Bound by Abbey
Bookbinding Co.,
Cardiff, South Wales
Tel: (01222) 395882

The Automatic Generation of Software Test Data Using Genetic Algorithms

by

Harmen - Hinrich Sthamer

A thesis submitted in partial fulfilment of the requirements of the University of Glamorgan / Prifysgol Morgannwg for the degree of a Doctor of Philosophy.

November 1995

University of Glamorgan

Declaration

I declare that this thesis has not been, nor is currently being, submitted for the award of any other degree or similar qualification.

Signed [signature]

Harmen - Hinrich Sthamer

Acknowledgements

I wish to thank my director of studies, Prof. Dr. Bryan F. Jones for his thorough guidance and support throughout the research and his whole-hearted efforts in providing the necessary help and many useful discussions and suggestions for the research project. With gratitude I would also acknowledge my second supervisor, David Eyres especially for his help during the research time and for the encouragement provided.

Many thanks go to Professor Dr.-Ing. Walter Lechner from the Fachhochschule Hannover and Professor Darrel C. Ince from the Open University for valuable discussions and suggestions at meetings.

I am especially indebted to my colleagues of the software testing research group Mrs. Xile Yang and Mr. Steve Holmes for providing invaluable discussions.

Special thanks go to Dr. David Knibb for providing commercial software programs which were used during the course of the investigation as software to be tested.

In particular thanks go also to Professor Dr.-Ing. Walter Heinecke from the Fachhochschule Braunschweig/Wolfenbüttel for his efforts in establishing the collaboration between the German academic institute and its British counterpart, the University of Glamorgan, which paved the way for German students to study at British Universities.

Last but not least, I would like to thank my parents, my brothers, sisters and sisters in law who supported me through out my stay in Britain in any aspect, inspiration and understanding and especially my grandparents, Eija and Ofa, without them I would not be here.

Abstract

Genetic Algorithms (GAs) have been used successfully to automate the generation of test data for software developed in ADA83. The test data were derived from the program's structure with the aim to traverse every branch in the software. The investigation uses fitness functions based on the Hamming distance between the expressions in the branch predicate and on the reciprocal of the difference between numerical expressions in the predicate. The input variables are represented in Gray code and as an image of the machine memory. The power of using GAs lies in their ability to handle input data which may be of complex structure, and predicates which may be complicated and unknown functions of the input variables. Thus, the problem of test data generation is treated entirely as an optimisation problem.

Random testing is used as a comparison of the effectiveness of test data generation using GAs which requires up to two orders of magnitude fewer tests than random testing and achieves 100% branch coverage. The advantage of GAs is that through the search and optimisation process, test sets are improved such that they are at or close to the input subdomain boundaries. The GAs give most improvements over random testing when these subdomains are small. Mutation analysis is used to establish the quality of test data generation and the strengths and weaknesses of the test data generation strategy.

Various software procedures with different input data structures (integer, characters, arrays and records) and program structures with '*if*' conditions and loops are tested i.e. a quadratic equation solver, a triangle classifier program comprising a system of three procedures, linear and binary search procedures, remainder procedure and a commercially available generic sorting procedure.

Experiments show that GAs required less CPU time in general to reach a global solution than random testing. The greatest advantage is when the density of global optima (solutions) is small compared to entire input search domain.

Table of contents

CHAPTER 1 .... 1-1 - 1-6

1. Introduction 1-1

1.1 Objectives and aims of the research project 1-2
1.2 Hypotheses 1-3
1.3 Testing criteria 1-4
1.4 Structure of Thesis 1-4

CHAPTER 2 .... 2-1 - 2-13

2. Background of various automatic testing methods 2-1

2.1 Testing techniques 2-1
2.1.1 Black box testing 2-1
2.1.2 White box testing 2-1
2.2 Automatic test data generator 2-2
2.2.1 Pathwise generators 2-5
2.2.2 Data specification generators 2-10
2.2.3 Random testing 2-11

CHAPTER 3 .... 3-1 - 3-27

3. Genetic Algorithm 3-1

3.1 Introduction to Genetic Algorithms 3-1
3.2 Application of Genetic Algorithms 3-2
3.3 Overview and basics of Genetic Algorithms 3-5
3.4 Features of GAs 3-8
3.5 Population and generation 3-9
3.5.1 Convergence and sub optima solutions 3-9
3.6 Seeding 3-10
3.7 Representation of chromosomes 3-10
3.8 The way from one generation P(t) to the next generation P(t+1) 3-11
3.8.1 Fitness 3-11
3.8.2 Selection 3-12
3.8.2.1 Selection according to fitness 3-13
3.8.2.2 Random selection 3-14
3.8.3 Recombination operators 3-14
3.8.3.1 Crossover operator 3-14
3.8.3.1.1 Single crossover 3-15
3.8.3.1.2 Double crossover 3-16
3.8.3.1.3 Uniform crossover 3-16
3.8.3.2 Mutation operator 3-17
3.8.3.2.1 Normal mutation 3-17
3.8.3.2.2 Weighted mutation 3-18
3.8.4 Survive 3-19
3.8.4.1 SURVIVE_1 3-20

5.1.5.2 Gaussian function 5-10
5.1.5.3 Hamming distance function 5-11
5.1.6 Gray code 5-13
5.1.6.1 Results of using Gray code 5-15
5.1.7 Zero solution 5-16
5.1.8 Comparison of different crossovers 5-18
5.1.8.1 Results of crossover 5-18
5.1.9 Different mutations 5-20
5.1.10 The EQUALITY procedure 5-21
5.1.11 Using mutation only 5-22
5.1.12 Results of the quadratic equation solver 5-22
5.1.13 Random testing 5-23
5.1.14 Comparison between GA and Random testing 5-25
5.1.15 Interim Conclusion quadratic 5-26
5.2 Triangle classification procedure 5-29
5.2.1 Description of the triangle procedure 5-29
5.2.2 Result for the triangle classifier 5-31
5.2.2.1 Different Fitness functions and survive probabilities 5-31
5.2.2.2 Different crossover operator 5-31
5.2.3 Comparison with random testing and probabilities 5-32
5.2.3.1 Results Random Test 5-33
5.3 Interim conclusion triangle 5-35
5.4 Interim Conclusion 5-36

CHAPTER 6 ..... 6-1 - 6-30

6. The application of GAs to more complex data structure 6-1
6.1 Search procedures 6-1
6.1.1 Linear Search_1 procedure 6-1
6.1.1.1 Description 6-2
6.1.1.2 Different experiments with single loop condition 6-3
6.1.1.3 Experiments with full '*while ... loop*' testing 6-10
6.1.1.4 Random testing of LINEAR_1 6-12
6.1.1.5 Interim conclusion of LINEAR_1 6-14
6.1.2 Linear Search 2 6-15
6.1.2.1 Random testing of LINEAR_2 6-16
6.1.2.2 Interim conclusion LINEAR_2 6-16
6.1.3 Binary Search 6-17
6.1.3.1 Results of binary search 6-18
6.1.3.2 Full loop testing 6-20
6.1.3.3 Random testing of binary search 6-20
6.1.4 Using character in LINEAR_1 and BINARY_SEARCH 6-21
6.1.4.1 Conclusion of search procedures 6-22
6.2 Remainder procedure 6-24
6.2.1 Description 6-24
6.2.2 Results of Remainder 6-25
6.2.3 Random testing using REMAINDER procedure 6-27

6.2.4 Interim Conclusion 6-28
6.3 Conclusion of procedures with loop conditions 6-28

CHAPTER 7 ..... 7-1 - 7-15

7. Testing generic procedure 7-1
7.1 Generic Sorting Procedure: Direct Sort 7-1
7.2 Generic feature 7-3
7.3 Test strategy and data structure 7-4
7.4 Different Tests 7-8
7.5 Results of DIRECT_SORT 7-9
7.6 Test results 7-10
7.7 Interim Conclusion 7-14

CHAPTER 8 ..... 8-1 - 8-20

8. Adequate test Data 8-1
8.1 Adequacy of Test Data 8-1
8.1.1 Subdomain boundary test data 8-2
8.2 Mutation Testing and analysis 8-3
8.2.1 Overview of mutation analysis 8-3
8.2.2 Detection of mutants 8-3
8.2.3 Construction of mutants 8-5
8.3 Application of mutation testing to measure test data efficiency 8-6
8.3.1.1 Different mutants 8-7
8.3.1.2 First mutation results 8-10
8.3.1.3 Improving the testing tool with regard to mutation testing 8-12
8.3.1.4 Test results 8-13
8.4 Interim conclusion 8-18

CHAPTER 9 ..... 9-1 - 9-8

9. Review and Conclusion 9-1
9.1 Review of the project 9-1
9.2 Summary 9-1
9.2.1 Operators 9-1
9.2.2 Data types, fitness function and program structures 9-3
9.2.3 Representation; Gray vs. binary 9-4
9.2.4 Adequacy criteria and mutation testing 9-4
9.2.5 Random testing vs. GA testing 9-4
9.3 Conclusion 9-5
9.4 Contribution to published Literature 9-7
9.5 Further studies 9-7

REFERENCES..**R-1 - R-8**

APPENDIX A: Listing of TRIANGLE classifier function ....**A-1 - A-2**

APPENDIX B: Results for LINEAR SEARCH procedure ....**B-1 - B-1**

APPENDIX C: Listing of REMAINDER procedure ....**C-1 - C-1**

APPENDIX D: Listing of DIRECT_SORT procedure ....**D-1 - D-3**

Table of Figures

Figure 2.1: Sibling nodes. 2-6
Figure 2.2: Control flow tree for the 2-7
Figure 2.3: Example of an input space partitioning structure in the range of -15 to 15 2-8
Figure 3.1: Single crossover with $k = 5$. 3-15
Figure 3.2: Double crossover with $k = 2$ and $n = 5$. 3-16
Figure 3.3: Uniform crossover with crossing points at 1, 4, 5 and 7. 3-17
Figure 3.4: Before and after mutation. 3-18
Figure 3.5: Survival method. 3-20
Figure 3.6: Block diagram of GA. 3-23
Figure 3.7: Pseudo code of GA. 3-23
Figure 4.1: Overall structure of testing tool. 4-6
Figure 4.2: Software and control flow tree for the example. 4-7
Figure 4.3: Example with generated test data for generation G1 to G5. 4-12
Figure 4.4: Control flow tree of an '*if...then....else*' condition and the corresponding original software 4-13
Figure 4.5: Control flow tree of an '*if...then....else*' condition and the corresponding original (bold) software and instrumentation 4-14
Figure 4.6: Example of original software (displayed in bold) and the instrumentation. 4-15
Figure 4.7: Test data for the nodes 2 and 3. 4-16
Figure 4.8: Control flow trees of a '*while*' loop-statement with the corresponding software. 4-18
Figure 4.9: Control flow graph of a '*loop ... exit*' condition. 4-20
Figure 4.10: Loop testing with '*if*' statement inside. 4-21
Figure 4.11: Example of calculating Hamming distance. 4-22
Figure 5.1: Control flow tree for the quadratic procedure. 5-1
Figure 5.2: Illustrating global and local optima with regard to D = 0 using integers. 5-3
Figure 5.3: Required tests for different survival procedures and probabilities using reciprocal fitness function to give branch coverage. 5-6
Figure 5.4: Required tests for different survival procedures and probabilities using Hamming fitness function to give branch coverage. 5-7
Figure 5.5: Binary to Gray conversion. 5-15
Figure 5.6: Gray to Binary conversion. 5-15
Figure 5.7: Distribution of global solutions using binary coded representation where solution for $A = 0$ has been filtered out 5-17
Figure 5.8: Distribution of global solutions using Gray coded representation where solution for $A = 0$ has been filtered out 5-17
Figure 5.9: Distribution of global solutions using random testing where solution for solution for $A = 0$ has been filtered out 5-18
Figure 5.10: Pseudo code of EQUALITY procedure 5-21
Figure 5.11: CPU time over various input ranges for using random numbers and GA. 5-24
Figure 5.12: Individual fitness over a test run using GAs and Random Testing 5-25
Figure 5.13: Histogram of successful test runs. 5-26
Figure 5.14: The complete triangle control flow tree. 5-30
Figure 5.15: Executed branch distribution in log for random testing. 5-33
Figure 5.16: CPU time over various input ranges for using random numbers and GA. 5-34

Figure 5.17: Fitness distribution using Genetic Algorithms. 5-35
Figure 6.1: Control flow graph of LINEAR_1 search procedure. 6-2
Figure 6.2: Converging process towards global optimum using weighted Hamming 6-5
Figure 6.3: Converging process towards global optimum using unweighted Hamming 6-5
Figure 6.4: Converging process towards global optimum using reciprocal fitness. 6-6
Figure 6.5: Typical fitness distribution of linear search with full loop testing. 6-11
Figure 6.6: Comparison of random testing and Genetic Algorithm testing. 6-13
Figure 6.7: Control flow graph of LINEAR_2 procedure 6-15
Figure 6.8: Control flow graph of the binary search function 6-18
Figure 6.9: Required tests using reciprocal and Hamming fitness function 6-19
Figure 6.10: Control flow tree of the REMAINDER. 6-24
Figure 6.11: Distribution of off-line performance for the remainder procedure using GA. 6-27
Figure 7.1: Control flow graph of DIRECT_SORT 7-2
Figure 7.2: Control flow graph of procedure PARTITION. 7-2
Figure 7.3: Control flow graph of procedure INSERT. 7-2
Figure 7.4: Control flow graph of procedure SWAP. 7-2
Figure 7.5: Data structure of the new chromosome. 7-6
Figure 7.6: Usage of different array sizes as defined by *index_type* 7-6
Figure 7.7: Example of a chromosome using different data types. 7-8
Figure 8.1: Original and mutated statement causing shifting of subdomain boundary. 8-2
Figure 8.2: Definition of sub-expression for the quadratic equation solver problem. 8-8

Table of Listings

Listing 2.1: Example of software. 2-7
Listing 4.2: Example with instrumentation. 4-7
Listing 4.1: Listing of CHECK_BRANCH 4-14
Listing 4.2: Listing of LOOKING_BRANCH. 4-15
Listing 4.3: Listing of procedure calls for boundary testing approach. 4-16
Listing 4.4: Fitness function for different nodes. 4-17
Listing 4.5: Software listings for the instrumented procedures for a loop condition. 4-19
Listing 4.6: *'while'* loop condition with instrumented software. 4-20
Listing 4.7: Instrumented procedures in to a *'loop ... exit'* condition. 4-21
Listing 5.1: Code for the quadratic procedure. 5-1
Listing 6.1: Code of LINEAR_1 search procedure 6-2
Listing 6.2: Code of LINEAR_2 search procedure 6-15
Listing 6.3: Code of the binary search function 6-18
Listing 6.4: Code of a part of the REMAINDER 6-24
Listing 7.1: Type declaration of the chromosome. 7-6
Listing 7.2: Generic type declaration. 7-7

Table of Tables

Table 3.1 Binary coded representation of a chromosomes. 3-11
Table 3.2: Chromosomes with fitness values for the initial population. 3-11
Table 3.3: Population with different fitness values. 3-13
Table 3.4: Selected chromosomes after selection procedure. 3-13
Table 3.5: Pseudo code of procedure SELECT_F. 3-14
Table 3.6: Pseudo code of procedure SELECT_R. 3-14
Table 3.7: Result after crossover. 3-16
Table 3.8: Mutated chromosome (mutation at first bit position). 3-18
Table 3.9: Offspring population. 3-19
Table 3.10: Offspring, who survive into the next generation. 3-19
Table 3.11: Pseudo code of the basic survive procedure. 3-21
Table 3.12: Building blocks at bit position 1 and 2. 3-23
Table 4.1: Settings for the GA. 4-7
Table 4.2: First generation. 4-8
Table 4.3: Second generation. 4-9
Table 4.4: Offspring population generated by GA. 4-9
Table 4.5: Survival of offspring members. 4-10
Table 4.6: Third generation. 4-11
Table 4.7: Fourth generation. 4-11
Table 4.8: Fifth generation. 4-12
Table 4.9: Possible set-ups. 4-23
Table 5.1: Difference between binary-plus-sign code and two's complement representation. 5-4
Table 5.2: Results using different population sizes. 5-8
Table 5.3: Different Hamming fitness functions. 5-11
Table 5.4: Results from using different Hamming fitness functions. 5-12
Table 5.5: Comparison of binary and Gray code with MSB on the right hand side. 5-13
Table 5.6: Results of using different crossover operators. 5-19
Table 5.7: Results of using different mutation probability P_m. 5-20
Table 5.8: Results of using different values for P_E. 5-21
Table 5.9: Results using random and GA testing. 5-24
Table 5.10: Summary table of most significant results. 5-27
Table 5.11: Different crossover for the triangle procedure. 5-32
Table 5.12: Results using random and GA testing. 5-34
Table 5.13: Results of triangle using GA and random testing. 5-36
Table 6.1: Results of linear procedure for $A(1) = 1$. 6-3
Table 6.2: Results of generating $A(1)$ randomly for each test run in the range ±20000. 6-8
Table 6.3: Results of linear procedure for *zero* and *more than zero* iterations where the elements of the array are also changed by the GAs 6-9
Table 6.4: Results of LINEAR_1 procedure for full loop testing. 6-11
Table 6.5: Results using random and GA testing for full loop testing. 6-13
Table 6.6: Results of LINEAR_2 procedure for full loop testing using binary coding. 6-16
Table 6.7: Results of binary search procedure for full loop testing. 6-20
Table 6.8: Results of random testing with predefined number of iterations $NITS = 1$. 6-20

Table 6.9: Results for full loop testing using REMAINDER. 6-25
Table 6.10: Results of remainder procedure using different crossover operator. 6-26
Table 6.11: Results of random and GA testing. 6-28
Table 7.1: Results of testing DIRECT_SORT using integer data type. 7-11
Table 7.2: Results using integer data type without CONTROL_PARENTS. 7-12
Table 7.3: Results of testing DIRECT_SORT using record type of integer and. 7-13
Table 7.4: Results of DIRECT_SORT using record type of character and integer. 7-14
Table 8.1: First level of mutation analysis: Statement Analysis. 8-7
Table 8.2: Second level of mutation analysis: Predicate Analysis. 8-8
Table 8.3: Third level of mutation testing: Domain Analysis. 8-9
Table 8.4: Fourth level of mutation testing: Coincidental Correctness Analysis. 8-9
Table 8.5: Results of statement analysis. 8-14
Table 8.6: Results of predicate analysis. 8-14
Table 8.7: Results of domain analysis. 8-15
Table 8.8: Results of coincidental correctness analysis. 8-17

List of Abbreviations

P_C	Crossover probability
P_S	Survive probability
P_m	Mutation probability
P_{SZ}	Population size
P_E	Equality probability
Nits	Number of iterations
NoRT	Number of Random Tests
GA	Genetic Algorithm
P_{m_w}	Weighted mutation probability
S	Chromosome length
H_x	Hamming fitness function$_x$
C	Chromosome
LCSAJ	Linear Code Sequence And Jump
CPU	Central Processor Unit
MSB	Most Significant Bit
LSB	Least Significant Bit
F	Fitness value
M_G	MAX_GENERATION
ES	Evolutionstrategie

CHAPTER 1

Introduction

Between 40% and 50% of the software production development cost is expended in software testing, Tai [1980], Ince [1987] and Graham [1992]. It consumes resources and adds nothing to the product in terms of functionality. Therefore, much effort has been spent in the development of automatic software testing tools in order to significantly reduce the cost of developing software. A test data generator is a tool which supports and helps the program tester to produce test data for software.

Ideally, testing software guarantees the absence of errors in the software, but in reality it only reveals the presence of software errors but never guarantees their absence, Dijkstra [1972]. Even, systematic testing cannot prove absolutely the absence of errors which are detected by discovering their effects, Clarke and Richardson [1983]. One objective of software testing is to find errors and program structure faults. However, a problem might be to decide when to stop testing the software, e.g. if no errors are found or, how long does one keep looking, if several errors are found, Morell [1990].

Software testing is one of the main feasible methods to increase the confidence of the programmers in the correctness and reliability of software, Deason [1991]. Sometimes, programs which poorly tested, perform correctly for months and even years before some input sets reveal the presence of serious errors, Miller [1978]. Incorrect software which is released to market without being fully tested, could result in customer dissatisfaction and moreover it is vitally important for software in critical applications that it is free of software faults which might lead to heavy financial loss or even endanger lives, Hamlet [1987]. In the past decades, systematic approaches to software testing procedures and tools have been developed to avoid many difficulties which existed in ad hoc techniques. Nevertheless, software testing is the most usual technique for error detection in today's software industry. The main goal of software testing is to increase one's confidence in the correctness of the program being tested.

In order to test software, test data have to be generated and some test data are better at

finding errors than others. Therefore, a systematic testing system has to differentiate good (suitable) test data from bad test (unsuitable) data, and so it should be able to detect good test data if they are generated. Nowadays testing tools can automatically generate test data which will satisfy certain criteria, such as branch testing, path testing, etc. However, these tools have problems, when complicated software is tested.

A testing tool should be general, robust and generate the right test data corresponding to the testing criteria for use in the real world of software testing, Korel [1992]. Therefore, a search algorithm must decide where the best values (test data) lie and concentrate its search there. It can be difficult to find correct test data because conditions or predicates in the software restrict the input domain which is a set of valid data.

Test data which are good for one program are not necessarily appropriate for another program even if they have the same functionality. Therefore, an adaptive testing tool for the software under test is necessary. Adaptive means that it monitors the effectiveness of the test data to the environment in order to produce new solutions with the attempt to maximise the test effectiveness.

1.1 Objectives and aims of the research project

The overall aim of this research project is to investigate the effectiveness of Genetic Algorithms (GAs) with regard to random testing and to automatically generate test data to traverse all branches of software. The objectives of the research activity can be defined as follows:

- The furtherance of basic knowledge required to develop new techniques for automatic testing;
- To assess the feasibility of using GAs to automatically generate test data for a variety of data type variables and complex data structures for software testing;
- To analyse the performance of GAs under various circumstances e.g. large systems.
- Comparison of the effectiveness of GAs with pure random testing for software developed in ADA;
- The automatic testing of complex software procedures;
- Analysis of the test data adequacy using mutation testing;

The performance of GAs in automatically generating test data for small procedures is assessed and analysed. A library of GAs is developed and then applied to larger systems. The efficiency of GAs in generating test data is compared to random testing with regard to the number of test data sets generated and the CPU time required.

This research project presents a system for the generation of test data for software written in ADA83. The problem of test data generation is formed and solved completely as a numerical optimisation problem using Genetic Algorithms and structural testing techniques.

Software testing is about searching and generating certain test data in a domain to satisfy the test criteria. Since GAs are an established search and optimisation process the basic aim of this project is to generate test sets which will traverse all branches in a given procedure under test.

1.2 Hypotheses

In order to make my objectives clear several hypotheses are suggested and justified in the following chapters by evolving experiments which are described in section 4.6.

1. **Hypothesis:**

   Genetic Algorithms are more efficient than random testing in generating test data, see section 2.2.3. The efficiency will be measured as the number of tests required to obtain full branch coverage.

2. **Hypothesis:**

   A standard set of parameters for Genetic Algorithms can be established which will apply to a variety of procedures with different input data types. In particular, the following will be investigated:

   2_1 which of the following bit patterns is most appropriate for representing the input test-set: twos complement, binary with sign bit or Gray code; see also section 3.7;

   2_2 which of the following reproduction strategies is most efficient: selection at random or according to fitness), see section 3.8.2;

2_3 which crossover strategy is most efficient: single, double or uniform crossover, see section 3.8.3.1;

2_4 what size of population gives the best result, see section 3.5.1;

2_5 what mutation probability gives the best results, see section 3.5.1.

These investigations are described in detail in chapter 3. A standard set is determined in chapter 5 and confirmed in chapters 6 and 7;

3. **Hypothesis:**
   Test cases can be generated for loops with *zero*, *one*, *two* and *more than two* iterations, see section 4.7.2. The confirmation is in chapters 6 and 7.

4. **Hypothesis:**
   Genetic Algorithms generate adequate test data in terms of mutation testing and generating test data for the original (unmutated) software is better. A detailed description is in section 2.2.1. This is confirmed in chapter 8;

These hypotheses will be under close investigation through out the chapters and will be discussed in more detail in the chapter 3 and 5 where these different operators and parameters are introduced.

1.3 Testing criteria

The criterion of testing in this thesis is branch testing, see section 2.1.2. Our aim is to develop a test system to exercise every branch of the software under test. In order to generate the required test data for branch testing Genetic Algorithms and random testing are used. These two testing techniques will be compared by means of the percentage of coverage which each of them can achieve and by the number of test data which have to be generated before full branch coverage has been attained.

1.4 Structure of Thesis

Following this introductory chapter, Chapter 2 reviews various testing methods and applications for software testing. The advantages and disadvantages of these techniques

are examined and explained.

Chapter 3 describes the overall idea of GAs. An introduction to GAs is given and how and why they work is explained using an example. Various operators and procedures are explained which are used within a GA. Important and necessary issues of GAs are described.

Chapter 4 describes the technique which has been applied to test software. A detailed description of the application of GAs to software testing is explained and is shown with brief examples. Instrumentation of the software under test is explained.

The validity of any technique can only be ascertained by means of experimental verification. A significant part of the work reported in this thesis is the conduct of experiments which yield results which can be compared to the method of random testing.

Chapter 5 describes these experiments for a quadratic equation solver procedure and a triangle classifier procedure using different GAs by means of various settings. These experiments are conducted in order to investigate the effectiveness of using GA for software testing. Both procedures under test handle integer variables which are involved in complex predicates which makes the search for test data difficult. In addition the triangle procedure comprises various nested procedure declarations.

In Chapter 6, various linear search procedures, a binary search and a remainder procedure have been tested. Moreover, these procedures have '*loop*' conditions as well as '*if*' conditions. In contrast to the previous chapter they consist of more complex data types such as characters, strings and arrays.

Chapter 7 uses a commercially available generic sort procedure, DIRECT_SORT, which has nested procedure declarations and complex data structures such as records of integer and character variable arrays where the arrays have to be of variable length.

Chapter 8 describes an error - based testing method, also called mutation testing. The goal is to construct test data that reveal the presence or absence of specific errors and to measure the adequacy of the test data sets and so of the testing tool.

Chapter 9 gives an overall conclusion of the project. One main conclusion is that the proposed technique represents a significant improvement over random testing with regard to the required number of tests. The technique required up to two orders of magnitude fewer tests and less CPU time.

CHAPTER 2

Background of various automatic testing methods

Software testing is widely used in many different applications using various testing strategies. This chapter explains and gives an overview of the fundamental differences between several approaches to software testing.

2.1 Testing techniques

There are two different testing techniques; *black box* and *white box testing.*

2.1.1 Black box testing

In black box testing, the internal structure and behaviour of the program under test is not considered. The objective is to find out solely when the input-output behaviour of the program does not agree with its specification. In this approach, test data for software are constructed from its specification, Beizer [1990], Ince [1987] and Frankl and Weiss [1993]. The strength of black box testing is that tests can be derived early in the development cycle. This can detect *missing logic* faults mentioned by Hamlet [1987]. The software is treated as a black box and its functionality is tested by providing it with various combinations of input test data. Black box testing is also called *functional* or *specification based testing.* In contrast to this is white box testing.

2.1.2 White box testing

In *white box* testing, the internal structure and behaviour of the program under test is considered. The structure of the software is examined by execution of the code. Test data are derived from the program's logic. This is also called *program-based* or *structural testing*, Roper [1994]. This method gives feedback e.g. on coverage of the software.

There are several white box (structural) testing criteria:

- *Statement Testing*: Every statement in the software under test has to be executed at least once during testing. A more extensive and stronger strategy is branch testing.
- *Branch testing*: Branch coverage is a stronger criterion than statement coverage. It requires every possible outcome of all decisions to be exercised at least once Huang [1975], i.e. each possible transfer of control in the program be exercised. This means that all control transfers are executed, Jin [1995]. It includes statement coverage since every statement is executed if every branch in a program is exercised once. However, some errors can only be detected if the statements and branches are executed in a certain order, which leads to path testing.
- *Path testing*: In path testing every possible path in the software under test is executed; this increases the probability of error detection and is a stronger method than both statement and branch testing. A path through software can be described as the conjunction of predicates in relation to the software's input variables. However, path testing is generally considered impractical because a program with loop statements can have an infinite number of paths. A path is said to be '*feasible*', when there exists an input for which the path is traversed during program execution, otherwise the path is unfeasible.

2.2 Automatic test data generator

Extensive testing can only be carried out by an automation of the test process, claimed by Staknis [1990]. The benefits are a reduction in time, effort, labour and cost for software testing. Automated testing tools consist in general of an *instrumentator*, *test harness* and a *test data generator*.

Static analysing tools analyse the software under test without executing the code, either manually or automatically. It is a limited analysis technique for programs containing array references, pointer variables and other dynamic constructs. Experiments have shown that this kind of evaluation of code inspections (visual inspections) has found static analysis is very effective in finding 30% to 70% of the logic design and coding errors in a typical software, DeMillo [1987]. *Symbolic execution* and *evaluation* is a

typical static tool for generating test data.

