Thus, a path that contains these basic blocks with that particular order and no other uses of *M* cannot yield a killing test case for the mutants depicted in the figure. Apart from detecting partially equivalent mutants, DifferentBB-UD can also detect equivalent ones: in this case, (1) the previously stated conditions must hold for all paths connecting the using and defining basic blocks and (2) no path should exist that connects the using basic block with another one that uses the respective variable and does not include an intermediate basic block that defines the corresponding variable. It should be mentioned that this last condition was not included in the original definition of this pattern and was added to address a corner case belonging to a studied test subject. Figure 5.2d, which depicts a code fragment of the `decodeName` method of the `XStream` test subject, presents an instance of equivalent mutant detection. The problematic pattern resides in lines 127 and 118. At the former, variable *c* is used and at the latter it is defined. The application of AOIS at this specific code location will lead to the generation of two equivalent mutants, which are discovered by the DifferentBB-UD pattern. Another example of equivalent detection based on this pattern was presented at the beginning of this subsection.

The aforementioned patterns search for uses of variables that can reach a definition. As a special case, the Use-Ret (UR) category of patterns searches for uses that do not reach another use.

5.1.2 Use-Ret (UR) Category of Patterns

The Use-Ret (UR) family of patterns, introduced in Section 4.2.2, searches for uses of variables that do not reach another use. Thus, the application of the AOIS mutation operator at these specific code locations will lead to the generation of equivalent or partially equivalent mutants. This category includes three patterns that are analogous to the previously presented ones.

```
     ...
187: if (divisor == 1) {
188:     return this;
189: }
190: return mins(getVal()/ divisor );
     Δ               .../divisor++);
     Δ               .../divisor−−);
     ...
```

(a) `Joda-time`: SameLine-UR – Equiv.

```
     ...
83:  if (position != -1) {
84:      ...rmElementAt( position );
     Δ                ...(position++);
     Δ                ...(position−−);
85:      return true;
86:  } else {
     ...
88:  }
```

(b) `Pamvotis`: SameBB-UR – Equiv.

```
     ...
214: for (...; i < isize; i++) {
215:     if ( ch == delimiters[i]) {
     Δ     (ch++ ...)
     Δ     (ch−− ...)
216:         return true;
217:     }
218: }
219: return false;
     ...
```

(c) `Commons`: DifferentBB-UR – Partially Eq.

```
     ...
49:  else {
50:      if (tr == 3 && b + c>a) {
     Δ          ... && b++ ...
     Δ          ... && b−− ...
51:          return ISOSCELES;
52:      }
53:  }
     ...
55:  return INVALID;
```

(d) `Triangle`: DifferentBB-UR – Equiv.

Figure 5.3: Problematic Situations Detected by the Use-Ret (UR) Category of Patterns. Each part presents a code fragment of a studied test subject, the name of the discovering pattern and the type of the detected mutants (denoted by the Δ symbol).

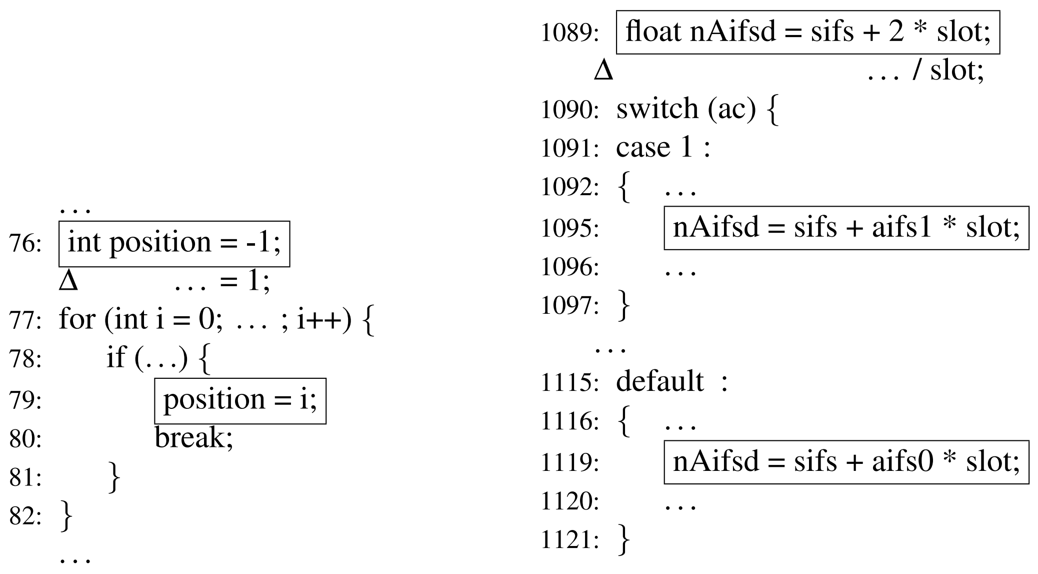
- **SameLine-UR Problematic Pattern.** This pattern targets equivalent mutants that relate to problematic situations where a variable is used at an exiting statement, e.g. a `return` statement. An example of such a case is present in Figure 5.3a, which illustrates a code fragment of the `dividedBy` method of the `Joda-time` test subject. It can be seen that variable *divisor* is used at the `return` statement of line 190; the application of AOIS at this particular line will result in two equivalent mutants (depicted in the figure) that are detected by this pattern.

- **SameBB-UR Problematic Pattern.** The SameBB-UR pattern is analogous to the SameBB-UD one, but instead of searching for uses of a variable that coexist with definitions of the same variable inside a basic block, it searches for basic blocks that contain exiting statements and include uses of variables that do not reach other uses. An instance of this situation is illustrated in Figure 5.3b, which presents a code fragment of the `removeSource` method of the `Pamvotis` test subject. It can be seen that the highlighted use of variable *position* does not reach another use before the `return` statement of line 85. Thus, the application of the AOIS mutation operator will generate two equivalent mutants that are discovered by this pattern.

- **DifferentBB-UR Problematic Pattern.** This pattern constitutes a special case of the DifferentBB-UD one in that it searches for uses of variables at a basic block that can reach an exiting basic block without any intermediate uses or definitions. In this particular circumstance, the application of AOIS can lead to the generation of partially equivalent mutants or equivalent ones. An example of the former case is depicted in Figure 5.3c. This code fragment belongs to the `isDelimiter` method of the `Commons` test subject. It can be seen that the only use of variable *ch* is at line 215 which lies inside a `for` block. Consequently, any path that does not contain more than one loops, i.e. more than one uses of this variable, cannot produce killing test cases for the AOIS mutants. The DifferentBB-UR pattern identifies this fact and marks this code location as problematic and the corresponding mutants as partially equivalent. Figure 5.3d presents an instance of a code location that will generate equivalent mutants. This figure illustrates a code fragment of the `classify` method of the `Triangle` test subject. It can be seen that variable *b* is used at line 50 and has no other uses after this line. Thus, the mutants created by the insertion of the post-increment and decrement arithmetic operators can never be killed. The DifferentBB-UR pattern discovers this problematic situation.

5.1.3 Def-Def (DD) Category of Patterns

The Def-Def (DD) category of patterns, presented in Section 4.2.3, targets problematic situations that are caused by definitions of variables instead of uses. This



```
    ...
76: int position = -1;
    Δ         ... = 1;
77: for (int i = 0; ... ; i++) {
78:     if (...) {
79:         position = i;
80:         break;
81:     }
82: }
    ...
```

(a) `Pamvotis`: DD – Partially Eq.

```
1089: float nAifsd = sifs + 2 * slot;
      Δ                       ... / slot;
1090: switch (ac) {
1091: case 1 :
1092: {   ...
1095:     nAifsd = sifs + aifs1 * slot;
1096:     ...
1097: }
      ...
1115: default :
1116: {   ...
1119:     nAifsd = sifs + aifs0 * slot;
1120:     ...
1121: }
```

(b) `Pamvotis`: DD – Equiv.

Figure 5.4: Problematic Situations Detected by the Def-Def (DD) Category of Patterns. Each part presents a code fragment of a studied test subject, the name of the discovering pattern and the type of the detected mutants (denoted by the Δ symbol).

constitutes the main difference between this category and the aforementioned ones. The only pattern that belongs to this family is the DD problematic pattern.

- **DD Problematic Pattern.** This pattern detects problematic situations that arise from the existence of two consecutive definitions of a variable, belonging to different basic blocks, with no intermediate uses. Such being the case, any mutation operator that changes the first definition is bound to generate partially equivalent mutants or equivalent ones. In the former situation, the two definitions must be reached by at least one path with no intermediate uses – these paths cannot produce a killing test case for the respective mutants. In the latter case, every path reaching the first definition must reach a second one (with no intermediate uses), thus, the change induced by mutation operators affecting the first definition cannot be discerned. Examples of such mutation operators are: the Arithmetic Operator Deletion Unary (AODU) and the Arithmetic Operator Replacement Binary (AORB) mutation operators of the MUJAVA framework. An instance of a code location that will generate partially equivalent mutants is presented in Figure 5.4a. This code fragment belongs to the `removeSource` method of the `Pamvotis` test subject. It can be seen that variable *position* is defined twice, at lines 76 and 79 respectively, and there is no use of that variable prior to the second definition. Due to the fact that these two definitions can be reached by at least one path and there is no use between them, it can be concluded that mutants affecting the definition of line 76 are partially equivalent. The depicted mutant, produced by the AODU mutation operator which deletes unary arithmetic operators, falls into this category. The DD pattern can also detect equivalent mutants: Figure 5.4b illustrates an example belonging to the `addNode` method of the `Pamvotis` test subject. In this code fragment, variable *nAifsd*, which is defined at line 1089, is later redefined at every `case` block and at the `default` block of the `switch` statement, without any intermediate uses. Consequently, every path reaching the definition of line 1089 will definitely reach a second one. The DD pattern identifies this fact and reports that the mutants affecting the right expression of this definition are equivalent ones. An instance of such a mutant, generated by the AORB mutation operator which replaces binary arithmetic operators, is presented in the figure.

5.1.4 Def-Ret (DR) Category of Patterns

The Def-Ret (DR) category of patterns, introduced in Section 4.2.3, constitutes a special case of the aforementioned one. The patterns of this category search for definitions of variables that do not reach a use. In such a case, the induced change of the mutants affecting that particular definition is indistinguishable. Unfortunately, this implies the existence of unused variables in the program under test, which is or should be scarce in a real-world application. The empirical assessment of these patterns showed no instances of equivalent mutant detection (see Section 5.4 for more details), thus, their description is not accompanied by appropriate source code examples.

- **SameBB-DR Problematic Pattern.** The SameBB-DR pattern searches for definitions of variables at a basic block that contains (1) an exiting statement and (2) no use of those variables between the considered definition and the

```
...
r = x;
mResult = r;      // mResult is not a local variable
Δ     ... = -r;
return r;
```

Figure 5.5: SameBB-DR Pattern: Handling Non-local Variables. A detected problematic situation based on the original definition of SameBB-DR. The depicted mutant (denoted by the Δ symbol) is killable because *mResult* is not a local variable. The refined definition of this pattern rectifies this situation.

exiting statement. It is obvious that such a case will generate equivalent mutants. The empirical evaluation of this pattern revealed an additional requirement: (3) it should not be possible to access the variable whose definition is affected after the exit of the corresponding method, e.g. the case of a non-local variable. Consider for example Figure 5.5. This figure presents a code fragment of the `Bisect` test subject. According to the original definition of the SameBB-DR pattern, the highlighted definition of variable *mResult* will be detected as a problematic code location that will generate equivalent mutants. Upon closer inspection, it becomes apparent that these mutants can be easily killed by examining the value of *mResult* after the end of the respective method since it is not a local variable. The newly added requirement refines SameBB-DR's definition and rectifies the aforementioned situation.

- **DifferentBB-DR Problematic Pattern.** The DifferentBB-DR pattern searches for definitions of variables at one basic block that reach an exiting basic block, without any intermediate uses. This pattern can detect both equivalent and partially equivalent mutants. In the first case, every path reaching the considered definition must also reach an exiting basic block (with no intermediate uses) and in the second one, at least one such path must exist between the defining and exiting basic blocks. The empirical evaluation of this pattern revealed no cases of equivalent mutant detection, similarly to the SameBB-DR one, although it did reveal instances of partially equivalent mutants.

5.2 MEDIC – Mutants' Equivalence DIsCovery

The primary focus of this chapter is the empirical evaluation of the problematic patterns described in Chapter 4. To fulfil this, an automated framework, named Mutant's Equivalence Discovery (MEDIC), incorporating these patterns has been implemented. MEDIC is written in the Jython programming language and leverages several frameworks to perform its analyses. MEDIC's components and implementation details are presented in the following sections.

MEDIC utilises the Static Single Assignment (SSA) form [159, 160] of a program under test to perform its analysis. As mentioned at the beginning of Section 5.1, the SSA form is an internal representation of a program whose basic characteristic is that every variable has exactly one definition. MEDIC obtains such a representation by leveraging the T. J. Watson Libraries for Analysis (WALA) framework [164].

5.2.1 T. J. Watson Libraries for Analysis (WALA)

The WALA framework [164] is a static analysis tool for the Java and the JavaScript programming languages. It can perform various analyses, control and data flow alike. The following information is obtained by the application of WALA to the program under test:

- **SSA form of the artefact under test.** WALA transforms the source code of the input program into SSA instructions which form its SSA representation. An instance of this transformation was depicted in Figure 5.1, which presents a code fragment of the `Commons` test subject, along with the generated SSA instructions. WALA applies several optimisations to the transformation process. Most notably, it constructs pruned SSA forms [165] and employs copy propagation [166]. Note that these optimisations are not a prerequisite for the application of MEDIC. In fact, their employment prevents MEDIC from discovering all problematic source code locations that the implemented patterns would have in theory[2].

[2]This results in MEDIC's missing 7 equivalent mutants, cf. Table 5.3.

- **Control Flow Graph of the SSA form.** WALA divides the produced SSA instructions into basic blocks, creating an SSA-based control flow graph. MEDIC utilises this graph to examine the requirements of each implemented pattern.

- **Definitions and uses per SSA instruction.** Typically, each SSA instruction has a single definition and one or more uses. These definitions and uses refer to variables in the SSA representation of the program under test and do not necessarily map to ones in its source code. By examining the second part of Figure 5.1, it becomes evident that even though the uses of the SSA form match the ones of the corresponding code fragment (first part of the figure), the definitions do not. For instance, the definitions of lines 3 and 4 of the source code do not directly correspond to appropriate ones in the SSA form. Instead, these definitions appear as phi statements, or more precisely as ϕ-functions, in the SSA representation. A ϕ-function is a special form of an assignment which is added to the SSA representation of a program when there are variables in its source code that are defined along two converging paths [167]. In other words, two or more definitions of a variable in the source code can reach the same use of that variable via different paths. Such a case is present in Figure 5.1 where variable *i* is defined at the initialisation expression of the `for` statement (`i = 0`) and it is redefined at its increment expression (`i++`). These two definitions both reach the use of *i* at the termination expression of the `for` statement (`i < strLen`) via different paths. Thus, WALA adds an appropriate ϕ-function ($v31$ `= phi` $v10$`:#0,`$v29$) before that particular use in the produced SSA representation. A similar situation pertaining to the definitions of variable `uncapitalizeNext` (lines 3, 8, 12) is treated analogously, as shown in the figure.

5.2.2 MEDIC's Implementation Details

The previously described data form the basis for the operation of MEDIC. In order to increase MEDIC's extensibility, these data are not used in their raw format. Instead, a custom data model has been developed that encapsulates all the necessary information for MEDIC's operation.

The main advantage of such an approach is that MEDIC is decoupled from the internal mechanics of WALA and can leverage other program analysis frameworks that can potentially support different programming languages. Due to the fact that the data to be modelled were graph-centric, i.e. interconnected basic blocks containing uses and definitions of variables, the utilisation of graph databases was deemed appropriate. In particular, MEDIC utilises the NEO4J graph database [168].

Graph databases model the underlying data based on *nodes* and *relationships* which can have *properties*. A property augments the corresponding model with additional information pertinent to the respective node or relationship. MEDIC defines two kinds of nodes in its data model, the `Basic Block` nodes and the `Variable` ones, and introduces three types of relationships, the `goes` relationship that connects two `Basic Block` nodes and the `uses` and `defines` relationships that connect a `Basic Block` node with a `Variable` one.

Figure 5.6 presents an illustrative example of the aforementioned data model that belongs to the `Bisect` test subject. By examining this figure, it becomes apparent that the developed model clearly captures both control and data flow information of basic block `bb2`. This figure also presents the properties that individual nodes and relationships can possess. For instance, a `Basic Block` node can contain only one property, the `id` property, whereas a `Variable` node can contain more. Regarding the corresponding relationships, `uses` and `defines` include similar properties and the `goes` relationship includes none.

The information described by the previously presented data model suffices for the application of MEDIC, i.e. MEDIC examines this information to discover problematic code locations in the source code of the program under test that can generate equivalent or partially equivalent mutants. Note that even though this analysis is based on the SSA representation of the examined program, the discovered code locations refer to its source code.