Many automated test data generators are based on symbolic execution, Howden [1977], Ramamoorthy [1976]. Symbolic execution provides a functional representation of the path in a program and assigns symbolic names for the input values and evaluates a path by interpreting the statements and predicates on the path in terms of these symbolic names, King [1976]. Symbolic execution requires the systematic derivation of these expressions which can take much computational effort, Fosdick and Osterweil [1976]. The values of all variables are maintained as algebraic expressions in terms of symbolic names. The value of each program variable is determined at every node of a flow graph as a symbolic formula (expression) for which the only unknown is the program input value. The symbolic expression for a variable carries enough information such that, if numerical values are assigned to the inputs, a numerical value can be obtained for the variable, this is called symbolic evaluation. The characteristics of symbolic execution are:

- Symbolic expressions are generated and show the necessary requirements to execute a certain path or branch, Clarke [1976]. The result of symbolic execution is a set of equality and inequality constraints on the input variables; these constraints may be linear or non-linear and define a subset of the input space that will lead to the execution of the path chosen;
- If the symbolic expression can be solved the test path is feasible and the solution corresponds to a set of input data which will execute the test path. If no solution can be found then the test path is unfeasible;
- Manipulating algebraic expressions is computationally expensive, especially when performed on a large number of paths;
- Common problems are variable dependent loop conditions, input variable dependent array (sometimes the value is only known during run time) reference subscripts, module calls and pointers, Korel [1990];
- These problems slow down the successful application of symbolic execution, especially if many constraints have to be combined, Coward [1988] and Gallagher [1993].

Some program errors are easily identified by examining the symbolic output of a program if the program is supposed to compute a mathematical formula. In this kind of event, the output has just to be checked against the formula to see if they match.

In contrast to *static analysis*, *dynamic testing* tools involve the execution of the software under test and rely upon the feedback of the software (achieved by instrumentation) in order to generate test data. Precautions are taken to ensure that these additional instructions have no effect whatever upon the logic of the original software. A representative of this method is described by Gallagher *et al.* [1993] who used instrumentation to return information to the test data generation system about the state of various variables, path predicates and test coverage. A penalty function evaluates by means of a constraint value of the branch predicate how good the current test data is with regard to the branch predicate. There are three types of test data generators; *pathwise*, *data specification* and *random test data generator*.

A test set is run on the software under test, and the output is saved as the actual output of that test case. The program tester has to examine the output and decides whether it is correct, by comparing the actual output with the *expected-output*. If the output is incorrect, an error has been discovered, the program must be changed and testing must start again. This leads to *regression testing* executing all previous test data to verify that the correction introduced no new errors. BCS SIGIST [1995] defined regression testing as:

Retesting of a previously tested program following modification to ensure that faults have not been introduced or uncovered as a result of the changes made.

To finish testing, the tester will manually examine the output of the test cases to determine whether they are correct.

Deason [1991] investigated the use of rule-based testing methods using integers and real variables. His system uses prior tests as input for the generation of additional tests. The test data generator assigns values directly to input variables in conditions with constants and then increments and decrements them by small amounts to come closer to the boundary. The input values are doubled and halved resulting in much faster movements through the search space. Finally one input variable at a time is set to a random number.

The result of this project is that the rule-based method performed almost always better than random. Deason called his method *multiple-condition boundary coverage* where *multiple-condition coverage* means that test data exercise all possible combinations of condition (true and false) outcomes in every decision. Boundary here means that the test data has to be as close as possible to switching the conditions from true to false. He mentioned that it is not possible to generate test data which causes the execution of all branches in any arbitrary software, i.e. no algorithm exists for solving general non-linear predicates. In addition, his approach is restricted to numeric types such as integer data types. A rule based approach has always the drawback that a rule should exist for unforeseen problems which can be difficult to realise. If such a rule does not exist, the generation of test data can end in a local optimum solution and not in a global solution which will traverse a branch.

2.2.1 Pathwise generators

Pathwise test data generators are systems that test software using a testing criterion which can be path coverage, statement coverage, branch coverage, etc. The system automatically generates test data to the chosen requirements. A pathwise test generator consists of a program control flow graph construction, path selection and test data generation tool.

Deterministic heuristics have been used by Korel [1990, 1992]. He used a dynamic test data generation approach which is based on a pathwise test data generator to locate automatically the values of input variables for which a selected path is traversed. His steps are program control flow graph construction and test data generation. The path selection stage is not used because if unfeasible paths are selected, the result is a waste of computational effort examining these paths. Most of these methods use symbolic evaluation to generate the test data. Korel's method is based on data flow analysis and a function minimisation approach to generate test data which is based on the execution of the software under test. Since the software under test is executed, values of array indexes and pointers are known at each point in the software execution and this overcomes the problems and limitations of symbolic evaluations.

In Korel's approach a *branch function* is formed out of the branch predicates where the

control should flow. These functions are dependent on the input variables which can be difficult to represent algebraically, but the values can be determined by program execution. The idea is now to minimise these branch functions which have a positive value when the desired branch is not executed. As soon as the value becomes negative the branch will be traversed. The minimisation of the branch function demands that the path, up to the node where the sibling node should be executed, will be retained for the next test data.

A boolean condition has two branches with a true and a false node, see Figure 2.1. A reference to the sibling node means, the other node corresponding to the current executed node. For example the sibling node of 'True branch' is 'False branch'.

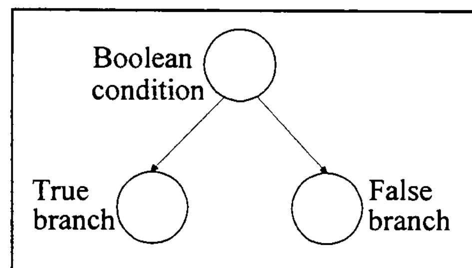


Figure 2.1: Sibling nodes.

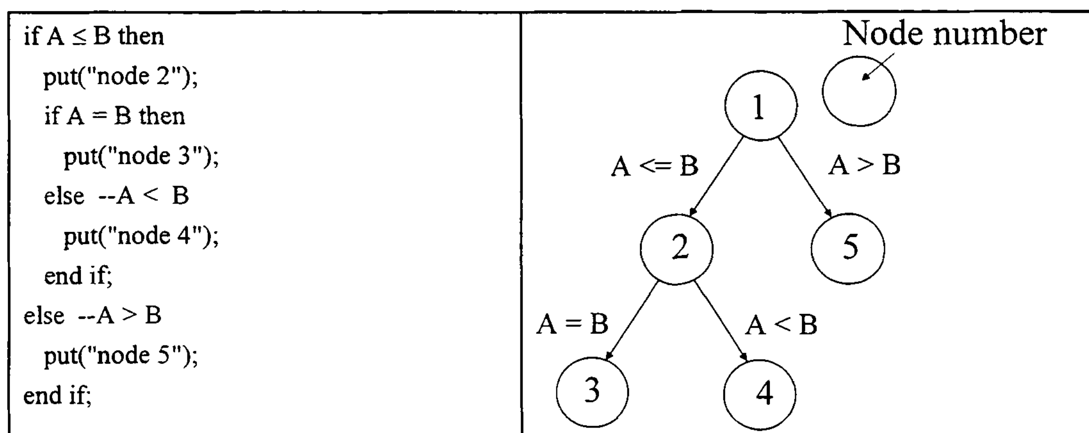
Korel's method of generating test data is based on the *alternating variable method* which consists of minimising the current branch function. Each input variable in turn is increased or decreased by a small amount in an *exploratory search*; and by larger amounts in a *pattern search*. The effect of this is one of the following:

- a decrease in the branch function value so that the direction in which to proceed for changing a variable is known, and keep changing in this direction and the new test data and value replaces the old one;
- an increase of the branch function value which results in changing the direction of manipulating the variable;
- no effect so that the next variable will be manipulated.

If one cycle is completed, the method continuously cycles around the input variables until the desired branch is executed or no progress (decreasing the branch function) can be made for any input variable. To reduce the search time significantly for the *alternating variable* approach, Korel applies a *dynamic data flow analysis* to determine

those input variables which have an influence for the current branch function value on a given program input in order to reduce the number of unnecessary tries. Therefore, only these variables need to be manipulated during the minimisation process. The disadvantage of this approach is that it is not a general approach to software testing because his approach can fail depending on the initial test set, because the subdomain of a branch may comprise small and disconnected regions, see e.g. section 5.1 and Figure 5.2. In this case, this local search technique has to be replaced by a global optimisation technique, otherwise only local minima for the branch function value may be found which might not be good enough traverse the desired branch. This is where Genetic Algorithms gain their advantages and strength as a global optimisation process because they do not depend on a continuous and connected domain.

The basic idea of domain testing, White and Cohen [1978, 1980], is that each path of the software belongs to a certain subdomain, which consists of those inputs which are necessary to traverse that path.



```
if A ≤ B then
  put("node 2");
  if A = B then
    put("node 3");
  else --A < B
    put("node 4");
  end if;
else --A > B
  put("node 5");
end if;
```


Listing 2.1: Example of software.

Figure 2.2: Control flow tree for the example.

An example of these subdomains are shown in Figure 2.3 for the software example in Listing 2.1 and the control flow tree in Figure 2.2.

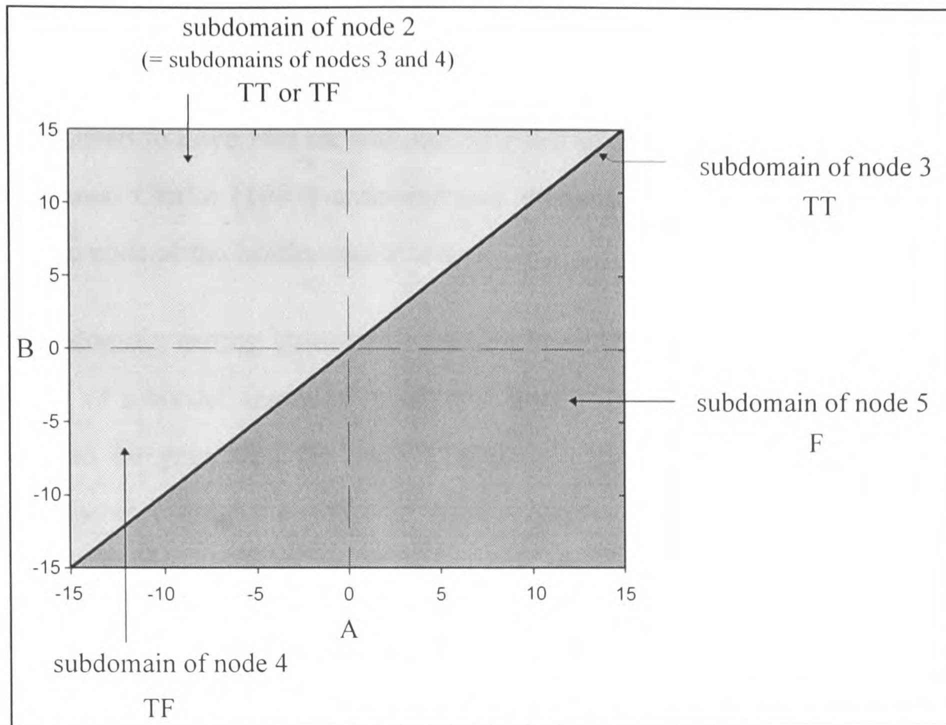


Figure 2.3: Example of an input space partitioning structure in the range of -15 to 15.

The domain is the set of all valid test sets. It is divided into subdomains such that all members of a subdomain cause a particular branch to be exercised. Alternatively, a different division of subdomains is formed for path testing etc. The domain notation may be based upon which branch (true or false) has been taken. A character code specifies the branch (here also path), e.g. TT, TF, F. In addition the respective node is also mentioned. The subdomain of node 5 is the dark grey area, the subdomain of node 3 is the diagonal line, the subdomain of node 4 is the light grey area whereas the subdomain of node 2 includes the light grey area (node 2) plus the diagonal line (node 3).

Domain testing tries to check whether the border segments of the subdomains are correctly located by the execution of the software with test data to find errors in the flow of the control through the software. These test data belong to an input space which is partitioned into a set of subdomains which belong to a certain path in the software. The boundary of these domains is obtained by the predicates in the path condition where a border segment is a section of the boundary created by a single path condition. Two types of boundary test points are necessary; *on* and *off* test points. The *on* test points are on the border within the domain under test, and the *off* points are outside the border

within an adjacent domain which means if the software generates correct results for all these points then it can be considered that the border locations are correct. White and Cohen proposed to have two *on* and one *off* point where the off point is in between the two *on* points. Clarke [1982] extended this technique and suggested having two *off* points at the ends of the border under test.

Therefore, domain testing strategies concentrate on *domain errors* which are based on the shifting of a border segment by using a wrong relational operator. This means test data have to be generated for each border segment (predicate) to see whether the relational operator and the position of the border segment are correct, White and Cohen [1980] and see chapter 4 for further detail. Hence points close to the border (called boundary test data) are the most sensitive test data for analysing the path domains and revealing domain errors, Clarke and Richardson [1983].

Domain testing, therefore, is an example of partition testing. It divides the input space into equivalent domains and it is assumed that all test data from one domain are expected to be correct if a selected test data from that domain is shown to be correct.

25% of all errors (bugs) arise out of structural and control flow errors according to Beizer [1990], pp. 463. Two different types of errors were identified by Howden [1976]. A *domain error* occurs when a specific input takes the wrong path because of an error in the control flow of the program which will end in a different subdomain. A '*computational error*' is based on an input which follows the correct path, but an error in some assignment statement causes the wrong output. In complex systems with several input variables it is usually hard to find data points which belong to a small subdomain because the subdomain does not have many possible data points. Zeil *et al.* [1992] and White and Cohen [1978] used domain testing in their strategies but restrict it to linear predicates handling floating point variables. They use a symbolic analysis for the paths and a geometrical approach for test data generation. An example is in chapter 4 of generating test data using Genetic Algorithms to check these subdomains and boundaries of a small program.

Mutation testing is an implementation of an error-based testing method, DeMillo [1978]. It is based on the introduction of a single syntactically-correct fault e.g. by

manipulation of conditions and statements. This new program is called mutant. Mutation testing is used to show the absence of prespecified faults, Morell [1990]. After checking the output of the original program to be correct (by some oracle), the same test data is input to the mutant and if the output of the mutant differs from the expected output the mutant is killed by the test data because the error is detected. If the mutant has not been killed and it is said to be still alive and more test data have to be generated to kill it. If a mutant cannot be killed then either it is an equivalent mutant (no functional change) or the test data sets are not of sufficient quality. This revealed a weakness in the test data (low quality test data). By using test data which do not kill the mutants, it can be said that either the generating tool for test data is not good enough and the original program has to be re-examined or additional test data have to be produced until some threshold is met where it appears that it is impossible to reveal a difference. The checking of the correctness is a major factor in the high cost of software development. Checking correctness of test data can be automated by using an oracle or post conditions, Holmes [1993] or from input - output specification. The main task is to generate test data that reveals a difference in the mutant's behaviour corresponding to the original software. A detailed description and application is given in chapter 8. Mutation testing shows only the absence of certain faults. However, it is very time consuming to generate and test a large number of mutant programs. Hypothesis 4 is formulated which states that GAs are robust to generate test data and that it is better to generate test data for the original or the mutant program.

2.2.2 Data specification generators

Deriving test data from specification belongs to the '*black-box*' testing method. Such a strategy generate test cases and test data e.g. from formal Z specification, Yang [1995]. The test data can then be applied to software and the effectiveness can be measured, e.g. using ADATEST (ADATEST is an automatic testing system for Ada software which measures for example the percentage of statements executed or branches covered).

A disadvantage is the need for a formal specification for the software which does not often exist, Gutjahr [1993].

2.2.3 Random testing

Random testing selects arbitrarily test data from the input domain and then these test data are applied to the program under test. The automatic production of random test data, drawn from an uniform distribution, should be the default method by which other systems should be judged, Ince [1987]. Statistical testing is a test case design technique in which the tests are derived according to the expected usage distribution profile.

Taylor [1989], Ould [1991] and Duran [1981] suggested that the distribution of selected input data should have the same probability distribution of inputs which will occur in actual use (operational profile or distribution which occurs during the real use of the software) in order to estimate the operational reliability.

Hamlet [1987] mentioned that the operational distribution for a problem may not be known and a uniform distribution may choose points from an unlikely part of the domain which can lead to inaccurate predictions, however, he still favours this technique. Duran [1981] had the opinion that an operational profile is not as effective for error detection as a uniform distribution. Taylor [1989] mentioned that concentrating on a certain feature using partition testing tended to be easier and simpler to generate test data than actual user inputs (operational profile) because they are focused on a particular feature. Partitioning testing is less effective than random testing in detecting faults which cause a printer controller to crash, Taylor [1989]. Random testing is the only standard in reliability estimation, Hamlet and Taylor [1990], in the user application because it can use data which resemble the user's operational profile. Partition testing in general can not supply this information because it focuses on test data in partitions that are more likely to fail, so that the failure rate for partition testing would be higher than that in expected actual use. If it is not known where the faults are likely to be, partition testing is not significantly better than random testing.

Hamlet and Taylor [1990] mentioned that there is not much difference between partition and random testing in terms of finding faults. Hamlet showed that random testing is superior to partition testing with regard to human effort especially with more partitions and if confidence is required. For a small number of sub-domains partition testing will perform better than random testing.

On the contrary Deason [1991] commented that random number generators are ineffective in that they rarely provide the necessary coverage of the program. Myers [1979] strengthened this comment and is of the opinion that random testing is probably the poorest methodology in testing. However, Duran and Ntafos [1984] and Duran [1981] stated that many errors are easy to find, but the problem is to determine whether a test run failed. Therefore, automatic output checking is essential if large numbers of tests are to be performed. They also said that partition testing is more expensive than performing an equivalent number of random tests which is more cost effective because it only requires a random number generator and a small amount of software support.

DeMillo [1978] proved that the adequacy of random data is very dependent on the interval (range) from which the data is generated. Data from poorly chosen intervals are much worse than those from well chosen intervals. Duran and Ntafos [1984] agreed that the change of range for random testing has a great effect. Further they mentioned a disadvantage of random testing which is to satisfy equality values which are difficult to generate randomly.

Moranda [1978], Bertolino [1991] commented, the advantage of random testing is normally that it is more stressing to the program under test than hand selected test data, but on the other hand random inputs may never exercise both branches of a predicate which tests for equality. Even in the case that random testing is cheaper than partition testing, the slight advantage of random testing could be compensated for by using more random tests and there is no assurance that full coverage can be obtained, e.g. if equality between variables are required. And secondly it may mean examining the output from thousands of tests.

Random testing was especially recommended for the final testing stage of software by Tsoukalas [1993] and Girard and Rault [1973]. Duran and Ntafos [1984] recommended a mixed final testing, starting with random testing, followed by a special value testing method (to handle exceptional cases). Ince [1986] reported that random testing is a relatively cheap method of generating initial test data.

It is decided to use random testing as a benchmark for our Genetic Algorithm testing system as suggested by Ince [1987]. It offers a good comparison between the systems so

that also other testing tool system can be easily compared indirectly to our system. Whether the comparison of GA's with random testing is appropriate, especially when generating test data for disconnected subdomains, will be examined and discussed in chapters 5, 6, 7 and 8. Therefore, the hypothesis 1 is formulated, see section 1.2. Are using GAs in order to generate test data more effective than using random testing?

The next chapter explains the method of Genetic Algorithms and their features and characteristics. An example shows the method of working of the Gas.

CHAPTER 3

Genetic Algorithm

Optimisation problems arise in almost every field, especially in the engineering world. As a consequence many different optimisation techniques have been developed. However, these techniques quite often have problems with functions which are not continuous or differentiable everywhere, multi-modal (multiple peaks) and noisy. Therefore, more robust optimisation techniques are under development which may be capable of handling such problems. In the past biological and physical approaches have become of increasing interest to solve optimisation problems, including for the former neural networks, genetic algorithms and evolution strategies (ESs) and for the second simulated annealing, Hills and Barlow [1994], Rayward-Smith and Debuse [1994], Bayliss [1994], Golden and Skiscim [1986], Hoffmann *et al.* [1991], Osborne and Gillett [1991].

Other optimisation techniques are:

- Tabu search, Glover [1989], Reeves *et al.* [1994], Rayward-Smith and Debuse [1994];
- Simplex method, Box [1965];
- Hooke Jeeves, Hooke and Jeeves [1961];
- Gradient method, Donne *et al.* [1994].

This chapter explains the features and methods of Genetic Algorithms. An introduction to genetic algorithms is followed by an optimisation example using genetic algorithms.

3.1 Introduction to Genetic Algorithms

Genetic algorithms (GAs) represent a class of adaptive search techniques and procedures based on the processes of natural genetics and Darwin's principal of the survival of the fittest. There is a randomised exchange of structured information among a population of artificial chromosomes. GAs are a computer model of biological evolution. When GAs are used to solve optimisation problems, good results are obtained

surprisingly quickly. In the context of software testing, the basic idea is to search the domain for input variables which satisfy the goal of testing.

3.2 Application of Genetic Algorithms

Creatures are the perfect problem solver. In the amount of tasks which they have to cope with (e.g. adaptation, changing environment), they do better by far than the best computer programs to the frustration of programmers because these organisms acquire their ability by the apparently aimless mechanism of evolution.

GAs have been used in many different applications as an adaptive search method, e.g. by Grefenstette *et al.* [1985 b], Allen and Lesser [1989], and Jog *et al.* [1989].

The fundamental concept of GAs is to evolve successive generations of increasingly better combinations of those parameters which significantly effect the overall performance of a design. The GAs come from the evolution strategy. Perhaps the slowness of biological evolution has lead to the fallacy that evolution strategies are in principle time consuming and less efficient.

However, the Berlin Professor for the science of engineering, Rechenberg, successfully developed independently and applied a selection - mutation - strategy, with the name *Evolutionstrategie (ES)*, on the basis of trial and error principle in the early 1960s. Rechenberg [1965] and Schwefel [1989] developed an optimal solid shape for the flow technique and achieved astonishing shapes for a nozzle which are distinguished by their high efficiency. Mutation was the key operator in his investigation. He also applied ES to determine the optimum configuration of five plates of steel in which each of them could have fifty one different positions corresponding to a search space consisting of some 3.45×10^8 plate configurations. An optimal solution was achieved by using the ES. By selecting an experiment with a known optimal solution Rechenberg successfully demonstrated the capabilities of an evolutionary algorithm.

This result is very impressive because the experimental method was quite simple and the mathematical approach failed due to the complexity. The disadvantage of a random method which is that no step builds upon another is avoided by using these evolution strategies. Its steps are based on the experience which has been gained from previous

trials, Abblay [1987]. Many other projects have used evolutionary strategies, among them are the development of a right-angled pipe with minimum flow resistance and other structural elements Parmee [1992].

A parallel development of evolutionary algorithms has also taken place in the USA. Seminal work concerning the formulation and behaviour of GAs was pioneered by Holland [1975] in his research on adaptation in natural and artificial systems at the University of Michigan (USA). Three basic operators are responsible for GAs: *selection*, *crossover* and *mutation*. The main genetic operator is crossover which performs recombination (mixing) of different solutions to ensure that the genetic information of a child life form is made up of the elements (genes) from each parent. He simulated the methods used when biological systems adapt to their environment in computer software models to solve optimisation problems. Also in the former USSR the method of evolution has been an accepted technique for many years, Zhigljavsky [1991].

Evolution avoids one of the most difficult obstacles which the software designer is confronted: the need to know in advance what to do for every situation which may confront a program. The advantage of GAs is the fact that they are adaptive. These GAs have already achieved epoch-making solutions for complex tasks like the construction of an aeroplane turbine. Evolution is under the influence of two fundamental processes; natural selection and recombination. The former determines which individual member of a population is selected, survives and reproduces, the latter ensures that the genes (or entire chromosome) will be mixed to form a new one. Human beings have used a combination of crossbreeding and selection, to breed more productive corn, faster racehorses or more beautiful roses for thousands of years, Holland [1992].

Goldberg [1989] mentioned that various engineering projects had applied GAs to solve problems, e.g. to optimise a gas pipeline control. This problem was controlled by non-linear state transition equations that impose the pressure drop through the pipelines and pressure rise across compressors.

Other applications describe the use of GAs to the optimisation of a ten member plane truss, Goldberg and Samtani [1986]. The objective of this problem is to minimise the

weight of the structure under the condition of maximum and minimum stress constraints on each member. As reported the GA always showed optimal solutions.

Grefenstette and Fitzpatrick [1985 a] considered a medical imaging system problem where the problem lies in the registration of digital images. The functions which are to be optimised in image registration are the measures of the difference between (in this case) two x-ray images, one taken prior to the injection of dye into the artery and one taken following the injection. The images differ because of motion which has taken place between the two acquisition times. The two images are digitised and subtracted pixel by pixel with the desired end result being a difference image that clearly outlines the interior of the subject artery. By performing a geometrical transformation which warps one image relative to the other it is possible to improve the registration of the images so that the difference which is due to the motion is reduced.

GAs are also applied to the classical problem of the Prisoner's Dilemma problem, studied by Mühlenbein [1991 a], Fujiki and Dickinson [1987] and Wilson [1987]. In its simplest form, each of the two players have a choice of co-operating with the other or defecting. Grefenstette *et al.* [1985 b] and Oliver *et al.* [1987] applied GAs to the well known combinatorial optimisation Travelling Salesman Problem (TSP). The optimisation problem consists in finding the shortest distance (normally Euclidean distance) between n cities. Shultz *et al.* [1992, 1993] used GA in order to test autonomous vehicle software controllers. The task for this application is to search for combinations of faults that produce abnormal vehicle controller performance by comparing a controller to a chosen set of fault scenarios within a vehicle simulator. They concluded that this approach using GA is an effective method compared to manual testing of sophisticated software controllers.

In addition, GAs have been applied to the optimisation for example of the design of a concrete shell of an arch dam (large scale hydropower scheme) Parmee [1994]; the design of digital filters, Suckley [1991], Roberts and Wade [1994]; the design of cooling hole geometry of gas turbine blades, Parmee *et al.* [1993], Parmee and Purchase [1991]; design of microwave absorbers (low-profile radar absorbing materials) which results in a reduction of the radar signature of military hardware, Tennant and Chambers [1994]

and the generation of test patterns for VLSl circuits, O'Dare *et al.* [1994].

3.3 Overview and basics of Genetic Algorithms

GAs offer a robust non-linear search technique that is particularly suited to problems involving large numbers of variables. The GA achieves the optimum solution by the random exchange of information between increasingly fit samples and the introduction of a probability of independent random change. Compared to other search methods, there is a need for a strategy which is global, efficient and robust over a broad spectrum of problems. The strength of GAs is derived from their ability to exploit in a highly efficient manner, information about a large number of individuals. This search method is modelled on natural selection by Holland [1992] whose motivation was to design and implement a robust adaptive system. GAs are being used to solve a variety of problems and are becoming an important tool in machine learning and function optimisation, Goldberg [1989]. Natural selection is used to produce adaptation.

GAs derive their name from the fact that they are loosely based on models of genetic change in a population of individuals, in order to effect a search mechanism with surprising power and speed. These algorithms apply genetically inspired operators to populations of potential solutions in an iterative fashion, creating new populations while searching for an optimum solution. The key word here is population. The fact that many points in the space are sampled in parallel shows that genetic algorithms are a global optimisation technique. GAs do not make incremental changes to a single structure, but maintain a population of structures from which new structures are created using genetic operators. The evolution is based on two primary operators: *mutation* and *crossover*. The power of genetic algorithms is the technique of applying a recombination operator (crossover and mutation) to a population of individuals. Despite their randomised nature, GAs are not a simple random search. GAs take advantage of the old knowledge held in a parent population to generate new solutions with improved performance. Thereby, the population undergoes simulated evolution at each generation. Relatively good solutions reproduce; relatively bad ones die out and are replaced by fitter offspring.

An important characteristic of genetic algorithms is the fact that they are very effective

when searching or optimising spaces that are not smooth or continuous. These are very difficult or impossible to search using calculus based methods, e.g. hill climbing.

Genetic algorithms may be differentiated from more conventional techniques by the following characteristics:

1. A representation for the sample population must be derived;
2. GAs manipulate directly the encoded representation of variables, rather than manipulation of the variables themselves;
3. GAs use stochastic rather then deterministic operators;
4. GAs search blindly by sampling and ignoring all information except the outcome of the sample;
5. GAs search from a population of points rather than from a single point, thus reducing the probability of being stuck at a local optimum which make them suitable for parallel processing, see section 3.5;

GAs are iterative procedures that produce new populations at each step. A new population is created from an existing population by means of performance evaluation, selection procedures, recombination and survival. These processes repeat themselves until the population locates an optimum solution or some other stopping condition is reached, e.g. number of generation or time.

The initial population comprises a set of individuals generated randomly or heuristically. The selection of the starting generation has a significant effect on the performance of the next generation. In most GAs, individuals are represented by a fixed-length string over a finite alphabet. The binary alphabet is one of many possible ways of representing the individuals. GAs work directly with this representation and they are difficult to fool because they are not dependent upon continuity of the parameter space and existence of a derivative.

The process is similar to a natural population of biological creatures where successive generations are conceived, born and raised until they themselves are ready to reproduce. This population-by-population approach is very different from the more typical search methods of engineering optimisation. In many search methods, we move gingerly from

a single point in the decision space to the next, using some decision rule to tell us how to get to the next point (hill climbing). This point-by-point method is dangerous because it often locates local peaks in the search space. GAs work from a population of points (individuals) simultaneously climbing many peaks in one generation (parallel), thus reducing the probability of finding a local optimum. To get a starting population, we can generate a number of strings at random, or if we have some special prior knowledge of good regions of the decision space, we may plant seeds within the population to help things along. Regardless of the starting population, the operators of genetic algorithm have found members of high fitness quickly in many applications studied to date.

A string of a population can be considered as concatenated sub-strings (input variables) to represent a chromosome. The individual bits of the string represent genes. The length of a string is S and a population of strings contains a total of P_{SZ} strings.

Once the initial population has been created the evaluation phase begins. The GAs require that members of the population can be differentiated according to the string's fitness. The parameter combinations are then processed by a model of the system under test. The relative fitness of each combination is determined from the model's output. Fitness is defined as a non negative function which is to be maximised. An increase in the population average fitness is the overall effect of genetic algorithms.

The members that are fitter are given a higher probability of participating during the selection and reproduction phases and the others are more likely to be discarded. Fitness is measured by decoding a chromosome in the corresponding variables to an objective function (which is specific to the problem being solved). The value returned by the objective function is used to calculate a fitness value. The fitness is the only feedback facility which maintains sufficient selective differences between competing individuals in a population stated by DeJong [1993]. The genetic algorithms are blind; they know nothing of the problem except the fitness information.

In the selection phase, chromosomes of the population may be chosen for the reproduction phase in several ways: for example, they may be chosen at random, or preference may be given to the fitter members.

During the reproduction phase, two members are chosen from the generation. The evolutionary process is then based on the genetic or recombination operators, crossover and mutation, which are applied to them to produce two new members (offspring) for the next generation.

The crossover operator couples the items of two parents (chromosomes) to generate two similar offspring, which are created by swapping corresponding substrings of its parents. The idea of crossover is to create better individuals by combining genetic material (genes) of fitter parents. The mutation operator alters one or more genetic cells (genes) of a selected structure with a low probability. This ensures a certain diversity in the genetic chromosomes over long periods of time and prevents stagnation near a local optimum. This means a complete new population of offspring is formed. A predefined survival strategy determines which of the parent and offspring survive.

The whole process is repeated generation by generation until a global optimum is found or some other stopping condition is reached. One of the disadvantages can be the excessive number of iterations required and therefore the amount of computational time.

3.4 Features of GAs

GAs are quite successful in solving problems of the type that are too constrained for more conventional strategies like hill climbing and derivative based techniques. A problem is to maximise a function of the kind $f(x_1, x_2, ..., x_m)$ where $(x_1, x_2, ..., x_m)$ are variables which have to be adjusted towards a global optimum. The bit strings of the variables are then concatenated together to produce a single bit string (chromosome) which represents the whole vector of the variables of the problem. In biological terminology, each bit position represents a gene of the chromosome, and each gene may take on some number of values called alleles.

In the following sections the method of GAs is explained and how and why they work. The basic structure, a variety of operators and control parameters are explained. An example will be taken of a function which is to be optimised. An explanation regarding the population and chromosome, fitness, selection, crossover, mutation and survival procedure will be given.

3.5 Population and generation

A population is like a list of several guesses (database). It consists of information about the individuals. As in nature, a population in GAs has several members in order to be a healthy population. If the population is too small inbreeding could produce unhealthy members. DeJong [1988] mentioned that the population size should be generally in the range of 50 - 100 members, although we find out that a different size can be beneficial, see section 6.1.1.2. The population changes from one generation to next. The individuals in a population represent solutions. The advantage of using a population with many members is that many points in a space are searched in one generation. GAs are therefore highly suited for parallel processing, Robertson [1987], Mühlenbein [1989], Georges-Schleuter [1989] and Goldberg [1989]. This sets the GAs apart from other search methods.

3.5.1 Convergence and sub optima solutions

A generation is said to have premature by converged when the population of a generation has a uniform structure at all positions of the genes without reaching an optimal structure, Baker [1985]. This means that the GA or the generation has lost the power of searching and generating more better solutions.

As we shall see later in 5.1.4, generally small populations can quickly find good solutions because they require less computational effort (fewer evaluations per generation). However, premature convergence is generally obtained in a small population and the effect is that the population is often stuck on a local optimum. This can be compensated by an increased mutation probability, see section 5.18, which would be similar to a random testing method. Larger populations are less likely to be caught by local optima, but generally take longer to find good solutions and an excessive amount of function evaluation per generation is required. A larger population allows the space to be sampled more thoroughly, resulting in more accurate statistics. Samples of small populations are not as thorough and produce results with a higher variance. Therefore, a method must be set up in order to find a strategy which will avoid converging towards a non optimum solution. Hypothesis 2_4 (see section 1.2), therefore, investigates the size of a population. Hypothesis 2_5 studies the percentage of

probability of mutation on average per chromosome.

3.6 Seeding

In order to start the optimisation method, the first population has to be generated. It can be seeded with a set of parameter values which can influence the search through the space. It can help to speed up the location of an optimum. Some systems have used parameter values from the previous experiments to provide a portion of the initial population, Powell [1989]. Alternatively values can be used which the user believes are in the right area of the search space to find an optimum faster. Normally the seeding is performed by random selection which means that random data are generated.

3.7 Representation of chromosomes

DeJong [1993] found out that the representation of the chromosome can itself affect the performance of a GA-based function optimiser. There are different methods of representing a chromosome in the genetic algorithm, e.g. using binary, Gray, integer or floating data types. The two main representations which will be used in this project are binary with sign bit and Gray code representation, hypothesis 2_1.

The most common representation, invented by Holland [1975], is the bit format. The variable values are encoded as bit strings, composed of characters copied from the binary alphabet {0, 1}. This kind of representation has turned out to be successful and was applied by Holland. He suggested that GAs are most effective when each gene takes on a small number of values and that binary genes are optimal for GA adaptive searching. A binary representation is not only convenient because of the GA's nature, but also for implementation by computers. In general, all bit strings within a population have the same format. A bit string format describes how it is sub-divided into contiguously placed binary bit fields, see Table 3.1. A single chromosome is the solution to a problem which can consist of a set of variables. If the problem consists of three input variables A, B and C, then the chromosome could look like the example in Table 3.1. This implies that all bit strings in the population have the same length. Each of these bit fields (A, B and C) represent an input variable value and its smallest unit is one bit which carries the information, Lucasius and Kateman [1993].

Chromosome												
A				B				C				
0	1	0	1	0	0	1	1	1	0	1	0	A = 5 B = 3 C = 9
0	0	1	1	0	0	1	0	1	0	1	0	A = 3 B = 2 C = 10
0	1	1	0	1	1	1	0	1	1	1	1	A = 6 B = 14 C = 15
0	0	0	0	0	0	0	1	1	0	0	0	A = 0 B = 1 C = 8

Table 3.1 Binary coded representation of a chromosomes.

3.8 The way from one generation P(t) to the next generation P(t+1)

This section shows an example of a working GA, to explain the function of various parameter settings and the GAs property.

3.8.1 Fitness

Fitness expresses how good the solution of the chromosome is in relation to the global optimum. This kind of value will be calculated for each chromosome in each population by a fitness function. The fitness value is used to compare the individuals and to differentiate their performance. An individual which is near an optimum solution gets a higher fitness value than an individual which is far away. The fitness value is the only feedback from the problem for the GA. The GA does not need any knowledge about the problem and it is blind in all other respects. A difficult issue in using GA is often the attempt to find a suitable fitness function which calculates the fitness value, and expresses the problem as well as possible. Every point in the search space must be represented by a valid fitness value.

For example , suppose that the function to optimise is $f(A) = A^2$ with ($A \in [0,15]$) and the fitness function has in this case the same form:

$$fitness_i = A^2 \qquad (4.1.)$$

The initial population is generated randomly. The population will only consist of one input variable per chromosome and four individuals per generation.

Chromosome	A_i	Fitness (f_i)
C_1	5	25
C_2	3	9
C_3	6	36
C_4	1	1

Table 3.2: Chromosomes with fitness values for the initial population.

Table 3.2 shows the chromosomes with their fitness values calculated by the fitness function (4.1). The total fitness of the population is calculated in equation (4.2):

$$fitness_{total} = \sum_{i=1}^{4} f_i = 71 \qquad (4.2)$$

The higher the fitness value, the better and closer the individual is towards the global optimum, which is in this case a value of $A = 15$.

3.8.2 Selection

The selection operator chooses two individuals from a generation to become parents for the recombination process (crossover and mutation). There are different methods of selecting individuals, e.g. randomly or with regard to their fitness value. This issue is formalised in hypothesis 2_3 which asks whether random selection or selection according fitness is better and in which instances this will be.

If the individuals are selected with regard to their fitness value, this guarantees that the chromosomes with a higher fitness value have a higher likelihood of being selected, the others are more likely to be discarded. Using an elitist method, the individual with the highest fitness value has to be selected. The user has the choice in deciding what kind of selection procedure should be taken.

A ranking system is necessary when the individuals are selected according to their fitness performance. There are many different ways to realise a ranking system. One method is using the fitness value in order to calculate the $f_{i,norm}$ equation 4.3 and then the $f_{i,accu}$ equation 4.4. The result can be seen in Table 3.3. We define:

$$f_{i,norm} = \frac{f_i}{\sum_{i=1}^{P_{sz}} f_i} \qquad (4.3)$$

where $f_{i,norm}$ is the normalised fitness for the ith chromosome
and P_{SZ} is the Population size.

$$f_{i,accu} = \sum_{k=1}^{i} f_{k,norm} \qquad (4.4)$$

where $f_{i,accu}$ is the accumulative normalised fitness of the ith chromosome.

Chromosomes	A_i	f_i	$f_{i,norm}$	$f_{i,accu}$
C_1	$A_1 = 5$	25	0.352	0.352
C_2	$A_2 = 3$	9	0.126	0.478
C_3	$A_3 = 6$	36	0.508	0.986
C_4	$A_4 = 1$	1	0.014	1.0
Total fitness		**71**	**1.0**	

Table 3.3: Population with different fitness values.

Random numbers are now generated between 0.0 and 1.0. The individual is selected which has the next highest $f_{i,accu}$ value with regard to the random number. For example, in order to select chromosome C_1 a random number between 0.0 and 0.352 must be generated. Therefore, as can be clearly seen from the Table 3.3 individual C_3 has the highest probability of being chosen, because it has the highest fitness value and is the closest value with regard to the global optimum. This will ensure that the member with the highest fitness value gets a high chance of being selected. In this example the individual with the index number C_3, C_1, C_2 and C_3 are selected, as shown in Table 3.4. Individual C_3 has been selected twice. This is justified by its high fitness value f_3, which also has the biggest range of the normalised accumulated fitness value ($f_{3,accu}$ - $f_{2,accu}$). Individual C_4 which has the smallest fitness value and, therefore, the smallest range of the normalised accumulated value has not been selected.

Random numbers	0.8547	0.1258	0.4317	0.9416
Chromosomes	C_3	C_1	C_2	C_3

Table 3.4: Selected chromosomes after selection procedure.

Selection procedures which will be investigated in further experiments are described in the following sections.

3.8.2.1 Selection according to fitness

This select procedure SELECT_F (uppercase names are names of procedures) will select the parents according to their fitness value, see Table 3.5. The advantage of this method is to prefer the fitter members of the population in order to guarantee that the best members are chosen with regard to fitness. The offspring should have increased fitness which means that they are closer to the global optimum.

```
Provide the normalised accumulated fitness for offspring population;
for population size loop;
    rand = random number;
        loop
            if rand ≤ F_offspring, i, accu then
                select this offspring individual;
                exit loop;
            end if;
        end loop;
```

Table 3.5: Pseudo code of procedure SELECT_F.

3.8.2.2 Random selection

The selection of the parents could be made randomly using SELECT_R, so that every member of the population has an equal chance of being selected for recombination, see Table 3.6.

```
rand = random number;
select this offspring individual;
```

Table 3.6: Pseudo code of procedure SELECT_R.

This method would guarantee diversity and healthy mating. Selecting only members with a high fitness (SELECT_F) can lead to inbreeding which can cause strong convergence towards a local optimum and a loss on diversity. It can be difficult to leave that local optimum in order to find the global optimum. A pseudo random number generator is used with uniform distribution to select the members of a generation to become parents for the mating process.

3.8.3 Recombination operators

These operators, crossover and mutation, are the key to the power of GAs. They are the operators which create new individuals with the idea that the new individuals will be closer to a global optimum.

3.8.3.1 Crossover operator

Crossover operates at the individual level. Before the crossover operator may be applied, the individual can be converted into a binary representation. During crossover, the two parents (chromosomes) exchange sub string information (genetic material) at a random position in the chromosome to produce two new strings (offspring). The

crossover operators search for better genes (building blocks) within the genetic material. The objective here is to create better individuals and a better population over time by combining material from pairs of (fitter) members from the parent population. Crossover occurs according to a crossover probability P_C. The easiest form of crossover is the *single crossover* operator. This matter will be investigated in Hypothesis 2_3 to find the optimum crossover operator.

3.8.3.1.1 Single crossover

A crossover point is randomly chosen for two chromosomes (parents). This point occurs between two bits and divides each individual into left and right sections. Crossover then swaps the left (or right) section of two individuals which can be seen in Figure 3.1. For example, if the two parents are $[v_1,...,v_m]$ and $[w_1,...,w_m]$, then crossing the chromosomes after the kth gene ($1 \leq k \leq m$) would produce the offspring: $[v_1,...,v_k, w_{k+1},...,w_m]$ and $[w_1,...,w_k, v_{k+1},...,v_m]$.

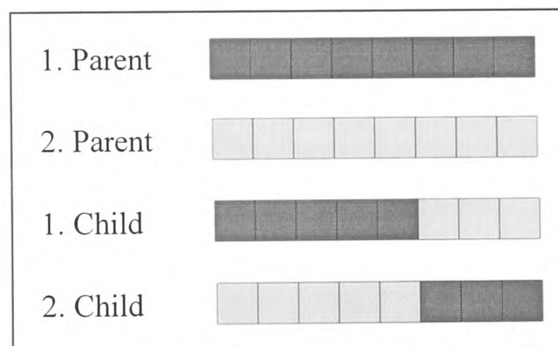


Figure 3.1: Single crossover with $k = 5$.

The selected chromosomes are then applied to the crossover operator and the new offspring can be seen in Figure 3.1 and in Table 3.7. As can be seen the total fitness of the offspring has increased to 118.

						A	f_i
C3	1. parent	**0**	**1**	**1**	**0**	6	36
C1	2. parent	0	1	0	1	5	25
	1. child	**0**	**1**	**1**	1	7	49
	2. child	0	1	0	**0**	4	16
	with k = 3						
C2	3. parent	**0**	**0**	**1**	**1**	3	9
C3	4. parent	0	1	1	0	6	36
	3. child	**0**	**0**	1	0	2	4
	4. child	0	1	**1**	**1**	7	49
	with k = 2						
	$f_{total, parent}$						71
	$f_{total, offspring}$						118

Table 3.7: Result after crossover.

Various other crossover methods exist, such as double and uniform crossover.

3.8.3.1.2 Double crossover

Double Crossover operates by selecting two random genes within the parent strings with subsequent swapping of material between these two genes (Figure 3.2). For example, if the two parents are $[v_1,....,v_m]$ and $[w_1,...,w_m]$, and the first randomly chosen point is k with $(1 \le k \le m-1)$ and the second random point is n with $(k+1 \le n \le m)$ would produce the offspring: $[v_1,...,v_k, w_{k+1},...,w_n, v_{n+1},....v_m]$ and $[w_1,...,w_k, v_{k+1},...,v_n, w_{n+1},....w_m]$.

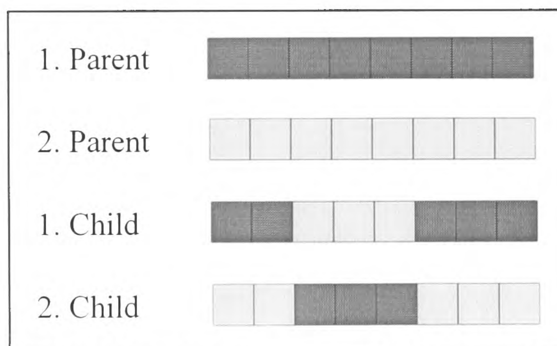


Figure 3.2: Double crossover with $k = 2$ and $n = 5$.

3.8.3.1.3 Uniform crossover

Uniform crossover is the extended method of 1-point crossover to n-point crossover where n is the number of crossover points. Uniform crossover, Syswerda [1989] and Spears and DeJong [1991, 1992], means that each bit of the parents can be selected according to some probability P_c so that these two bits are exchanged to create

offspring, displayed in Figure 3.3. The number of genes exchanged during uniform crossover is on average ($\frac{S}{2}$) crossings on strings of the length S for $P_c = 0.5$.

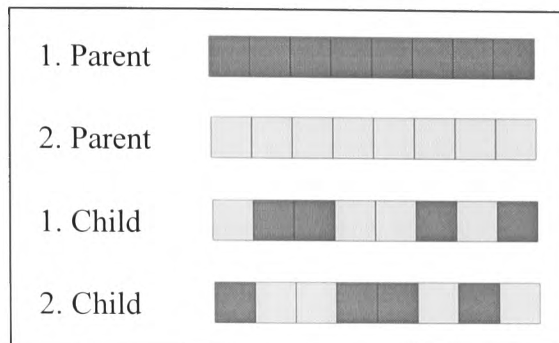


Figure 3.3: Uniform crossover with crossing points at 1, 4, 5 and 7.

3.8.3.2 Mutation operator

Mutation is the occasional random alteration of a bit value which alters some features with unpredictable consequences. In a binary code, this simply means changing the state of a gene from a 0 to a 1 or vice versa. Mutation is like a random walk through the search space and is used to maintain diversity in the population and to keep the population from prematurely converging on one (local) solution. Mutation avoids local optima and creates genetic material that may not be present in the current population (loss of important material) because it was never present or because it was lost by the crossover and survival operators.

3.8.3.2.1 Normal mutation

Mutation always works after the crossover operator. This kind of mutation is called here *normal mutation* which operates on chromosomes created during crossover, and flips each bit with the pre-determined probability. Mutation provokes randomly chosen genes to change (flip) bits (see Figure 3.4), whereas crossover allows random exchange of information of two chromosomes.

Schaffer [1987], Mühlenbein *et al.* [1991 b] suggested that the optimum mutation probability P_m is the reciprocal of the chromosome size $P_m = \frac{1}{S}$ so that it would be unlikely for the code to have on average more than one bit of a chromosome mutated. If the mutation probability P_m is too low, there will be insufficient global sampling to

prevent (premature) convergence to a local optimum. If the rate of mutation is significantly increased, the location of global optima is delayed. It is then a pure random search technique.

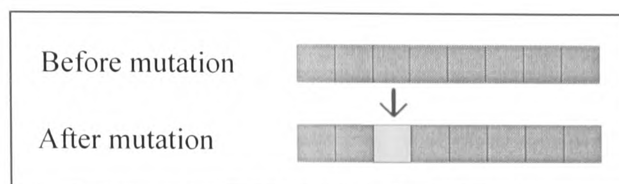


Figure 3.4: Before and after mutation.

A random number in the range from 0.0 to 1.0 is generated for each gene and as soon as a random number is less or equal to P_m (here $P_m = 0.25$), the gene will be mutated, see Table 3.8. Mutation can be turned off by using the menu option or by setting the mutation probability to zero.

	Chromosome	Random numbers			
2. child	**0** 1 0 0	**0.01**	0.607	0.253	0.893
	1 1 0 0				

Table 3.8: Mutated chromosome (mutation at first bit position).

In the example, the second child is mutated at the first bit position, Table 3.8. This is a good example of how new genetic material is created. The first bit positions of the current and offspring population had always the same bit state '0', displayed in Table 3.7. Without mutation it would be impossible to create such new genetic material. This means that the global optimum ($A = 15$) could have never been generated. After mutation the value of the input variable A has increased from 4 to 12. Therefore the fitness value of this chromosome has increased from 16 to 144. Another method of modifying single bit values is using a *weighted mutation*.

3.8.3.2.2 Weighted mutation

Weighted mutation, W_MUTATE, however, is only to be executed when the population seems to be stuck. W_MUTATE increases the probability of mutating certain bits depending on the chromosomes representation. Those are usually the Most Significant Bit, if a sign bit exists (MSB: sign bit) and some of the Least Significant Bits (LSBs). This has an effect similar to a local search because W_MUTATE causes only small changes to the variables. The threshold of starting W_MUTATE can be controlled by a

parameter P_E which specifies the percentages of equal chromosomes which must be obtained before W_MUTATE starts to work.

3.8.4 Survive

The survive method decides which chromosome of the offspring and parent population will survive and which will be discarded or die. To accomplish this, the procedure may copy parts of the offspring population to the parent population, with regard to e.g. the fitness of the individuals similar to the selection procedure. There are many different methods of survival, e.g. random survival, elite survival, etc.

In the example the offspring population will determine a new parent population according to the fitness of the individuals like in the selection procedure. Four random numbers are generated between 0.0 and 1.0 to select four individuals of the offspring population for the next generation. Table 3.9 shows the chromosomes of the offspring population after crossover and mutation with their different fitness.

					A_i	f_i	$f_{i,norm}$	$f_{i,accu}$
$C_{1,offspring}$	0	1	1	1	$A_1 = 7$	49	0.1763	0.1763
$C_{2,offspring}$	1	1	0	0	$A_2 = 12$	144	0.5180	0.6943
$C_{3,offspring}$	0	1	1	0	$A_3 = 6$	36	0.1294	0.8237
$C_{4,offspring}$	0	1	1	1	$A_4 = 7$	49	0.1763	1.0
Total fitness						**278**	**1.0**	

Table 3.9: Offspring population.

Table 3.10 shows the selected chromosomes.

Random numbers	0.6789	0.9347	0.3835	0.5194
Chromosomes	C_2	C_4	C_2	C_2

Table 3.10: Offspring, who survive into the next generation.

The offspring that has the next highest $f_{i,accu}$ value with regard to the random number, survives. In this case it is chromosome 2 (C_2) three times and C_4 once. The total fitness of the new current population is 481 compared with 71 of the previous generation. Several other survival methods are investigated in order to find out which are the most appropriate. They are explained in the following sections.

3.8.4.1 SURVIVE_1

This procedure will select good individuals more likely than bad ones of the offspring population according their fitness to overwrite bad individuals (selected after probability) from the parent generation according their fitness. The survival of an individual also depends on the probability P_s. A survival probability P_s of, e.g. $P_s = 0.1$ indicates that the probability of survival into the next generation of the offspring is only 10%. 90% of the parents survive unchanged whereas 10% are overwritten by the offspring which is demonstrated in Figure 3.5.

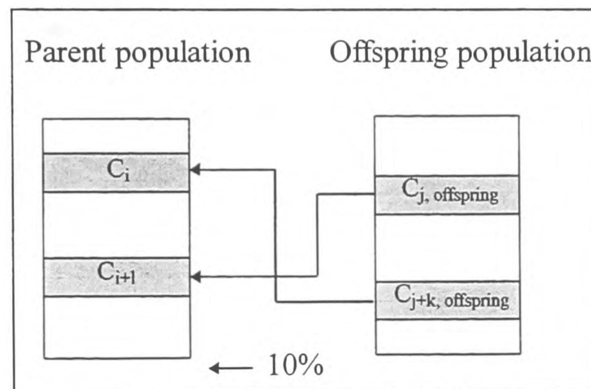


Figure 3.5: Survival method.

On the left side in Figure 3.5 the parent population is displayed, on the right side the offspring population which is generated by crossover and mutation. In the survive procedure certain individuals of the offspring population are selected, e.g. according their fitness which means that better individuals (higher fitness) have a better chance of being selected, in this case they are $C_{j,\ offspring}$ and $C_{j+k,\ offspring}$. These will then overwrite individuals of the parent population which are selected according their fitness where bad individuals (lower fitness) have a better chance of being chosen, e.g. C_i and C_{i+l}. By chance a survivor from the offspring can be overwritten by another survivor from the offspring population. In Figure 3.5 only two survivals are displayed, however, the survival rate depends on the survival probability P_s which expresses a percentage of the population size. Table 3.11 displays the pseudo code of the survive procedure.

```
Provide the normalised accumulated fitness for offspring population;
Provide the reciprocal normalised accumulated fitness for parent population (bad members
high fitness);
for population size loop;
    if random number < P_S then
        rand = random number;
        loop
            if rand ≤ F_offspring,i,accu then
                select this offspring individual;
                exit loop;
            end if;
        end loop;
        loop;
            if rand ≤ F̄_parent,i,accu then
                select this parent individual;
                exit loop;
            end if;
        end loop;
    end if;
selected offspring overwrites selected parent and fitness value
end loop;
```

Table 3.11: Pseudo code of the basic survive procedure.

If the probability is high then there is a strong likelihood that many individuals from the offspring population will survive. It is also possible that an individual could be selected several times to survive or to be overwritten. This could mean that survivors of the offspring population with high fitness can be overwritten again.

3.8.4.2 SURVIVE_2

SURVIVE_2 selects only the very best individual with regard to the fitness value of the offspring population, and overwrites the very worst individual from the parent generation. This is also called the elite survival. The reason for using this kind of survival is to have more exploitation and less exploration which works quite well for some functions being optimised, mentioned by Whitley [1989]. The disadvantage is that it can result in suboptimal hill climbing on multi-peaked functions. Since the fittest individual always survives it could mean that after a couple of generations the population comprises several copies of the same very dominant individual which can lead to inbreeding and loss of genetic material. This survival method is independent of the survival probability P_s because only the best individual will survive.

3.8.4.3 SURVIVE_3

This procedure is similar to SURVIVE_1. The only difference is that an individual from the offspring population can only be selected once. A chromosome of the parent population can only be overwritten once. The survival probability should be less than in the SURVIVE_1 procedure because otherwise too many low fitness chromosomes will survive.

3.8.4.4 SURVIVE_4

SURVIVE_4 is similar to the SURVIVE_3 procedure. The only difference is that an individual of the offspring population can be selected more than once, with regard to its fitness value, but an individual can only be chosen once from the parent generation to be overwritten. The advantage of this procedure is that no survivors will be overwritten again. However, the first offspring to survive, will have been chosen via the elite method like the SURVIVE_2 procedure. An additional condition is that the fitness value of the offspring must be at least equal to or better than the fitness value of the selected individual from the parent generation in order to survive and to overwrite it. If this is not the case the offspring will be not copied into the parent generation. This has an effect on the number of survivals which will be less than P_s because not all selected offspring individuals have a higher fitness than the selected individuals from the parent population so that these will not survive.

3.8.4.5 SURVIVE_5

SURVIVE_5 is similar to SURVIVE_4 but without the stipulation that the offspring must be equal to or better than the selected individual of the parent generation. This should prevent a too strong converging process as might happen in SURVIVE_4, because stronger diversity is guaranteed. Several experiments have been conducted using these survive procedures, which are described in chapter 5.

3.9 Why Do GAs work?

GAs search for similarities at certain bit positions, which are also called building blocks Bayer and Wang [1991]. In the example, chromosomes C_1 and C_3 of the initial

population (Table 3.12) have the highest fitness values. They have similar building blocks (bits 1 and 2), even if the building blocks have not got the final optimum structure, i.e. the $MSB = 1$. Table 3.12 shows the population before the selection for reproduction.

					A_i	F_i
C_1	**0**	**1**	0	1	5	25
C_2	0	0	1	1	3	9
C_3	**0**	**1**	1	0	6	36
C_4	0	0	0	1	1	1

Table 3.12: Building blocks at bit position 1 and 2.

The first two bit positions of these two chromosomes are the same. The GA assumes now that the pattern 0 1 is a good building block for the start of the chromosomes. These chromosomes are selected preferentially for reproduction because of their high fitness values. It cannot know yet that the first bit must be bit state of 1.

3.10 Structure of Genetic Algorithm

The above described steps and structure of the GA can be seen as a block diagram in Figure 3.6, the associated pseudo code is displayed in Figure 3.7 where t is the generation number and P the population.

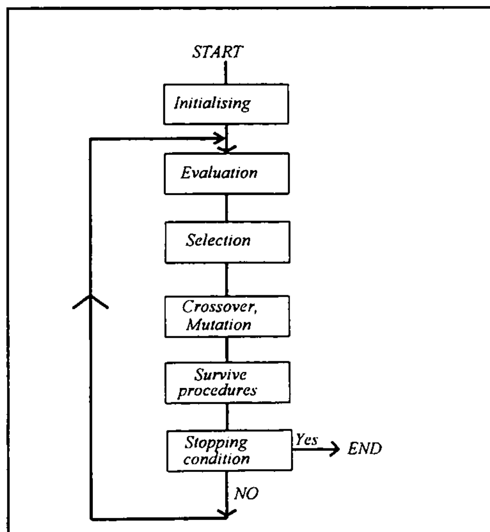


Figure 3.6: Block diagram of GA.

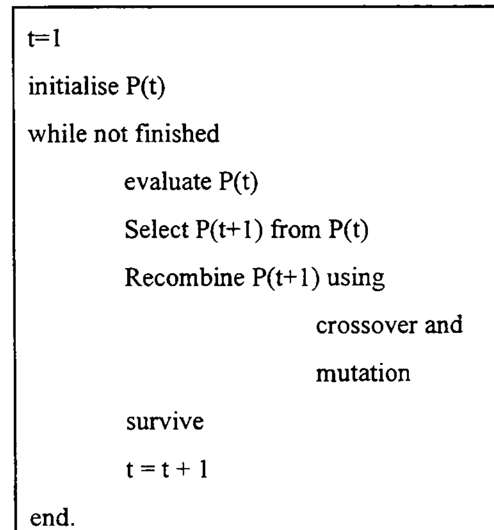


Figure 3.7: Pseudo code of GA.