In the following subsections, the generic algorithm that MEDIC employs for

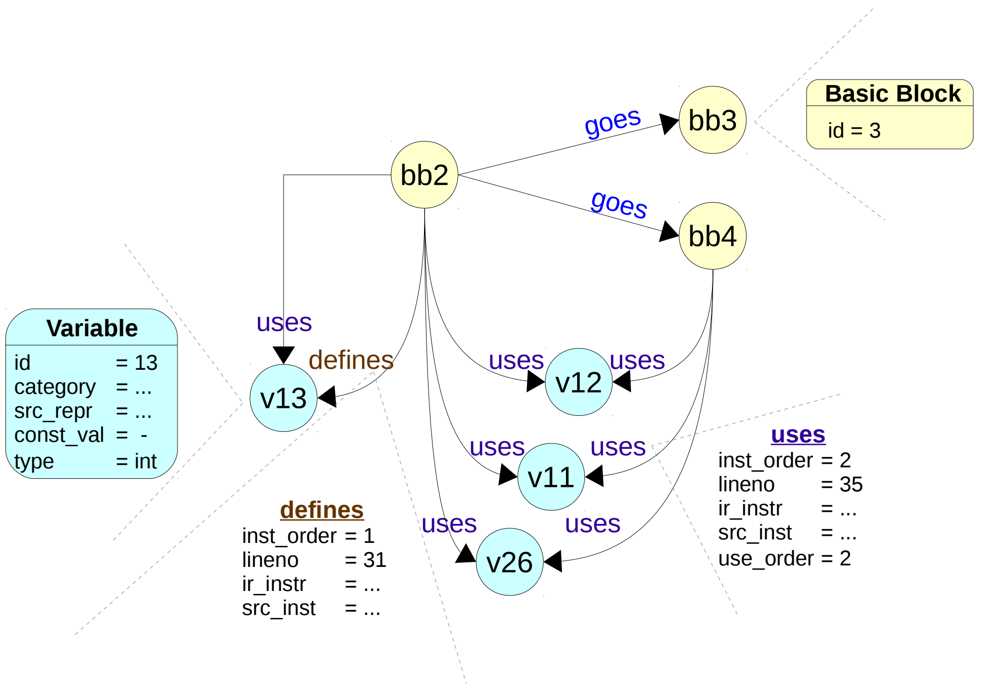


Figure 5.6: MEDIC's Data Model. The model is represented as a graph which has two types of nodes (`Basic block` and `Variable`) and three kinds of edges/relationships (`goes`, `uses`, and `defines`); each node and relationship can contain properties that augment the modelled information.

equivalent and partially equivalent mutant identification is described and the specific instantiation of this algorithm for the case of the SameLine-UD problematic pattern is detailed.

5.2.2.1 MEDIC's Generic Detection Algorithm

MEDIC implements all the problematic patterns detailed in Section 5.1 based on their formal definitions (introduced in Chapter 4). Algorithm 5.1 presents the pseudocode of MEDIC's generic algorithm for equivalent and partially equivalent mutant identification.

The algorithm operates on a NEO4J database (denoted by *db*) which is based on MEDIC's data model and encapsulates WALA's output for the program under test. MEDIC queries this database utilising the input query (denoted by *q*) and examines whether the obtained results satisfy the conditions imposed by the corresponding data flow pattern (denoted by *p*). MEDIC's detection algorithm includes

Algorithm 5.1 MEDIC's Generic Algorithm for Equivalent and Partially Equivalent Mutant Identification.

```
Let $p$ represent a problematic data flow pattern
Let $q$ represent a Cypher query for $p$
Let $db$ represent a NEO4J database modelling WALA's output

1: function EQUIVALENTMUTANTDIAGNOSIS($q$, $p$, $db$)
2:     $qres \leftarrow execute(q, db)$
3:     foreach $r \in qres$ do
4:         if ISVALIDPROBLEMATICSITUATION(R,P) then
5:             return DESCRIBEPROBLEMATICSITUATION(R,P)
6:         end if
7:     end for
8: end function
```

three generic parts that are instantiated differently based on the employed data flow pattern:

- **Input query.** The first step in MEDIC's identification process is the execution of the specified query on the target database (line 2 of Algorithm 5.1). This query is written in Cypher, NEO4J's graph query language. Cypher is a declarative, SQL-inspired language that describes patterns of connected nodes and relationships in a graph. In Cypher's syntax, nodes are represented by pairs of parentheses and relationships by pairs of dashes. An example of a Cypher query that is based on MEDIC's data model and returns all variables that are used in basic block 2 of a program under test is illustrated in Figure 5.7. The presented query has three clauses: a `MATCH` clause that searches for the specified pattern in the underlying graph; a `WHERE` clause that filters the previously matched results based on the *id* property of the matched `Basic Block` nodes; and a `RETURN` clause that returns the value of the `src_repr`[3] property of all matched `Variable` nodes. It should be mentioned that an appropriate Cypher query has been created and incorporated into MEDIC for each implemented data flow pattern.

- **Evaluation of input query's results.** The next generic step in MEDIC's de-

[3]The `src_repr` property of a `Variable` node refers to the source code name of the modelled variable.

```
MATCH (bb:BasicBlock)-[:uses]->(var:Variable)
WHERE bb.id = 2
RETURN var.src_repr
```

Figure 5.7: Example Cypher Query based on MEDIC's Data Model. The query returns all variables that are used in basic block 2 of the program under test.

tection algorithm is the evaluation of the results obtained by the execution of the input query (line 4 of Algorithm 5.1). More precisely, it is examined, per obtained result, whether it describes a problematic source code location that could generate equivalent or partially equivalent mutants. Each considered data flow pattern necessitates several conditions in order to detect equivalent and partially equivalent mutants. Thus, the first objective of this step is to examine whether these conditions hold. Additionally, certain corner cases that were revealed during the problematic patterns' empirical evaluation are also handled in this step. For instance, in the case of the UD and UR categories of patterns some code locations were identified as problematic even though they were not valid targets for the examined mutation operators (e.g. a `boolean` variable erroneously considered a valid target for AOIS). MEDIC filters out these corner cases and reports only valid problematic source code locations that could generate equivalent and partially equivalent mutants.

- **Description of problematic situations.** The final step in MEDIC's generic algorithm pertains to the description of the discovered problematic situations (line 5 of Algorithm 5.1). Recall that MEDIC's data model contains information regarding both the SSA representation of the program under test and its source code. These data, which can be returned by the `RETURN` clauses of the corresponding Cypher queries, are utilised by MEDIC in order to describe the detected problematic source code locations. Since problematic situations that belong to different data flow patterns require different amounts of information in order to be adequately described, MEDIC incorporates appropriate descriptive functions per problematic pattern. For instance, in order to report a problematic source code location that is detected by the SameLine-UD pattern, MEDIC utilises the name of the examined variable and the number of the source code line of the statement that includes the problematic use.

5.2.2.2 A Concrete Example

The previous subsection presented the generic algorithm that forms the basis for MEDIC's operation. This subsection delineates the concrete algorithm that MEDIC employs to detect problematic situations that belong to the SameLine-UD data flow pattern. The detection algorithms of the remaining problematic patterns are implemented in an analogous fashion.

As mentioned earlier, MEDIC's identification algorithm consists of three generic parts that are instantiated differently per data flow pattern. Figure 5.8 depicts the instantiation of these parts for the SameLine-UD problematic pattern. The first part of the figure presents the corresponding input query; the second part, the evaluation algorithm; and the third one, the function that reports the detected problematic source code locations. Next, these parts are presented in greater detail:

- **Input query.** As can be seen from the first part of Figure 5.8, the input query for the SameLine-UD problematic pattern consists of three clauses. The `MATCH` clause matches definitions and uses of variables inside the same basic blocks. The `WHERE` clause filters these matches according to the `src_repr` property of the *var1* and *var2* matched nodes and the `inst_order` property of the `use` and `def` matched relationships. The first condition of this clause ensures that the matched definition and use refer to the same variable and the second one that they belong to the same statement. Finally, the `RETURN` clause returns per matched result: the name of the corresponding variable (as `vname`); the number of the source code line that contains the problematic use and definition (as `uline`); and, the corresponding source code statement (as `src_inst`). Note that these data will be utilised to describe the discovered problematic situations of this pattern.

- **Evaluation of input query's results.** The second part of Figure 5.8 depicts the evaluation algorithm that examines whether the results obtained by the

```
MATCH (var1:Variable)<-[use:uses]-(:BasicBlock)-[def:defines]->(var2:Variable)
WHERE var1.src_repr = var2.src_repr AND use.inst_order = def.inst_order
RETURN var1.src_repr as vname, use.lineno as uline, use.src_inst as src_inst
```

(a) The input query q utilised by MEDIC for the SameLine-UD problematic pattern.

```
1: function IsValidProblematicSituation($r$, 'SameLine-UD')
2:     $invalid\_cases \leftarrow [r.get('vname').concat('++'), \ldots]$
3:     foreach $invalid\_case \in invalid\_cases$ do
4:         if $r.get('src\_inst').contains(invalid\_case)$ then
5:             return $False$
6:         end if
7:     end for
8:     return $True$
9: end function
```

(b) The evaluation algorithm utilised by MEDIC for the purposes of SameLine-UD.

```
function DescribeProblematicSituation($r$, 'SameLine-UD')
    $des \leftarrow$ 'Problematic use and def of variable '
    $var\_name \leftarrow r.get('vname')$
    $lineno \leftarrow r.get('uline')$
    return $des.concat(var\_name).concat(' at ').concat(lineno)$
end function
```

(c) The function that MEDIC utilises to describe the problematic situations that belong to the SameLine-UD pattern.

Figure 5.8: SameLine-UD Pattern: Instantiation of MEDIC's Generic Algorithm. Each part of the figure corresponds to an instantiated part of MEDIC's generic algorithm for the purposes of the SameLine-UD data flow pattern (see also Algorithm 5.1).

execution of the input query are valid problematic situations based on the SameLine-UD pattern. It should be mentioned that the `WHERE` clause of the input query covers the conditions imposed by SameLine-UD[4] – the presented algorithm handles certain corner cases that were revealed during the empirical evaluation of this pattern. For instance, the `i++` source code expression is transformed into an assignment that uses and defines the same variable in the SSA form of the program under test. Thus, it is matched by the corresponding input query. It is obvious that this expression is not problematic based on the

[4]Note that this is not the case for all problematic patterns.

considered data flow pattern. Such invalid cases are stored in the *invalid_cases* variable of the algorithm (line 2 of the second part of Figure 5.8). At line 4 of the algorithm, the source code statement (accessible via the `src_inst` property of matched result *r*) is examined in order to determine whether it contains an invalid case. If it does, the corresponding matched result is discarded; in the opposite situation, it is returned as a valid problematic source code location that will generate equivalent mutants.

- **Description of problematic situations.** The final part of MEDIC's generic algorithm corresponds to the description of the discovered problematic situations. In the case of SameLine-UD, MEDIC utilises the name of the variable that is involved in the problematic use and definition and the number of the corresponding source code line, as can be seen from the last part of Figure 5.8. Recall that this information is returned by the `RETURN` clause of the respective input query. To exemplify, a problematic source code location that is detected by the SameLine-UD pattern could be described by the following: `Problematic use and def of variable` *b* `at line 10`. It should be mentioned that this description is intended to be human-friendly; the same information can be utilised in various ways by MEDIC or other automated frameworks.

5.3 Empirical Study

The primary goal of this work is to provide insights regarding MEDIC's effectiveness and efficiency in detecting equivalent mutants. Additionally, it investigates the cross-language nature of the implemented data flow patterns and the killability of partially equivalent mutants, i.e. whether the detected partially equivalent mutants are easy-to-kill or stubborn ones.

The conducted empirical study is the first one that provides evidence for automated stubborn mutant detection and equivalent mutant detection in the context of different programming languages. This section begins by outlining the posed research questions and continues by detailing the corresponding empirical study.

5.3.1 Research Questions

The research questions that this study attempts to answer are summarised in the following:

- **RQ 5.1** *How effective is MEDIC in detecting equivalent mutants? How efficient is this process?*
- **RQ 5.2** *Can MEDIC detect equivalent mutants in different programming languages?*
- **RQ 5.3** *What is the nature of partially equivalent mutants? Do they tend to be killable? How easily can they be killed?*

The first research question examines both the effectiveness and efficiency of MEDIC. It is important to quantify these two properties for any automated framework in order to investigate the tool's practicality. The second research question is relevant to the applicability of MEDIC and examines its cross-language nature. The final research objective aims at providing insights into the nature of partially equivalent mutants. More precisely, it explores their killability, i.e. whether or not they can be killed and the difficulty in performing this task.

5.3.2 Experimental Procedure

In order to answer the above-mentioned research questions an empirical study was conducted. This study was based on test subjects of various size and complexity that are implemented in different programming languages, namely the Java and JavaScript languages. These two languages were chosen because they are natively supported by WALA and their application domains differ substantially.

5.3.2.1 RQ 5.1: Experimental Design

To address the first research question, a set of manually analysed mutants was created. This set resulted from the application of all method-level mutation operators of the MUJAVA mutation testing framework (version 3) [19, 163] to specific classes of the Java test subjects. Note that these test subjects are the same as the ones utilised in Chapter 4.

Table 5.1: Java Test Subjects' Details.

Program	**Short Description**	**LOC**	**Manual Analysis**	
			Killable	Equivalent
`Bisect`	Square root calculation	36	118	17
`Commons`	Various utilities	19,583	110	28
`Joda-Time`	Date and time utilities	25,909	42	4
`Pamvotis`	WLAN simulator	5,149	411	47
`Triangle`	Triangle classification	32	314	40
`XStream`	XML object serialisation	16,791	127	29
Total	-	67,500	1,122	165

The main difference between this chapter's study and the one presented in Chapter 4 is that this study evaluates the examined patterns based on an automated framework whereas the previous one applied them manually. Additionally, this study considers approximately twice the number of manually identified equivalent mutants.

Table 5.1 describes the Java test subjects in more detail. The table is divided into two parts. The first part presents information regarding the application domain of the studied programs and the corresponding number of source code lines. In total, six test subjects were considered, ranging from small programs to real-world libraries.

The second part of the table presents the results of the manual analysis of the examined methods' mutants, i.e. the number of the equivalent and killable ones. Note that this set of mutants was based on the one utilised for the purposes of the manual evaluation of the respective data flow patterns, presented in Chapter 4.

From the table, it can be seen that 1,122 mutants were identified as killable and 165 as equivalent; the evaluation of MEDIC's effectiveness and efficiency is based on this set of equivalent mutants, hereafter referred to as the *manually identified set*. It must be noted that this set is one of the largest manually identified sets of equivalent mutants in the literature (cf. Table 4 in the study of Yao et al. [106]).

To further investigate the manually identified set and its relationship to the employed mutation operators, Figure 5.9 illustrates the proportion of equivalent mu-

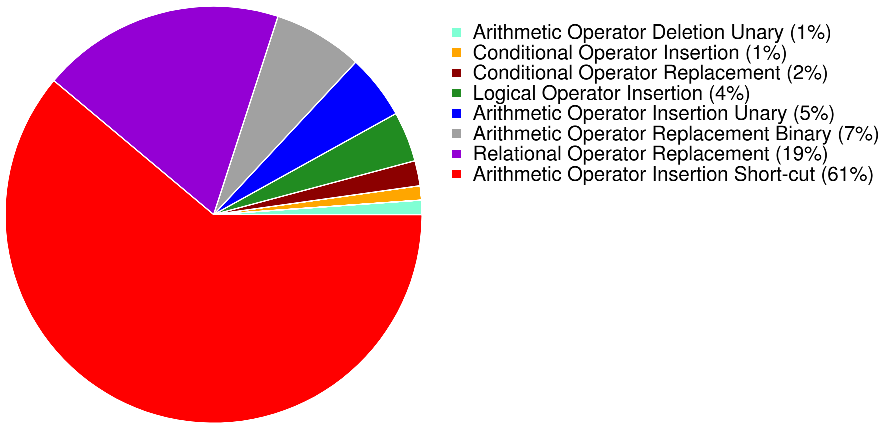


Figure 5.9: Equivalent Mutants Per Mutation Operator. Contribution of each mutation operator to the manually identified set of equivalent mutants.

tants per mutation operator (without including the ones that did not generate such mutants). Recall that the employed mutation operators are all the method-level operators of the MUJAVA framework. The depicted data suggest that the Arithmetic Operator Insertion Short-cut (AOIS) and the Relational Operator Replacement (ROR) mutation operators generated most of the studied equivalent mutants, with AOIS generating more than 50% of them.

In order to measure MEDIC's effectiveness, MEDIC was employed to the studied test subjects and the resulting set of automatically identified equivalent mutants was compared to the manually identified one. Figure 5.10 presents this process. In essence, the following steps were performed per test subject:

Step 1. WALA was applied to the classes that contained the manually identified equivalent mutants of the corresponding subject.

Step 2. The output of WALA was automatically transformed into a format compatible with MEDIC's data model and then stored in a graph database.

Step 3. MEDIC utilised these data to detect the underlying equivalent and partially equivalent mutants.