3.11 Performance

Although the goal is clearly to achieve an optimum solution, It is undesirable that the entire population should converge to the same value. This is because valuable information which is developed in part of the population is often lost. Therefore, the population needs to be diverse, so that a wide search of the input domain is guaranteed. If the population converges prematurely or too fast, the penalty will be to lose information which restricts the exploration of the search space. DeJong [1975] defined a converged allele, when a particular gene has at least 95% of all individuals the same value in a population. Since the characteristics of the function which is to be optimised, are unknown, such a restriction may prevent the finding of the optimum solution. Baker [1985] mentioned three metrics for the performance of genetic algorithms which were proposed by Grefenstette [1986]. They are:

1. The *on-line* performance is the average fitness value of all individuals that have been generated and evaluated. It penalises those search methods which have to test many poor solutions (structures) before generating a solution for the global optimum. In order to have a high on-line performance the GA has to concentrate on those areas in the search space where the best values lie.
2. The *off-line* performance is the average of the best individual fitness from each generation. This method will not penalise exploring poor regions of the search space which may lead to better solutions.
3. The *best individual* is the individual with the highest fitness that has been generated.

If the diversity is increased, the on-line performance measure will be affected quite badly. A restricted convergence impairs the off-line performance. A usual reason for fast convergence is the existence of a very fit (super) individual that dominates the population surviving many more times and hence reducing the variety of genetic material available. In a small number of generations the super individual and its descendants can dominate the entire population. To avoid this phenomenon Baker places a threshold on an individual's expected number of offspring.

3.12 Exploiting the power of genetic algorithms

The key feature of GAs is their capability to exploit information gathered about an initially unknown search space. This directs other searches into useful sub-spaces. If the space of legal structural changes is not too large, an enumerative search strategy can be developed with appropriate heuristic cut-offs in order to keep the computation time under control. However, if the search space is large, much time and effort can be spent in developing domain knowledge heuristics. It is exactly in these occasions (large, extremely non-linear, complex, poorly understood search spaces) where the GAs have been used successfully. Even for large search spaces (e.g. 10^{30} points), DeJong [1988] mentioned that suitable combinations are found after only a couple of simulated generations.

3.12.1 The role of feedback

So far a description of how GAs work and how their power can be exploited has been given. In this section the focus is on one of the issues in the optimisation process - the role of feedback.

GAs can be used as an adaptive sampling strategy to search large and complex spaces. This sampling strategy is adaptive with regard to feedback from the samples (offspring) being used to bias subsequent sampling into regions with high expected performance (global optimum). This means that, even if a good solution has been generated, the effectiveness of GAs in optimising parameters also depends on the usefulness of the information obtained via the feedback. It is important that the right feedback mechanism is selected to enable an adaptive search strategy.

Such feedback mechanisms have been shown to be very effective, Schaffer [1985] and DeJong [1988]. Feedback mechanisms are called *fitness*, *cost* or *pay-off functions*. This form of feedback uses a reward and punishment method, in which performance evaluation is stated in terms of a fitness function. GAs can employ this information directly, to influence the selection of parents who will be used to produce new offspring or for the survival of the offspring. Not all fitness functions are equally suited. A good function will provide useful information early in the search process to help focus

attention. For example, a fitness function that almost always gives zero fitness, provides almost no information for directing the search process. Therefore suitable fitness functions must be found which describe the environment of the problem in order to exploit the search space and therefore the power of the GA.

3.12.2 The use of domain knowledge

GAs are normally categorised as domain-independent search and optimisation methods so that they can be applied without any knowledge of the space being searched. However, although no domain knowledge is required, there are possibilities and opportunities to incorporate domain knowledge. A good example of domain knowledge involves the choice of the initial population, which is described earlier as randomly selected, but there is no reason not to use available information that permits seeding the initial population with individuals who have a certain knowledge about the problem and which may be close to a global solution.

Another obvious method to exploit domain knowledge is by means of the feedback mechanism. As described earlier, the effectiveness of the GAs relies on the usefulness of the feedback information (fitness function) provided.

3.13 Interim conclusion

As the example in this chapter shows, the obvious desire is to achieve an optimum solution for a particular function. How a GA works is shown with a simple problem.

The main characteristics of GAs are listed below:

1. Concentrates on chromosomes with above average fitness.
2. Exploits information about a large number of values while processing a small population.
3. Prevents search from stagnating at a local optimum.
4. They take advantage of old knowledge held in a population of solutions to generate new solutions with improved performance.

In the case that a fitness-proportional selection procedure is the only active part of a

optimisation, an initial random generated population of size N will quite rapidly create a population which will only contain N duplicates of the best individual (highest fitness). The GAs counterbalance this selective pressure by the genetic operator (crossover and mutation) toward a uniformity by generating diversity in the form of new alleles and their combination. GAs rapidly locate the area in which a global optimum could be found, but need much more time to pinpoint it, DeJong [1993].

In the next chapter, the approach of software testing is described. The method covers the testing of 'if' conditions, various loops and different data types.

CHAPTER 4

A strategy for applying GAs and random numbers to software testing

GAs form a method of adaptive search in the sense that they modify the test data from one generation to the next, in order to optimise a fitness function. In contrast random testing generates test data without using any knowledge of previous test data.

This chapter describes the interface between the software under test and testing tool which uses either the GA or random numbers. The method random numbers is used as a comparison of the GA testing strategy.

4.1 Testing using Random Testing

In order to measure the effectiveness of GA testing, random testing is carried out. The random generation of tests identifies members of the subdomains arbitrarily, with a homogeneous probability which is related to the cardinality of the subdomains. Under these circumstances, the chances of testing a function, whose subdomain has a low cardinality with regard to the domain as a whole, is much reduced. A pseudo random number generator generates the test data with no use of feedback from previous tests. The tests are passed to the procedure under test, in the hope that all branches will be traversed. Watt's [1987] pseudo random number generator, written in Ada, has been used and tested and has a uniform distribution. The test harness used for random testing is the same as that used for GAs. The only difference is the way data is generated.

4.2 Subdomains

A search space is defined and the GAs and random numbers probe for the global optimum (goal). In this case the search space is the domain D of input variables x_i for the software under test, and is given by the set $D = \{x_1, x_2, ..., x_m\}$. The domain D may be split into a group of subdomains, d_i, displayed in Figure 2.2.

Each path through the program identifies a unique subdomain. The conditions and

statements in a software program partitions the input space into a set of exclusive domains. Each of these subdomains belongs to a certain software path and identifies a unique function. They consist of input data which will cause a certain path to be executed. In this case there are only two input variables A and B. The domain is split up into several subdomains and each of them cause one specific path in the software to be traversed where early branches in the control flow usually have a higher cardinality than subsequent branches which tend to be smaller because of the filtering effect of successive branches.

The goal for the GAs is typically to search for members of these particular subdomains $d_s = \{x_j,...,x_k\}$. One way of generating high adequacy test data is, therefore, to find test sets which fall at or near the boundaries of a subdomain in order to identify whether the boundary between subdomains is wrongly located, see Figure 2.2. A test data set is considered to be a set of values $\{x_1, x_2, ..., x_m\}$. Each value corresponds to an input variable of the procedure to be tested. The problem remains how the boundary of a subdomain may be identified. This problem may be acute when the subdomains are multi-dimensioned, disconnected or isolated. The solution of the problem is an example of partition testing, and it lies in the location of a member of the subdomain boundary, d_s^b, which is a proper subset, i.e. $d_s^b \subseteq d_s$.

4.2.1 Fitness functions adapted from predicates

On the basis of the preceding argument, subdomains of functionality align with the path structure of the program, and their boundaries may be found by examining the predicates at different points along the path. A predicate is a Boolean expression involving functions of the input variables, constants, related variables and relational operators. The aim of this work is to identify test sets which, when changed by a small amount (where small is defined in terms of the underlying data type), cause the predicate to switch from true to false, or vice versa. It is these pivotal values which form the basis of the genetic algorithm fitness function. By choosing the fitness function to give higher fitness rating for boundary test sets (closer to boundary), GAs will identify test sets which are more likely to reveal faults, Clarke [1976]. These test sets are called boundary test data because they are the next to the boundaries defined by the predicates.

The fitness functions which are used in the next chapters are based on the predicates of the software under test, and the system attempts to exercise every branch. A fitness function is applied to predicates involving the input variables. Each predicate has its own fitness function in order to evaluate the test data performance. For example, a predicate function has the form of:

$$h(X) \quad rop \quad g(X) \tag{4.1}$$
where $X = \{x_1, x_2, \ldots, x_m\}$

where h and g may be complex functions of the test set (input variables) $\{x_1, x_2, \ldots, x_m\}$ and rop is one of the relational operator $\{<, >, \leq, \geq, , =, \neq\}$. The power of GAs and the testing tool is that the form of h and g need not be known explicitly, only their values, which are made available by suitable instrumentation of software at that point where the predicate is executed. A possible fitness function, F, is the reciprocal of the distance between the two functions, i.e.

$$F = (|h(X) - g(X)| + \delta)^{-n} \tag{4.2}$$
where n is a positive integer and δ is a small quantity to prevent numeric overflow.

Whatever relational operator is involved, this approach will assign higher fitness measures to boundary test sets. This function has been adapted to use $n = 1$, $n = 3$ or the Gaussian function. In general, none of these performed better than the inverse square law ($n = 2$).

The GAs will be used to generate those data which are close to the boundary in order to traverse all branches, because the closer the test data are to the boundary, the more information is provided about the correctness of the condition under test. Another advantage of boundary test data is that if one of two branches of the same condition has not been executed, test data closer to boundaries are usually more likely to lead to test data which crosses the boundary and covers the opposite branch. Each branch will have a different fitness function with regard to its predicate. Those branches which are traversed, do not need to be visited so reducing computational time. The system looks for the next untraversed branch and will concentrate on that node in order to execute it.

The execution of a branch, only once, is appropriate because every test set generated from the same subdomain will execute the same functions and follow the same branch, so that all remaining test sets of that subdomain will work correctly too. Therefore, no more information is gained by executing more than one test set from the same sub - domain. The exception is when boundary test data have to be generated to check the boundary between sub - domains because an error in the boundary can lead to a shifting of it (using '>' instead of '≥') which can be located with boundary test data.

4.3 Control flow tree and graph

The structure of a program or procedure can be shown by a control flow diagram. The control flow diagram may be represented as a tree or a graph whose nodes represent sequences of statements followed by a jump initiated by a selection such as an if - condition or the condition of a loop. The jump is indicated by the edges of the nodes. A control flow tree / graph divides a program into nodes and edges. A control flow tree compared to a graph has no edges back from a later node to a previous node, i.e. it exists no loop statement. The nodes represent statements in a program, the edges depict the actions of a program to get from one node to another. The edges express the flow of the control and they are between each of these statements. The combination of a node and branch is, therefore, equivalent to the LCSAJ (**l**inear **c**ode **s**equence **a**nd **j**ump). A LCSAJ is defined as a sequence of code where the flow of control is sequential and terminates by a jump in the control flow. Nodes which have no following nodes are called leaf nodes.

A structured database equivalent to the control flow tree is created, i.e. information with regard to the nodes can be stored. This information includes nodes that have been executed and not been executed, test sets which executed the nodes and fitness values of the test sets.

A path is defined by White and Cohen [1980], by executing the node with the initial statement (entry node) and the path terminates with the node of the last statement (exit node). There must be only one entry node, but there could be several exit nodes.

Two control flows through a program, which differ only in the number of times a

particular loop has been executed, are two distinct paths. Therefore the number of paths in a program with loops can be infinite because loops may iterate any number of times. In general path testing is impossible.

4.4 Effectiveness measure of test sets

In order to compare different testing systems, the effectiveness or coverage of test sets can be measured in different metrics. Woodward, Headley and Hennel [1980] defined different levels of structural testing by quantifying *Test Effectiveness Ratios* (TER). TER1 and TER2 describe the percentage of statements and branches being executed respectively. The third measure is TER3 which is the percentage of linear code sequences and jumps (LCSAJs) being traversed which is in between branch and path testing.

Since the testing tool has been developed to execute every branch in the software, the metric to measure the performance of the testing tool is TER2 including the four (or three) branches for loop testing. In addition the number of function evaluations required (tests) is also taken as a measure.

4.5 Instrumentation

Howden [1975] described systems which automatically insert instrumentation statements into a program. The instrumentation statements monitor and keep a record of the branches and statements that are executed during the testing of a program, i.e. the dynamic (performance) rather than its static (structure) behaviour can be examined. In our case, instrumentation is used in order to return information regarding values of the fitness; it has to be done manually, but it could be automated, since strict rules are applied. The software probes are inserted at strategic points in the program. They are sited around control flow jumps which can be called nodes. The instrumentation process is similar to the case of a programmer inserting additional print statements in a program for debugging purposes.

When an *'if'* - condition is used as a branch condition, CHECK_BRANCH will be implemented to record whether the branch has been executed. LOOKING_BRANCH calculates the fitness value in the case the sibling node or one of its successors has not

been executed. The instrumentation requires among other things, the number of the node currently being executed and its sibling node. The values of the constraints (i.e. g and h, equation 4.1) and which operator is used, are fundamental information required to form the fitness functions. Information about the number of attempts to traverse a certain node before it gives up to generate test sets for the next node, is essential. This information is important so that the testing system will not be stuck at a node that can not be executed. Similar procedures are instrumented when using a '*loop*' conditions. A detailed description of all software procedures is given below, see section 4.8.

4.6 Overall structure of testing tool

In Figure 4.1 the structure of the GA and random testing tool is displayed where the darker boxes emphasise the main parts of the tool.

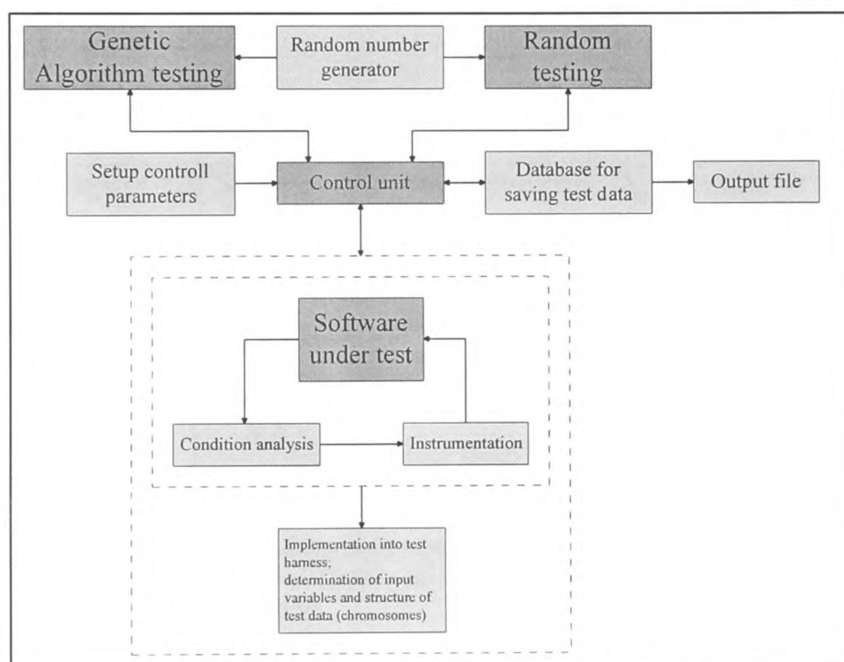


Figure 4.1: Overall structure of testing tool.

The entire software under test has to be inserted into the testing tool's harness. Predicate analysis is carried out in order to instrument the procedures and monitor the test. The control unit is responsible for the whole testing process, i.e. putting test data, either generated from the GA tool or random testing tool, through the software under test by calling it. Once a branch has been traversed by a test data, the test data will be copied into a database together with information that this node has been executed. After the entire procedure has been tested, the information about the performance and test data

can be obtained in a file (Output file).

4.7 Applying the testing strategy on an example

To help understand how GAs are used in the automatic generation of test data, a hand worked example for the control flow tree given in Figure 2.2 (page 2-7) will be explained. The example is intended to illustrate the general principle of the process and not its detailed working. The detailed working of the strategy and of the instrumented procedures are explained in more detail in section 4.8. Figure 4.2 repeats the example from chapter 2 (Figure 2.2) to remind the reader.

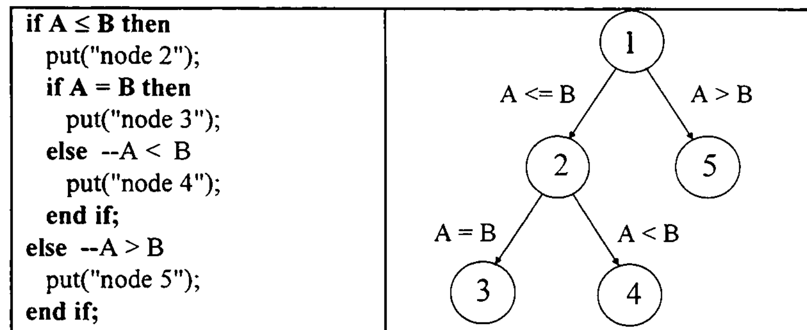


Figure 4.2: Software and control flow tree for the example.

Listing 4.1 displays the example with the instrumented procedures.

```
if A ≤ B then
    CHECK_BRANCH(2);
    LOOKING_BRANCH(5, A, B + 1);
    if A = B then
        CHECK_BRANCH(3);
        LOOKING_BRANCH(4, A, B - 1);
    else --A < B
        CHECK_BRANCH(4);
        LOOKING_BRANCH(3, A, B);
    end if;
else --A > B
    CHECK_BRANCH(5);
    LOOKING_BRANCH(2, A, B);
end if;
```

Listing 4.1: Example with instrumentation.

The most important parameter settings for the GA are given in Table 4.1.

Selection of parents for recombination is random
The mutated genes (bits) are bold in the offspring population
Fitness is calculated according reciprocal fitness function
Single crossover
Survive probability $P_s = 0.5$
Mutation probability $P_m = 0.1$

Table 4.1: Settings for the GA.

Table 4.2 shows the first generation which is randomly generated by the testing tool. Each row in the table represents a member of the population whose size is 4. The columns in Table 4.2 have the following meaning:

- P_i indicates a member of the parent population;
- A and B are the values of the identifiers representing the input variables;
- *look* (short for *looking*) gives the node number to be traversed;
- *Path* indicates which nodes have been traversed by this current test data of A and B;
- *chromosome* displays the bit pattern of the test data in binary-plus-sign bit format;
- *fitness* gives the fitness value calculated according to the test data and the node required to be traversed;
- $f_{i,norm}$ is the normalised fitness;
- $f_{i,accu}$ is the accumulated normalised fitness value;
- F_t indicates the population total fitness value.

P_i	A	B	*look*	*Path*	*chromosome*	*fitness*	$f_{i,norm}$	$f_{i,accu}$	
P_1	4	10	2	1, 2, 4	00100 01010	0.0278	0.365	0.365	
P_2	-7	-15	2	1,5	11101 11111	0.0156	0.205	0.570	
P_3	8	15	2	1, 2, 4	00010 11110	0.0204	0.268	0.838	
P_4	3	-6	2	1, 5	11000 01101	0.0123	0.162	1.0	$F_t = 0.076$

Table 4.2: First generation.

There are two points to note concerning the fields in Table 4.2 which are:

(i) A 5 bit representation per input test data has been chosen. Therefore, the chromosome size is 10 bits where the first five bits represents the input data A and the rest the input data B. The least significant bit is stored on the left hand side and the most significant bit (sign bit) on the right hand side of the two substrings within the chromosome. This representation conforms to the conversion function that is provided by Ada.

(ii) A large $f_{i,norm}$ value indicates that these population members have a high fitness and hence have a higher probability of surviving into the next generation.

The first test data (P_1) is put into the software under test. The first node required to be executed is node 2 (see *look* in first generation).

The fitness function f, which calculates the test data performance and is based on the

conditions in the code (see chapter 3.8.1) is for this node $f = \frac{1}{(|A - B| + 0.01)^2}$ because the boundary test data to traverse the condition $A \leq B$ (node 2) is $A = B$. The test sets in the first generation execute nodes 1, 2, 4, and 5 leaving only node 3 untraversed. This fitness function ensures that test data where A and B are numerical close to each other have a higher fitness. When a *looking* node is executed with a test data (e.g. in this case node 2, first test data set in the first generation), the fitness values of the remaining test data (here second, third and fourth test data sets in the first generation) will be still calculated for the *looking* node and no offspring population will be generated in this case. Therefore, the first generation now becomes the starting point in the search for test data which will execute node 3 (see Table 4.3). By chance, the predicate controlling access to node 3 is the same as that for node 2, and hence the test data and the fitness values shown in Table 4.3 for the second generation are the same as those in Table 4.2.

P_i	*A*	*B*	*look*	*Path*	*chromosome*	*fitness*	$f_{i,norm}$	$f_{i,accu}$	
P_1	4	10	3	1, 2, 4	00100 01010	0.0278	0.365	0.365	
P_2	-7	-15	3	1,5	11101 11111	0.0156	0.205	0.570	
P_3	8	15	3	1, 2, 4	00010 11110	0.0204	0.268	0.838	
P_4	3	-6	3	1, 5	11000 01101	0.0123	0.162	1.0	$F_t = 0.076$

Table 4.3: Second generation.

Since the *looking* nodes (node 3) has not been traversed within the second generation, the GA now generates an offspring population using crossover and mutation as shown in Table 4.4.

O_i	P_i	P_i	*look*	*Path*	*chromosome*	*fitness*	$f_{i,norm}$	$f_{i,accu}$	*A*	*B*	*k*
O_1	P_2	P_4	3	1, 5	11101 011***1***1	0.0204	0.289	0.289	-7	-14	5
O_2			3	1, 5	11***1***00 11111	0.0021	0.029	0.318	7	-15	
O_3	P_1	P_4	3	1, 5	00***0***00 01101	0.0278	0.393	0.711	0	-6	3
O_4			3	1, 2, 4	11000 01010	0.0204	0.289	1.0	3	10	
									$F_t = 0.071$		

Table 4.4: Offspring population generated by GA.

In Table 4.4 the new offspring test data are indicated by O_i and the parents which have been used for reproduction are indicated by P_i. These parents are chosen randomly. Two parent members generate two offspring members during the recombination phase. The columns *look, Path, chromosome, fitness,* $f_{i,norm}$ and $f_{i,accu}$ have the same meaning as for the parent population. *A* and *B* represent the new test data values and *k* indicates the single crossover point. The genes displayed in bold and italics are the result of mutation.

The mating process has resulted in an offspring population which includes the member O_3 which is the same distance from node 3 as P_1 in the parent population. This is manifested by both these members having the same fitness value *(0.0278)*. Additionally, O_3 has the highest fitness value among the offspring population and is rewarded with a high value for $f_{i,norm}$ which in turn results in a high probability of this member surviving into the next parent generation. However, the total fitness value F_t of the offspring population is less than that of the parent population indicating that an overall improvement from one population to the next is not guaranteed.

We now have two populations (parent and offspring) each containing 4 members which will provide the members of the next generation. Because the probability of survival (P_s in Table 4.1) is 0.5, on average the next generation will be made up from two members of each population. Table 4.5 shows how the members 1 - 4 of the next generation are selected. For each member of the new population a random number is generated. This is shown in the *parent vs. offspring* row in the Table 4.5. If the random number is > 0.5 (> P_s) the parent population is selected, otherwise the offspring population is used. Once the population has been selected, another random number in the range 0.0 to 1.0 is generated to select which member of the chosen population survives to the next generation.

	member 1		member 2		member 3		member 4	
parent vs. offspring	0.678		0.298		0.978		0.457	
Survived parents	*0.257*	P_1	---	---	*0.710*	P_3	---	---
Survived offspring	---	--	0.026	O_1	---	--	0.609	O_3

Table 4.5: Survival of offspring members.

For example, when selecting member 1 for the next generation, the *parent vs. offspring* random number generated is 0.678 which means the parent population is selected. The next random number generated is 0.257 which selects member P_1 using the $f_{i,accu}$ column of Table 4.3. This process is repeated for each member of the new population. The new generation is shown in the top part of Table 4.6.

The whole process repeats itself again, until all nodes are traversed. Table 4.6 presents the third generation of the test run.

P_i	A	B	*look*	*Path*	*chromosome*	*fitness*	$f_{i,norm}$	$f_{i,accu}$			
P_1	4	10	3	1, 2, 4	00100 01010	0.0277	0.288	0.288			
P_2	-7	-14	3	1, 5	11101 01111	0.0204	0.212	0.500			
P_3	8	15	3	1, 2, 4	00010 11110	0.0204	0.212	0.712			
P_4	0	-6	3	1, 5	00000 01101	0.02278	0.288	1.0	F_t = 0.096		
O_i	P_i	P_i	—	—	—	—	—	—	A	B	k
O_1	*P3*	*P1*	3	1, 2, 4	00010 11010	0.1111	0.689	0.689	8	11	7
O_2			3	1, 2, 4	*1*0100 11*1*10	0.0099	0.062	0.751	5	15	
O_3	*P2*	*P4*	3	1, 2, 4	11*00*0 01101	0.0123	0.077	0.828	3	-6	4
O_4			3	1, 5	000*1*1 01111	0.0278	0.172	1.0	-8	-14	
									F_t =0.161		

	member 1		member 2		member 3		member 4	
parent vs. offspring	0.034		0.295		0.785		0.546	
Survived parents	---	---	---	---	*0.540*	P_3	*0.952*	P_4
Survived offspring	0.158	O_1	0.331	O_1	---	---	---	---

Table 4.6: Third generation.

The third generation of the parent population has a total fitness increase over the second generation which can be seen in F_t. The offspring population, produced by crossover and mutation, generated a test data O_1 which is only three integer units ($11 - 8 = 3$) away from the global optimum according to node 3. A high fitness value is calculated for this member and is chosen to survive twice into the next generation. Table 4.7 presents the fourth generation.

P_i	A	B	*look*	*Path*	*chromosome*	*fitness*	$f_{i,norm}$	$f_{i,accu}$			
P_1	8	11	3	1, 2, 4	00010 11010	0.1111	0.411	0.411			
P_2	8	11	3	1, 2, 4	00010 11010	0.1111	0.411	0.822			
P_3	8	15	3	1, 2, 4	00010 11110	0.0204	0.075	0.897			
P_4	0	-6	3	1, 5	00000 01101	0.0278	0.103	1.0	F_t = 0.27		
Oi	P_i	P_i	—	—	—	—	—	—	A	B	k
O_1	P_1	P_2	3	1, 2, 4	*1*0010 11010	0.2499	0.199	0.199	9	11	2
O_2			3	1, 5	00010 1101*1*	0.0028	0.002	0.201	8	-11	
O_3	P_4	P_3	3	1, 2, 4	00000 01110	0.0051	0.004	0.205	0	14	8
O_4			3	1, 2, 4	0001*1* 11101	0.9990	0.795	1.0	-8	-7	
									F_t = 1,26		

	member 1		member 2		member 3		member 4	
parent vs. offspring	0.691		0.124		0.753		0.498	
Survived parents	*0.356*	P_1	---	---	*0.861*	P_3	---	---
Survived offspring	---	---	*0.551*	O_4	---	---	*0.050*	O_1

Table 4.7: Fourth generation.

In the offspring population, two test sets (O_1 and O_4) have been generated which are close to satisfying the goal. O_4 is actually closer to the global optimum and, therefore, has a higher fitness. The total fitness F_t has improved by 280% from the third to the fourth generation. Table 4.8 presents the fifth generation.

P_i	A	B	look	Path	chromosome	fitness	$f_{i,norm}$	$f_{i,accu}$			
P_1	8	11	3	1, 2, 4	00010 11010	0.1111	0.081	0.081			
P_2	-8	-7	3	1, 2, 4	00011 11101	0.9990	0.724	0.805			
P_3	8	15	3	1, 5	00010 11110	0.0204	0.015	0.820			
P_4	9	11	3	1, 2, 4	10010 11010	0.2499	0.180	1.0	F_t = 1.38		
O_i	P_i	P_i	---	---	---	---	---	$f_{i,accu}$	A	B	k
O_1	P_4	P_1	3	1, 2, 3	11010 11010	100.0			11	11	9
O_2					00010 11011				8	-11	
O_3	P_3	P_4			00010 10010				8	9	6
O_4					10110 11110				13	15	

Table 4.8: Fifth generation.

In general the total fitness value F_t increases over several generations. Node 3 has been traversed in the fifth generation with the test data set of O_1 *with* $A = B = 11$. As soon as the last node has been traversed the test run finishes.