The first step of the aforementioned process entailed the application of the WALA framework to randomly selected methods of the classes that were mutated

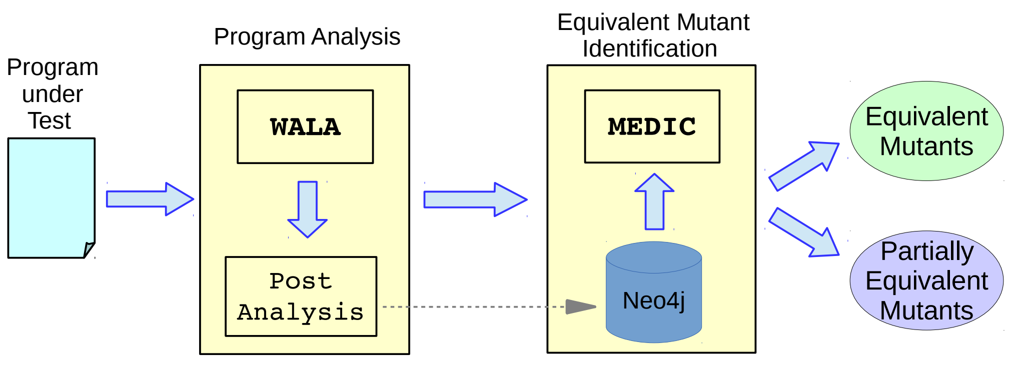


Figure 5.10: MEDIC's Application Process. First, the program under test is analysed by WALA; second, WALA's output is transformed into a format compatible with MEDIC's data model and is stored in a NEO4J database; finally, MEDIC utilises this model to identify the equivalent and partially equivalent mutants of the examined program.

during the manual analysis phase. Next, the output of WALA was processed in order to transform it into an appropriate format that was compatible with the data model of MEDIC. This transformation was performed automatically by a script and the adjusted output was stored in a NEO4J database. Finally, this database was given as input to the MEDIC system in order to perform its analysis.

This process resulted in two sets of mutants: the set of automatically identified equivalent mutants and the set of the partially equivalent ones. The former of these sets is contrasted with the manually identified one in order to investigate MEDIC's effectiveness and the latter is utilised for the purposes of the RQ 5.3 research question.

To study the efficiency of MEDIC, the run-time of the above-mentioned steps was measured. The experiment was conducted on a physical machine running GNU/Linux, equipped with an i7 processor (3,40 GHz, 4 cores) and 16GB of memory. Note that since the detection of partially equivalent mutants is integral to the detection of equivalent ones, the corresponding findings refer to the time that both these analyses required.

Table 5.2: JavaScript Test Subjects' Details.

Program	Short Description	LOC
`dojox.calendar`	Calendar widget	8,524
`D3`	Visualisation library	11,594
`mathjs`	Mathematics library	13,112
`DateJS`	Date library	29,880
Total	-	63,110

5.3.2.2 RQ 5.2: Experimental Design

This research question examines whether MEDIC can detect equivalent and partially equivalent mutants in programs implemented in different programming languages (apart from Java). To answer this question, MEDIC was also applied to a set of test subjects written in JavaScript. This particular language was chosen because WALA natively supports it and its application domain differs greatly from the one of Java.

Table 5.2 presents details regarding the corresponding test subjects in a similar fashion to the Java test subjects (cf. Table 5.1). As can be seen, a total of four test subjects were considered, which vary in size and application domain; the latter of these being the primary reason for their selection.

Owing to the fact that the studied research question is solely concerned with the feasibility of detecting equivalent and partially equivalent mutants in different programming languages, no exhaustive manual analysis of mutants was performed, but rather the mutants that were identified by MEDIC as equivalent or partially equivalent were manually inspected to ensure the correctness of the analysis.

The undertaken steps, for the purposes of this research question, are the same as the steps of the first one with two exceptions. At the first step, WALA was applied to randomly selected functions and, at the second step, the transformation of WALA's output was performed in a semi-automated fashion.

To elaborate on this, WALA's support for the JavaScript programming language did not cater for all the necessary information pertinent to MEDIC's data model. Specifically, it did not report the type of the examined variables. This fact is not due to a limitation of the tool, but rather it is an inherent characteristic of the dynamic nature of JavaScript. To circumvent this issue, the corresponding information was added manually, based on either available comments in the corresponding source code or by inspecting the variables' usage. The rest of WALA's output was transformed via an automated script.

5.3.2.3 RQ 5.3: Experimental Design

The final research question refers to the partially equivalent mutants and investigates their killability. Recall that the examined set of partially equivalent mutants is the one generated by MEDIC when applied to the Java test subjects.

The first step in addressing this question was to examine whether this set consisted of killable or equivalent mutants based on the results of the manual analysis (performed for the purposes of RQ 5.1). Next, the difficulty in killing these mutants was investigated. To quantify such an intangible property the concept of *stubborn* mutants [124] was utilised.

For the purposes of this study, a stubborn mutant is considered to be a killable mutant that remains alive by a test suite that covers all the feasible branches of the control flow graph of the program under test. The same definition was also adopted in the study of Yao et al. [106]. Since a stubborn mutant cannot be killed by a branch adequate test suite, it is considered harder to kill than a non-stubborn one. Thus, if the partially equivalent mutant set consisted mainly of stubborn mutants then it would contain hard-to-kill mutants, or, in the opposite situation, easy-to-kill ones.

The investigation of this research question is based on three metrics: (1) the proportion of the partially equivalent mutants that are equivalent; (2) the proportion of the partially equivalent mutants that are stubborn; and, (3) the proportion of the stubborn mutants that are partially equivalent. In order to calculate these metrics, the subsequent process was followed per test subject:

Step 1. The corresponding test subject was executed with the mutation adequate test suite to discover the remaining uncovered branches.

Step 2. The discovered branches were manually inspected to determine their (in)feasibility.

Step 3. The mutants of the test subject were executed against a set of five manually constructed branch adequate test suites in order to determine the stubborn ones.

Step 4. The stubborn partially equivalent mutants were discovered.

Step 5. The final results were averaged over the five repetitions.

The previously described process entails the identification of the branches of the considered test subjects that were not covered by the mutation adequate test suites and their manual inspection to determine their (in)feasibility. Note that the mutation adequate test suites were created for the purposes of RQ 5.1.

Next, five branch adequate test suites were constructed in order to discover the underlying stubborn mutants. These test suites were created in such a way that they did not overlap each other. The reason for utilising five branch adequate test suites instead of one is to cater for discrepancies caused by high quality test suites, i.e. branch adequate test suites that kill more mutants than other analogous ones.

The next stage was to execute the mutants of each test subject with the previously constructed branch adequate test suites to determine the stubborn ones. The stubborn mutants were the ones that remained alive and were not equivalent. After the identification of the stubborn mutants, the stubborn partially equivalent ones were determined. Finally, the aforementioned metrics were calculated based on all five executions.

5.4 Empirical Findings

This section details the empirical findings of the conducted experimental study. The corresponding results are presented according to the relevant research question.

5.4.1 RQ 5.1: MEDIC's Effectiveness and Efficiency

The first research question, RQ 5.1, investigates the effectiveness and efficiency of MEDIC in detecting equivalent mutants. Table 5.3 presents the corresponding findings with respect to the tool's effectiveness.

Table 5.3: Automatically Identified Equivalent Mutants per Data Flow Pattern and Java Test Subject. The middle part of the table presents the corresponding findings grouped by the relevant categories of the considered patterns.

Program	**Categories of Problematic Patterns**									**Total**
	UD			*DD*	*UR*			*DR*		
	SL	SB	DB		SL	SB	DB	SB	DB	
`Bisect`	-	4	2	-	2	-	-	-	-	8
`Commons`	-	-	12	-	-	-	4	-	-	16
`Joda-Time`	-	-	-	-	-	-	4	-	-	4
`Pamvotis`	-	-	-	11	-	-	32	-	-	43
`Triangle`	4	-	-	-	-	-	14	-	-	18
`XStream`	-	-	4	-	-	-	-	-	-	4
Total	4	4	18	11	2	-	54	-	-	93

The table is divided into three parts: the first part refers to the Java test subjects; the middle part presents the automatically identified equivalent mutants per data flow pattern; and the last one depicts the automatically identified equivalent mutants per test subject. It should be mentioned that the results presented in the middle part of the table are grouped by the corresponding categories of the studied patterns. To exemplify, the *UD* column of the table refers to the Use-Def category of patterns and its *SL*, *SB* and *DB* columns to the SameLine-UD, SameBB-UD and DifferentBB-UD patterns, respectively. The results of the remaining patterns are presented analogously.

By examining the table, it becomes obvious that MEDIC manages to automatically identify 93 equivalent mutants for the Java test subjects, which corresponds to a **56%** reduction in the number of the examined equivalent mutants that have to be manually analysed (cf. Table 5.1). Additionally, it can be seen that the UD and UR categories of patterns identified the most equivalent mutants, followed by the DD category of patterns.

Interestingly, three problematic patterns did not identify any equivalent mutant for the Java test subjects. This fact does not limit their usefulness; the SameBB-UR problematic pattern detected equivalent mutants of the JavaScript test subjects and DifferentBB-DR identified partially equivalent ones belonging to the examined

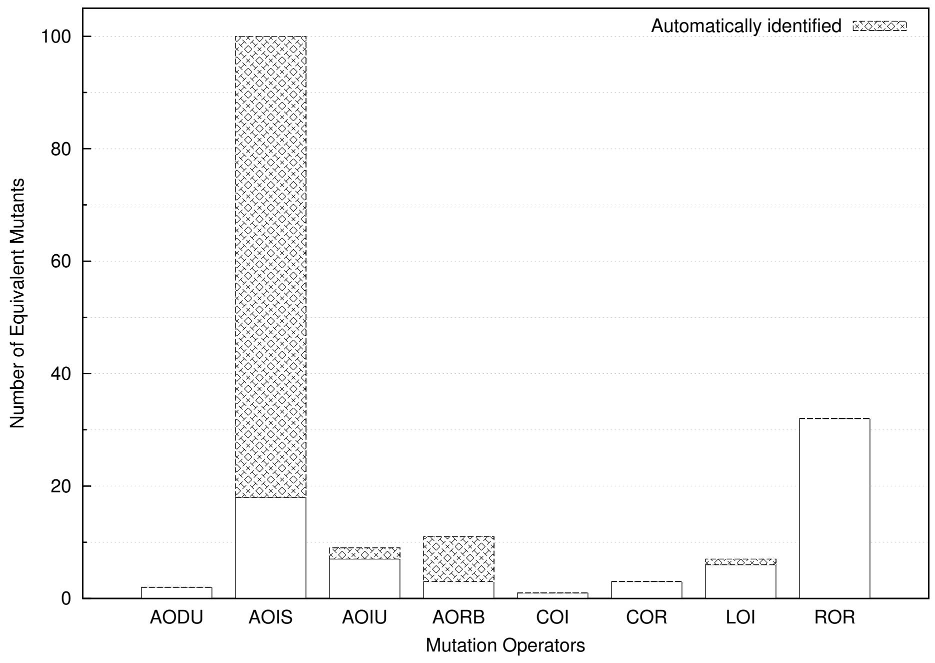


Figure 5.11: Automatically Identified Equivalent Mutants per Mutation Operator. The figure depicts the proportion of the automatically identified equivalent mutants per mutation operator for the Java test subjects.

Java programs. The only pattern that did not detect equivalent or partially equivalent mutants for all test subjects is the SameBB-DR pattern.

In order to better investigate the nature of the automatically identified equivalent mutants, Figure 5.11 visualises the proportion of these mutants (with respect to all studied equivalent ones) per mutation operator. It is evident that the majority of the equivalent mutants produced by the Arithmetic Operator Insertion Short-cut (AOIS) and Arithmetic Operator Replacement Binary (AORB) mutation operators were automatically identified. Recall that AOIS was the operator that produced the most equivalent mutants (cf. Figure 5.9).

Additionally, equivalent mutants created by the Arithmetic Operator Insertion Unary (AOIU) and Logical Operator Insertion (LOI) were also detected, although in a smaller scale. It should be mentioned that all mutants detected by MEDIC as equivalent were indeed equivalent ones and, thus, they can be weeded out safely.

The previous results lend colour to MEDIC's effectiveness in detecting equivalent mutants. Even though these findings are encouraging, the practicality of any

Table 5.4: Run-time of MEDIC's Equivalent Mutant Detection Process for the Java Test Subjects (results are presented in seconds).

Program	WALA Analysis	MEDIC Analysis	Total
	(*seconds*)		
`Bisect`	3	7	10
`Commons`	5	7	12
`Joda-Time`	4	3	7
`Pamvotis`	10	18	28
`Triangle`	3	15	18
`XStream`	4	46	50
Total	29	96	125

automated framework depends greatly on its efficiency. To provide insights regarding the performance of MEDIC, Table 5.4 depicts the run-time of the corresponding analysis. More precisely, it presents the run-time of the WALA framework when applied to the examined test subjects and the respective one of the MEDIC system. Note that all figures are in seconds.

It can be seen that MEDIC required approximately 96 seconds to complete the equivalent mutant detection, utilising the program analysis data that had been collected in 29 seconds. Recall that the program analysis was performed only for the classes of the considered test subjects that contained the manually identified equivalent mutants.

By examining the table, it becomes apparent that most of the studied classes were analysed in under 30 seconds, with `XStream`'s one being the exception. The increased run-time for the corresponding class is attributed to its internal complexity and the large number of the available combinations of uses and definitions of variables that MEDIC had to evaluate, which exceeded 150,000!

To summarise, MEDIC managed to automatically detect **93** equivalent mutants in just **125** seconds. Assuming an equivalent mutant requires approximately 15 minutes of manual analysis [79], the analysis of the examined equivalent ones would necessitate $165 \times 15 = 41$ man-hours! The utilisation of MEDIC decreases this cost from 41 to 18 man-hours, a **56%** reduction in the manual effort involved, thus boosting the practical adoption of mutation.

Table 5.5: Automatically Identified Equivalent Mutants per Data Flow Pattern and JavaScript Test Subject. The middle part of the table presents the corresponding findings grouped by the relevant categories of the considered patterns.

Program	**Categories of Patterns**							**Total**
	UD			*DD*	*UR*			
	SL	SB	DB	-	SL	SB	DB	
`nthRoot`	4	-	-	-	-	4	4	12
`BisectJS`	-	-	8	-	4	-	-	12
`StorageManager`	-	-	-	-	-	2	2	4
`DateJS`	-	-	-	-	-	-	2	2
Total	4	-	8	-	4	6	8	30

Table 5.6: Automatically Identified Partially Equivalent Mutants per Data Flow Pattern and JavaScript Test Subject. The middle part of the table presents the corresponding findings grouped by the relevant categories of the considered patterns.

Program	**Data Flow Patterns**			**Total**
	DifferentBB-UD	*DD*	*DifferentBB-UR*	
`nthRoot`	-	-	16	16
`BisectJS`	4	-	8	12
`StorageManager`	-	-	2	2
`DateJS`	-	-	-	0
Total	4	-	26	30

5.4.2 RQ 5.2: Equivalent Mutant Detection in Different Programming Languages

The results of this subsection are relevant to the cross-language nature of the MEDIC framework, i.e. its capability to detect equivalent and partially equivalent mutants in programs implemented in different programming languages. The corresponding findings are depicted in Table 5.5 and Table 5.6. The former one presents the automatically identified equivalent mutants and the latter, the partially equivalent ones per studied data flow pattern and JavaScript test subject. Note that the SameBB-DR and DifferentBB-DR patterns are not included in the tables because they did not detect any such mutant.

From Table 5.5, which is structured in a similar fashion to Table 5.3, it can be seen that 30 equivalent mutants were automatically identified, supporting the

Table 5.7: Partially Equivalent Mutants' Killability. Proportion of equivalent and stubborn mutants w.r.t. the partially equivalent ones (column *Part. Equivalent Mutants*) and proportion of the stubborn partially equivalent mutants w.r.t. the total stubborn ones (column *Stubborn Mutants*).

Program	**Part. Equivalent Mutants**		**Stubborn Mutants**
	% Equivalent	*% Stubborn*	*% Part. Equivalent*
`Bisect`	5	4	11
`Commons`	43	0	0
`Joda-Time`	0	65	17
`Pamvotis`	0	19	3
`Triangle`	27	17	20
`XStream`	0	4	5
Grand Total	16	14	6

statement that MEDIC can detected equivalent mutants in different programming languages. The findings of Table 5.6 lead to the same conclusion but in this case for partially equivalent mutant detection.

The results of this subsection regarding the JavaScript test subjects and the findings of the previous one regarding the examined Java programs provide clear evidence to support the cross-language nature of the MEDIC framework. MEDIC is the first tool that has been empirically evaluated to achieve such a task.

5.4.3 RQ 5.3: Partially Equivalent Mutants' Killability

The final research question investigates the killability of the partially equivalent mutants. Table 5.7 presents the corresponding findings. The table is divided into two groups of columns: the first group presents the partially equivalent mutant set's proportion of equivalent and stubborn mutants; and the second one, the proportion of the stubborn mutants that are partially equivalent ones.

It can be seen that 16% of the partially equivalent mutant set is composed of equivalent mutants and 14% of stubborn ones, on average. Furthermore, these stubborn mutants account for 6% of the total stubborn ones.

Figure 5.12 presents a Venn diagram illustrating the detected partially equivalent mutant set (denoted as *PE*) and the corresponding killable (*K*), equivalent (*E*) and stubborn (*S*) ones, in order to better visualise the relation between each of

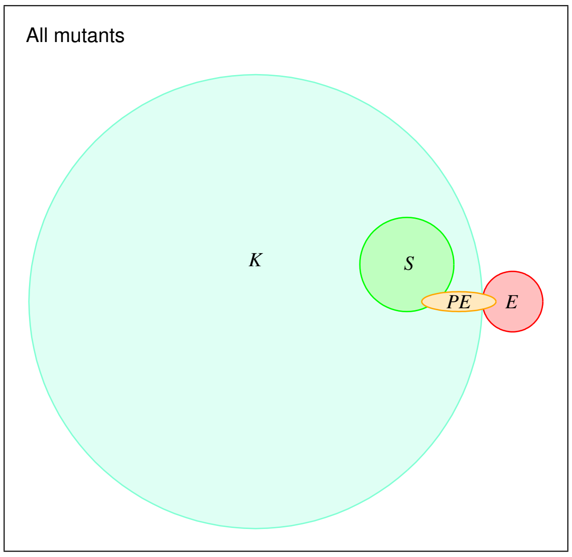


Figure 5.12: Relation between *PE* and *K*, *E* and *S* Mutant Sets. The relation between the Partially Equivalent (*PE*) mutant set and the corresponding Killable (*K*), Equivalent (*E*) and Stubborn (*S*) ones. (The size of the shapes is analogous to the cardinality of the illustrated sets.)

them. From the depicted data, it becomes clear that the partially equivalent mutant set contains equivalent and stubborn mutants, but consists largely of non-stubborn ones, i.e. easy-to-kill ones.

Considering the above findings, one might decide to discard this set altogether. Such a decision would result in a 12% additional reduction in the number of equivalent mutants that have to be manually analysed and a 9% reduction in the number of killable ones, for the studied test subjects. Although, such an act is not without its perils, i.e. the removal of valuable mutants, the fact that only a small portion of the killable mutants needs to be targeted in order to kill the whole generated set seems to mitigate the underlying risk (see also Section 2.3.2.3).

To recapitulate this section's findings, MEDIC managed to automatically detect equivalent and partially equivalent mutants in the Java test subjects. MEDIC identified **56%** of the corresponding equivalent mutants in just **125** seconds. A reduction that can be further increased by **12%** if the discovered partially equivalent mutant set is discarded. These results indicate that MEDIC is a very cost-effective tool, managing to detect a considerable number of equivalent mutants in a negligible amount of time. Additionally, MEDIC identified equivalent and partially equivalent mutants in the JavaScript test subjects. These findings support the cross-language nature of the tool and suggest that the aforementioned benefits are not bound to a specific programming language.

5.4.4 Threats to Validity

All empirical studies inevitably face specific limitations on the interpretation of their results, this one is no exception. The present subsection discusses the corresponding threats and presents the actions taken to ameliorate their effects. First, threats to the construct validity are described and subsequently, the ones to the external and internal validity are discussed.

- **Threats to Construct Validity.** This particular category is concerned with the appropriateness of the measures utilised in the conducted experiments. One threat that belongs to this category is relevant to the investigation of the difficulty in killing the partially equivalent mutants. For the purposes of this investigation, the proportion of the stubborn partially equivalent mutants was utilised. Owing to the fact that a stubborn mutant is harder to kill than a non-stubborn one, this metric is considered adequate for gaining insights regarding the nature of the partially equivalent mutants.

- **Threats to External Validity.** This category of threats refers to the generalisability of the obtained results. No empirical study can claim that its results are generalisable in their entirety. Indeed, different studied programs or programming languages could yield different results for any empirical study. To mitigate these threats, the conducted empirical study was based on test subjects of various size and application domain and a considerable number of manually identified mutants. It should be mentioned that many of the studied programs have also been utilised in previous research studies, e.g. [79, 145].

- **Threats to Internal Validity.** The threats to internal validity pertain to the correctness of the conclusions of an empirical study. One such threat is relevant to the manual analysis of the examined mutants and more precisely to the detection of equivalent ones. To control this threat, a mutant was evaluated thoroughly in order to be identified as equivalent. It should be mentioned that this threat is a direct consequence of the undecidability of the equivalent mutant problem and affects all the relevant mutation testing studies. Analogous considerations arise from the detection of stubborn mutants and, by extension, the detection of stubborn partially equivalent ones. To mitigate the effects of this threat, the corresponding process was based on five, non-overlapping branch adequate test suites. A final threat to the internal validity of the presented work is the correctness of the implementation of the WALA and MEDIC frameworks. In order to cater for this threat, the results of both tools were manually inspected to ascertain their correctness.

5.5 Summary

This chapter introduced an automated, static analysis framework for equivalent and partially equivalent mutant identification, named Mutants' Equivalence Discovery (MEDIC). MEDIC's analysis is based on the problematic data flow patterns proposed in the previous chapter whose presence in the source code of the program under test leads to the generation of equivalent and partially equivalent mutants.

In order to investigate MEDIC's effectiveness and efficiency, an empirical study was conducted based on a manually analysed set of mutants from real-world programs written in the Java programming language. In particular, this set consisted of 1,122 killable mutants and 165 equivalent ones. The obtained results indicate that MEDIC detected 56% of the considered equivalent mutants in just 125 seconds, a run-time cost that is far from comparable to the corresponding manual effort which approximates 23 man-hours (93 mutants $\times$ 15 minutes).

Apart from evaluating the detection power and performance of MEDIC, this chapter was also concerned with the cross-language capabilities of the tool, i.e. it was examined whether or not it could detect equivalent and partially equivalent mutants in programs written in different programming languages. For this reason, MEDIC was additionally applied to test subjects written in JavaScript. The respective findings suggest that MEDIC can indeed detect such mutants in the studied

JavaScript programs, indicating that the tool's benefits are not confined to a specific programming language.

The final research question that this chapter addresses pertains to the killability of the partially equivalent mutants, i.e. whether or not they tend to be killable, and the difficulty in performing such a task. To answer this question, (a) the proportion of the partially equivalent mutants that are equivalent, (b) the proportion of the partially equivalent mutants that are stubborn and (c) the proportion of the stubborn mutants that are partially equivalent were calculated.

The obtained data indicate that 16% of the partially equivalent mutant set is composed of equivalent mutants and 14% of stubborn ones, which account for 6% of the total stubborn mutants. Thus, this set consists largely of non-stubborn mutants, while containing equivalent ones. Based on these findings, one might decide to discard the partially equivalent mutant set completely, realising a total reduction of 68% in the number of the equivalent mutants that have to be manually analysed. This translates into an additional 5 man-hour reduction in the involved manual effort, salvaging a total of 28 man-hours that would have been wasted otherwise. Apart from the cross-language nature, the automated stubborn mutant detection constitutes another unique feature of MEDIC.

Most of the previously introduced techniques for detecting equivalent mutants require the generation, compilation and analysis of the corresponding mutants of the program under test. In contrast, MEDIC is only applied to the original program. Thus, it can be argued that MEDIC has a clear advantage over these techniques, as far as efficiency is concerned.

The next chapter presents another approach to deal with the equivalent mutant problem in the presence of software clones. To this end, the chapter introduces the concept of *mirrored mutants* denoting mutants that belong to similar code fragments of the examined program. It is postulated that such mutants exhibit similar behaviour with respect to their equivalence and, thus, knowledge about the equivalence of one of them could be utilised to classify others as possibly equivalent or possibly killable ones. The conducted empirical investigation supports this intuition and suggests that considerable effort savings can be achieved.

Chapter 6

Eliminating Equivalent Mutants via Code Similarity

As mentioned in Chapter 2, mutation testing is a very powerful technique for testing software, but is considered prohibitively expensive for practical adoption. This cost is primarily attributed to the computational resources required for the execution of the generated mutants and the human effort involved in finding appropriate test cases to kill these mutants or determine their equivalence.

This chapter argues that knowledge about the already identified killable and equivalent mutants can reduce mutation's cost in the presence of software clones. More precisely, given two similar code fragments, this work investigates whether the killability or equivalence of the mutants of the one code fragment can determine the killability or equivalence of the mutants of the other.

To this end, the concept of *mirrored mutants* is introduced, that is mutants that belong to similar code fragments and, more precisely, to analogous code locations within these fragments. The intuition behind this idea is that mirrored mutants exhibit analogous behaviour with respect to their equivalence. If this argument is true, then knowledge about the equivalence of one of them could be used to determine the equivalence of the others. Thus, effort savings can be achieved by manually analysing only one of the mirrored mutants and automatically inferring the killability or equivalence of the others.

The contributions of the present chapter can be summarised in the following points:

1. The introduction of the concept of *mirrored mutants* for alleviating the effects of the equivalent mutant problem.

2. An empirical study, based on a set of approximately 800 manually analysed mutants[1] from several real-world programs, which provides evidence to support the usefulness of mirrored mutants at both the intra- and inter-method level.

3. Experimental results pertaining to the utilisation of mirrored mutants for test case generation purposes.

The rest of the chapter is organised as follows. Section 6.1 introduces the necessary background information and Section 6.2 elaborates on the concept of mirrored mutants. In Section 6.3, details about the conducted empirical study, the experimental procedure, the obtained results and possible threats to their validity are presented. Finally, Section 6.4 concludes this chapter.

6.1 Background: Code Similarity

This section describes the necessary concepts with respect to code similarity, along with examples from the conducted study.

Similar code fragments, which are termed *code clones* or *software clones*, exist in software systems [169–171]. Their existence is attributed to the reuse of already developed code, by means of copy and paste, with or without minor modifications. The detection of these fragments is achieved by the employment of appropriate code detection techniques [170, 171].

In clone detection terminology, a code fragment is any sequence of code lines, with or without comments. A code clone of a code fragment $cf1$ is another code fragment, $cf2$, which is similar to $cf1$ by a given definition of similarity, i.e. given a similarity function g, $g(cf1) = g(cf2)$ [170]. The code fragments $cf1$ and $cf2$ form the *clone pair* $(cf1, cf2)$. Note that code clones can appear at any level of granularity (e.g. class level, method level, etc.).

[1]This set, along with the rest of the data of this chapter, is publicly available at: `http://pages.cs.aueb.gr/~kintism/#apsec2013`

Clone detection techniques are based on two primary definitions of similarity between code fragments, similarity based on program text and similarity based on functionality [170]. In the former case, the syntactic similarity of their source code is examined, whereas, in the latter, their semantic similarity is evaluated.

From the aforementioned definitions, different types of code clones are derived (adapted from [170]):

- **Type-1.** *Identical code fragments, except for variations in whitespace, layout and comments.*
- **Type-2.** *Syntactically identical fragments, except for variations in identifiers, literals, types, whitespace, layout and comments.*
- **Type-3.** *Copied fragments with further modifications such as changed, added or removed statements, in addition to variations in identifiers, literals, types, whitespace, layout and comments.*
- **Type-4.** *Two or more code fragments that perform the same computation, but are implemented by different syntactic variants.*

This chapter considers syntactic clones only, i.e. Type-1 to Type-3, and characterises them as intra-method or inter-method according to whether or not they belong to the same method. Type-4 code clones, although interesting, are left for future research.

To denote a clone pair belonging to one file, the following notation is used:

$$([\mathbf{sl}_1 : sc_1 - \mathbf{el}_1 : ec_1], [\mathbf{sl}_2 : sc_2 - \mathbf{el}_2 : ec_2])$$

where sl_1 and sc_1 are the starting line and column of the first code fragment and el_1 and ec_1 the corresponding ending ones. Accordingly, sl_2, sc_2, el_2 and ec_2 refer to the starting and ending lines and columns of the second code fragment. Note that in the case of clone pairs that belong to different files, an identifier of the corresponding files must be added to this notation.

Figure 6.1 presents the source code of the well-studied `Triangle` program. The `classify` method takes as input the length of the three sides of a triangle and classifies it as scalene, isosceles, equilateral or invalid. The source code of this program contains several similar code fragments, such as $([\mathbf{6}:0-\mathbf{7}:22],[\mathbf{8}:0-\mathbf{9}:22])$ and $([\mathbf{19}:0-\mathbf{20}:21],[\mathbf{21}:5-\mathbf{22}:21])$.

In particular, it contains six clone pairs[2], as determined by the CCFINDERX clone detection tool [172] (Section 6.3.2.1 describes the tool in greater detail). These clone pairs involve the `if-blocks` starting at lines 6, 8, 10 and at lines 19, 21, 23, respectively.

It becomes apparent that even for this small program, similar code fragments do exist. Thus, if the equivalence of the mutants of one of these fragments can provide information about the equivalence of the mutants of the others, then the manual effort involved in identifying equivalent mutants can be considerably reduced.

6.2 Mirrored Mutants

The primary focus of this chapter is to ameliorate the unfavorable effects of the equivalent mutant problem. The proposed approach leverages software clones and examines if mutants belonging to these code fragments exhibit analogous behaviour with respect to their equivalence. First, this section introduces the concept of mirrored mutants and, then, it details the hypothesis of the present work.

6.2.1 Mirrored Mutants: Definition

Given two code fragments, $cf1$ and $cf2$, their generated mutant sets, $Muts_1$ and $Muts_2$, and two of their mutants $m_1 \in Muts_1$ and $m_2 \in Muts_2$, m_1 mirrors m_2 when the following conditions are satisfied:

- **Condition 1.** The code fragments must form a clone pair, i.e. given a similarity function g:

$$g(cf1) = g(cf2)$$

- **Condition 2.** The examined mutants must affect analogous code locations in

[2]For the purposes of this study, the clone pairs $(cf1, cf2)$ and $(cf2, cf1)$ are considered identical.

```
classify (int a, int b, int c) {
    int trian;
    if (a <= 0 || b <= 0 || c <= 0)
        return INVALID;
    $trian = 0$;
    if (a == b)
        $trian = trian + 1$;
    if (a == c)
        $trian = trian + 2$;
    if (b == c)
        $trian = trian + 3$;
    if (trian == 0)
        if (a + b < c || a + c < b || b + c < a)
            return INVALID;
        else
            return SCALENE;
    if (trian > 3)
        return EQUILATERAL;
    if (trian == 1 && a + b > c)
        return ISOSCELES;
    else if (trian == 2 && a + c > b)
        return ISOSCELES;
    else if (trian == 3 && b + c > a)
        return ISOSCELES;
    return INVALID;
}
```

Figure 6.1: Source Code of the `Triangle` test subject.

these fragments, i.e. given $l_1 \in cf1$ and $l_2 \in cf2$ the lines that are affected by m_1 and m_2, respectively, and *linemap*, a mapping[3] between the lines of $cf1$ and $cf2$:

$$linemap(l_1) = l_2$$

- **Condition 3.** The mutants must induce analogous syntactic changes, i.e. given op_1 and op_2 the mutation operators of m_1 and m_2, and a similarity function f:

$$op_1 = op_2 \wedge f(l_1) = f(l_2)$$

Mutants m_1 and m_2 are termed mirrored mutants. According to whether or not

[3]Techniques to automatically generate such a mapping exist in the literature, cf. [173].

Mirrored Mutants	**Mutated Statement**
`AOIS_25`	7: $trian = trian\boxed{++}+1;$
`AOIS_37`	9: $trian = trian\boxed{++}+2;$
`AOIS_105`	19: $\textbf{if}\ (trian == 1\ \texttt{\&\&}\ a+b\boxed{++} > c)$
`AOIS_121`	21: $\textbf{if}\ (trian == 2\ \texttt{\&\&}\ a+c\boxed{++} > b)$
`AORB_4`	7: $trian = trian\boxed{-}1;$
`AORB_12`	11: $trian = trian\boxed{-}3;$

Figure 6.2: Examples of Mirrored Mutants from the `Triangle` test subject.

$cf1$ and $cf2$ belong to the same method, mirrored mutants can be characterised as intra-method or inter-method ones.

Figure 6.2 presents three instances of mirrored mutants from the `Triangle` test subject (presented in Figure 6.1). For each mutant, its name, the number of the affected line, the induced change and the resulting statement are depicted. For instance, the first pair, `AOIS_25` and `AOIS_37`, which belongs to the $([\mathbf{6}:0-\mathbf{7}:22],[\mathbf{8}:0-\mathbf{9}:22])$ clone pair[4], is generated by inserting the post-increment arithmetic operator (e.g. `var++`) at lines 7 and 9 of Figure 6.1, respectively.

Note that the mutation operator of the first pair of mirrored mutants, Arithmetic Operator Insertion Short-cut (AOIS), generates three additional mutants per considered line at these specific code locations (`++trian`, `--trian` and `trian--`), resulting in a total of four mutants per line. Although all these mutants affect the same lines employing the same mutation operator, they form different mirrored mutant sets.

By examining Figure 6.2 closely, it can be seen that the presented mutants affect analogous code locations belonging to similar code lines of similar code fragments, thus, they constitute mirrored mutants. It is argued that mirrored mutants exhibit analogous behaviour with respect to their equivalence; the next subsection discusses this hypothesis and presents a motivating example.

[4]The other mutants belong to: $([\mathbf{19}:0-\mathbf{20}:21],[\mathbf{21}:5-\mathbf{22}:21])$ and $([\mathbf{6}:0-\mathbf{7}:22],[\mathbf{10}:0-\mathbf{11}:22])$ clone pairs, respectively.

6.2.2 Mirrored Mutants and Equivalent Mutant Discovery

This work is based on the intuition that if a mutant *mirrors* other mutants and has been identified as equivalent (or killable), then its *mirrored* ones could also be equivalent (or killable). More formally, given two mirrored mutants, m_1 and m_2:

$$m_1 \in equivs \Rightarrow m_2 \in equivs$$

where *equivs* is the set of equivalent mutants of the original program. Note that although this statement does not constitute a mathematical theorem, its empirical investigation suggests that it manages to provide substantial guidance in detecting more equivalent mutants from the already identified ones (cf. Section 6.3.3).

Consider again Figure 6.2, the first two mirrored mutant pairs consist solely of equivalent mutants (determined by manual analysis). In the first case, the value of variable *trian* is used unmodified, then it is incremented by one (due to the post-increment operator) and finally, it is redefined by the evaluation of the whole statement. Thus, the induced change can never be detected. Although, the equivalent mutants of the first pair can be considered trivial, i.e. they are relatively easy to identify, the ones of the second pair require a more thorough examination and a better understanding of the internal mechanics of the program.