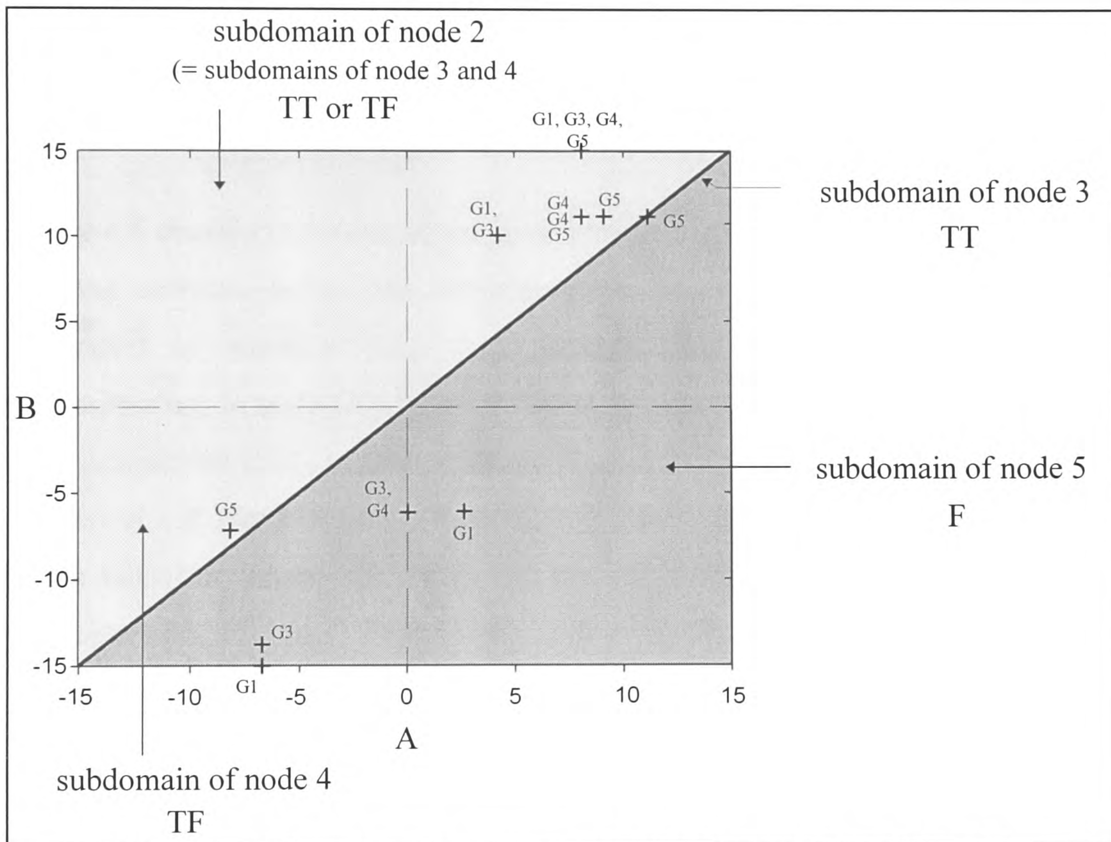


Figure 4.3: Example with generated test data for generation G1 to G5.

Figure 4.3 shows the test data in each parent population which were generated using the GA in the different subdomains. The abbreviation '*Gn*' means that the test data is generated in the *n*th generation. As can be seen the test data get closer to the domain of the path 1, 2, 3 (the diagonal). The test data which traversed node 3 is point (11, 11) in Figure 4.3. No test points are drawn for the second generation *G2*, because they are

identical to the first generation $G1$.

4.8 Method of testing

In this section the test strategy is explained in more detail with examples for i.e. 'if' conditions and loop statements. The task of the instrumented procedures are described and the method of generating boundary test data are outlined.

4.8.1 Testing '*if ... then ... else*' conditions

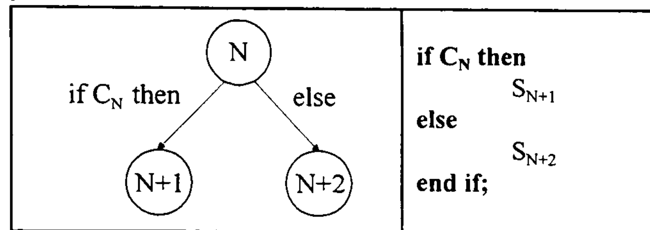


Figure 4.4: Control flow tree of an '*if...then....else*' condition and the corresponding original software.

Figure 4.4 shows an example of the control tree of a simple '*if ... then ... else*' condition and the software before the instrumentation. C_N represents a predicate function (described in equation 4.1), S_{N+1} (corresponding to node ($N+1$)) and S_{N+2} (corresponding to node ($N+2$)) are different sequences of statements to be executed. S_{N+1} is executed if C_N is true otherwise S_{N+2} is executed. Suppose the condition C_N denotes $A = B$ (see example in Figure 2.2, using the condition of node 2) where A and B are unknown integer identifiers and may be complicated functions of the input parameters $\{x_1, x_2, ...,x_m\}$. To traverse S_{N+1} in node ($N+1$), A must have a value of B. A may have any value not equal to B ($A \neq B$) to execute S_{N+2} in node ($N+2$). A preferable value for A is $B \pm 1$ since it is next to the subdomain boundary and, therefore, more likely to reveal errors than any other values for A. In terms of GAs this means that the closer the value of A is to B for node ($N+1$), the higher the fitness should be. Unfortunately these subdomain boundary values are quite often difficult to generate. In order to know which node has already been executed, the program under test is controlled by a test harness, and has to be instrumented. All necessary input parameters $\{x_1, x_2, ...,x_m\}$ are stored in a record containing the input parameters. Figure 4.5 shows the kind of instrumentation that takes place for the code segment shown in Figure 4.4.

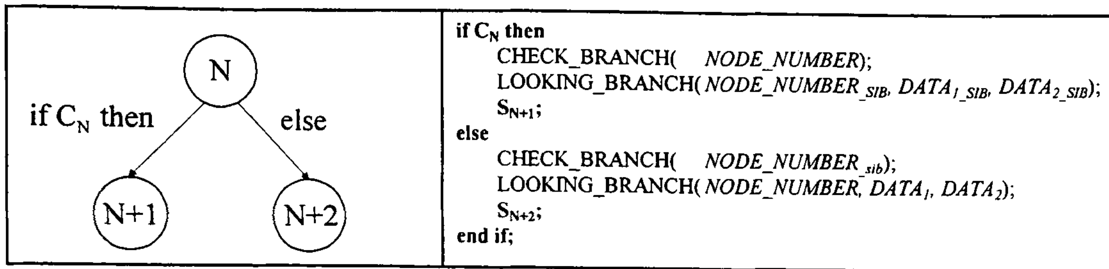


Figure 4.5: Control flow tree of an '*if...then....else*' condition and the corresponding original (bold) software and instrumentation.

CHECK_BRANCH is a procedure with one input parameter of the type integer (*NODE_NUMBER*) which records whether this particular node has been executed and if so stores the related test data. If the node has been executed, a flag will be set to true (*PV(NODE_NUMBER).BOO* := true) and the associated test data is stored, so that the testing system can start to generate test sets for the next untraversed node. The suffix '_SIB' means the properties of the sibling node in relation to the current node number. The CHECK_BRANCH procedure is given in Listing 4.1.

```
procedure CHECK_BRANCH (NODE) is
begin
  if not PV(NODE).BOO then                 -- condition whether node has been executed
     PV(NODE).BOO := true;                 -- identifier that the node has been executed
     PV(NODE).DATA.TEST := (DATA.A);       -- storing of test data
     TRI_FIT := true;                      -- identifier that a new node has been executed
  end if;
end CHECK_BRANCH;
```

Listing 4.1: Listing of CHECK_BRANCH.

LOOKING_BRANCH is a procedure with three input parameters (one for the node number, one of the left (*h*) and one of the right (*g*) predicate function, see equation 4.1) which calculates the fitness value of the sibling node when it has not been traversed. Therefore, it looks at the sibling node ($NODE_{sib}$) whether it is the next node which has to be traversed according to the variable *LOOKING*. The procedure LOOKING_BRANCH is displayed in Listing 4.2. The variable *LOOKING* holds the next untraversed node number.

```
procedure LOOKING_BRANCH(NODE_SIB, DATA_1, DATA_2) is
begin
  if LOOKING = NODE_SIB then                  -- is sibling node next node to traverse?
     BRANCH := true;                          -- identifier that a fitness value is calculated
     FITNESS_FUNCTION(DATA_1, DATA_2);        -- calling of fitness function
  end if;
end LOOKING_BRANCH
```

Listing 4.2: Listing of LOOKING_BRANCH.

The values of $DATA_1$ (evaluated by $g(x_1, x_2, \ldots, x_m)$) and $DATA_2$ (evaluated by $h(x_1, x_2, \ldots, x_m)$ depend only on the predicate, so that no other knowledge is needed. In the above example with the condition for C_N ($A = B$) with regard to execute node ($N+1$), $DATA_1$ will have the value of A and $DATA_2$ will be B. $DATA_1$ for node ($N+2$) will be unchanged whereas $DATA_2$ will have a value of the predecessor of B ($B - 1$). The symbol S_n indicates the actual statement. A more explicit example is shown in Figure 4.6.

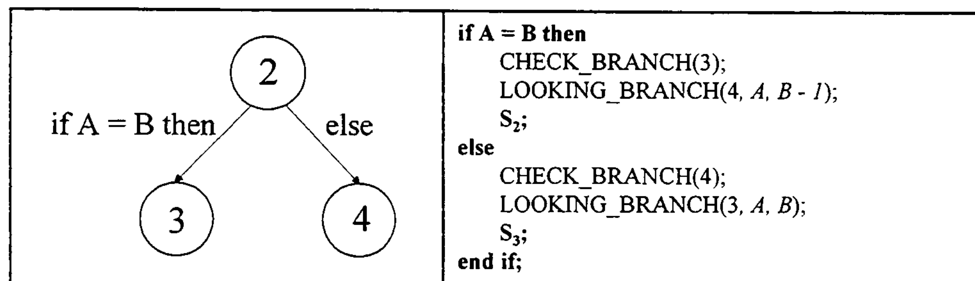


Figure 4.6: Example of original software (displayed in bold) and the instrumentation.

In the case of using either '>' or '<' in an *'if'* condition the successor and predecessor are used in order to calculate the fitness. In the case of using '>' (e.g. *'if A > B then'*) the fitness function for the true branch looks like:

FITNESS_FUNCTION(A, $B + 1$); [1]

In this case the successor of B is chosen to match A because it is the closest data with regard to A and vice versa the predecessor is chosen if using *'if A < B'*.

4.8.2 Boundary test data

Boundary test data are specially generated for mutation testing in chapter 8. The only difference to the branch testing approach is that a node is not set to be traversed with any test data which executes the node. The test data has also to be very close to the predicate's condition, that means the node is only being "executed", when by changing

[1] If test system is automated, Ada syntax: FITNESS_FUNCTION(*A*, *integer'succ(B)*);

the value of the test data by a small amount, the sibling node is being traversed. The instrumented procedures are similar to those already described (CHECK_BRANCH and LOOKING_BRANCH). An example is shown in Listing 4.3.

```
if C_N then
    CHECK_BRANCH_BOUNDARY(      NODE NUMBER, NO_OF_DATA, DATA_1, DATA_2, MAX_GENERATION);
    LOOKING_BRANCH_BOUNDARY(    NODE NUMBER_SIB, NO_OF_DATA_SIB, DATA_1_SIB, DATA_2_SIB,
                                MAX_GENERATION_SIB);
    S_N+1;
else
    CHECK_BRANCH_BOUNDARY(      NODE NUMBER_SIB, NO_OF_DATA_SIB, DATA_1_SIB, DATA_2_SIB,
                                MAX_GENERATION_SIB);
    LOOKING_BRANCH_BOUNDARY(    NODE NUMBER, NO_OF_DATA, DATA_1, DATA_2, MAX_GENERATION);
    S_N+2;
end if;
```

Listing 4.3: Listing of procedure calls for boundary testing approach.

As can be seen more information is needed for the approach of generating boundary test sets. In the CHECK_BRANCH_BOUNDARY procedure the variable *NODE_NUMBER* and values of the predicate are requested. In addition there are two new parameters *NO_OF_DATA* and *MAX_GENERATION*. *NO_OF_DATA* is an indicator of the relational operator used in the predicate and holds the number of test data sets required to be generated for this node. In the cases of the equality ('=') and inequality ('≠') relational operator, two test sets are required in order to test both sides of this boundary. If the example from Figure 4.6 is taken, test data will be generated as displayed in Figure 4.7. The crosses display test data and the labels indicate to which nodes the test data belong. This is similar to White and Cohen's approach where they use points *on* and *off* the border.

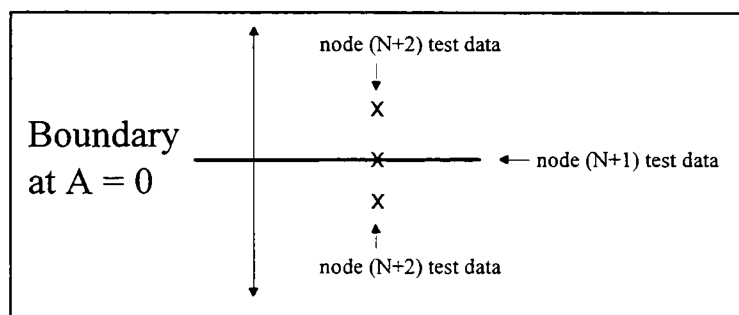


Figure 4.7: Test data for the nodes 2 and 3.

In general if boundary test data can not be found, the search will be terminated and if available the best test set according to the fitness value will be taken instead. *MAX_GENERATION* is, therefore, a limit for the number of generations which try to generate boundary test data for the node. The same applies to the procedure

LOOKING_BRANCH_BOUNDARY. The two test sets labelled in Figure 4.7 with '*node (N+2) test data*' have to be generated for node (*N+2*) in order to be sure that both sides of the boundary are tested. Node (*N+1*) just needs one test data in this case, labelled with '*node (N+1) test data*'. This means there are two different fitness functions for node (*N+2*), which use the predefined attributes *succ* (successor) and *pred* (predecessor). The fitness functions in this case are shown in Listing 4.4.

```
FITNESS_FUNCTION(A, 1);     -- fitness function for test data above the boundary (N+2)
FITNESS_FUNCTION(A, 0);     -- fitness function for test data on the boundary (N+1)
FITNESS_FUNCTION(A, -1);    -- fitness function for test data below the boundary (N+2)
```

Listing 4.4: Fitness function for different nodes.

4.8.3 Testing loops

Two different types of loops are going to be tested, the '*while ... loop*' and the '*loop ... exit*'. They will be tested for a predefined number of times a loop will iterate. In our tool the number of iterations to be tested is predefined. The testing condition is that a loop has to perform *zero*, *one*, *two* and *more than two* iterations, if possible, before it is successfully tested. This corresponds to the Defence Standard 00-55 section 33.2 [1991]:

All statements must be exercised, all branch outcomes must be tested, and all loops must be tested for zero, one and many iterations as appropriate (clause 23.2). Instrumentation of the code is required, so that coverage can be reliably checked.

Zero times mean that the loop condition is not entered which is not possible for '*loop exit*' conditions. Therefore, hypothesis 3 investigates whether GAs are able to generate test data to test a loop condition.

4.8.3.1 '*While ... loop*' testing

Two control flow trees and typical software of a '*while C loop*' statement is shown in Figure 4.8. The second control flow tree is a reduced control flow tree where the first indicates the different separate nodes in a '*while*' loop which have to be tested. These nodes indicate at the same time the exit node of the loop condition. *N* indicates the node number on entering the '*while*' loop. When the '*while*' loop condition *C* is false, the

control flows to node number $N+1$ (i.e. $n = 0$ for zero iteration and then exits the loop), otherwise to $(N+2)$, $(N+3)$ or $(N+4)$ depending on the number of iterations. In the reduced control flow tree, the middle part of Figure 4.8, the nodes are $(L = N+n+1)$, where n is the number of iterations. If the condition is false the loop terminates. S in the software represents some linear statement sequence inside the loop which executes in node *N*.

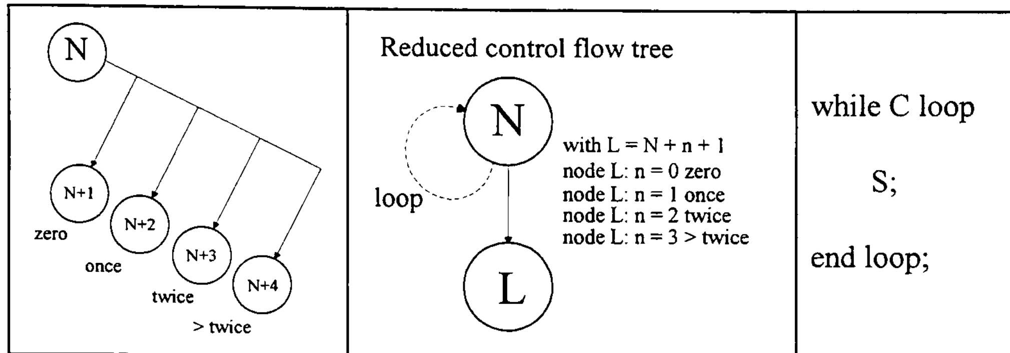


Figure 4.8: Control flow trees of a '*while*' loop-statement with the corresponding software.

Iterations are handled in a similar way as '*if*' - statements. However, a '*while ... loop*' statement will be tested for zero, one, two and more than two iterations, displayed in Figure 4.8. The loop is displayed as a dashed line in the reduced control flow tree where the control flow returns from the end of the loop back to the start of the loop condition. The additional nodes for the loop iteration testing are numbered as shown in the control flow tree with *L*, where $L = N+n+1$ and represents the exit node. The '+ 1' expression is important since the loop is tested for zero iteration which will be a separate node from the other loop testing nodes. The required number of iterations is analogous to proof by induction, which means if it is true (true referring to successful testing) for *N* and *N+1* iterations and then true for 1 iteration, it is likely to be true for 2, 3, ..., *N* iterations.

Therefore, the loop will be handled as four separate nodes. The instrumentation can be seen in Listing 4.6. Two different procedures have to be instrumented at each node which are similar to those for an '*if*' - statement but which control the number of iterations of a conditional loop. The first one is CHECK_BRANCH_LOOP which checks whether the loop iterated the predefined number of times according to the node under test. The second one is LOOKING_BRANCH_LOOP which calculates the fitness value for the node under consideration. The software is displayed in Listing 4.5.

```
procedure CHECK_BRANCH_LOOP(NODE, NITS, LOOP_COUNT) is
begin
if not PV(NODE).BOO and Nits = LOOP_COUNT then
  PV(NODE).BOO := true;
  PV(NODE).DATA.TEST := (DATA.A);
  TRI_FIT := true;
end if;
end CHECK_BRANCH_LOOP;

procedure LOOKING_BRANCH_LOOP(NODE, NITS, LOOP_COUNT) is
begin
if LOOKING = NODE then
  BRANCH := true;
  FITNESS_FUNCTION(NITS, LOOP_COUNT);
end if;
end LOOKING_BRANCH_LOOP;
```

Listing 4.5: Software listings for the instrumented procedures for a loop condition.

Two methods are used to calculate the fitness for the untraversed loop nodes, both are similar to the instrumentation for an '*if*-statement. The default one is CONTROL_BRANCH_LOOKING where *NITS* has to be the same value as *LOOP_COUNT* (line 3 in Listing 4.5) in order to execute the desired node. *LOOP_COUNT* is the desired number of iterations (predefined) required to execute a node (i.e. zero, once, twice and more than twice) and *NITS* is the actual number of iterations which the loop performs.

The second approach is used when arrays are under consideration. The array elements are used instead of the iteration number. The instrumented software is the same, only the values for the calculations of the fitness are different. This has the advantage that if an array is being used in the condition, the array elements can be accessed directly which can reduce the amount of required test data.

Each node has a different fitness function which is based on the integer variables *NITS* and *LOOP_COUNT*. The reciprocal fitness function for *zero* iteration is therefore:

$$F = \frac{1}{(NITS - LOOP_Count + \delta)^n} = \frac{1}{(NITS + \delta)^n} \tag{4.3}$$

where NITS is the number of loop iterations, δ is a small quantity to prevent numeric overflow and $n = 2$ which gave best results.

This means the closer *NITS* is to *LOOP_COUNT*, the higher the fitness and, therefore,

the closer to the desired branch being traversed. A value of 3 is chosen for *LOOP_COUNT* which corresponds to more than two iterations because it is the boundary data. A complete instrumentation for loop testing is shown in Listing 4.6.

```
while C loop
      Nits := Nits + 1;
      S;
end loop;

CHECK_BRANCH_LOOP(N + 1, NITS, 0);
CHECK_BRANCH_LOOP(N + 2, NITS, 1);
CHECK_BRANCH_LOOP(N + 3, NITS, 2);
CHECK_BRANCH_LOOP(N + 4, NITS, 3);

LOOKING_BRANCH_LOOP(N + 1, NITS, 0);
LOOKING_BRANCH_LOOP(N + 2, NITS, 1);
LOOKING_BRANCH_LOOP(N + 3, NITS, 2);
LOOKING_BRANCH_LOOP(N + 4, NITS, 3);
```

Listing 4.6: *'while'* loop condition with instrumented software.

4.8.3.2 '*Loop ... exit*' testing

The '*loop ... exit*' testing is very similar to the '*while ... loop*' testing. The only difference is that the loop can not be tested for zero iteration since the control has to enter the loop at least once. This means that the loop can only be tested for *one*, *two* and *more* than two iterations, represented in Figure 4.9 with the control flow tree and the reduced control flow tree; the instrumented software is shown in Listing 4.7.

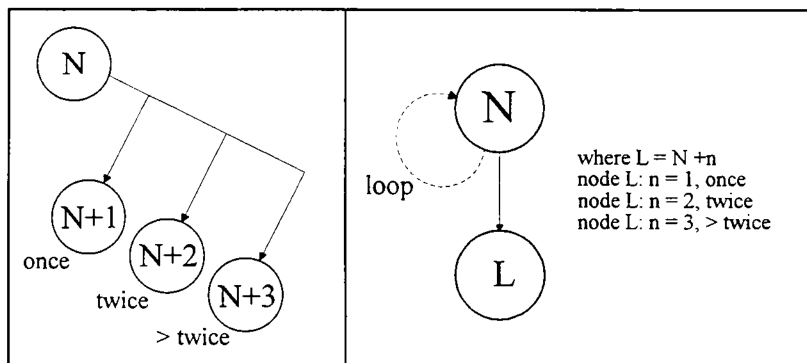


Figure 4.9: Control flow graph of a '*loop ... exit*' condition.

The only difference to the previous loop testing approach is that no test is done for zero iterations.

```
loop
    nits := nits + 1;
    S;
    exit when C̄
end loop;

Check_Branch_Loop(N + 1, NITS, 1);
Check_Branch_Loop(N + 2, NITS, 2);
Check_Branch_Loop(N + 3, NITS, 3);

Looking_Branch_Loop(N + 1, NITS, 1);
Looking_Branch_Loop(N + 2, NITS, 2);
Looking_Branch_Loop(N + 3, NITS, 3);
```

Listing 4.7: Instrumented procedures in to a '*loop ... exit*' condition.

4.8.4 Additional conditions in a loop

The testing tool has been developed to execute every branch and a predefined number of iterations. These two approaches are decoupled which means that when '*if*' conditions are inside a loop condition, the loop has to be tested for the predefined number of iterations and the '*if*' conditions for true and false. This is done separately in the way that all true and false branches of '*if*' conditions have to be executed at least once (in the case of branch testing) and not for every predefined loop iteration, i.e. the execution of the branches inside the loop is independent of the number of iterations. A control flow tree of an '*if*' condition inside a '*while*' loop is displayed in Figure 4.10.

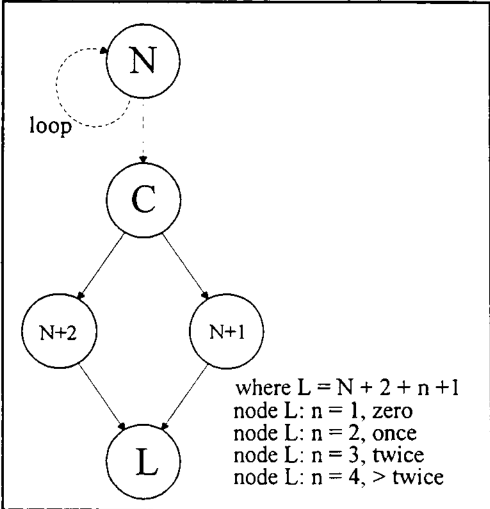


Figure 4.10: Loop testing with '*if*' statement inside.

The '*if*' condition inside the loop only gets different node numbers for the two branches, true ($N+1$) and false ($N+2$). The '*if*' condition itself does not get a separate node

number as in Figure 4.4, since the '*if* condition must be executed in order to traverse the true and false node.

4.8.5 Testing of complex data types

In the example above only simple data types such as integers were used in conjunction with a reciprocal fitness function, see equation 4.2. In the case of more complex data types and structures such as characters, records or arrays a more general fitness function based on the Hamming distance between the functions h and g is used. The advantage of the Hamming distance is that it uses the bit pattern of the predicate's function instead of their values. The Hamming distance is evaluated using the *exclusive* - OR (xor) operator of the two binary patterns, see Figure 4.11. The Hamming distance is the total number of bits, which are different, within the two strings; it is evaluated by counting the bit state '1' of a bit string which originates from combining two bit strings with an XOR operator.

Example: Two bit-strings:	1	*0*	0	1	1	*1*	0	*1*	
	1	*1*	0	1	1	*0*	0	*0*	
H_d =		*1*		+		*1*	+	*1*	= *3*

Figure 4.11: Example of calculating Hamming distance.

This fitness function is, therefore, more suitable for predicates which rely on other than numeric variables, or which involve variables of complex data structures rather than primitive data types.

4.9 Implementation (ADA, VAX, ALPHA, PC)

The programming language ADA83 was chosen to implement the GA and the test procedures. The program works on a VAX 8650 and recently it was transferred to a DEC (Digital Equipment Corporation) ALPHA computer with a 64 bit RISC processor. With small adjustments to the software testing tool, the package could also run on a Personal Computer.

4.10 Motivation of experiments

In order to verify the hypotheses from section 1.2 in the following chapters, several experiments will be carried out. In total there are many possible ways of setting up the

testing tool. In order to get an overview of how many different settings are possible, the following Table 4.9 is created.

Possible changes of set-up	Number of combination
Different crossover	3
Crossover probability P_C	10
Different mutation combination	4
Mutation probability P_m	10
Selection procedure	3
Survive procedure	5
Survive probabilities	10
Fitness functions	9
Gray or binary code	2
Threshold of weighted mutation P_E	5

Table 4.9: Possible set-ups.

There is a minimum of about $16.2 * 10^6$ different combinations for the settings using different methods in GAs, without taking into consideration the size of the population and the parameter for *BITS* which determines how many bits should get a higher probability in W_MUTATE to flip over. This amount of experiments with all different kind of combinations of parameter and procedures are of course not possible to carry out. Therefore, selected experiments are carried out, where only one parameter is changed at the time. The results of these experiments will give knowledge about the parameter settings and how the GAs react to certain settings. However, additional tests are required to make sure that the different parameter values do not influence each other, so that an optimal solution can be found.

These experiments are carried out for all the procedures under test. Only the most interesting results are listed in the following chapters, where the experiments for the quadratic procedure are explained in more detail.

Experiments were performed on alternative procedures with the GA settings the same as those for the quadratic. Those produced by the quadratic procedure and hence are not mentioned explicitly.

4.11 Interim conclusion

The technique of this approach is white box testing, which means the actual software is needed for instrumentation and execution (dynamic testing).

The above technique (instrumentation and information transfer to the testing tool) makes the basic interface possible between the program under test and the test harness. The testing tool does not need any knowledge of the program's predicates. It needs only to know what kind of input parameters are used, the values of the predicates at run time and the relational operator used. The adequacy of a test set performance which is directly related to the fitness value, according to a certain node is obtained via the predicates.

The number of required iterations can be controlled by *LOOP_COUNT* and can be changed. As mentioned earlier the traversing of branches inside a loop is independent of the number of loop iterations.

In the following chapter experiments are carried out in order to investigate the feasibility of the applied approach. Several experiments are carried out on two different procedures under test.

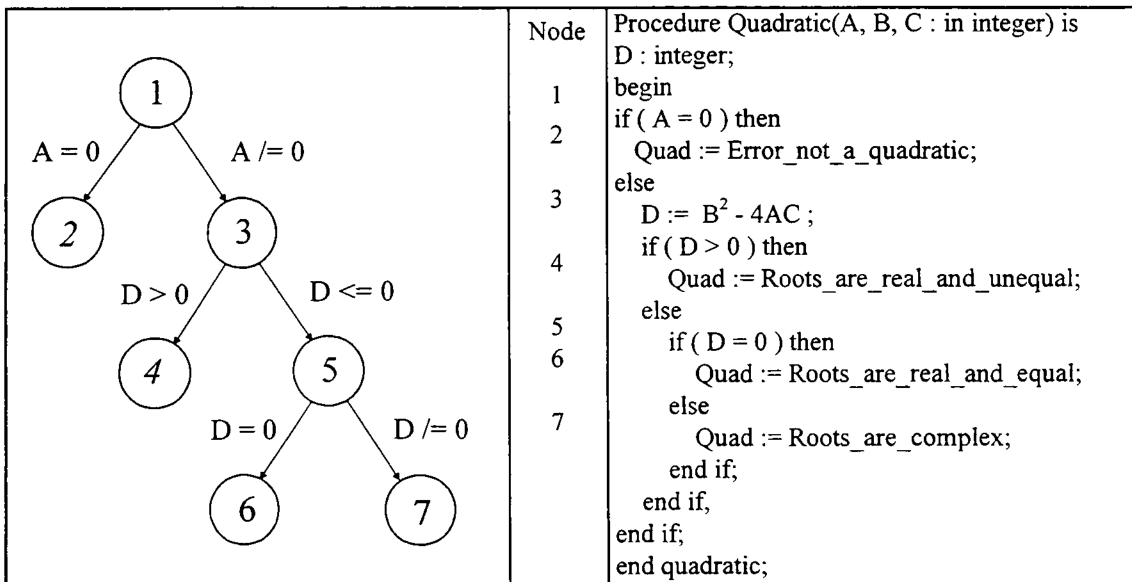
CHAPTER 5

Investigation of the use of GA to test procedures without loop conditions

The aim of this chapter is to explain the experimental investigation into software testing using two different procedures under test; the quadratic equation solver problem and the triangle classifier problem. Several experiments with various settings are conducted to find out the strength of the operators and parameter settings.