In both cases, the effort involved in manually analysing the examined mutants could be considerably reduced by leveraging the previously described property; instead of manually analysing four mutants, the analysis could be restricted to two mutants that *mirror* the others, e.g. `AOIS_25` and `AOIS_105`, and thus the equivalence of the *mirrored* ones, i.e. `AOIS_37` and `AOIS_121`, could be automatically determined.

This statement also holds true in the case of automated equivalent mutant identification. For example, since `AOIS_25` can be automatically detected as equivalent by the SameLine-UD data flow pattern, described in Section 4.2.2.1, in the presence of mirrored mutants, the automated detection of one of these mutants suffices.

The last mirrored mutant pair of Figure 6.2 demonstrates the opposite situation. It can be easily seen that `AORB_4` and `AORB_12` can be killed, thus, knowledge about the non-equivalence of the one of them could be used to determine the non-equivalence of the other. In this study, experimental results suggesting that mirrored mutants can be beneficial to test case generation processes are also provided.

More precisely, it is postulated that a test case that kills a mutant can be transformed into an appropriate one that kills its *mirrored* ones. For instance, the test case $(a = 2,\ b = 2,\ c = 1)$ that kills `AORB_4` can be appropriately transformed to kill `AORB_12` based on information derived from the corresponding clone pair. By examining the $([\mathbf{6}:0-\mathbf{7}:22],[\mathbf{10}:0-\mathbf{11}:22])$ clone pair, it becomes evident that variable a is replaced with b and b with c, thus, a similar transformation at the test case level could produce a test case able to kill `AORB_12`. Indeed, the resulting test case $(a = 1,\ b = 2,\ c = 2)$ manages to kill the corresponding mutant. Although finding such an automatic transformation technique is out of the scope of this work, it is presented as another interesting aspect of mirrored mutants and a possible direction for future research.

To summarise, mirrored mutants contribute to the elimination of equivalent mutants and potentially to test case generation processes that target these particular mutants. The next section furnishes a detailed view of the experimental study, along with the research questions that are being investigated.

6.3 Empirical Study and Results

The present study examines whether mirrored mutants can be of assistance in discovering more equivalent mutants from the already identified ones. To this end, an experimental study based on a set of manually analysed mirrored mutants was conducted. This section describes the underlying experimental procedure, the obtained results and the actions taken to mitigate possible threats to validity.

6.3.1 Research Questions

The research questions that are investigated by this study are the following:

- **RQ 6.1** *Do mirrored mutants exhibit analogous behaviour with respect to their equivalence?*

- **RQ 6.2** *In the case of killable mutants, can mirrored mutants contribute to the test case generation process?*

Although the above research objectives are sound, an additional point should be investigated: *Do mirrored mutants appear in adequate numbers in real-world programs?*

This is an important question because if mirrored mutants appear scarcely in software systems, then their underlying benefits would be negligible. In a different case, significant effort savings could be achieved. By definition, mirrored mutants are closely related to the number of similar code fragments in the program under test. Thus, the above question can be restated as: *To what extent do real world programs contain duplicated code?*, or equally, *Does a considerable number of clone pairs exist in software systems?*

Fortunately, this question has already been answered in the literature of clone detection. In particular, studies suggest that the percentage of cloned code of a typical software system lies between 7% and 23% [169, 174]. Considering that applying mutation testing to a program of 30 lines could produce over 300 mutants, then its application to even the 7% of the lines of a large software system would produce a considerable number of mirrored mutants.

6.3.2 Experimental Study

6.3.2.1 Supporting Tools

For the purposes of this study, the CCFINDERX clone detection tool [172, 175] (version 10.2.7.4) and the MUJAVA mutation testing framework [19, 163] (version 3) were utilised. A brief description of these tools follows:

- **Clone Detection.** CCFINDERX is a state-of-the-art token-based clone detection tool and constitutes a major upgrade of CCFINDER [175]. The tool supports various programming languages, e.g. Java, C, COBOL, etc., and has been applied to large software systems [175]. Several experimental studies have evaluated its ability to detect software clones, e.g. [170], and concluded that it manages to successfully detect all types of syntactic clones. In this study, CCFINDERX was employed to detect similar code fragments in the considered test subjects with the `minimumclonelength` and `minimumTKS` options set to 10.

- **Mutant Generation.** The MUJAVA testing framework is a tool for applying mutation testing to programs implemented in the Java programming language. It supports method-level and class-level mutation operators. The method-level operators target the unit level and were designed based on the selective mutation approach [81] (see also Table 4.1), whereas the class-level operators target specific object-oriented features. The MUJAVA tool is a rather mature framework that has been utilised by many research studies, e.g. [87, 176]. In this study, the considered mutants were generated by applying all method-level mutation operators of the tool.

6.3.2.2 Test Subjects

This empirical study was conducted on a set of six test subjects (written in Java), most of which have been utilised in previous research studies, e.g. [78]. Table 6.1 presents details about the corresponding programs.

The first four columns of the table outline the id of the test subjects that uniquely identifies them and will be used in subsequent tables, e.g. Table 6.3, their name, a brief description of their usage and the corresponding source code lines[5]. The last column presents the number of the corresponding clone sets, as determined by CCFINDERX. Note that a clone set contains one or more clone pairs.

It should be mentioned that some minor modifications to `Pamvotis` were performed in order to enable the application of the MUJAVA framework. This was necessary due to specific limitations of the tool, e.g. it cannot handle programs utilising the generics feature of Java. These modifications did not affect the semantics of the program.

[5]Generated by SLOCCOUNT (`http://www.dwheeler.com/sloccount/`).

Table 6.1: Test Subjects' Details.

Id	**Program**	**Description**	**LOC**	**Clone Sets**
1	`Bisect`	Square root calculation	36	1
2	`Commons`	Various utilities	19,583	1,126
3	`Joda-Time`	Date and time utilities	25,909	1,678
4	`Pamvotis`	WLAN simulator	5,149	468
5	`Triangle`	Triangle classification	32	3
6	`Xstream`	XML object serialisation	16,791	710
-	Total	-	**67,500**	**3,986**

6.3.2.3 Experimental Design

The experimental procedure of this study necessitated two steps; the discovery of a random sample of mirrored mutants and its corresponding manual analysis. These steps allowed the investigation of whether or not mirrored mutants share common characteristics with respect to their equivalence.

The process of finding a random sample of mirrored mutants is illustrated in Figure 6.3. For each test subject, the CCFINDERX tool was employed to detect all possible similar code fragments. Next, a clone pair was chosen at random and its mutants were generated by MUJAVA. If their number was greater than 40, the corresponding mirrored mutants were discovered by mapping the mutants of the one code fragment onto the ones of the other. Recall that a clone pair comprises two similar code fragments. This restriction on the number of mutants was imposed in order to prohibit the selection of clone pairs that produced very few mutants. The aforementioned process was repeated, until a suitable match was found.

Table 6.2 presents information on the obtained mirrored mutant pairs. Column "Rand. CPs" refers to the number of the randomly selected clone pairs per test subject, column "MMPs" to the number of the respective mirrored mutant pairs, column "Mutants" to the number of mutants that were manually analysed and column "Test Cases" to the number of test cases that were generated during the manual analysis process. It should be mentioned that these test cases do not form a minimum test set that is able to kill the corresponding mutants.

As can be seen from the table, the previously described procedure yielded 409

```
foreach test subject ts
    foreach clone pair of ts
        select a random clone pair cp
        generate the mutants of cp
        if (mutants > 40)
            create the mirrored mutants of cp
            return the mirrored mutants
        end if
    end for
end for
```

Figure 6.3: Generating a Random Sample of Mirrored Mutants.

Table 6.2: Randomly Selected Mirrored Mutants' Details.

Id	Program	Rand. CPs	MMPs	Mutants	Test Cases
1	`Bisect`	1	22	44	4
2	`Commons`	1	69	138	16
3	`Joda-Time`	1	23	46	6
4	`Pamvotis`	2	76	152	18
5	`Triangle`	4	142	213	30
6	`Xstream`	3	77	154	22
-	Total	12	409	747	96

mirrored mutant pairs, with a total of 747 mutants. Note that the number of mutants is not 818 because several mutants of the `Triangle` test subject belong to more than one mirrored mutant pairs.

It should be mentioned that the mapping between the mutants of the code fragments of a clone pair is necessary in order to find mutants that affect analogous code locations (cf. Section 6.2.1). This mapping was straightforward in the conducted experiments: the clone pairs contained sequential lines of code and for each line, the mutants had been generated in the same order. One exception was the `QuickWriter` class of the `Xstream` test subject, where two mutants of the considered clone pair could not be mapped onto any other. Upon inspection, the corresponding mutation operator could not be applied to the other code fragment at the specific code location.

After finding the mirrored mutant pairs, the manual analysis of these mutants was performed, i.e. the mutants were manually inspected in order to find a test case

Table 6.3: Manual Analysis of Mirrored Mutants.

Gran.	**Class(es)**	**Killable**	**Equiv.**
Method	`1:Bisect`	40	4
	`5:Triangle`	183	30
	`6:XmlFriendlyNameCoder`	72	8
Class	`2:WordUtils`	110	28
	`6:QuickWriter`	74	0
I-Class	`3:Minutes,Seconds`	42	4
	`4:Simulator,SourceManager`	142	10
Total	-	663	84

able to kill them. If such a test case could be found, the mutant was identified as killable. In the opposite situation, it was classified as equivalent.

The results are presented in Table 6.3. The corresponding mirrored mutants are divided into three categories according to the granularity level of their respective clone pairs: the ”Method” and ”Class” categories, which refer to the intra-method and intra-class levels and the ”I-Class” category, which denotes the inter-class level. In the first category, mirrored mutants belong to the same method, in the second, to different methods of the same class, and in the last one, to different methods of different classes.

The first column of the table presents the aforementioned categories, the subsequent ones, the id of the corresponding test subject, along with the name of the considered class (or classes in the case of I-Class) and the number of killable and equivalent mirrored mutants. In summary, 747 mirrored mutants were manually analysed, 663 of which were determined killable and 84 equivalent.

In order to answer RQ 6.1, i.e. whether mirrored mutants can be of benefit when dealing with the equivalent mutant problem, the following procedure was undertaken: For each mirrored mutant pair (m_1, m_2), m_2 was classified as equivalent (or killable) based on the result of the manual analysis for m_1. Note that the results of the manual analysis were used only for one of the mutants of the considered mirrored mutant pair. The remaining one was classified accordingly, heuristically (cf. Section 6.2.2).

Afterwards, these classification results were evaluated against those of the manual analysis and the ratio of the correctly classified equivalent (or killable) mirrored mutant pairs to the total number of classified mirrored mutant pairs of the specific category was calculated. This metric is widely used in the area of Information Retrieval [156] and is termed *precision*. The formal definition of this metric is given in Equation 3.1.

Precision has been utilised in several, previous studies, evaluating different mutant classification techniques, e.g. [78, 79]. A high precision score indicates that the classification outcome of a mutant will most likely be the same as the one of the respective manual analysis. A low one indicates the opposite situation.

It should be mentioned that in the cases of `Bisect`, `Triangle` and `XmlFriendlyNameCoder`, some mutants could be differently classified based on the order the corresponding mutants of the respective mirrored mutant pairs were examined, i.e. some mirrored mutant pairs contained both killable and equivalent mutants and, thus, the classification process would lead to different results according to which mutant's manually analysed results will be used. In these cases, the classification process was employed to both mutants of the corresponding pairs and the average precision was calculated.

The precision metric is usually complemented by the *recall* value, which measures the retrieval capability of a classifier [156]. In this study, the recall metric was not utilised based on two reasons. First, the examined approach is not a classifier; the examined property of mirrored mutants necessitates previous knowledge of the equivalence of the underlying mirrored mutants. Second, in this particular case, the precision and the recall values are closely intertwined in such a way that a high precision corresponds to a high recall score. To elaborate, in the case of equivalent mutants for instance, if mirrored mutants exhibit the sought behaviour in their equivalence, then the mutants classified as equivalent will be equivalent, leading to a high precision score, but, at the same time, most equivalent mutants will also be retrieved, leading to a high recall score (see also Equation 3.2 for the formal definition of this metric).

In order to investigate RQ 6.2, i.e. whether mirrored mutants can contribute to test case generation processes that target them, the subsequent steps were followed: for each mirrored mutant pair (m_1, m_2) in which m_1 was determined killable by manual analysis, the transformation of the corresponding test case that killed m_1 based on information derived from the respective clone pair was attempted (an example demonstrating such a transformation was given in Section 6.2.2). If a transformation was found, then the ability of the resulting test case to kill m_2 was examined. Thus, the employed metric is the ratio of the number of mirrored mutant pairs for which such a transformation was possible to the number of all killable mirrored mutant pairs.

6.3.3 Experimental Results

The obtained experimental results are depicted in Table 6.4 and Table 6.5. The former details the obtained results pertaining to RQ 6.1 and RQ 6.2 and the latter, an estimation of the cost reduction achieved by the presence of mirrored mutants.

Table 6.4 is divided into two parts. The first part (column "Precision") presents the precision metric with respect to both killable and equivalent mirrored mutants. Note that, for `QuickWriter`, the precision metric was not calculated in the case of equivalent mirrored mutants because all of its mutants were killable.

It can be seen that mirrored mutants can be leveraged to discover equivalent and killable mutants based on the already identified ones. Specifically, in the case of killable mirrored mutants at the intra-method level, an average precision of 98% is realised, whereas at the intra- and inter-class levels a precision of 100% is achieved, indicating that the results of the classification process are tantamount to the ones of the manual analysis.

In the case of equivalent mirrored mutants, the corresponding results are 88%, 100% and 100%, respectively, suggesting a reasonable equivalent mutant classification process. At this point, it should be mentioned that none of the examined clone pairs was of *Type-1*, i.e. the corresponding code fragments were not identical (cf. Section 6.1). Thus, the results cannot be attributed to the examination of identical source code.

Table 6.4: Mirrored Mutants: Experimental Results.

Class(es)	Precision		Test Data
	Killable	*Equivalents*	**Transformation**
`1:Bisect`	100%	100%	60%
`5:Triangle`	97%	84%	89%
`6:XmlFriendlyNameCoder`	97%	80%	89%
Average (Method)	98%	88%	79%
`2:WordUtils`	100%	100%	100%
`6:QuickWriter`	100%	-	100%
Average (Class)	100%	100%	100%
`3:Minutes,Seconds`	100%	100%	100%
`4:Simulator,SourceManager`	100%	100%	100%
Average (I-Class)	100%	100%	100%

The second part of Table 6.4 (column "Test Data Transformation") presents results regarding RQ 6.2, i.e. whether or not a test case that kills a mutant of a mirrored mutant pair can be transformed to kill the other mutant(s) of the corresponding pair, based on information derived from the respective clone pair.

The obtained data suggest that this transformation is feasible and the resulting test cases are indeed able to kill the respective mutants. At the intra-method level, 79% of the total number of killable mirrored mutant pairs could produce such a test case, on average. For the remaining categories, this transformation was always possible (i.e. 100% in all cases).

To better understand the cost reduction achieved by leveraging mirrored mutants, Table 6.5 presents the ratio of equivalent mutants that are automatically classified as such to the total number of equivalent mutants. More precisely, the table depicts the number of equivalent mutants per considered class, the number of the manually analysed ones, the number of the automatically determined ones and the corresponding cost reduction measure.

It can be seen that approximately 50% of the total equivalent mutants of the considered test subjects can be automatically classified as such. Note that the number of the automatically determined equivalent mutants of the `Triangle` test subject is greater than the one of the manually analysed equivalent mutants due to the

Table 6.5: Mirrored Mutants: Cost Reduction w.r.t. Manual Analysis of Equivalent Mutants.

Class(es)	**CR Analysis**			**Cost Reduction**
	Equiv.	*Man.*	*Auto.*	
`1:Bisect`	4	2	2	50%
`5:Triangle`	30	10	17	56%
`6:XmlFriendlyNameCoder`	8	4	3	38%
Average (Method)	-	-	-	48%
`2:WordUtils`	28	14	14	50%
`6:QuickWriter`	-	-	-	-
Average (Class)	-	-	-	50%
`3:Minutes,Seconds`	4	2	2	50%
`4:Simulator,SourceManager`	10	5	5	50%
Average (I-Class)	-	-	-	50%

fact that several equivalent mutants belong to more than one mirrored mutant pairs.

Conclusively, from the presented results, it can be argued that mirrored mutants can be beneficial to the equivalent mutant identification process by reducing the number of equivalent mutants that have to be manually analysed. In addition, they can be potentially valuable to test case generation processes by providing a way to transform the already available killing test cases into appropriate ones that can kill other mirrored mutants.

6.3.4 Threats to Validity

Every research study has limitations concerning the interpretation of its results and is exposed to possible threats related to its validity. This subsection discusses the underlying threats and presents the actions taken to mitigate their effects.

- **Threats to External Validity.** This category refers to threats that affect the generalisation of the obtained results. To weaken these threats, the conducted experiments were based on approximately 800 manually identified mirrored mutants, belonging to several open source projects of various size and complexity that have been previously used in similar research studies, e.g. [78, 79]. Additionally, results based on small test subjects, e.g. `Triangle` and `Bisect`, were only reported at the intra-method level. At this particular granularity level, the size of the examined program should not be of importance. Although no study can claim that its results are widely generalisable, the examined property of mirrored mutants is believed to be independent of the studied projects and more related to the similar structure of cloned code.