5.1 Quadratic Equation Solver

To apply genetic algorithms to generate test data automatically for software testing, a series of experiments is carried out. In this section a quadratic equation solver problem (called the procedure under test) is chosen. This procedure has three predicates involving both linear and non-linear functions of the input variables. The control flow tree is displayed in Figure 5.1 and the Ada code is listed in Listing 5.1. It is important to indicate that there are three integer input variables (A, B and C) and four paths through the procedure under test.



Node	
	Procedure Quadratic(A, B, C : in integer) is
	D : integer;
1	begin
	if (A = 0) then
2	Quad := Error_not_a_quadratic;
	else
3	D := B^2 - 4AC ;
	if (D > 0) then
4	Quad := Roots_are_real_and_unequal;
	else
5	if (D = 0) then
6	Quad := Roots_are_real_and_equal;
	else
7	Quad := Roots_are_complex;
	end if;
	end if,
	end if;
	end quadratic;

Figure 5.1: Control flow tree for the quadratic procedure.

Listing 5.1: Code for the quadratic procedure.

The quadratic equation solver problem is derived from the solution of a quadratic equation of the form equation (5.1). The solution is shown in equation (5.2).

$$Ax^2 + Bx + C = 0 \tag{5.1}$$

$$x_{1,2} = \frac{-B}{2A} \pm \frac{\sqrt{B^2 - 4AC}}{2A} \tag{5.2}$$

$$D = B^2 - 4AC \tag{5.3}$$

The type of result for a quadratic equation depends on the relationship represented in equation (5.3). The nodes of the control flow tree represent a linear code sequence of statements between each selection. The leaf nodes 2, 4, 6 and 7 finish with an *end if* and will eventually exit the procedure. These nodes represent the different alternatives which the roots can have (e.g. real, complex, etc.) which will be decided by equation (5.3). If the conditions are true the next left child node will be executed, if not then the right node. Nodes 1, 3 and 5 are the branch nodes and they determine the next branch to be executed depending on its condition and input data. Points to note about the procedure under test are:

1. One of the input variables, A, is involved directly in an equality condition ($A = 0$);
2. D is a non-linear function of the input variables, and is involved in two conditions controlling a total of three paths;
3. D is involved in an equality ($D = 0$);

If the condition $A = 0$ is true, node 2 is executed which means that the input variable A has the value of the constant ($A = 0$) and indicates that it is not a quadratic equation, because the first term of equation (5.1) which represents the quadratic characteristic is 0.

Figure 5.2 illustrates global optima ($D=0$) and local optima (e.g. $D = 1$). The figure shows a section from the search space in the range from 0 to 40 in only two dimensions for the input variables A and B with regard to node 6. The default search range is limited to ± 100 for each of the three input variables for the first generation. However, using GAs and, therefore, crossover and especially mutation operators, test data may be generated which lie outside of the software input's domain. Those test are invalid for the software, but it is necessary to use those data to determine the software's response, Weyuker [1983].

Different symbols indicate different results for D. Circles (o) indicate a global optimum, cross symbols (x) display solutions for $D = \pm 1$, star symbols ($*$) display solutions with $D = \pm 2$, plus symbols (+) displays $D = \pm 3$ and points ($\cdot$) indicate solutions for $D = \pm 4$. The numbers at the circles (global optima solutions, $D = 0$) indicate the value of the third variable C for that particular global optima solution. This section displays only the solutions in the first quadrant. Figure 5.2 shows that the global optima are disconnected. This means the global optima are surrounded with test data of low fitness so that the fitness landscape is not linear.

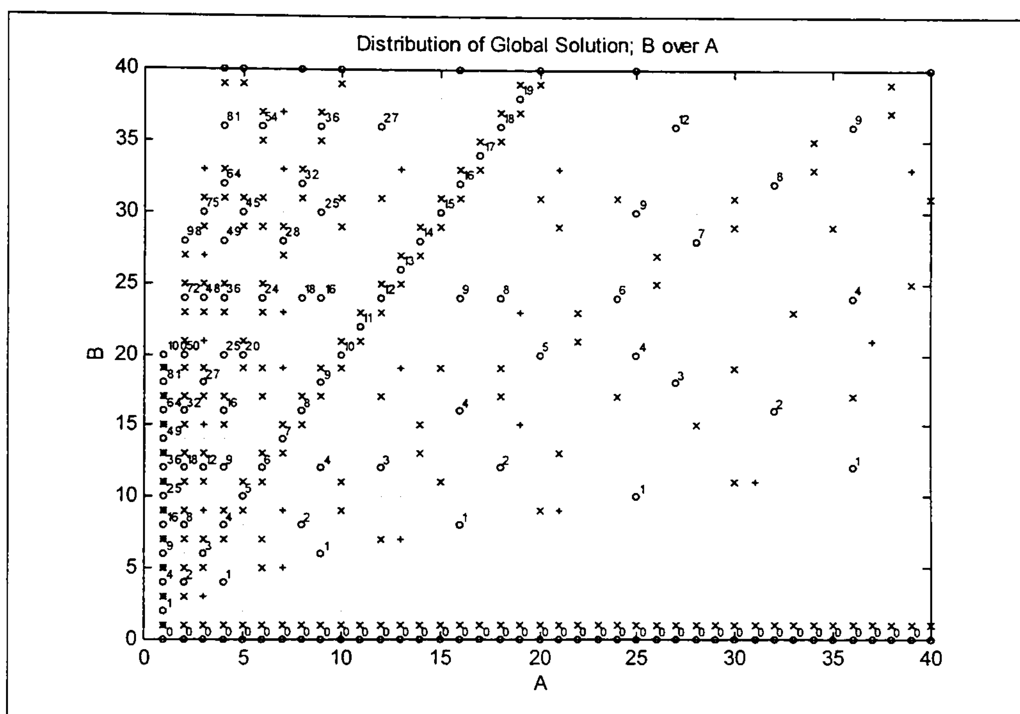


Figure 5.2: Illustrating global and local optima with regard to D = 0 using integers.

5.1.1 Experiments and investigation of GA for branch coverage and testing

In this section different experiments and settings are suggested and tested. Detailed explanations of the control parameters of the GAs are given and discussed. The results are shown below in the subsections. The experiments are derived by changing control parameters like the probability of survival into the next generation or by changing a complete operator such as the crossover operator.

The input data consists of three integer variables which are converted to chromosomes

(binary strings) by the generic ADA utility UNCHECKED_CONVERSION.

5.1.1.1 The generic Unchecked_Conversion procedure

The generic UNCHECKED_CONVERSION procedure of ADA, converts any data type into a two's complement representation. One of the most important features of ADA is the generic definition. Generic procedures or packages are written in such a general way that the same algorithm can be applied to variables of any data type. There is no need to know all the details of these generic types being manipulated. These types together with procedures which manipulate variables of these types are passed to the generic unit as parameters when the generic unit is instantiated, Feldman [1993].

An integer conversion will lead to a 32 binary bit array in two's complement format. This kind of representation is quite different from the representation in binary format plus sign bit which is shown in Table 5.1 for the numeric value of -1 and +1 with a 8 bit representation.

Bit array								Code type	decimal value
1	1	1	1	1	1	1	1	two's complement	-1
1	0	0	0	0	0	0	0	two's complement	1
1	0	0	0	0	0	0	1	binary-plus-sign	-1
1	0	0	0	0	0	0	0	binary-plus-sign	1

Table 5.1: Difference between binary-plus-sign code and two's complement representation.

In the case where a two's complement representation is chosen for mating (crossover), (e.g. for a negative integer value -1 and positive integer value 1) the offspring are in all probability totally different from the parents. This is because the patterns of both parent arrays are very different, compared with the numeric values, see Table 5.1. To avoid such an effect, a procedure with the name CONTROL_PARENT has been written, which checks whether a parent has a negative value. In the case of a negative value, it will be converted into a normal binary with sign coded representation. The MSB represents the sign bit and is stored by UNCHECKED_CONVERSION on the right side of the bit array and the LSBs are on the left side.

The patterns of both arrays are now similar as are their numeric values.

5.1.2 Different select procedure

Two chromosomes are selected from the current population for submission to the crossover and mutation operators. The selection may be made in many ways, either purely at random (SELECT_R) or according to the chromosomes' fitness (SELECT_F). These selection procedures are described in chapter 3.8.2.

5.1.2.1 Results of selection procedures

Experiments are performed with these selection procedures (random and selection according fitness) in order to find the best way to choose parents for the reproduction phase. The results show that if the parents with a higher fitness have a better chance of being selected, they are not as good as an alternative approach where the parents are completely chosen at random using SELECT_R. In agreement with Lucasius and Kateman [1993], it is found that the best strategy is to select the parents purely at random, especially under the present circumstances where there are many global optima ($D = 0$) of equal fitness value. Suppose, two chromosomes in one generation might aim for two different global optima which are in totally different domain areas, so that although both chromosomes have a high fitness value, the bit patterns are completely different. If those two chromosomes are selected for recombination, the resulting offspring could have a very low fitness, because the offspring might be in fact far away from any global optima, because the offspring might be totally mixed up.

This result is surprising at first sight, but on reflection, random selection maintains a diversity in the population and this encourages healthy offspring. As has been shown in other experiments by Lucasius, inbreeding leads to premature convergence at local optimum solutions which means that the search space is not explored widely enough. When the parents are selected according to fitness, performance deteriorated. Only 94% of test runs give complete branch coverage at an average generation of 19.4, giving at least 2342 tests. This compared to full branch coverage in 13.4 generation (1286 tests) for random selection. This means that nearly double the number of tests are required in order to traverse every branch when parents are selected according fitness.

The results, therefore, give a clear statement for hypothesis 2_2 that random selection is

better at least in the cases when several global optima exists.

5.1.3 Different survive procedure

One of the most important operators in the process of GAs is the method of how parents and offspring will survive into the next generation, i.e. which individuals of the parent population are dying and being overwritten by the offspring. In total, five different survive methods, which are described in chapter 3, are tested thoroughly with different survive probabilities P_S.

5.1.3.1 Results

The following diagram shows the results of all of the different survive procedures using the reciprocal fitness function. Figure 5.3 shows the required tests in average over the probability of survival. The survive procedure which needs fewest tests is the best one, because it finds a global optimum faster than the others with regard to function evaluation effort. In order to get a good statistical result, 500 test runs are carried out for each set-up.

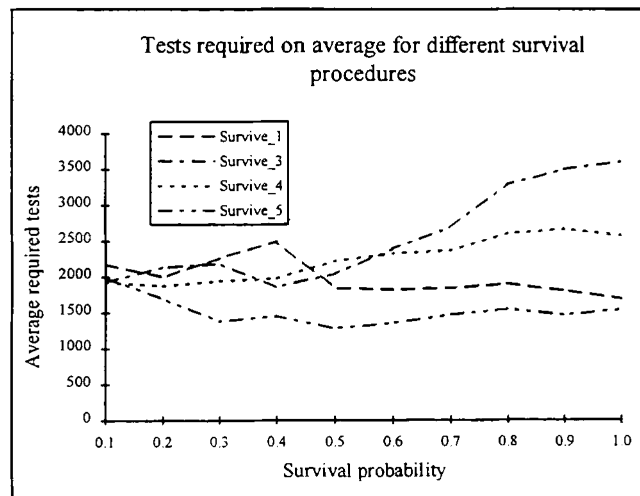


Figure 5.3: Required tests for different survival procedures and probabilities using reciprocal fitness function to give branch coverage.

The graph for the results of SURVIVE_2 are omitted from Figure 5.3 because its survival is independent of P_S. The result is about 3254 tests using SURVIVE_2. As can be seen the best survival strategy is SURVIVE_5 using a reciprocal fitness function which required fewer tests on average than all other survival procedures. It is not only the best strategy associated with successful test runs (always 100% success at $P_S = 0.5$),

but it is also the method which generates the most steady and consistent results whatever the survival probability is. SURVIVE_1 only achieves a similar good result with a very high survive probability of $P_S = 1.0$. The same experiment is repeated using the Hamming fitness function. The results are shown in Figure 5.4.

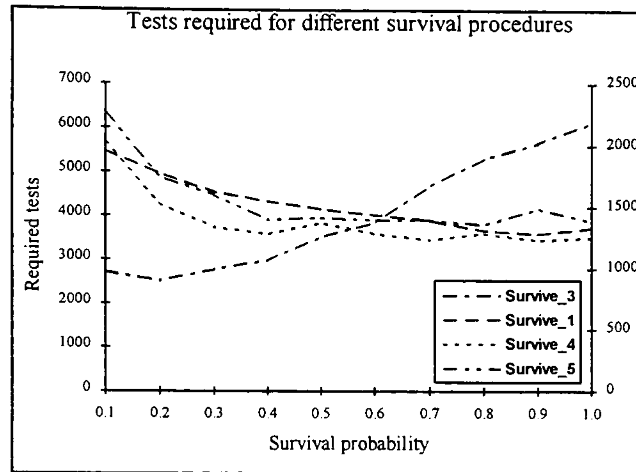


Figure 5.4: Required tests for different survival procedures and probabilities using Hamming fitness function to give branch coverage.

The figure for SURVIVE_3 uses the left Y-axis, all other results use the right for clarity. SURVIVE_2 needed about 2669 tests for full branch coverage. SURVIVE_4 procedure turns out to be the best suited survival procedure using Hamming fitness function. The only survival probability at which full branch coverage is achieved, is $P_S = 0.5$ using SURVIVE_4.

5.1.4 Different population size P_{SZ}

The population size P_{SZ} is chosen according to the size of the chromosome. Normally there are as many chromosomes in a population as there are bits (genes) in a chromosome itself. The chromosome length (S) is the product of the number of bits (n_i) which a data type represents times the number of input variables (N) which are to be optimised by the GA, e.g. if there are only the same input type variables, the number of bits can be calculated by equation (5.4):

$$S = \sum_{i}^{N} n_i \tag{5.4}$$

In this case the chromosome length is 96 bits, i.e. three integers where an integer has 32

bits. The decision to use a population which has a square array of bits for the three 32 bit input integers, has been shown to be successful. This is demonstrated by the next set of experiments. Multiples of the integer size are chosen as the basis for the population size. Experiments are carried out with a population size of 32, 64, 96, 128 and 160 and the results are shown in Table 5.2.

Experiment No.	Population size P_{SZ}	Results	
P_1	32	91.0% in 31.8,	> 1214
P_2	64	99.0% in 19.4,	> 1294
P_3	96	100% in 13.4,	1286
P_4	128	100% in 11.8,	1510
P_5	160	100% in 9.1,	1456

Table 5.2: Results using different population sizes.

As can been seen, the results vary with the size of the population. A good indicator of the performance of different experiments (settings) are the number of tests which are needed to satisfy all branches.

In Table 5.2 three different results are displayed in the column 'Results'. The first number refers to the percentage of successful branch coverage achieved during an experiment (success(%)). The second number states the number of generations required for the experiment (result_gen) and the last number indicates how many times the actual procedure under test is called or how many test data are generated (tests). The number of tests are evaluated from the number of required generations times the number of chromosomes per generations. If full branch coverage is not achieved (less than 100%), an expected number of required generations are calculated with the help of the maximum allowed number of generations per test run (max_gen). It is obvious that the higher maximum generation is, the more accurate is the result for the number of tests, especially if full branch coverage is not achieved, see equation (5.5). In this case the greater than sign ' > ' is used to indicate more than this number of tests are essential to get full branch coverage. In the first two experiments (P_1 and P_2) the greater than sign '>' indicates that more tests are needed than the stated number of tests.

$$tests = \frac{success(\%) * result_gen + (100\% - success(\%)) * max_gen}{100} * P_{SZ} \qquad (5.5)$$

The smaller populations produce full branch coverage in only 91% of test runs at an

average generation of 31.8. This enables a minimum value of 1214 to be assigned to the number of test sets needed for full branch coverage.

The third experiment shows that the method of using a population size which depends on the chromosome length, i.e. there are as many chromosomes in a population as there are bits in the chromosome itself, is better than a populations with a smaller or larger number of members, which defines hypothesis 2_4. The suggested population size give improved results in the sense that full coverage is obtained in all test runs at an average of 13.4 generations, corresponding to an average of 1286 tests.

Although, the average number of generations for full branch coverage decreases (100% in 11.8 generations) the number of required tests (1510) increase, because of the increase in number of the population size to 128 members.

Small populations usually find solutions quickly, but tend to converge prematurely to a local optimum. Although in the context of locating members of suitable subdomains, there may be many goals of equal value, there may be no global optimum in the normally accepted sense. There is a tendency for the whole population to take the same value, and this loss of diversity effectively disables the search for the required goal. Larger populations allow the search space to be sampled more thoroughly and they are therefore less likely to be trapped by a sub-optimal solution, but the penalty is increased processing effort (more function evaluation) and it does not mean under any circumstances that the solution is found in fewer tests. For all future experiments of the quadratic equation solver a population size of 96 is chosen.

5.1.5 Different fitness functions

The fitness value is calculated by the program under test. The fitness value of an individual is used to compare an individual with other individuals in the same population to differentiate their performance with regard to the problem under test. If the resulting individual is near to the optimum solution, it will get a high fitness value and if it is far away from the optimum it will get a low fitness value. The better individuals (higher fitness) usually replicate for mating purposes with a higher probability than the worse ones which tend to die.

All fitness functions, whether reciprocal or Hamming distance, are derived directly from the condition of the predicate (objective function).

5.1.5.1 Reciprocal fitness function

The easiest of all the fitness functions used is the reciprocal function. This function is the reciprocal of the variable to be optimised, see equation (4.2). In trying to satisfy the predicate $D = 0$ the fitness of an individual, which has a value of $D = 1$, reaches a higher level of fitness than an individual with the value of $D = 2$ (Fitness($D = 1$) > Fitness($D = 2$)) because the first individual is closer to satisfying the predicate. Experiments have consistently shown that the best value for n using equation (4.2) is 2. The reciprocal fitness function for node 6 is formulated in equation (5.6).

$$Fitness = \frac{\alpha}{(h-g)^2 + \delta} = \frac{\alpha}{(D-0)^2 + \delta} \tag{5.6}$$

where δ is a small quantity to prevent numeric overflow,
α is a constant (default value is 1) and
h and g defines the predicate (see section 4.2.1).

The default setting achieves full branch coverage in 13.4 generations (1286 tests).

5.1.5.2 Gaussian function

The Gaussian distribution is used in order to calculate the fitness of the chromosomes. The only difference is the shape of the function after the fitness has been calculated.

$$f(x) = \frac{250}{\sqrt{2\pi}} e^{-\phi x^2} \tag{5.7}$$

where ϕ is a factor in order to change the width of the function and x is here e.g. $D - 0$.

Various parameter values for ϕ are chosen in order to obtain the best setting. The disadvantage of the Gaussian and reciprocal approach is that these fitness functions are only valid for numeric functions. In order to calculate the fitness for non numeric optimisation problems (characters, records and arrays) a new approach has to be taken.

5.1.5.3 Hamming distance function

The Hamming distance has been implemented using the *exclusive OR operator* (XOR). Different variations of the Hamming distances are under investigation; unweighted, weighted, reciprocal and non-reciprocal.

The simplest form of the Hamming distance is where the bits which have a state of '1' are counted. This is to be called *unweighted* Hamming distance (H_4 in Table 5.3) . If the position of the '1' bits are taken into consideration, it is called *weighted* Hamming distance. There are different ways of calculating a weighted Hamming distance using these bit state positions of '1's which are reflected in the fitness value. H_2 squares the bit position and adds them up whereas H_3 only adds up the bit positions. The bit position of the LSB is 1. H_5 calculates the actual bit values of the '1' bits positions and adds these together. In all these cases, after the distance is determined, the reciprocal of the distance has to be taken, because the smaller the distance the higher the fitness and the nearer it is to the global optimum. Another method is to look for bits with the bit state of '0' after combining two bit strings with an XOR operator (fitness function H_1). The effect now is that the closer the solution is to the global optimum, the higher the total amount of '0's. Consequently the higher number of '0' is now directly related to the fitness so that there is no need to take the reciprocal of that value. For node 6 the fitness function could look like that displayed in Table 5.3 where S is the size of the bit string.

H_1 = D XOR 0	with adding the 0 bit states:	$Fitness = \delta + \sum_{i=1}^{S} \begin{cases} 1 & if\ H_1(i) = 0 \\ 0 & if\ H_1(i) = 1 \end{cases}$

Referring to the *i*th '1' bit state position and using reciprocal:

H_2 = D XOR 0	with adding the bits with i^2:	$\frac{1}{Fitness} = \delta + \sum_{i=1}^{S} \begin{cases} i^2 & if\ H_2(i) = 1 \\ 0 & if\ H_2(i) = 0 \end{cases}$
H_3 = D XOR 0	with adding the bits with i:	$\frac{1}{Fitness} = \delta + \sum_{i=1}^{S} \begin{cases} i & if\ H_3(i) = 1 \\ 0 & if\ H_3(i) = 0 \end{cases}$
H_4 = D XOR 0	with adding the bits with 1;	$\frac{1}{Fitness} = \delta + \sum_{i=1}^{S} \begin{cases} 1 & if\ H_4(i) = 1 \\ 0 & if\ H_4(i) = 0 \end{cases}$
H_5 = D XOR 0	with adding the bits with 2^i:	$\frac{1}{Fitness} = \delta + \sum_{i=1}^{S} \begin{cases} 2^i & if\ H_5(i) = 1 \\ 0 & if\ H_5(i) = 0 \end{cases}$

Table 5.3: Different Hamming fitness functions.

The experiments show that the fitness function H_2 gives the best results among the different Hamming fitness functions; the results are shown in Table 5.4.

Fitness function	Result	Tests
H_1	100% in 18.3 generation	1757
H_2	100% in 14.3 generation	1373
H_3	100% in 15.2 generation	1460
H_4	100% in 15.9 generation	1527
H_5	96.3% in 15.1 generation	>1752

Table 5.4: Results from using different Hamming fitness functions.

The result when using fitness function H_4 is worse than when using the weighted method H_2 or H_3, because it does not take into consideration at which position the difference occurs. A Hamming distance of one between two binary strings can mean in this case that the numerical difference may be very small (e.g. 2^0) but it can also mean that the difference may be quite large (e.g. 2^{31}) and that the chromosome is numerically far away from the global optimum.

Using a weighted Hamming fitness avoids this and is used by H_2, H_3 and H_4. This method will distinguish between chromosomes which are actually close to or far from the goal using different weighting methods. The results using H_5 fitness are not as good as the other weighted fitness functions. This may be explained by the method being too strongly weighted. This result is reflected in the experiment when a fitness function is chosen which is similar to fitness H_2, the only difference is that the ith bit position is not quadrupled (like in H_2), it is tripled. An over weighted method will decrease the performance of the GAs, because the fitness value will always be low until the individual gets very close to the global optimum.

A comparison between the reciprocal H_4 and non reciprocal H_1 method, using the same weighting method, turns out to favour the reciprocal method. The results for the experiments using H_1 are not as good as for the Hamming reciprocal version. The non reciprocal version H_1 needs at least 400 tests more than H_2 and about 230 tests more than H_4 until full branch coverage is achieved. The reciprocal effect on the fitness functions is that closer values (of h and g, see equation (4.1)) are more favoured so that the GA is directed to these data sets.

A comparison between the different fitness functions shows that using a Hamming

distance as the basis for a fitness function produces more consistent results. By increasing the range of the initial randomly generated population from ±100 to the range ±200, on average more function evaluations are needed. The reciprocal fitness function needs at least 3122 tests (91.2% in 26 generations) to obtain full branch coverage whereas the Hamming distance only needs 1978 tests (20.6 generations) and full branch coverage is always achieved.

5.1.6 Gray code

The Hamming distance is effective in comparing patterns rather than values. However, the numbers 7, 8 and 9 are close numerically, but 7 and 8 are separated by a larger Hamming distance (using binary code) than 8 and 9, this can make the search difficult for the GA. To avoid such an effect and to achieve a change of one unit in the underlying data type using a Hamming distance of exactly one unit everywhere, the Gray code is implemented, where the Hamming distance in Table 5.5 refers always to the previous bit pattern.

Decimal Number	Binary code		Gray code	
	Bit string	Hamming distance	Bit string	Hamming distance
0	0000	-	0000	-
1	1000	1	1000	1
2	0100	2	1100	1
3	1100	1	0100	1
4	0010	3	0110	1
5	1010	1	1110	1
6	0110	2	1010	1
7	1110	1	0010	1
8	0001	4	0011	1
9	1001	1	1011	1
10	0101	2	1111	1
11	1101	1	0111	1
12	0011	3	0101	1
13	1011	1	1101	1
14	0111	2	1001	1
15	1111	1	0001	1

Table 5.5: Comparison of binary and Gray code with MSB on the right hand side.

A Gray code represents each number in the sequence of integers as a binary string of length S in such an order that adjacent integers in Gray code representations differ by only one bit position, see Table 5.5. Stepping through the integer sequence only requires the flipping of one bit at a time in the code. Basically, a Gray code takes a binary

sequence and shuffles it to form a new sequence with the property.

When a bit of a binary code mutates, the corresponding real variable is perturbed. The size of the perturbation depends on the bit or bits chosen for mutation. Caruana [1988] mentioned that a Gray coded representation improves a mutation operator's chance of gaining incremental advantages. In a binary coded string of length S, a single mutation in the most significant bit (MSB) alters the number by 2^{k-1} (where k is the kth bit mutated, and k starts to count from LSB). Through mutating in a Gray coded representation, less significant bits can lead to a change of this size.

In the example above, a single mutation of the extreme right bit (MSB) changes a zero to a 15 and vice versa, whereas the largest change in the corresponding binary coded representation of a single mutation is always eight (for $S = 4$). Using Gray coded representation, the kth bit can affect all bits of the corresponding binary code from the kth bit to the *MSB* bit, so that the magnitude of the corresponding perturbation can be up to 2^k and perturbations of all sizes from 2^0 up to this maximum are possible. The advantage is that most mutations will make only small changes, while the occasional mutation that effects a truly big change may initiate exploration of an entirely new region in the search space.

The direction of the perturbation is determined by the value of the bit that is mutated. Using binary coded representation, changing the bit state from 0 to a 1 will always yield a perturbation in the positive direction, and changing a 1 to 0 will always produce a perturbation in the negative direction. Using Gray coded representation a change from 0 to 1 may perturb the variable in either direction.

In order to produce a Gray code, the binary coded representation is converted into the new code representation. After crossover and mutation the Gray coded representation is converted back to the binary coded representation. The conversion processes are as follows and are displayed in Figure 5.5 and Figure 5.6. The bits of the binary coded string B[i] and the Gray coded string G[i] are labelled in such a way that the larger represent the more significant bits. The most significant bit is copied into the new string. In order to convert from binary to Gray *code* $G[i] = B[i+1]\ xor\ B[i]$, in the case of converting back from Gray to binary, use $B[i] = G[i+1]\ xor\ G[i]$.

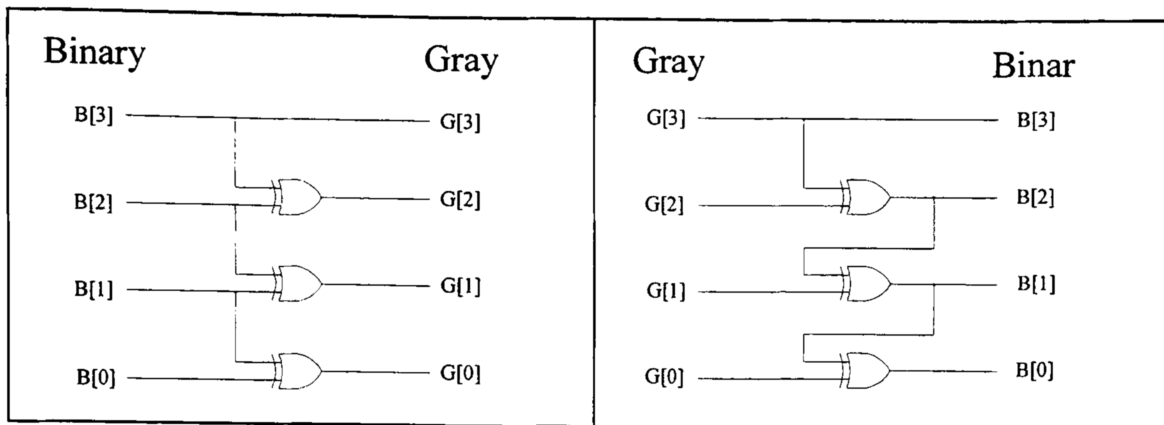


Figure 5.5: Binary to Gray conversion. **Figure 5.6:** Gray to Binary conversion.

Wright [1991] and DeJong [1993] investigated the use of GAs for optimising functions of two variables and claimed that using a Gray coded representation worked slightly better than the binary coded representation. DeJong attributed this difference to the adjacent property of the Gray code representation. The step from the value three to four requires the flipping of all the bits in the binary representation, as can be seen in the above example in Table 5.5. In general, adjacent integers in the binary representation often lie many bit flips apart. This fact makes it less likely that a mutation operator can effect small changes for a binary coded individual.

5.1.6.1 Results of using Gray code

The results of the experiments using the Gray code are not as good as expected. Experiments are carried out for both fitness functions. The best results are obtained using the reciprocal fitness function with only 99.6% success rate in 16.6 generations (> 1626 tests compared to 1286 tests using binary code), but zero solutions ($A \neq 0$, $B = 0$, $C = 0$) are only 27% of all test solutions. Since there are fewer zero solutions than using Gray code means that the pressure towards small values for the input variables A, B and C is less, and the chance to generate an optimum solution deteriorates because the highest density of global optima is near the origin.

Using the Hamming fitness function H_2, only 97.8% successful test runs are achieved in 18.1 generations (> 1911 tests compared to 1372 tests and 100% success rate using binary code), however, only 21% zero solutions are generated. For both experiments the strategy of using the Gray code instead of the binary code increase the number of tests;

in the first case about 350 tests, in the second experiment about 500 tests in order to achieve full branch coverage.

The results change when W_MUTATE is switched off. Using the reciprocal fitness function with binary code, the results are much worse. Only 23% of all test runs are successful in 5.3 generations, compared to using the Gray code, where the success rate is 62.3% in 18.4 generations. By not allowing *zero solutions* to be a global optima and using a reciprocal fitness function and binary coding achieved full coverage in 19.7 generations which is about 6.4 generations more than allowing zero solutions, because there are fewer global optima. However, using Gray code representation achieved slightly better results in 18.5 generations. This result indicates that Gray code could be better than binary code (defining hypothesis 2_1) in some cases, especially when zero values can be avoided. This will be further investigated in the triangle procedure in section 5.2.

5.1.7 Zero solution

In seeking to satisfy the predicate $D = 0$ (equation (5.3)) the GA led to 43% of all combinations having $B = C = 0$ (zero values for A are already filtered before this predicate), compared with 200 or 17.6% out of the possible 1104 solutions in the range of ±100. These are called here *zero solutions*. The high percentage of zero solutions for the GA is because smaller values for B and C naturally lead to smaller values for $B^2 - 4AC$, and therefore higher fitness. This produces a pressure leading to the case when $B = C = 0$. Figure 5.7 shows a distribution of global solution to the problem of $D = 0$ which represents node 6. The dots represent all possible global solutions in the displayed search range. The numbers next to the dots indicate how often those particular solutions are generated by the GA. The zero solutions are along the A-axis where $B = 0$ (C is also zero for these solutions), as can been seen in Figure 5.2.

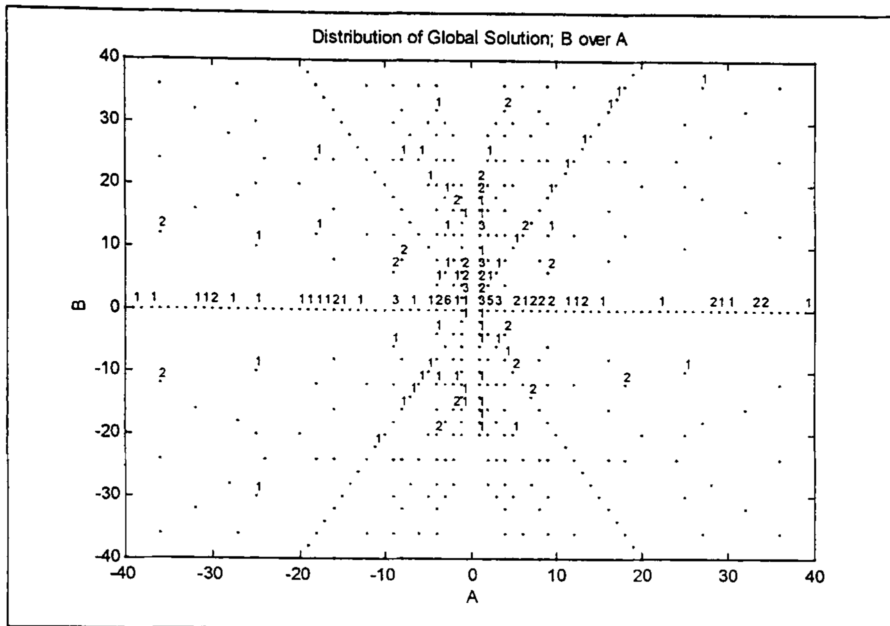


Figure 5.7: Distribution of global solutions using binary coded representation where solution for $A = 0$ has been filtered out.

Instead of using a binary code, a Gray code is used in the next experiment to see whether using a Gray coded representation still prefers smaller values. As stated earlier in the experiments using Gray code (section 5.1.6.1) fewer zero solutions are generated. This can be seen in Figure 5.8. There are clearly fewer entries on the B-axis with $B = 0$. The results of a random test are shown in Figure 5.9.

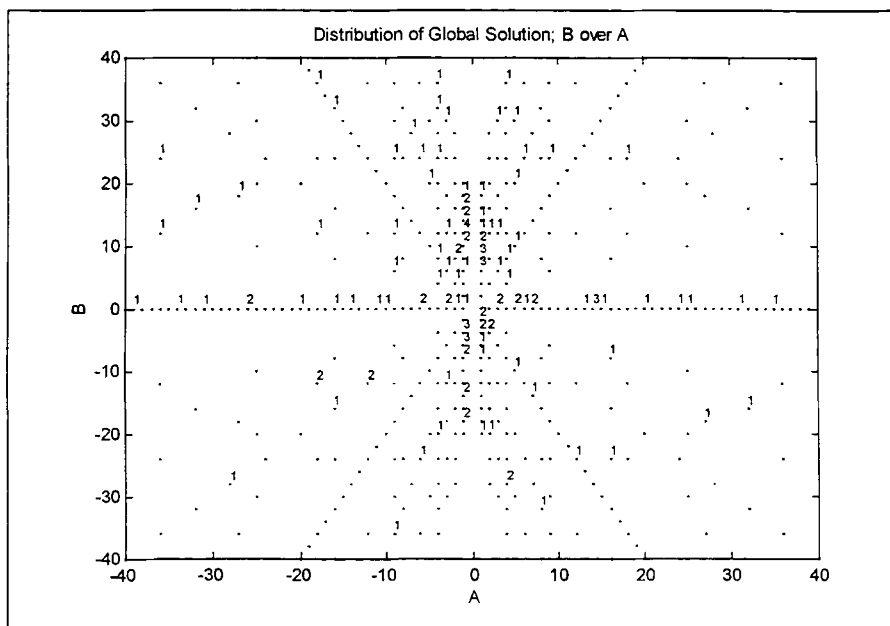


Figure 5.8: Distribution of global solutions using Gray coded representation where solution for $A = 0$ has been filtered out.

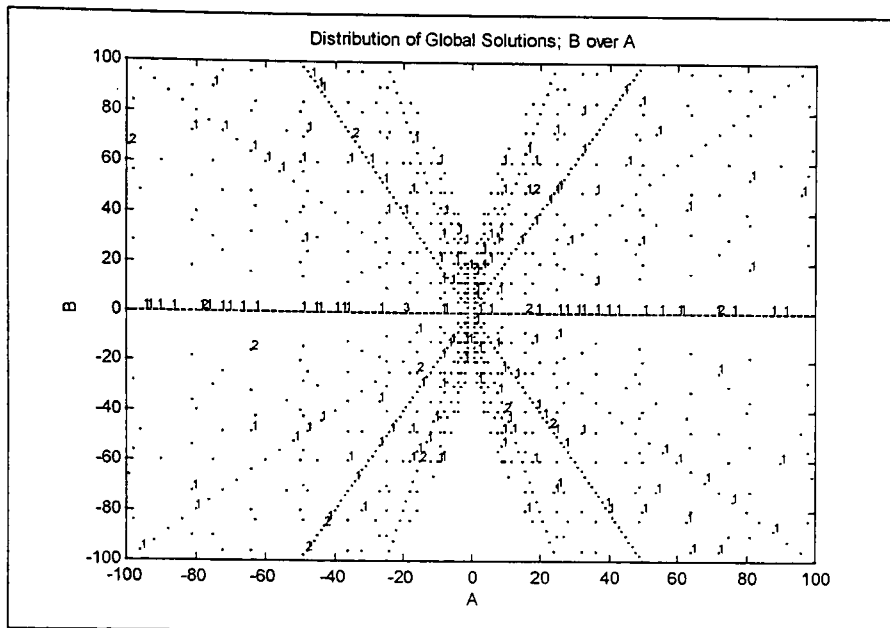


Figure 5.9: Distribution of global solutions using random testing where solution for $A = 0$ has been filtered out.

As can be seen in the random experiment, Figure 5.9, the generated global solutions are evenly distributed, whereas the solutions for using GA tends to favour points near the origin. The results are shown in Figure 5.7 and Figure 5.8 with a limited range. The entire range is shown for the random experiment.

5.1.8 Comparison of different crossovers

The crossover operator is a process of mixing bit patterns from two guesses (chromosomes) which may have been chosen because they have a high fitness. Arbitrary points along the bit string are chosen at random and the tails of the two chromosomes are exchanged so that two new offspring are produced. The number of those points depends on the different kinds of crossover operators which are explained in chapter 3. The selection can be made by the fitness or through random selection.

5.1.8.1 Results of crossover

Experiments are carried out for all three crossover operators, single, double and uniform crossover. For each operator, different crossover probabilities P_C are chosen. The crossover probability of the variants had different effects. The crossover probability of the single and double crossover operator decides whether the crossover is carried out for the two selected parents strings. The crossover probability for the uniform crossover

operator decides whether or not each bit of the parent string should be swapped. The results are shown in Table 5.6.

Prob. P_c	Single crossover	Double crossover	uniform Crossover
0.1	96.4% in 18.9	95.4% in 19.5	99.1% in 15.9
0.2	97.6% in 17.9	96.7% in 18.9	99.6% in 16.0
0.3	97.5% in 16.8	97.0% in 18.8	100% in 14.9
0.4	98.0% in 16.9	97.5% in 17.4	100% in 14.8
0.5	98.4% in 16.4	98.2% in 18.2	100% in 13.4
0.75	98.6% in 17.2	98.3% in 16.3	99.4% in 15.4
0.9	98.1% in 17.4	98.0% in 16.8	99.0% in 16.2

Table 5.6: Results of using different crossover operators.

For the uniform crossover the results in the probability range from $P_C = 0.6$ to $P_C = 0.9$ are similar to those from $P_C = 0.4$ to $P_C = 0.1$, because the probability P_C identified whether a bit position should be swapped or not, so that a high probability is likely to achieve a similar offspring as a low probability, when both offspring are used in the next steps of the GAs.

A direct comparison between the crossover operators favours uniform crossover. The reason for this can be explained by the more exploitative method of uniform crossover compared with the single and double crossover operators. The chance of combining good building blocks is better with uniform crossover.

Single crossover may only change one input variable at a time and double crossover either one or two, but never three variables. The predicate functions involve all three variables and a de-coupling of any two variables will reduce the effectiveness of the search for the optimum. In general, uniform crossover explores more of the domain than 1- or 2-point crossover.

Uniform crossover also achieves better results when the input variables are handled separately and not in one single bit string, so that crossover is applied to each single input variable (bit string). This can be explained by the length of the input variable and the range for the first randomly generated population. In order that the offspring are different from their parents after using single crossover, the crossing point has to be in the region where bits (genes) have values of '1' which is in most cases the lower significant bit regions since the input variables have relatively small numeric values

compared to the maximum of + 2^{31} to ($-2^{31}-1$). However, if the crossover point is outside this region the offspring will not change their pattern and thus can not improve their genetic material. The chance that the crossover point is in the preferred region is ,therefore, smaller. Uniform crossover does not have this problem because each bit has a chance of being swapped.

These experiments results conclude that uniform achieves in fewer tests branch coverage than the other two methods of crossover, defining hypothesis 2_3.

5.1.9 Different mutations

Two different mutation operators are used, MUTATE and W_MUTATE, which are both described in chapter 3. The best mutation probability turns out to be $P_m = 0.01$ in the experiments which means that on average every *100*th gene is swapped, so that there will be about one mutation per chromosome. This is in agreement with Schaffer's [1987] and Mühlenbein's [1991 b] suggestion of taking the reciprocal value of the length of a chromosome as the mutation probability. Therefore, the hypothesis 2_5 is confirmed. Several tests shown in Table 5.7 are conducted in order to find out which parameter settings deliver good results.

Probability of P_m	Results	Tests
0.05	82.2% in 36.9	> 4621
0.025	95.6% in 28.2	> 3011
0.01	100.0% in 13.4	1287
0.005	87.4% in 17.3	> 2662
0.002	63.2% in 14.4	> 4407

Table 5.7: Results of using different mutation probability P_m.

As can be seen if the mutation probability increases the results are worsen. This is similar to random generated test data, because the GAs cannot use their power to produce better building blocks because of the changes to the chromosomes are too big. The same effect regarding the results happens if the mutation probability decreases, because then there is not enough disruption in the population.

To decide whether the population is stuck at sub-optimal solutions, the procedure EQUALITY is developed.

5.1.10 The EQUALITY procedure

This procedure determines how many individuals of the current population have the same value by comparing their fitness values. A population which has many members of the same individual is unhealthy and risks being stuck at a sub-optimum. If a certain number of individuals are the same, a flag parameter is set and after the next normal mutation procedure W_MUTATE will start working. The threshold of starting W_MUTATE is controlled by the pre-defined parameter P_E the equality probability. Various tests are carried out with different values for P_E. The pseudo code of the EQUALITY procedure can be seen in Figure 5.10 and results in Table 5.8.

```
Determine how many individuals are the same;
if number of same individuals more than a predefined value P_E then
    use MUTATE and W_MUTATE;
else
    use only MUTATE;
```

Figure 5.10: Pseudo code of EQUALITY procedure.

Prob. of P_E	Results	Tests
0.1	99.4% in 15.6	1547
0.2	99.7% in 13.9	1360
0.3	100.0% in 13.4	1287
0.4	99.2% in 14.7	1477
0.5	98.2%% in 15.8	1663
0.75	86.2% in 26.2	3491

Table 5.8: Results of using different values for P_E.

If the value of P_E is too big the population has already converged on to a local optimum, before W_MUTATE can start working. The population has lost all diversity and it is difficult to leave that sub-optimal converged point in the domain.

On the other hand if P_E is too small, W_MUTATE will start too early with a high mutation rate for certain bit positions which is similar to a higher probability of the normal mutation operator P_m. This is then similar to a random search rather than an evolution towards a global optimum. A good value for P_E is 0.3 which always achieves complete branch coverage. The default factor turns out to be 20 ($P_{m_w} = 20 \cdot P_m$) where P_{m_w} is the probability after which some lower significant bit and the most significant bit positions are mutated.

5.1.11 Using mutation only

Using a GA with mutation but without crossover achieves a respectable result. This confirms the results of Spears and Anand [1991] who demonstrated that GAs without crossover can out-perform GAs with crossover for small populations where diversity is limited.

In our experiments the results achieve without crossover are not as good as those stated by Spears and Anand. Nevertheless, the results of the experiments show that 96% of test runs are successful in 17.7 generations using a Hamming fitness function H_2 and 90% of test runs are successful in 19.4 generations using the reciprocal fitness function. In this case the population is not small (96 members per population) as in Spears' case and good diversity is guaranteed through random selection of the parents and by using the weighted mutation operator and survive procedures. Mutation is a powerful operator of a GA, but without crossover, the GA is not always sufficient, which is confirmed by experimental results of DeJong [1990] and Schaffer and Eshelman [1991]. Neither mutation nor crossover alone should be advocated or dismissed. Each operator plays an important and different role in the search process where crossover is better for achieving good solutions because crossover shares information between fit individuals whereas mutation is better for disruption and exploration.

When comparing these results to pure random testing in section 5.1.13 it is found that the results without crossover are still good. The power of GAs is good at exploiting solutions even if crossover is not active.

5.1.12 Results of the quadratic equation solver

Many experiments are conducted to investigate which combinations of operator, probability and methods are best. The best set-up for the GAs for this kind of problem is:

Uniform crossover with a $P_C = 0.5$, population size of $P_{SZ} = 96$, mutation probability of $P_m = 0.01$, SURVIVE_5 with $P_S = 0.5$, equality probability $P_E = 0.3$, the reciprocal fitness function and binary coded sign and magnitude representation have been found to be the best setting. To check whether this default setting interacts between all other

parameters (probabilities and operators), several additional tests are carried out to demonstrate whether a good setting has been found.

5.1.13 Random testing

In order to compare the effectiveness of using GA, pure random experiments are carried out. The input test sets are generated across the range ±100 with a uniform probability. A total of 7354 random tests are needed to obtain full branch coverage (100% in 76.6 generations) where the limitation of maximum generation (*MAX_GEN*) per test run is set to 10000 to ensure that full branch coverage is achieved. If *MAX_GEN* is restricted to 100 generations only 73.2% of all tests achieve full branch coverage in 40.3 generations, compared to 1287 tests (100% in 13.4 generations) using GAs.

Poor performance of random testing on such a simple program arise because satisfying the predicate $D = 0$ is very difficult compared with the other inequalities. Within the range ±100, there are over 8 million possible input combinations of *A*, *B* and *C*, but only 1104 (0.014%) will satisfy this predicate. Therefore, the expected number of tests to execute node 6 can be calculated with equation (5.8):

$$NoRT = \frac{input \quad combination}{k} \tag{5.8}$$

where *k* is the number of solution for that particular goal and *NoRT* is the expected **N**umber **o**f **R**andom **T**ests.

The calculated number of random tests is 7356 which agrees closely with the above experimental result. As the input range increases, so the density of possible combinations decreases. For example, if the range of randomly generated test data is being doubled to ±200, the combinations of satisfied solutions are roughly doubled to 2472 solutions, but the range of all possible combinations is increased by the factor 8. Overall, the density of satisfied combinations is decreased by the factor 4. Using a range of ±200 for the random number testing, the result deteriorates by a big margin. If 100% success rate is achieved for random testing, 266 generations and 25536 tests are required. Only 30.8% of all tests in 46.9 generations generate test data for full branch testing if *MAX_GEN* is set to 100, compared to 100% successful test runs in 19.5 generations (1872 tests) using Hamming distance. Only 97.2% success rate in 17.3

generations (> 1884 tests) is achieved by using the reciprocal fitness function. It can be clearly seen that the results using the reciprocal fitness function are not as good as using Hamming fitness function with increasing input range.

Range of input	Number of solution and percent of input domain		Random testing		GA using Hamming	
	Number	Percentage	Tests	CPU	Tests	CPU
±100	1104	0.014%	7354	0.11s	1373	0.46s
±200	2472	0.0038%	25536	0.38s	1975	0.66s
±400	5480	0.0011%	92348	1.37s	2642	0.88s
±800	11976	0.00029%	329251	4.93s	3408	1.29s
±1000	15384	0.00019%	551924	7.70s	4247	1.47s

Table 5.9: Results using random and GA testing.

In Table 5.9 the first column expresses the range which is used for random testing and used for the first population of the GAs. The second column shows the total number of solutions in that search space defined by column 1 and column 3 shows the percentage of it with regard to the input domain. The results using random testing are displayed in columns four and five and columns six and seven show the results using GAs. In addition to the number of required tests for full branch coverage, the CPU time is presented in seconds per test run for full branch coverage. Figure 5.11 displays the rapid increase of CPU time for random testing compared to the slow increase of GA testing over the range of input values. In the comparison of the range ±100 and ±1000 random testing increases the used CPU time by a factor of 76.3, whereas GA testing increases it by a factor of 3.2. Random testing is very fast in the small range of ±100 compared to GAs, but at a range of ±270 the CPU times for both are comparable.

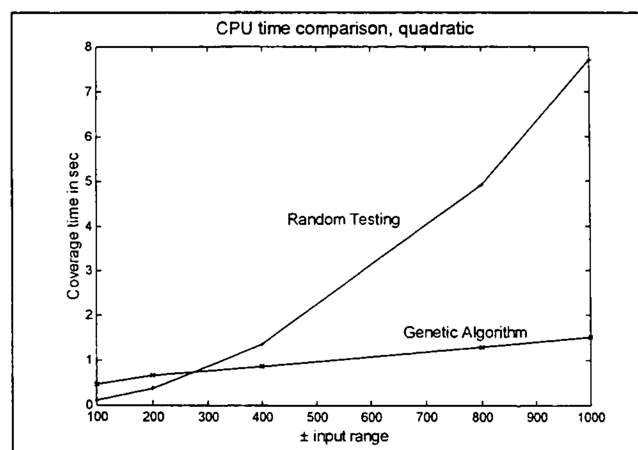


Figure 5.11: CPU time over various input ranges for using random numbers and GA.

5.1.14 Comparison between GA and Random testing

Figure 5.12 displays two test runs using GA and random testing. The global optima ($D = 0$) are found much earlier using GA with regard to the number of generations.

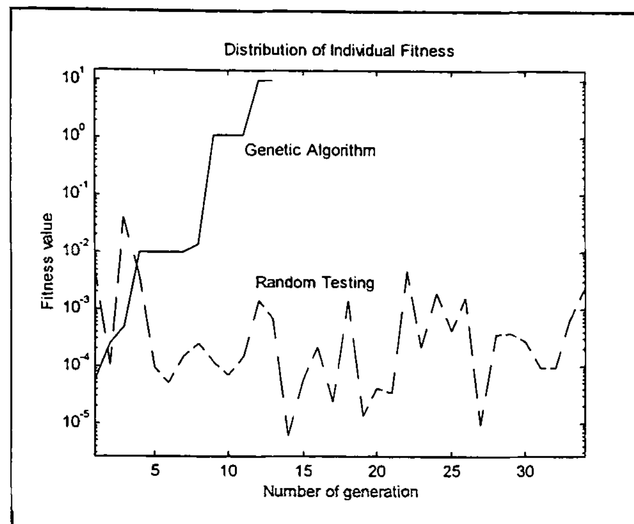


Figure 5.12: Individual fitness over a test run using GAs and Random Testing.

Figure 5.12 displays how fitness behaves over generations of a test run using GAs and random testing. The log-linear plot shows that GAs cause an improvement in fitness of several orders of magnitude over random testing.

The member with the highest fitness value within a population with GA and random testing is printed over the number of generations which displays the off-line performance (see chapter 3); the fitness values are not accumulated. Once the GA has started to work, a strong increase in fitness can be observed after only 4 generations respectively about 400 tests compared with the fitness values of the random testing method which oscillate around a certain low fitness value. This confirms DeJong's [1988] statement that typically between 500 and 1000 samples are required before GAs have sufficient information to explore useful subspaces. The increase in fitness is steady over the generations until it finds a global optimum in generation 13. The converging process towards the goal can be seen by the increasing fitness. The fitness values for the purely random tests are randomly distributed as would be expected.

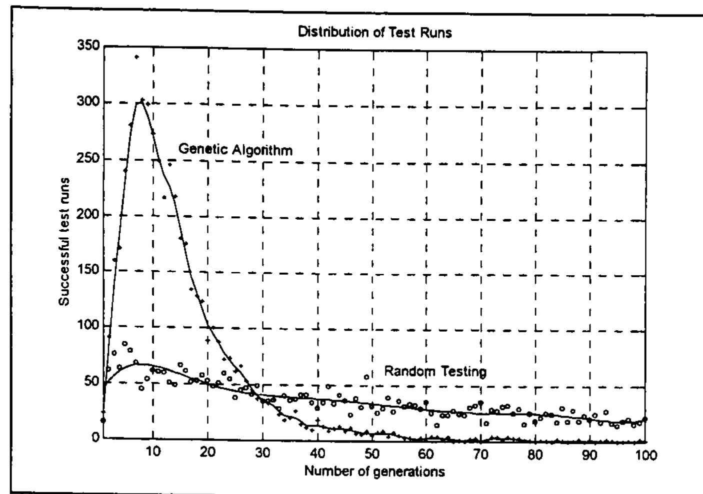


Figure 5.13: Histogram of successful test runs.

Figure 5.13 shows distribution / histograms of successful test runs using GAs and random testing. In both cases 5000 test runs are carried out to get a meaningful statistical result. The generation numbers in which full branch coverage is achieved are counted and plotted over the generation range allowable (1 to *maximum generation*). The plus (+) symbols indicate the results for the GA and the circles (o) of the random testing. As can be clearly seen, if using GAs, most of the test runs are successfully finished in the first 20 generations where its maximum is around generation 7. The figure strongly decreases after the maximum which is the sign that only a few test runs require more generations (or tests). However, random testing has not developed such a strong maximum which is also around generation 7 but it only decreases slowly which is a sign that many test runs require more generations.

As can be seen from these experiment results generating test data with GAs is more efficient than using random testing, especially when the solution sub-domains are small.

5.1.15 Interim Conclusion quadratic

The first set of experiments using the quadratic equation solver problem, indicate that it is useful to use GAs in order to generate test data for software branch testing compared to random testing, especially when the solution domain is small. This is demonstrated by the number of required tests and used CPU time for random and GA testing. The experiments are used to find out important characteristics of GAs and to find a default setting, which can be used for further experiments. The experiments show that a square

array for the population size and chromosome length is advantageous. Random selection of the parents is superior to the selection of parents according their fitness. Uniform crossover is better than single or double crossover. Both mutation operators are necessary for good results and binary coded representation is better than Gray coded representation.

Description	Results	Tests
GA, reciprocal	100% in 13.4	1286
GA Hamming	100% in 14.3	1373
GA reciprocal parent	94% in 19.4	> 2342
GA Hamming parent	100% in 15.6	1498
GA, reciprocal Gray	99.6% in 16.6	1626
GA Hamming Gray	97.8% in 18.1	> 1911
GA reciprocal ±200	97.2% in 17.3	1884
GA Hamming ±200	100% in 19.5	1872
Random ±100	100%	7354
Random ±200	100%	25536
GA Hamming without crossover	96% in 17.7	> 2016

Table 5.10: Summary table of most significant results.

Two main default settings have been found, depending on the fitness functions. In the case of reciprocal fitness function the SURVIVE_5 gives the best results, whereas using any Hamming fitness functions, SURVIVE_4 should always be used to achieve branch coverage. The reciprocal and Hamming fitness functions are similar in structure. The reciprocal fitness function needs roughly 90 tests less (full coverage in 13.4 generations) compared to the Hamming fitness (full coverage in 14.3 generations). However, using Hamming fitness functions the results are more consistent which can be seen for example in the experiments with the different initial range of the population, see section 5.1.13, where the performance using reciprocal fitness function deteriorated with increasing the size of the initial search range.

The results are promising in that the GAs are able to achieve complete branch coverage with fewer than 82% of the number of tests that pure random tests require. The results and analysis of random testing can be divided into two parts. Results which give a reasonable good performance with test data generated from a small range (±100) because the density of global solutions is quite high; on the other hand a larger range (±200) give much worse results because the density of global solutions decrease strongly and more tests and thus CPU time are required. The main hypothesis 2 can be

confirmed here. A standard setting has been found which will be applied to various programs under test to verify it and to try to tune and to describe it in more detail.

Both testing methods show that it is quite easy to generate test data for the linear condition nodes 2 and 3 and for the inequality condition nodes 4 and 7 but for both methods it is more difficult to generate test data for the non-linear and equality condition branch node 6. Most of the CPU time is spent producing test data for this particular node.

5.2 Triangle classification procedure

Another test procedure is chosen for testing which is similar to the quadratic equation solver. It is called the triangle classifier procedure and consists of several procedures.

5.2.1 Description of the triangle procedure

The triangle program comprises a combination of three procedures. This program was written by a member of the research group, Steve Holmes.

The triangle program involves both linear and non-linear functions of the input variables. Like the quadratic equation solver problem, the triangle also uses equality and inequality relational operators. The complete triangle program has three integer input variables A, B and C, one output variable TRI_KIND, 27 nodes, 14 paths and the longest path has 13 nodes through the software. It is a bigger and more complex procedure than the quadratic equation solver. The output variable returns the type of triangle corresponding to the three input variables. The triangle procedure decides whether the three input variables represent the lengths of the sides of a triangle and determines the type of the triangle, equilateral, isosceles, scalene or right angled scalene. The name of the main procedure is TRIANGLE and it has two sub procedures;
RIGHT_ANGLE_CHECK which is also a sub procedure of TRIANGLE_2. The input variables A, B ,C and the output variable TRI_KIND are global variables in all three procedures.

The TRIANGLE procedure checks whether the three variables represent a triangle (a scalene triangle). Therefore the variables have to be greater than the numeric value 0 (corresponding to node 3, 5 and 7, which involves only one variable and a constant at a time). In addition, twice the value of each single variable has to be less than the perimeter ($P = A + B + C$) value (corresponding node 9, 11 and 13 which involves linear conditions).

If the test data fulfil all these criteria then the procedure TRIANGLE_2 is called which determines whether the three variables form an isosceles triangle (represented by node 17, 18 and 21, involve only linear conditions) or an equilateral triangle (node 19).

In the case that the triangle is non of these types, the procedure RIGHT_ANGLE_CHECK is called which decides whether the current triangle is a right angled scalene triangle represented by the nodes 23, 25 and 27, which involves non-linear conditions).

The ADA software for the triangle procedure is listed in appendix A and the entire control flow tree is shown in Figure 5.14 with an indication of the parts that relate to the different procedures. The conditions for each node is printed next to the nodes.