- **Threats to Internal Validity.** Concerning potential threats pertaining to the internal validity, i.e. the ability to draw conclusions based on the studied factors, the manual classification of the mirrored mutants was an area that necessitated appropriate actions. More precisely, the manual identification of the equivalent mutants, due to the difficulty of the underlying problem, is subject to errors. To circumvent this problem, the mutants that were manually categorised as equivalent were examined thoroughly. Furthermore, all the results of this study are publicly available to support wider scrutiny.

6.4 Summary

This chapter presented another approach to ameliorate the adverse effects of the equivalent mutant problem in the presence of software clones. To this end, the concept of mirrored mutants is introduced.

Mirrored mutants are mutants that belong to similar code fragments of the program under test. It is posited that mirrored mutants exhibit analogous behaviour with respect to their equivalence and, thus, in the presence of such mutants, the manual cost of identifying equivalent mutants can be substantially reduced.

The chapter investigated whether or not mirrored mutants exhibit the aforementioned behaviour and whether they can be of assistance to test case generation processes. In order to answer the posed research questions, an empirical study based on approximately 800 manually analysed mirrored mutants belonging to several open source projects and different granularity levels was conducted.

The results of the study provide evidence supporting the aforementioned statement. More precisely, the obtained findings suggest that approximately 50% of studied equivalent mutants that belong to mirrored mutant pairs can be automatically classified as such. Additionally, the study presented experimental results indicating that test cases that kill a mutant of a mirrored mutant pair can be transformed into appropriate test cases that kill the remaining mirrored mutants of the corresponding pair.

It should be mentioned that the equivalent mutant detection techniques introduced in the previous chapters of this thesis, or in the literature of Mutation Testing in general, are orthogonal to the technique presented in this chapter. To elaborate, these approaches can be applied first to detect equivalent mutants that belong to mirrored mutant pairs and, next, the remaining mirrored mutants can be automatically classified as equivalent ones. Thus, the manual cost of identifying equivalent mutants could be further decreased.

Chapter 7

Conclusions and Future Work

Mutation testing is one of the most effective techniques in testing software. Unfortunately, its adoption in practice is hindered by its cost. One of the main sources of mutation's cost is the manual effort involved in the detection of equivalent mutants and, more precisely, the Equivalent Mutant Problem.

The Equivalent Mutant Problem is a well-known impediment to the adoption of mutation testing in practice. Its undecidable nature renders a complete automated solution unattainable. This situation is exacerbated further by the complexity of the underlying manual analysis and the large number of mutants that have to be considered. As a direct consequence, automated frameworks that can tackle this issue are scarce.

This thesis introduces several novel techniques that can automatically eliminate equivalent mutants, thus, reducing mutation's manual cost and improving its practical adoption. The dissertation's contributions can be summarised in the following points:

- **A Novel Mutant Classification Technique (Chapter 3)**

  This thesis proposed a novel mutant classification technique, named Higher Order Mutation (HOM) classifier, that utilises second order mutants to automatically classify first order ones. Additionally, the thesis introduced a new mutant classification scheme, named Isolating Equivalent Mutants (I-EQM) classifier, that combines effectively the state-of-the-art Coverage Impact classifier with the HOM classifier. The conducted experimental study that compared the effectiveness of the aforementioned classifiers, based on real-world test subjects, showed that I-EQM, with a precision score of 71% and a recall value of 81%, outperforms the examined approaches. The obtained results suggest that I-EQM manages to correctly classify approximately 20% more killable mutants with only a 2% loss on its precision, leading to a more thorough testing process. These findings are also supported by the accuracy metric and F_β scores of the classifier and by the conducted statistical analysis of the obtained results. Finally, the relationship between mutants' impact and mutants' killability was also investigated. The obtained findings indicate that mutants with the highest impact do not necessarily guarantee the highest killability ratios.

- **Data Flow Patterns for Equivalent Mutant Detection (Chapter 4)**

  Nine data flow patterns that can detect equivalent and partially equivalent mutants were introduced and formally defined in the present thesis. A partially equivalent mutant is a mutant that is equivalent to the program under test for a specific subset of paths. The main characteristic of their definition is that it is based on the Static Single Assignment (SSA) intermediate representation of the program under test. In essence, these patterns model specific problematic situations between variable definitions and uses whose existence in the program's source code will lead to the generation of equivalent mutants. An empirical study based on approximately 800 manually analysed mutants from real-world test subjects was conducted to examine the patterns' existence in real-world programs and their equivalent mutant detection power. The obtained results revealed that these patterns are indeed present in real-world software and that they can automatically detect approximately 70% of the studied equivalent mutants, thus, paving the way for the efficient application of mutation testing.

- **A Static Analysis Framework for Equivalent Mutant Detection (Chapter 5)**

The thesis introduced MEDIC (Mutants' Equivalence Discovery), a static analysis tool, written in the Jython programming language, that implements the aforementioned patterns and manages to automatically detect equivalent and partially equivalent mutants in different programming languages. To investigate MEDIC's effectiveness and efficiency, an empirical study based on approximately 1,300 manually analysed mutants from several real-world programs, written in the Java programming language, was conducted. The respective results indicate that MEDIC manages to detect 56% of the studied equivalent mutants in 125 seconds, providing strong evidence of the tool's effectiveness and efficiency. Additionally, MEDIC successfully detected such mutants in test subjects written in JavaScript, lending colour to the tool's cross-language nature. MEDIC's ability to detect equivalent mutants in different programming languages is a unique characteristic of the tool. Finally, the killability of the detected partially equivalent mutants was also examined. The respective findings reveal that 14% of these mutants are stubborn ones, suggesting that MEDIC can also detect automatically stubborn mutants.

- **Laveraging Software Clones to Eliminate Equivalent Mutants (Chapter 6)**

  This thesis introduced the concept of mirrored mutants, that is mutants belonging to similar code fragments and, particularly, to analogous code locations within these fragments. It is argued that mirrored mutants exhibit analogous behaviour with respect to their equivalence and that knowledge about the equivalence of one of them can be used to determine the equivalence of the others, thus, reducing the manual overhead of mutation. This assumption was empirically investigated based on 747 manually analysed mutants from real-world programs. The obtained results demonstrate that mirrored mutants can considerably reduce mutation's manual cost in the presence of software clones. Additionally, experimental results suggesting that test cases that kill mirrored mutants can be automatically transformed into appropriate ones that kill other mirrored mutants, with a success rate higher than 80%, were also presented.

Based on the aforementioned contributions, several future research directions can be pursued. Most notably:

Elimination of Higher Order Equivalent Mutants. One possible future research direction is the investigation of appropriate techniques to eliminate higher order equivalent mutants. Although higher order equivalent mutants are not as common as first order equivalent ones, such approaches could be beneficial to higher order mutation approximation strategies (cf. Section 2.3.1.1). Towards this direction, the mutant classification techniques presented in Chapter 3 seem to be a natural choice: since the HOM and I-EQM classifiers manage to isolate first order equivalent mutants based on second order ones, it would be interesting to explore whether this practice could be generalised, i.e. whether it is possible to isolate n order equivalent mutants via $(n+1)$ order mutants.

Mutation Approximation Techniques based on HOM and I-EQM Classifiers. Another potential research direction is the investigation of the effectiveness of mutation approximation techniques that are based on the HOM and I-EQM classifiers. Mutation approximation strategies based on the Coverage Impact classifier have been evaluated in the literature of mutation testing and have been found less effective than mutation (cf. Section 2.3.1.3). It would be interesting to explore whether the utilisation of the HOM and I-EQM classifiers will make a difference.

Complementing MEDIC's Equivalent Mutant Detection Process. MEDIC's empirical evaluation provides strong evidence of the tool's efficiency. Thus, an apparent future direction is the investigation of synergistic ways in which MEDIC can be combined with other equivalent mutant detection approaches. Based on the findings of the conducted experimental study, a prominent direction is the combination of MEDIC with techniques that can target equivalent mutants affecting branch predicates, since such equivalent mutants comprised approximately 20% of the generated ones (cf. Section 5.3.2.1). Due to MEDIC's efficiency, the analysis of the resulting equivalent mutant detection technique will not be hampered by the utilisation of more than one tools.

MEDIC and Different Programming Languages. Another avenue for further research is the application of MEDIC to additional programming languages. MEDIC has already been successfully applied to the Java and JavaScript programming languages. It would also be interesting to examine MEDIC's performance when applied to programs written in other programming languages. Although this will entail the utilisation of different program analysis frameworks, MEDIC relies on a language-agnostic data model that facilitates this task.

Generalising the Concept of Mirrored Mutants. Mirrored mutants have been shown to reduce mutation's cost in the presence of software clones. One particularly interesting research direction is the investigation of whether this concept can reduce the cost of other coverage criteria. For example, in the case of the branch coverage criterion, it would be interesting to investigate whether branches that belong to similar code fragments exhibit analogous behaviour with respect to their infeasibility, i.e. whether mirrored branches exist. If this is true for several coverage criteria, then the concept of mirrored mutants can be generalised to the concept of *mirrored test requirements*.

Mirrored Mutants and Different Programming Languages. Another possible research direction is the evaluation of the concept of mirrored mutants in other programming languages (apart from Java). Such languages could employ different mutation operators that affect the source code of the program under test in different ways. Thus, it would be useful to study whether mirrored mutants are beneficial to the reduction of mutation's manual cost in different programming languages.

Appendix A

Publications

A.1 Refereed Journal Papers

- M. Kintis and N. Malevris, “MEDIC: A static analysis framework for equivalent mutant identification,” *Information and Software Technology (IST)*, vol. 68, pp. 1 – 17, 2015

- M. Kintis, M. Papadakis, and N. Malevris, “Employing second-order mutation for isolating first-order equivalent mutants,” *Software Testing, Verification and Reliability (STVR), Special Issue on Mutation Testing*, vol. 25, no. 5-7, pp. 508–535, 2015

A.2 Refereed Conference and Workshop Papers

- M. Kintis and N. Malevris, “Using data flow patterns for equivalent mutant detection,” in *Proceedings of the 7th International Conference on Software Testing, Verification and Validation Workshops (ICSTW)*, March 2014, pp. 196–205

- M. Kintis and N. Malevris, “Identifying more equivalent mutants via code similarity,” in *Proceedings of the 20th Asia-Pacific Software Engineering Conference (APSEC), 2013*, vol. 1, December 2013, pp. 180–188

- M. Kintis, M. Papadakis, and N. Malevris, “Isolating first order equivalent mutants via second order mutation,” in *Proceedings of the 5th Interna-*

tional Conference on Software Testing, Verification and Validation Workshops (ICSTW), April 2012, pp. 701–710

- M. Kintis, M. Papadakis, and N. Malevris, "Evaluating mutation testing alternatives: A collateral experiment," in *Proceedings of the 17th Asia-Pacific Software Engineering Conference (APSEC), 2010*, November 2010, pp. 300–309

- M. Papadakis, N. Malevris, and M. Kintis, "Mutation testing strategies - A collateral approach," in *Proceedings of the 5th International Conference on Software and Data Technologies (ICSOFT), Volume 2*, July 2010, pp. 325–328

Bibliography

[1] G. Myers, *The Art of Software Testing*. New York: John Wiley & Sons, 1979.

[2] I. Sommerville, *Software Engineering*, 6th ed. New York: Addison Wesley, 2001.

[3] P. Ammann and J. Offutt, *Introduction to Software Testing*, 1st ed. New York, NY, USA: Cambridge University Press, 2008.

[4] R. Lipton, "Fault diagnosis of computer programs," Student Report, Carnegie Mellon University, 1971.

[5] R. A. DeMillo, "Test adequacy and program mutation," in *Proceedings of the 11th International Conference on Software Engineering*, ser. ICSE '89. New York, NY, USA: ACM, 1989, pp. 355–356.

[6] M. R. Woodward, "Mutation testing-an evolving technique," in *Software Testing for Critical Systems, IEE Colloquium on*, Jun 1990, pp. 3/1–3/6.

[7] M. Woodward, "Mutation testing — its origin and evolution," *Information and Software Technology*, vol. 35, no. 3, pp. 163 – 169, 1993.

[8] A. J. Offutt and R. H. Untch, "Mutation 2000: Uniting the orthogonal," in *Mutation Testing for the New Century*, ser. The Springer International Series on Advances in Database Systems, W. Wong, Ed. Springer US, 2001, vol. 24, pp. 34–44.

[9] Y. Jia and M. Harman, "An analysis and survey of the development of mutation testing," *Software Engineering, IEEE Transactions on*, vol. 37, no. 5, pp. 649–678, 2011.

[10] A. P. Mathur, *Foundations of Software Testing*. Pearson Education, 2008.

[11] T. A. Budd and F. G. Sayward, "Users guide to the Pilot mutation system." Department of Computer Science, Yale University, Tech. Rep. 114, 1977.

[12] A. T. Acree, T. A. Budd, R. A. DeMillo, R. J. Lipton, and F. G. Sayward, "Mutation analysis." School of Information and Computer Science, Georgia Institute of Technology, Tech. Rep. GIT-ICS-79/08, September 1979.

[13] K. N. King and A. J. Offutt, "A Fortran language system for mutation-based software testing," *Software: Practice and Experience*, vol. 21, no. 7, pp. 685–718, Jun. 1991.

[14] H. Agrawal, R. Demillo, R. Hathaway, W. Hsu, W. Hsu, E. Krauser, R. J. Martin, A. Mathur, and E. Spafford, "Design of mutant operators for the C programming language," Technical Report SERC-TR-41-P, Software Engineering Research Center, Purdue University, Tech. Rep., 1989.

[15] J. Maldonado, M. Delamaro, S. Fabbri, A. Silva Simão, T. Sugeta, A. Vincenzi, and P. Masiero, "Proteum: A family of tools to support specification and program testing based on mutation," in *Mutation Testing for the New Century*, ser. The Springer International Series on Advances in Database Systems, W. Wong, Ed. Springer US, 2001, vol. 24, pp. 113–116.

[16] Y. Jia and M. Harman, "Milu: A customizable, runtime-optimized higher order mutation testing tool for the full C language," in *Practice and Research Techniques, 2008. TAIC PART '08. Testing: Academic Industrial Conference*, Aug 2008, pp. 94–98.

[17] S. Kim, J. Clark, and J. McDermid, "Investigating the effectiveness of object-oriented strategies with the mutation method," in *Mutation Testing for the*

New Century, ser. The Springer International Series on Advances in Database Systems, W. Wong, Ed. Springer US, 2001, vol. 24, pp. 4–4.

[18] P. Chevalley, "Applying mutation analysis for object-oriented programs using a reflective approach," in *Software Engineering Conference, 2001. APSEC 2001. Eighth Asia-Pacific*, Dec 2001, pp. 267–270.

[19] Y.-S. Ma, J. Offutt, and Y. R. Kwon, "MuJava: an automated class mutation system," *Software Testing, Verification and Reliability*, vol. 15, no. 2, pp. 97–133, 2005.

[20] D. Schuler and A. Zeller, "Javalanche: Efficient mutation testing for Java," in *Proceedings of the the 7th Joint Meeting of the European Software Engineering Conference and the ACM SIGSOFT Symposium on The Foundations of Software Engineering*, ser. ESEC/FSE '09. New York, NY, USA: ACM, 2009, pp. 297–298.

[21] R. Just, "The Major mutation framework: Efficient and scalable mutation analysis for Java," in *Proceedings of the 2014 International Symposium on Software Testing and Analysis*, ser. ISSTA 2014. New York, NY, USA: ACM, 2014, pp. 433–436.

[22] L. Madeyski and N. Radyk, "Judy – a mutation testing tool for Java," *IET Software*, vol. 4, pp. 32–42, February 2010.

[23] M. Gligoric, S. Badame, and R. Johnson, "SMutant: A tool for type-sensitive mutation testing in a dynamic language," in *Proceedings of the 19th ACM SIGSOFT Symposium and the 13th European Conference on Foundations of Software Engineering*, ser. ESEC/FSE '11. New York, NY, USA: ACM, 2011, pp. 424–427.

[24] A. Derezińska and K. Hałas, "Experimental evaluation of mutation testing approaches to python programs," in *Software Testing, Verification and Validation Workshops (ICSTW), 2014 IEEE Seventh International Conference on*, March 2014, pp. 156–164.

[25] D. Le, M. A. Alipour, R. Gopinath, and A. Groce, "MuCheck: An extensible tool for mutation testing of Haskell programs," in *Proceedings of the 2014 International Symposium on Software Testing and Analysis*, ser. ISSTA 2014. New York, NY, USA: ACM, 2014, pp. 429–432.

[26] S. Mirshokraie, A. Mesbah, and K. Pattabiraman, "Efficient javascript mutation testing," in *Software Testing, Verification and Validation (ICST), 2013 IEEE Sixth International Conference on*, March 2013, pp. 74–83.

[27] S. Mirshokraie, A. Mesbah, and K. Pattabiraman, "Guided mutation testing for JavaScript web applications," *Software Engineering, IEEE Transactions on*, vol. 41, no. 5, pp. 429–444, May 2015.

[28] W. Chan, S. Cheung, and T. Tse, "Fault-based testing of database application programs with conceptual data model," in *Quality Software, 2005. (QSIC 2005). Fifth International Conference on*, Sept 2005, pp. 187–196.

[29] J. Tuya, M. Suarez-Cabal, and C. De La Riva, "SQLMutation: A tool to generate mutants of sql database queries," in *Mutation Analysis, 2006. Second Workshop on*, Nov 2006, pp. 1–1.

[30] J. Tuya, M. J. Surez-Cabal, and C. de la Riva, "Mutating database queries," *Information and Software Technology*, vol. 49, no. 4, pp. 398 – 417, 2007.

[31] C. Zhou and P. Frankl, "Mutation testing for java database applications," in *Software Testing Verification and Validation, 2009. ICST '09. International Conference on*, April 2009, pp. 396–405.

[32] C. Zhou and P. Frankl, "JDAMA: Java database application mutation analyser," *Software Testing, Verification and Reliability*, vol. 21, no. 3, pp. 241–263, 2011.

[33] T. A. Budd and A. S. Gopal, "Program testing by specification mutation," *Computer Languages*, vol. 10, no. 1, pp. 63 – 73, 1985.

[34] R. A. DeMillo, R. J. Lipton, and F. G. Sayward, “Hints on test data selection: Help for the practicing programmer,” *Computer*, vol. 11, no. 4, pp. 34–41, 1978.

[35] M. Delamaro, J. Maldonado, and A. Mathur, “Integration testing using interface mutation,” in *Software Reliability Engineering, 1996. Proceedings., Seventh International Symposium on*, Oct 1996, pp. 112–121.

[36] P. Mateo, M. Usaola, and J. Offutt, “Mutation at system and functional levels,” in *Software Testing, Verification, and Validation Workshops (ICSTW), 2010 Third International Conference on*, April 2010, pp. 110–119.

[37] P. R. Mateo, M. P. Usaola, and J. Offutt, “Mutation at the multi-class and system levels,” *Science of Computer Programming*, vol. 78, no. 4, pp. 364 – 387, 2013, special section on Mutation Testing and Analysis (Mutation 2010) &; Special section on the Programming Languages track at the 25th {ACM} Symposium on Applied Computing.

[38] S. Pinto Ferraz Fabbri, M. Delamaro, J. Maldonado, and P. Masiero, “Mutation analysis testing for finite state machines,” in *Software Reliability Engineering, 1994. Proceedings., 5th International Symposium on*, Nov 1994, pp. 220–229.

[39] R. Hierons and M. Merayo, “Mutation testing from probabilistic finite state machines,” in *Testing: Academic and Industrial Conference Practice and Research Techniques - MUTATION, 2007. TAICPART-MUTATION 2007*, Sept 2007, pp. 141–150.

[40] C. Jing, Z. Wang, X. Shi, X. Yin, and J. Wu, “Mutation testing of protocol messages based on extended TTCN-3,” in *Advanced Information Networking and Applications, 2008. AINA 2008. 22nd International Conference on*, March 2008, pp. 667–674.

[41] T. Mouelhi, Y. Le Traon, and B. Baudry, “Mutation analysis for security tests qualification,” in *Testing: Academic and Industrial Conference Practice*

and Research Techniques - MUTATION, 2007. TAICPART-MUTATION 2007, Sept 2007, pp. 233–242.

[42] E. Martin and T. Xie, “A fault model and mutation testing of access control policies,” in *Proceedings of the 16th International Conference on World Wide Web*, ser. WWW ’07. New York, NY, USA: ACM, 2007, pp. 667–676.

[43] Y. Le Traon, T. Mouelhi, and B. Baudry, “Testing security policies: Going beyond functional testing,” in *Software Reliability, 2007. ISSRE ’07. The 18th IEEE International Symposium on*, Nov 2007, pp. 93–102.

[44] C. Henard, M. Papadakis, G. Perrouin, J. Klein, and Y. Le Traon, “Assessing software product line testing via model-based mutation: An application to similarity testing,” in *Software Testing, Verification and Validation Workshops (ICSTW), 2013 IEEE Sixth International Conference on*, March 2013, pp. 188–197.

[45] C. Henard, M. Papadakis, and Y. Le Traon, “Mutation-based generation of software product line test configurations,” in *Search-Based Software Engineering*, ser. Lecture Notes in Computer Science, C. Le Goues and S. Yoo, Eds. Springer International Publishing, 2014, vol. 8636, pp. 92–106.

[46] C. Wright, G. Kapfhammer, and P. McMinn, “Efficient mutation analysis of relational database structure using mutant schemata and parallelisation,” in *Software Testing, Verification and Validation Workshops (ICSTW), 2013 IEEE Sixth International Conference on*, March 2013, pp. 63–72.

[47] C. Wright, G. Kapfhammer, and P. McMinn, “The impact of equivalent, redundant and quasi mutants on database schema mutation analysis,” in *Quality Software (QSIC), 2014 14th International Conference on*, Oct 2014, pp. 57–66.

[48] R. DeMillo and A. Offutt, “Constraint-based automatic test data generation,” *Software Engineering, IEEE Transactions on*, vol. 17, no. 9, pp. 900–910, Sep 1991.

[49] R. A. DeMillo and A. J. Offutt, "Experimental results from an automatic test case generator," *ACM Transactions on Software Engineering and Methodology*, vol. 2, no. 2, pp. 109–127, Apr. 1993.

[50] Y. Le Traon, B. Baudry, and J. Jezequel, "Design by contract to improve software vigilance," *Software Engineering, IEEE Transactions on*, vol. 32, no. 8, pp. 571–586, Aug 2006.

[51] M. Papadakis and N. Malevris, "Automatic mutation test case generation via dynamic symbolic execution," in *Software Reliability Engineering (ISSRE), 2010 IEEE 21st International Symposium on*, Nov 2010, pp. 121–130.

[52] L. Zhang, T. Xie, L. Zhang, N. Tillmann, J. de Halleux, and H. Mei, "Test generation via dynamic symbolic execution for mutation testing," in *Software Maintenance (ICSM), 2010 IEEE International Conference on*, Sept 2010, pp. 1–10.

[53] M. Papadakis and N. Malevris, "Mutation based test case generation via a path selection strategy," *Information and Software Technology*, vol. 54, no. 9, pp. 915 – 932, 2012.

[54] G. Fraser and A. Zeller, "Mutation-driven generation of unit tests and oracles," *Software Engineering, IEEE Transactions on*, vol. 38, no. 2, pp. 278–292, 2012.

[55] T. Xie, N. Tillmann, J. de Halleux, and W. Schulte, "Mutation analysis of parameterized unit tests," in *Software Testing, Verification and Validation Workshops, 2009. ICSTW '09. International Conference on*, April 2009, pp. 177–181.

[56] A. J. Offutt, J. Pan, and J. M. Voas, "Procedures for reducing the size of coverage-based test sets," in *In Proceedings of the Twelfth International Conference on Testing Computer Software*, 1995, pp. 111–123.

[57] L. Zhang, D. Marinov, L. Zhang, and S. Khurshid, "Regression mutation testing," in *Proceedings of the 2012 International Symposium on Software Testing and Analysis*, ser. ISSTA 2012. New York, NY, USA: ACM, 2012, pp. 331–341.

[58] M. Papadakis and Y. Le Traon, "Using mutants to locate "unknown" faults," in *Software Testing, Verification and Validation (ICST), 2012 IEEE Fifth International Conference on*, April 2012, pp. 691–700.

[59] S. Moon, Y. Kim, M. Kim, and S. Yoo, "Ask the mutants: Mutating faulty programs for fault localization," in *Software Testing, Verification and Validation (ICST), 2014 IEEE Seventh International Conference on*, March 2014, pp. 153–162.

[60] M. Papadakis and Y. Le Traon, "Metallaxis-fl: mutation-based fault localization," *Software Testing, Verification and Reliability*, vol. 25, no. 5-7, pp. 605–628, 2015.

[61] E. Alégroth, Z. Gao, R. Oliveira, and A. Memon, "Conceptualization and evaluation of component-based testing unified with visual gui testing: An empirical study," in *Software Testing, Verification and Validation (ICST), 2015 IEEE 8th International Conference on*, April 2015, pp. 1–10.

[62] R. Oliveira, E. Alégroth, Z. Gao, and A. Memon, "Definition and evaluation of mutation operators for gui-level mutation analysis," in *Software Testing, Verification and Validation Workshops (ICSTW), 2015 IEEE Eighth International Conference on*, April 2015, pp. 1–10.

[63] R. Geist, A. Offutt, and J. Harris, F.C., "Estimation and enhancement of real-time software reliability through mutation analysis," *Computers, IEEE Transactions on*, vol. 41, no. 5, pp. 550–558, May 1992.

[64] M. Daran and P. Thévenod-Fosse, "Software error analysis: A real case study involving real faults and mutations," in *Proceedings of the 1996 ACM SIG-*

SOFT International Symposium on Software Testing and Analysis, ser. ISSTA '96. New York, NY, USA: ACM, 1996, pp. 158–171.

[65] J. H. Andrews, L. C. Briand, and Y. Labiche, "Is mutation an appropriate tool for testing experiments?" in *Proceedings of the 27th International Conference on Software Engineering*, ser. ICSE '05. New York, NY, USA: ACM, 2005, pp. 402–411.

[66] J. Andrews, L. Briand, Y. Labiche, and A. Namin, "Using mutation analysis for assessing and comparing testing coverage criteria," *Software Engineering, IEEE Transactions on*, vol. 32, no. 8, pp. 608–624, Aug 2006.

[67] H. Do and G. Rothermel, "On the use of mutation faults in empirical assessments of test case prioritization techniques," *Software Engineering, IEEE Transactions on*, vol. 32, no. 9, pp. 733–752, Sept 2006.

[68] R. Just, D. Jalali, L. Inozemtseva, M. D. Ernst, R. Holmes, and G. Fraser, "Are mutants a valid substitute for real faults in software testing?" in *Proceedings of the 22Nd ACM SIGSOFT International Symposium on Foundations of Software Engineering*, ser. FSE 2014. New York, NY, USA: ACM, 2014, pp. 654–665.

[69] A. J. Offutt and J. M. Voas, "Subsumption of condition coverage techniques by mutation testing," Department of Information and Software Systems Engineering, George Mason University, Tech. Rep. ISSE-TR-96-100, 1996.

[70] N. Li, U. Praphamontripong, and J. Offutt, "An experimental comparison of four unit test criteria: Mutation, edge-pair, all-uses and prime path coverage," in *Software Testing, Verification and Validation Workshops, 2009. ICSTW '09. International Conference on*, April 2009, pp. 220–229.

[71] A. J. Offutt, J. Pan, K. Tewary, and T. Zhang, "Experiments with data flow and mutation testing." Department of Information and Software Systems Engineering, George Mason University, Tech. Rep. ISSE-TR-94-105, 1994.

[72] A. P. Mathur and W. E. Wong, "An empirical comparison of data flow and mutation-based test adequacy criteria," *Software Testing, Verification and Reliability*, vol. 4, no. 1, pp. 9–31, 1994.

[73] A. J. Offutt, J. Pan, K. Tewary, and T. Zhang, "An experimental evaluation of data flow and mutation testing," *Software: Practice and Experience*, vol. 26, no. 2, pp. 165–176, 1996.

[74] P. G. Frankl, S. N. Weiss, and C. Hu, "All-uses vs mutation testing: An experimental comparison of effectiveness," *Journal of Systems and Software*, vol. 38, no. 3, pp. 235 – 253, 1997.

[75] S. Rapps and E. J. Weyuker, "Data flow analysis techniques for test data selection," in *Proceedings of the 6th International Conference on Software Engineering*, ser. ICSE '82. Los Alamitos, CA, USA: IEEE Computer Society Press, 1982, pp. 272–278.

[76] S. Rapps and E. J. Weyuker, "Selecting software test data using data flow information," *IEEE Transactions on Software Engineering*, vol. SE-11, no. 4, pp. 367–375, April 1985.

[77] P. G. Frankl and E. J. Weyuker, "An applicable family of data flow testing criteria," *IEEE Transactions on Software Engineering*, vol. 14, no. 10, pp. 1483–1498, Oct 1988.

[78] D. Schuler and A. Zeller, "(Un-)Covering equivalent mutants," in *Software Testing, Verification and Validation (ICST), 2010 Third International Conference on*, April 2010, pp. 45–54.

[79] D. Schuler and A. Zeller, "Covering and uncovering equivalent mutants," *Software Testing, Verification and Reliability*, vol. 23, no. 5, pp. 353–374, 2013.

[80] L. Madeyski, W. Orzeszyna, R. Torkar, and M. Józala, "Overcoming the equivalent mutant problem: A systematic literature review and a comparative

experiment of second order mutation," *Software Engineering, IEEE Transactions on*, vol. 40, no. 1, pp. 23–42, Jan 2014.

[81] A. J. Offutt, A. Lee, G. Rothermel, R. H. Untch, and C. Zapf, "An experimental determination of sufficient mutant operators," *ACM Transactions on Software Engineering and Methodology*, vol. 5, no. 2, pp. 99–118, Apr. 1996.

[82] W. E. Howden, "Completeness criteria for testing elementary program functions," in *Proceedings of the 5th International Conference on Software Engineering*, ser. ICSE '81. Piscataway, NJ, USA: IEEE Press, 1981, pp. 235–243.

[83] W. E. Howden, "Weak mutation testing and completeness of test sets," *IEEE Trans. Softw. Eng.*, vol. 8, no. 4, pp. 371–379, Jul. 1982.

[84] M. Woodward and K. Halewood, "From weak to strong, dead or alive? an analysis of some mutation testing issues," in *Software Testing, Verification, and Analysis, 1988., Proceedings of the Second Workshop on*, Jul 1988, pp. 152–158.

[85] M. Polo, M. Piattini, and I. Garca-Rodrguez, "Decreasing the cost of mutation testing with second-order mutants," *Software Testing, Verification and Reliability*, vol. 19, no. 2, pp. 111–131, 2009.

[86] Y. Jia and M. Harman, "Higher order mutation testing," *Information and Software Technology*, vol. 51, no. 10, pp. 1379 – 1393, 2009, Source Code Analysis and Manipulation, {SCAM} 2008.

[87] M. Kintis, M. Papadakis, and N. Malevris, "Evaluating mutation testing alternatives: A collateral experiment," in *Proceedings of the 17th Asia-Pacific Software Engineering Conference (APSEC), 2010*, November 2010, pp. 300–309.

[88] M. Papadakis and N. Malevris, "An empirical evaluation of the first and second order mutation testing strategies," in *Software Testing, Verification,*

and Validation Workshops (ICSTW), 2010 Third International Conference on, April 2010, pp. 90–99.

[89] T. Budd and D. Angluin, "Two notions of correctness and their relation to testing," *Acta Informatica*, vol. 18, no. 1, pp. 31–45, 1982.

[90] R. G. Hamlet, "Testing programs with the aid of a compiler," *Software Engineering, IEEE Transactions on*, vol. SE-3, no. 4, pp. 279–290, 1977.

[91] R. A. DeMillo, D. S. Guindi, W. M. McCracken, A. J. Offutt, and K. N. King, "An extended overview of the Mothra software testing environment," in *Software Testing, Verification, and Analysis, 1988., Proceedings of the Second Workshop on*, Jul 1988, pp. 142–151.

[92] T. A. Budd, R. A. DeMillo, R. J. Lipton, and F. G. Sayward, "Theoretical and empirical studies on using program mutation to test the functional correctness of programs," in *Proceedings of the 7th ACM SIGPLAN-SIGACT Symposium on Principles of Programming Languages*, ser. POPL '80. New York, NY, USA: ACM, 1980, pp. 220–233.

[93] A. Offutt, "The coupling effect: Fact or fiction," in *Proceedings of the ACM SIGSOFT '89 Third Symposium on Software Testing, Analysis, and Verification*, ser. TAV3. New York, NY, USA: ACM, 1989, pp. 131–140.

[94] A. J. Offutt, "Investigations of the software testing coupling effect," *ACM Transactions on Software Engineering and Methodology*, vol. 1, no. 1, pp. 5–20, Jan. 1992.

[95] R. J. Lipton and F. G. Sayward, "The status of research on program mutation," in *the Workshop on Software Testing and Test Documentation*, 1978, pp. 355–373.

[96] L. J. Morell, "A theory of error-based testing," Ph.D. dissertation, University of Maryland, 1984.

[97] K. S. H. T. Wah, “Fault coupling in finite bijective functions,” *Software Testing, Verification and Reliability*, vol. 5, no. 1, pp. 3–47, 1995.

[98] K. S. H. T. Wah, “A theoretical study of fault coupling,” *Software Testing, Verification and Reliability*, vol. 10, no. 1, pp. 3–45, 2000.

[99] K. Kapoor, “Formal analysis of coupling hypothesis for logical faults,” *Innovations in Systems and Software Engineering*, vol. 2, no. 2, pp. 80–87, 2006.

[100] T. A. Budd, “Mutation analysis of program test data,” Ph.D. dissertation, Yale University, 1980.

[101] E. Barr, M. Harman, P. McMinn, M. Shahbaz, and S. Yoo, “The oracle problem in software testing: A survey,” *Software Engineering, IEEE Transactions on*, vol. 41, no. 5, pp. 507–525, May 2015.

[102] A. T. Acree, “On mutation,” Ph.D. dissertation, Georgia Institute of Technology, 1980.

[103] L. Morell, “A theory of fault-based testing,” *Software Engineering, IEEE Transactions on*, vol. 16, no. 8, pp. 844–857, Aug 1990.

[104] J. Offutt, “Automatic test data generation,” Ph.D. dissertation, Georgia Institute of Technology, 1988.

[105] J. M. Voas and G. McGraw, *Software Fault Injection: Inoculating Programs Against Errors*. New York, NY, USA: John Wiley & Sons, 1997.

[106] X. Yao, M. Harman, and Y. Jia, “A study of equivalent and stubborn mutation operators using human analysis of equivalence,” in *Proceedings of the 36th International Conference on Software Engineering*, ser. ICSE 2014. New York, NY, USA: ACM, 2014, pp. 919–930.

[107] M. Kintis, “Mutation testing and its approximations,” Master’s thesis, Department of Informatics, Athens University of Economics and Business, 2010, (in greek).

[108] H. Agrawal, “Dominators, super blocks, and program coverage,” in *Proceedings of the 21st ACM SIGPLAN-SIGACT Symposium on Principles of Programming Languages*, ser. POPL ’94. New York, NY, USA: ACM, 1994, pp. 25–34.

[109] M. Papadakis, N. Malevris, and M. Kintis, “Mutation testing strategies - A collateral approach,” in *Proceedings of the 5th International Conference on Software and Data Technologies (ICSOFT), Volume 2*, July 2010, pp. 325–328.

[110] K. Adamopoulos, M. Harman, and R. Hierons, “How to overcome the equivalent mutant problem and achieve tailored selective mutation using co-evolution,” in *Genetic and Evolutionary Computation GECCO 2004*, ser. Lecture Notes in Computer Science, K. Deb, Ed. Springer Berlin Heidelberg, 2004, vol. 3103, pp. 1338–1349.

[111] D. Baldwin and F. Sayward, “Heuristics for determining equivalence of program mutations.” Department of Computer Science, Yale University, Tech. Rep. 276, 1979.

[112] A. J. Offutt and W. M. Craft, “Using compiler optimization techniques to detect equivalent mutants,” *Software Testing, Verification and Reliability*, vol. 4, no. 3, pp. 131–154, 1994.

[113] M. Papadakis, Y. Jia, M. Harman, and Y. Le Traon, “Trivial compiler equivalence: A large scale empirical study of a simple, fast and effective equivalent mutant detection technique,” in *Proceedings of the 2015 International Conference on Software Engineering*, 2015, to appear.

[114] A. J. Offutt and J. Pan, “Automatically detecting equivalent mutants and infeasible paths,” *Software Testing, Verification and Reliability*, vol. 7, no. 3, pp. 165–192, 1997.

[115] A. J. Offutt and J. Pan, “Detecting equivalent mutants and the feasible path problem,” in *Computer Assurance, 1996. COMPASS ’96, Systems Integrity.*

Software Safety. Process Security. Proceedings of the Eleventh Annual Conference on, Jun 1996, pp. 224–236.

[116] S. Nica and F. Wotawa, "Using constraints for equivalent mutant detection," in *Formal Methods in the Development of Software, 2012. WS-FMDS 2012., Proceedings of the Second Workshop on*, 2012, pp. 1–8.

[117] S. Nica and F. Wotawa, "EqMutDetect – A tool for equivalent mutant detection in embedded systems," in *Intelligent Solutions in Embedded Systems, 2012. WISES 2012., Proceedings of the Tenth Workshop on*, 2012, pp. 57–62.

[118] S. Bardin, M. Delahaye, R. David, N. Kosmatov, M. Papadakis, Y. L. Traon, and J. Y. Marion, "Sound and quasi-complete detection of infeasible test requirements," in *Software Testing, Verification and Validation (ICST), 2015 IEEE 8th International Conference on*, April 2015, pp. 1–10.

[119] N. Malevris, "A path generation method for testing LCSAJs that restrains infeasible paths," *Information and Software Technology*, vol. 37, no. 8, pp. 435 – 441, 1995.

[120] M. N. Ngo and H. B. K. Tan, "Heuristics-based infeasible path detection for dynamic test data generation," *Information and Software Technology*, vol. 50, no. 7-8, pp. 641 – 655, 2008.

[121] M. Papadakis and N. Malevris, "A symbolic execution tool based on the elimination of infeasible paths," in *Software Engineering Advances (ICSEA), 2010 Fifth International Conference on*, Aug 2010, pp. 435–440.

[122] M. Weiser, "Program slicing," in *Proceedings of the 5th International Conference on Software Engineering*, ser. ICSE '81. Piscataway, NJ, USA: IEEE Press, 1981, pp. 439–449.

[123] J. M. Voas and G. McGraw, *Software Fault Injection: Inoculating Programs Against Errors*. New York, NY, USA: John Wiley & Sons, Inc., 1997.

[124] R. Hierons, M. Harman, and S. Danicic, "Using program slicing to assist in the detection of equivalent mutants," *Software Testing, Verification and Reliability*, vol. 9, no. 4, pp. 233–262, 1999.

[125] D. Binkley, "Computing amorphous program slices using dependence graphs," in *Proceedings of the 1999 ACM Symposium on Applied Computing*, ser. SAC '99. New York, NY, USA: ACM, 1999, pp. 519–525.

[126] M. Harman and S. Danicic, "Amorphous program slicing," in *Program Comprehension, 1997. IWPC '97. Proceedings., Fifth Iternational Workshop on*, Mar 1997, pp. 70–79.

[127] M. Harman, R. Hierons, and S. Danicic, "The relationship between program dependence and mutation analysis," in *Mutation Testing for the New Century*, ser. The Springer International Series on Advances in Database Systems, W. Wong, Ed. Springer US, 2001, vol. 24, pp. 5–13.

[128] M. Ellims, D. Ince, and M. Petre, "The Csaw C mutation tool: Initial results," in *Testing: Academic and Industrial Conference Practice and Research Techniques - MUTATION, 2007. TAICPART-MUTATION 2007*, Sept 2007, pp. 185–192.

[129] B. Grün, D. Schuler, and A. Zeller, "The impact of equivalent mutants," in *Software Testing, Verification and Validation Workshops, 2009. ICSTW '09. International Conference on*, April 2009, pp. 192–199.

[130] D. Schuler, V. Dallmeier, and A. Zeller, "Efficient mutation testing by checking invariant violations," in *Proceedings of the Eighteenth International Symposium on Software Testing and Analysis*, ser. ISSTA '09. New York, NY, USA: ACM, 2009, pp. 69–80.

[131] M. Papadakis and Y. Le Traon, "Mutation testing strategies using mutant classification," in *Proceedings of the 28th Annual ACM Symposium on Applied Computing*, ser. SAC '13. New York, NY, USA: ACM, 2013, pp. 1223–1229.

[132] M. Papadakis, M. Delamaro, and Y. Le Traon, "Mitigating the effects of equivalent mutants with mutant classification strategies," *Science of Computer Programming*, vol. 95, Part 3, pp. 298 – 319, 2014.

[133] W. E. Wong, "On mutation and data flow," Ph.D. dissertation, Purdue University, 1993.

[134] A. J. Offutt, G. Rothermel, and C. Zapf, "An experimental evaluation of selective mutation," in *Proceedings of the 15th International Conference on Software Engineering*, ser. ICSE '93. Los Alamitos, CA, USA: IEEE Computer Society Press, 1993, pp. 100–107.

[135] A. Mathur, "Performance, effectiveness, and reliability issues in software testing," in *Computer Software and Applications Conference, 1991. COMPSAC '91., Proceedings of the Fifteenth Annual International*, Sep 1991, pp. 604–605.

[136] E. F. Barbosa, J. C. Maldonado, and A. M. R. Vincenzi, "Toward the determination of sufficient mutant operators for C," *Software Testing, Verification and Reliability*, vol. 11, no. 2, pp. 113–136, 2001.

[137] A. Namin and J. Andrews, "Finding sufficient mutation operators via variable reduction," in *Mutation Analysis, 2006. Second Workshop on*, Nov 2006, p. 5.

[138] A. Namin and J. Andrews, "On sufficiency of mutants," in *Software Engineering - Companion, 2007. ICSE 2007 Companion. 29th International Conference on*, May 2007, pp. 73–74.

[139] A. Namin, J. H. Andrews, and D. J. Murdoch, "Sufficient mutation operators for measuring test effectiveness," in *Proceedings of the 30th International Conference on Software Engineering*, ser. ICSE '08. New York, NY, USA: ACM, 2008, pp. 351–360.

[140] W. Wong and A. P. Mathur, "Reducing the cost of mutation testing: An em-

pirical study," *Journal of Systems and Software*, vol. 31, no. 3, pp. 185 – 196, 1995.

[141] R. H. Untch, "On reduced neighborhood mutation analysis using a single mutagenic operator," in *Proceedings of the 47th Annual Southeast Regional Conference*, ser. ACM-SE 47. New York, NY, USA: ACM, 2009, pp. 71:1–71:4.

[142] L. Deng, J. Offutt, and N. Li, "Empirical evaluation of the statement deletion mutation operator," in *Software Testing, Verification and Validation (ICST), 2013 IEEE Sixth International Conference on*, March 2013, pp. 84–93.

[143] M. Delamaro, L. Deng, V. Serapilha Durelli, N. Li, and J. Offutt, "Experimental evaluation of sdl and one-op mutation for c," in *Software Testing, Verification and Validation (ICST), 2014 IEEE Seventh International Conference on*, March 2014, pp. 203–212.

[144] L. Zhang, S.-S. Hou, J.-J. Hu, T. Xie, and H. Mei, "Is operator-based mutant selection superior to random mutant selection?" in *Proceedings of the 32Nd ACM/IEEE International Conference on Software Engineering - Volume 1*, ser. ICSE '10. New York, NY, USA: ACM, 2010, pp. 435–444.

[145] L. Zhang, M. Gligoric, D. Marinov, and S. Khurshid, "Operator-based and random mutant selection: Better together," in *Automated Software Engineering (ASE), 2013 IEEE/ACM 28th International Conference on*, Nov 2013, pp. 92–102.

[146] N. Malevris and D. Yates, "The collateral coverage of data flow criteria when branch testing," *Information and Software Technology*, vol. 48, no. 8, pp. 676 – 686, 2006.

[147] P. Ammann, M. E. Delamaro, and A. J. Offutt, "Establishing theoretical minimal sets of mutants," in *Proceedings of the 2014 IEEE International Conference on Software Testing, Verification, and Validation*, ser. ICST '14. Washington, DC, USA: IEEE Computer Society, 2014, pp. 21–30.

[148] B. Kurtz, P. Ammann, M. Delamaro, J. Offutt, and L. Deng, "Mutant subsumption graphs," in *Software Testing, Verification and Validation Workshops (ICSTW), 2014 IEEE Seventh International Conference on*, March 2014, pp. 176–185.

[149] B. Kurtz, P. Ammann, and J. Offutt, "Static analysis of mutant subsumption," in *Software Testing, Verification and Validation Workshops (ICSTW), 2015 IEEE Eighth International Conference on*, April 2015, pp. 1–10.

[150] M. R. Girgis and M. R. Woodward, "An integrated system for program testing using weak mutation and data flow analysis," in *Proceedings of the 8th International Conference on Software Engineering*, ser. ICSE '85. Los Alamitos, CA, USA: IEEE Computer Society Press, 1985, pp. 313–319.

[151] J. R. Horgan and A. P. Mathur, "Weak mutation is probably strong mutation." Purdue University, Tech. Rep. SERC-TR-83-P, 1990.

[152] B. Marick, "The weak mutation hypothesis," in *Proceedings of the Symposium on Testing, Analysis, and Verification*, ser. TAV4. New York, NY, USA: ACM, 1991, pp. 190–199.

[153] A. J. Offutt and S. D. Lee, "How strong is weak mutation?" in *Proceedings of the Symposium on Testing, Analysis, and Verification*, ser. TAV4. New York, NY, USA: ACM, 1991, pp. 200–213.

[154] A. Offutt and S. Lee, "An empirical evaluation of weak mutation," *Software Engineering, IEEE Transactions on*, vol. 20, no. 5, pp. 337–344, May 1994.

[155] M. Kintis, M. Papadakis, and N. Malevris, "Isolating first order equivalent mutants via second order mutation," in *Proceedings of the 5th International Conference on Software Testing, Verification and Validation Workshops (ICSTW)*, April 2012, pp. 701–710.

[156] C. D. Manning, P. Raghavan, and H. Schütze, *Introduction to Information Retrieval*. Cambridge university press, 2008.

[157] G. Fraser and A. Zeller, "Mutation-driven generation of unit tests and oracles," in *Proceedings of the 19th International Symposium on Software Testing and Analysis*, ser. ISSTA '10. New York, NY, USA: ACM, 2010, pp. 147–158.

[158] D. Jackson and E. J. Rollins, "A new model of program dependences for reverse engineering," in *Proceedings of the 2Nd ACM SIGSOFT Symposium on Foundations of Software Engineering*, ser. SIGSOFT '94. New York, NY, USA: ACM, 1994, pp. 2–10.

[159] B. Alpern, M. N. Wegman, and F. K. Zadeck, "Detecting equality of variables in programs," in *Proceedings of the 15th ACM SIGPLAN-SIGACT Symposium on Principles of Programming Languages*, ser. POPL '88. New York, NY, USA: ACM, 1988, pp. 1–11.

[160] B. K. Rosen, M. N. Wegman, and F. K. Zadeck, "Global value numbers and redundant computations," in *Proceedings of the 15th ACM SIGPLAN-SIGACT Symposium on Principles of Programming Languages*, ser. POPL '88. New York, NY, USA: ACM, 1988, pp. 12–27.

[161] J. Dolby, M. Vaziri, and F. Tip, "Finding bugs efficiently with a SAT solver," in *Proceedings of the the 6th Joint Meeting of the European Software Engineering Conference and the ACM SIGSOFT Symposium on The Foundations of Software Engineering*, ser. ESEC-FSE '07. New York, NY, USA: ACM, 2007, pp. 195–204.

[162] R. Cytron, J. Ferrante, B. K. Rosen, M. N. Wegman, and F. K. Zadeck, "Efficiently computing static single assignment form and the control dependence graph," *ACM Trans. Program. Lang. Syst.*, vol. 13, no. 4, pp. 451–490, Oct. 1991.

[163] A. J. Offutt and N. Li. The μJava home page (version 3). Last Accessed April 2016. [Online]. Available: http://cs.gmu.edu/~offutt/mujava/index-v3-nov2008.html

[164] IBM T.J. Watson Research Center. T. J. Watson libraries for analysis. Last Accessed April 2016. [Online]. Available: http://wala.sourceforge.net

[165] J.-D. Choi, R. Cytron, and J. Ferrante, "Automatic construction of sparse data flow evaluation graphs," in *Proceedings of the 18th ACM SIGPLAN-SIGACT Symposium on Principles of Programming Languages*, ser. POPL '91. New York, NY, USA: ACM, 1991, pp. 55–66.

[166] M. Braun, S. Buchwald, S. Hack, R. Leia, C. Mallon, and A. Zwinkau, "Simple and efficient construction of static single assignment form," in *Compiler Construction*, ser. Lecture Notes in Computer Science, R. Jhala and K. De Bosschere, Eds. Springer Berlin Heidelberg, 2013, vol. 7791, pp. 102–122.

[167] P. Briggs, K. D. Cooper, T. J. Harvey, and L. T. Simpson, "Practical improvements to the construction and destruction of static single assignment form," *Software: Practice and Experience*, vol. 28, no. 8, pp. 859–881, 1998.

[168] Neo Technology. Neo4j graph database. Last Accessed April 2016. [Online]. Available: http://neo4j.com

[169] B. Baker, "On finding duplication and near-duplication in large software systems," in *Reverse Engineering, 1995., Proceedings of 2nd Working Conference on*, Jul 1995, pp. 86–95.

[170] C. K. Roy, J. R. Cordy, and R. Koschke, "Comparison and evaluation of code clone detection techniques and tools: A qualitative approach," *Science of Computer Programming*, vol. 74, no. 7, pp. 470–495, 2009.

[171] D. Rattan, R. Bhatia, and M. Singh, "Software clone detection: A systematic review," *Information and Software Technology*, vol. 55, no. 7, pp. 1165 – 1199, 2013.

[172] T. Kamiya. The official CCFinderX website. Last Accessed April 2016. [Online]. Available: http://www.ccfinder.net/ccfinderx.html

[173] E. Duala-Ekoko and M. Robillard, "Tracking code clones in evolving software," in *Software Engineering, 2007. ICSE 2007. 29th International Conference on*, May 2007, pp. 158–167.

[174] C. Roy and J. Cordy, "An empirical study of function clones in open source software," in *Reverse Engineering, 2008. WCRE '08. 15th Working Conference on*, Oct 2008, pp. 81–90.

[175] T. Kamiya, S. Kusumoto, and K. Inoue, "CCFinder: a multilinguistic token-based code clone detection system for large scale source code," *Software Engineering, IEEE Transactions on*, vol. 28, no. 7, pp. 654–670, Jul 2002.

[176] S. Wang and J. Offutt, "Comparison of unit-level automated test generation tools," in *Software Testing, Verification and Validation Workshops, 2009. ICSTW '09. International Conference on*, April 2009, pp. 210–219.

[177] M. Kintis and N. Malevris, "MEDIC: A static analysis framework for equivalent mutant identification," *Information and Software Technology (IST)*, vol. 68, pp. 1 – 17, 2015.

[178] M. Kintis, M. Papadakis, and N. Malevris, "Employing second-order mutation for isolating first-order equivalent mutants," *Software Testing, Verification and Reliability (STVR), Special Issue on Mutation Testing*, vol. 25, no. 5-7, pp. 508–535, 2015.

[179] M. Kintis and N. Malevris, "Using data flow patterns for equivalent mutant detection," in *Proceedings of the 7th International Conference on Software Testing, Verification and Validation Workshops (ICSTW)*, March 2014, pp. 196–205.

[180] M. Kintis and N. Malevris, "Identifying more equivalent mutants via code similarity," in *Proceedings of the 20th Asia-Pacific Software Engineering Conference (APSEC), 2013*, vol. 1, December 2013, pp. 180–188.