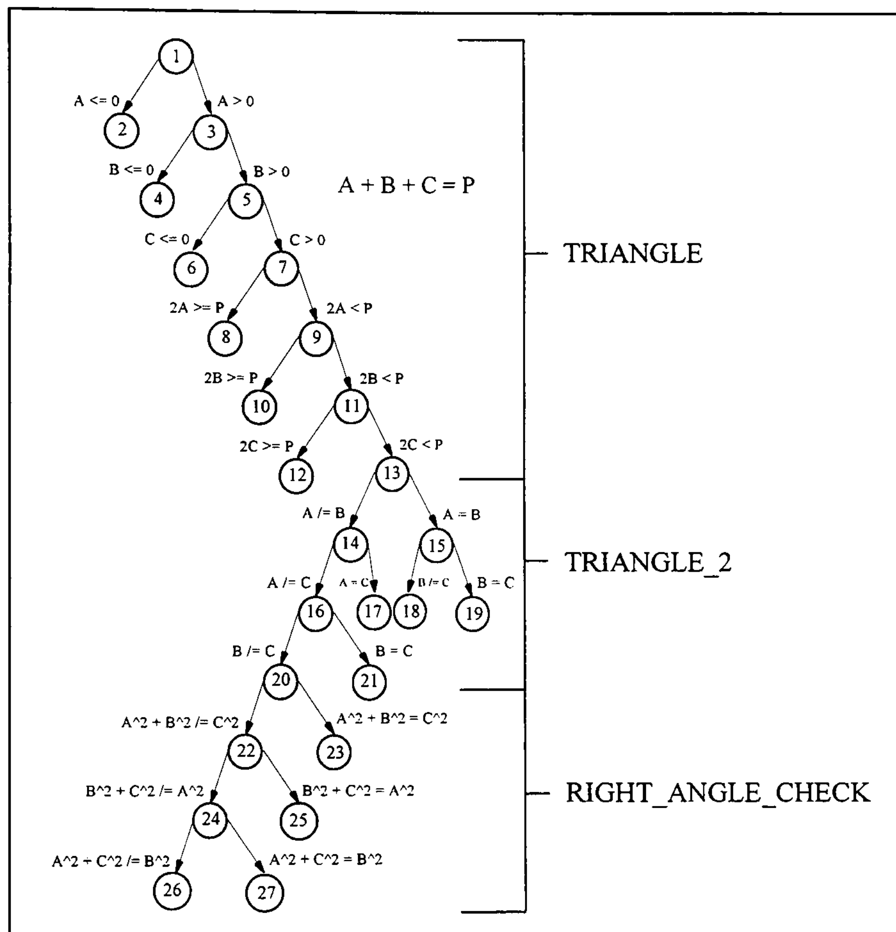


Figure 5.14: The complete triangle control flow tree.

The entire triangle procedure is used in the testing tool. The most difficult nodes to execute and to generate test data for are nodes 19, 23, 25 and 27. Node 19 is an equality predicate involving all three input variables of the form $A = B = C$. However, the high number of tests required reflects the presence of three non-linear predicates of the form $A^2 + B^2 = C^2$ and its permutations which are represented by nodes 23, 25 and 27. The main task will be to execute these branches. Not only are there few solutions for these,

but also the probability of traversing their opposite nodes is relatively small because many combinations of individuals are already filtered out via the pre-conditions at the start of the triangle procedure such as all negative values including zero.

5.2.2 Result for the triangle classifier

Several experiments are carried out in order to confirm the performance of the GA. In particular, different fitness functions and crossover operators are under intense investigation.

The maximum number of generations after which a test run is abandoned, is increased to 2000, because it is more difficult to generate test data which will satisfy all branches in the triangle procedure compared to the quadratic equation solver problem.

The results obtained using different fitness functions are similar to the previous set of experiments for the quadratic problem. The simple reciprocal fitness function achieves slightly better results than the Hamming fitness functions. The default set-up which has been derived from the quadratic problem is used for these experiments.

5.2.2.1 Different Fitness functions and survive probabilities

The reciprocal fitness function and default setting leads to 100% successful test runs in 276 generations (27876 tests). With a survival probability of $P_S = 0.5$, the Hamming fitness function achieves a success rate of 100%, and the average of the generations decreased to 270 generations (25945 tests).

5.2.2.2 Different crossover operator

By comparing the different crossover operators, the same kind of result is obtained as in the quadratic problem. The stated results are obtained with the default setting, which includes the reciprocal fitness function. Uniform crossover is superior to other crossover operators (single and double crossover), seen in Table 5.11 where the percentage of full branch coverage, the number of required generations and tests are displayed.

Uniform crossover	Double crossover	Single crossover
100% in 276 gen. (27876 tests)	96.3% in 363 gen. (> 40663 tests)	97.5% in 390 gen. (> 41304 tests)

Table 5.11: Different crossover for the triangle procedure.

Using uniform crossover, complete success (100%) is achieved in 276 generations (27876 tests). Double crossover is only 96.3% successful in 363 generations (> 40663 tests) and single crossover is 97.5% successful in 390 generations (> 41304 tests). Double and single crossover have almost the same performance, whereas uniform crossover shows a much better performance, so confirming hypothesis 2_3. When the crossover operator is completely switched off, only 86.8% of all test runs achieve full branch coverage in 437 generations. This means that more than 61834 tests must be completed for full branch coverage to be achieved.

Having used Gray code in the quadratic procedure which achieves slightly better results than binary code when *zero solutions* are not allowed, a surprising result is obtained by using Gray coded representation for the triangle procedure. Using the reciprocal fitness function, 99.5% of all test runs are successful in only 176 generations which corresponds to more than 17772 tests and 100% in only 185 generations (17789 tests) using the Hamming function. The Gray coded representation achieves much better results (half the number of required tests for branch coverage) than the binary coded representation for both fitness functions. This confirms hypothesis 2_1 that Gray code can achieve better results than binary representation.

5.2.3 Comparison with random testing and probabilities

Random testing is also applied to the triangle procedure, to obtain a comparison of the effectiveness of GAs. In the range ±100 there are only 104 solutions (0.0013%) which will satisfy the condition $A^2 + B^2 = C^2$ of node 23, including all pre-conditions. This means that for node 23 alone an average of 78083 random tests have to be generated in order to traverse this node. The same probability satisfies nodes 25 and 27 which have similar conditions, only in a different combination. Most of the CPU time is taken up traversing these three nodes. However, node 19 which has fewer solutions than any of these three nodes, is easily traversed by the GA because the predicate of node 19 is linear whereas the other three are non-linear; it is easier to find one of the global optima

for the linear predicate. Normally for linear conditions, the closer the test data is to the global optima the higher is the fitness. Thus, the fitness landscape is continuous increasing so that by favouring always the closer data with a higher fitness value will eventually generate the optima. On the other hand, if the condition is non-linear, the fitness landscape also can be non-linear, which means that test data close to a global optimum may not always have a higher fitness than test data further away, which can cause convergence towards a sub optimum instead of a global optimum.

5.2.3.1 Results Random Test

In the range of ±100 with a *MAX_GENERATION* of 2000 only 69.5% of test runs are successful in 1187 generations (> 167036 tests). If *MAX_GENERATION* increases so that 100% success is achieved, 1701 generations (163296 tests) are necessary which agrees closely with the theoretical result by generalising equation (5.8) provided that the probabilities of executing the four branches 19, 23, 25 and 27 are equal:

$$NoRT = \sum_{m=1}^{L} \frac{input \quad combination}{m * k_L} \qquad (5.9)$$

where L is the number of branches to consider (here $L = 4$), k_L is the number of solutions for that particular branch.

Therefore, NoRT = 162673. On increasing the initial range to ±200 the success rate is only 44.2% in 1533 generations whereas GA testing achieves 100% in 505 generations (48490 tests).

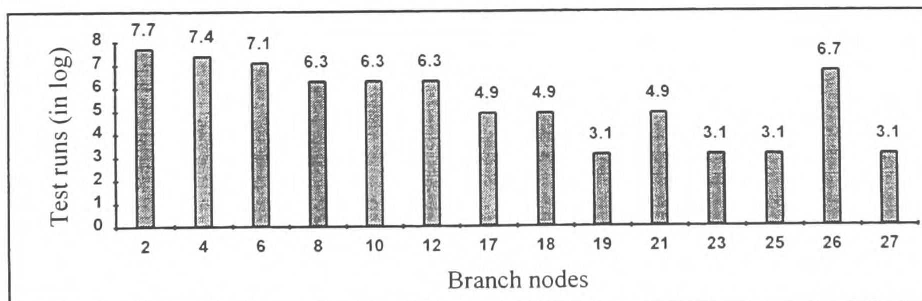


Figure 5.15: Executed branch distribution in log for random testing.

In Figure 5.15 the distribution of executed leaf nodes is displayed after 10^8 function evaluations with random generated numbers. After one test run, only one leaf node will have been executed. As can be seen the least executed nodes are node 19 (equilateral

triangle), 23, 25 and 27 (scalene right angled triangle). These four branches have about the same probability of being executed with random testing in the range of ±100 which is confirmed in Figure 5.15. This means that for random testing it is equally difficult to execute all these branches whereas using GA the most difficult nodes are only nodes 23, 25 and 27 because of the highly non-linear properties. A comparison of the required CPU times for the different testing methods are displayed in Table 5.12.

Range of input	**Random testing with 100% success rate**		**GA using Hamming**	
	Tests	CPU	Tests	CPU
±100	160752	3.0s	17789	8.4s
±200	571983	10.4s	48490	23.5s
±400	1967674	37.9s	126943	60.4s

Table 5.12: Results using random and GA testing.

It can be clearly seen in Table 5.12 that the random testing is in these ranges faster with regard to CPU time than GA. However, the factor increases with regard to the GA's CPU time slower than of random testing. In this case the GA needed only a factor of 10 less tests than random testing so that the total required CPU time for full branch coverage is in these input ranges higher. Figure 5.16 illustrates the required CPU time over various input ranges used in Table 5.12.

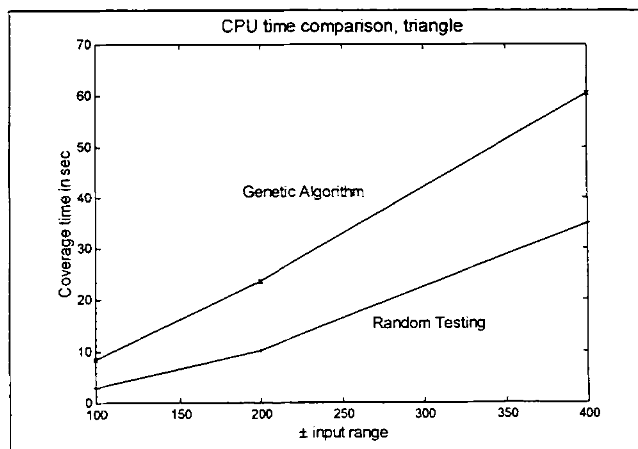


Figure 5.16: CPU time over various input ranges for using random numbers and GA.

It can be seen in Figure 5.16 that random testing in these ranges is faster than GAs. In this case random testing required a factor of 10 more tests than GAs so that the total CPU time required for full branch coverage in these input ranges is higher.

Hypothesis 1 can be confirmed for the triangle procedure according to the number of

required tests. The GAs need indeed fewer test data to generate for branch coverage than random testing, however, the GAs required more CPU time than the random generated test data.

5.3 Interim conclusion triangle

As for the quadratic problem, GAs are capable of generating and optimising test data in order to traverse all nodes in the control flow tree of a program. It is evident that the GA's performance is also the superior testing method for the triangle procedure in that it needs fewer tests. The importance of crossover is demonstrated and is more obvious than in the quadratic equation solver procedure. Not all of the experiments results are recorded here. Only the important experiments and results are mentioned in this section for the triangle procedure. The experiments, that are not explicitly listed in this section, had a similar outcome as for the quadratic equation procedure, e.g. the survive procedures and the survive probability.

After a node has been executed the fitness function changes, in order to optimise test data for the next node. This can be seen in the rapidly decreasing fitness value in Figure 5.17. The labels 'Node' express which node is executed at that stage. As earlier stated the four nodes (19, 23, 25 and 27) are the most difficult ones to execute so that only these are displayed. Node 23 is traversed in generation 42, node 25 in 63 and node 27 in generation 65. All other nodes including node 19 are executed in the first 23 generations.

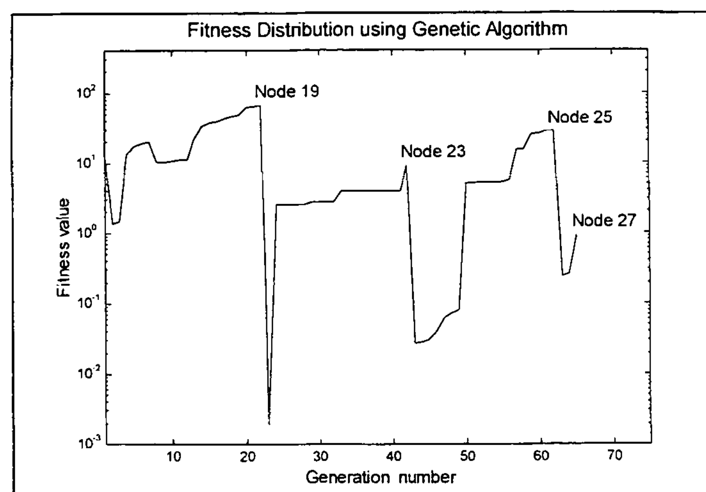


Figure 5.17: Fitness distribution using Genetic Algorithms.

An unexpected result is found when using the Gray code for the chromosomes, instead of binary format, compared to the results of the quadratic equation solver problem (see section 5.1.6.1). It indicates that using the Gray code representation of the test data set is not better than using binary representation if zero solutions are allowed. The better result obtained using Gray code coincides with those obtained by Schaffer and Caruana *et al.* [1991]. They found that using Gray code is often better than using binary coding for numeric variables. A summary of the most interesting results are shown in Table 5.13.

Setting and results		Tests
Default, reciprocal fitness	100% in 276 generations	27876
double crossover	96.3% in 363 generations	> 40663
single crossover	97.5% in 390 generations	> 41304
Hamming fitness	100% in 270 generations	25945
Gray, reciprocal fitness	99% in 176 generations	> 17772
Gray, Hamming fitness	100% in 185 generations	17789
Random Testing	69.5% in 1187 generations	> 167036
increased max. generation	100% in 1701 generations	163296

Table 5.13: Results of triangle using GA and random testing.

5.4 Interim Conclusion

The quadratic and triangle procedures have non-linear predicates, the size of the sub - domains have small cardinalities and some subdomains are not contiguous which makes testing very difficult. This latter point is supported by the results from random testing which are inferior in all cases with regard to the success rate and the average number of tests required to achieve full branch coverage.

Less CPU time is required for GAs despite the computational effort required to execute the coding, decoding, crossover, mutation, selection and survive procedures. The amount of CPU time per test (fitness function evaluation) is also an indicator of the complexity of the software under test. For example the average time for one test data set using GAs for the quadratic equation solver problem is about 0.33 msec whereas for the triangle classifier procedure 0.48 msec is required to have branch coverage on average. The same behaviour shows random testing for the CPU time which is only 14.8 μsec and 18.0 μsec per test data set respectively, however since many more random test data

have to be generated, it is lower for the quadratic equation solver procedure.

Uniform crossover has shown its strength and superiority over the other two crossover operators. This confirms several other authors' results. Holland [1975] has already analysed the single crossover theoretically and empirically. These are extended to n-point and uniform crossover by DeJong and Spears [1990]. Syswerda [1989] and Eschelman [1989] pointed out that a higher number of crossover points are beneficial. Uniform crossover has the additional feature that it has more exploratory power than n-point crossover, Eschelman [1989]. An example of this is where there are two chromosomes with one of them consisting of a string of *0*s and the other one consisting of *1*s. By using uniform crossover the new offspring can be anywhere in the domain, whereas one or two-point crossovers are restricted to smaller changes in the offspring. The advantage of a higher exploratory power is ensuring that the entire domain is well sampled, especially where the population size is small.

The importance of using a crossover operator is clear after the triangle experiments whereas the results for the quadratic experiments are similar for all crossover operators. Those results are verified by Schaffer *et al.* [1989], who mentioned in his work that a GA even without the assistance of the crossover operator is likely to be a powerful search algorithm. He also stated that the crossover has an important effect in the GA, which can be seen in the results of the triangle experiments with and without crossover. The results indicate that without a crossover operator, the GA is a better search method than initially expected, but crossover is important.

Having found a default setting for the GAs in this chapter the next chapter will conduct experiments on more complex data types and structures. Emphasis will be placed on testing loop conditions.

CHAPTER 6

The application of GAs to more complex data structure

In the previous chapter a quadratic equation solver and a triangle problem are investigated. Both programs require three integer input variables. The predicates of the branches are restricted to selections which contain equality and inequality predicates. In this chapter more complex data types and iterations are considered. Loops are considered as four different branches corresponding to *zero*, *one*, *two* and *more* iterations. Therefore, in this chapter hypothesis 3 is the main task to validate.

6.1 Search procedures

The application of searching is of great importance in computing, requiring the development of various techniques in order to test these applications. In this section two well- known and important algorithms, linear and binary search are tested.

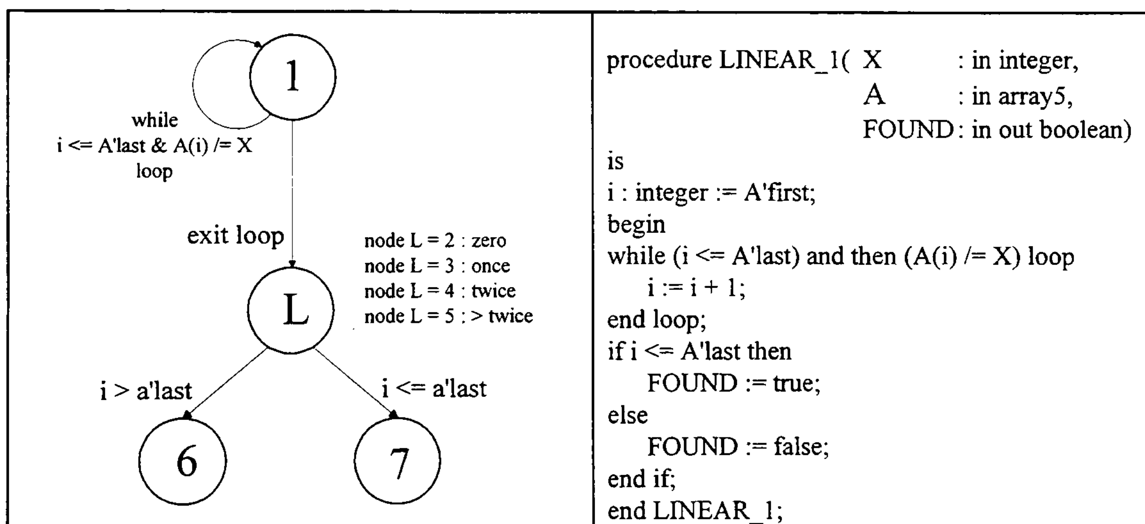
6.1.1 Linear Search_1 procedure

The linear search procedure has two input variables and one output variable. It searches for the first input variable, *X*, in an input array *A* of the size 1..N (second variable) of a predefined data type (e.g. integer) where the default value for N is 5 in this application. Using this search method the array element keys are compared with the target key (input variable *X*), starting with the first array element. The procedure terminates either when the target key is located or the end of the array is reached.

N comparisons have to be undertaken to determine the absence of the target key in the array of *N* elements. On average $N/2$ comparisons are performed when locating a target key in an array. The output variable of type boolean indicates whether the key is found (true) or not (false).

6.1.1.1 Description

The task of the GAs in this program is to adjust the target key (X) to equal one of the array elements. The default population size is $P_{SZ} = 32$ chromosomes since only one integer variable is to be optimised by the GA. Two different approaches are used to program the linear search, one using '*while ... loop*' and the other using '*loop ... exit*' constructs. The '*while ... loop*' has to perform *zero*, *one*, *two* and *more than two* iterations in order to satisfy the criteria for branch testing, see chapter 4. Zero iterations of the '*while ... loop*' statement means that the first element of the array is equivalent to the target key $X = A(1)$. *One* iteration of the loop statement is equivalent to the second element, i.e. $X = A(2)$. *Two* iterations of the loop statement is equivalent to the third element, i.e. $X = A(3)$ and *more than two* iterations of the loop statement is equivalent to the fourth, fifth, etc. array element or X is not represented within the entire array. The last one is the most likely event. This also applies when X is absent from the array. The control flow tree is displayed in Figure 6.1 and the corresponding code in Listing 6.1.




```
procedure LINEAR_1( X      : in integer,
                    A      : in array5,
                    FOUND  : in out boolean)
is
i : integer := A'first;
begin
while (i <= A'last) and then (A(i) /= X) loop
   i := i + 1;
end loop;
if i <= A'last then
   FOUND := true;
else
   FOUND := false;
end if;
end LINEAR_1;
```

Figure 6.1: Control flow graph of LINEAR_1 search procedure.

Listing 6.1: Code of LINEAR_1 search procedure.

'L' in the control flow tree in Figure 6.1 indicates the node numbers for the loop conditions. Examination of the search procedure reveals two unfeasible path in the code. The unfeasible paths are, in connection with the '*if*' condition after the loop condition has finished. If the target key X is not found in the array which contains the value to be searched, the '*else*' branch of the '*if*' condition is always executed and it is not possible to generate test data for the other path. The true branch of the '*if*' condition cannot be

executed. On the other hand if the key element is found in the array, the '*else*' branch of the '*if*' condition cannot be executed. Since this '*if*' condition has no influence on the input parameter *X*, the problem is neglected. Moreover this project is concerned with branch coverage and not path coverage. The fitness functions for the loop iterations are based on the array elements instead of a loop counter because it is difficult for the GA to find test data which traverses the required nodes, especially if the values in the array differ much from array element to array element.

Two main sets of experiments have been performed. Test sets for *zero* iteration are described in the next section whereas full loop testing is demonstrated in section 6.1.1.3 with *zero*, *one*, *two* and *more than two* iterations.

6.1.1.2 Different experiments with single loop condition

For the first set of experiments a '*while ... loop*' condition is used where the loop is only tested for *zero* and *more than zero* iterations which means that the target key (input variable *X*) has to be adjusted to be the same value as that of the first element in the array. In order to achieve this, the nodes 3 and 4 are not considered, so that no test data has to be generated for these nodes. The first element of the array is set to a numeric value of 1; the other elements are set to different values which are not important for the moment. These experiments show that GAs are suitable and capable of handling loop conditions and arrays, the results of which can be seen in Table 6.1. The mutation probability (which was defined earlier as $P_m = 1/P_{sz}$) is set to $P_m \approx 0.03$ due to the fact that the population size is only 32. The *MAX_GENERATION* is set to 500 before a test run terminates.

	Reciprocal fitness				Hamming fitness			
	SELECTION_R		SELECTION_F		SELECTION_R		SELECTION_F	
random	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
Binary	100% 8.0 256 tests	100% 9.6 308 tests	100% 6.6 212 tests	100% 7.4 237 tests	100% 7.6 243 tests	100% 8.3 266 tests	100% 5.7 183 tests	100% 5.8 186 tests
Gray	100% 9.5 304 tests	100% 10.8 347 tests	100% 9.2 295 tests	100% 8.8 282 tests	99.5% 49.1 > 1644 tests	100% 21.9 701 tests	95.0% 90.2 > 3561 tests	100% 20.4 653 tests

Table 6.1: Results of linear procedure for *A(1)* = 1.

Table 6.1 shows the results when the first element of the search array has a numeric

value of 1. Tests are carried out with the default set-up using the reciprocal fitness function and random selection. Columns three and four use selection of the parents according to their fitness values (SELECTION_F). Columns five and six use the Hamming fitness function for the random selection and SELECTION_F selection. The option '*5 bits*' and '*10 bits*' indicate how many lower significant bits are used for the weighted mutation operator W_MUTATE, see section 3.8.3.3.2. All these experiments are carried out for binary code and Gray code.

As can be seen from Table 6.1, the best results are achieved using the Hamming fitness function (183 tests) which require about 30 tests fewer than the reciprocal fitness function. Selection of parents according to fitness (SELECTION_F) produce better results for both fitness functions than random selection (SELECTION_R) alone. These are in contradiction to the results achieved with the quadratic and triangle procedures where SELECTION_F achieves worse results than random selection since there are many global optima for the nodes. However, in linear search there is just one global optimum for the node of *zero* iteration. This is valid for both fitness function methods, the reciprocal (256 tests) as well as the Hamming (243 tests) fitness functions. Experiments with Gray code are disappointing with worse results. More than 50 tests are required to completely achieve successful test runs using reciprocal fitness. The results deteriorate with the Hamming fitness in particular.

Figure 6.2 shows the population test data set values over the generations and displays the optimisation process towards the global optimum, which is in this case a value of 1 ($X = A(1) = 1$) for *zero* iterations using weighted Hamming fitness function. The plus symbols in the graph indicate the values of the key target X. Since the population size is 32, there should be 32 stars per generation. However, the scale of the y-axis is quite large (±20000) which means if the test data are close to each other, it is not possible to show all test data with separate symbols. This is especially obvious at the end of a test run where the test data converge towards the global optimum. As can clearly be seen this set-up avoids all negative values for the test data X (target key) after a few generations, because a negative number strongly decreases the fitness value due to the weighted structure of the fitness evaluation.

Assuming that only the MSB, which is the sign bit, has a wrong state (e.g. the current value is -1 instead of 1) the fitness value will be calculated to $\frac{1}{32^2}$ which results in a very small fitness value so that all negative values are discarded within a certain time. An example of a test run using the weighted Hamming fitness can be seen in Figure 6.2, an unweighted Hamming fitness test run is displayed in Figure 6.3 and a reciprocal fitness test run in Figure 6.4.

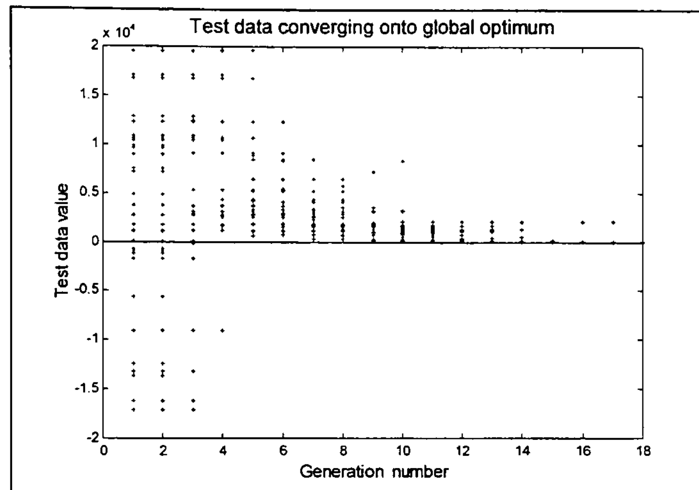


Figure 6.2: Converging process towards global optimum using weighted Hamming fitness.

Convergence is slower when negative values are not discarded and unweighted Hamming fitness is used, see Figure 6.2.

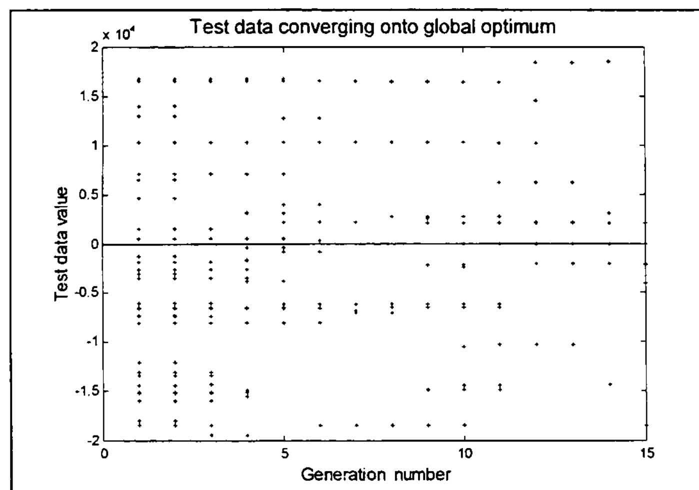


Figure 6.3: Converging process towards global optimum using unweighted Hamming fitness.

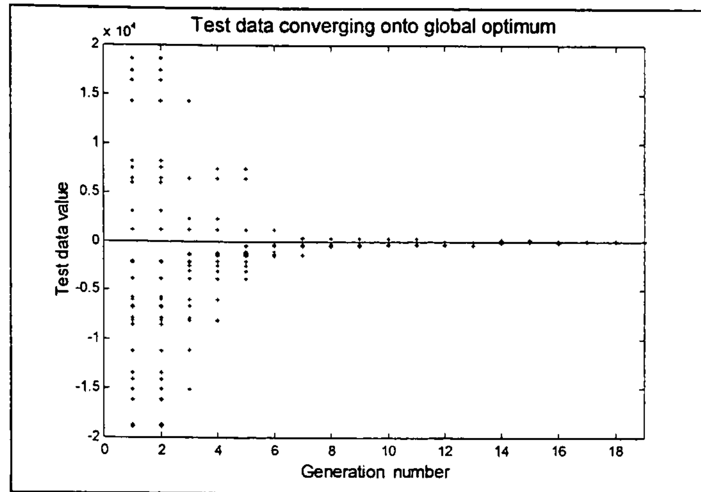


Figure 6.4: Converging process towards global optimum using reciprocal fitness.

The reciprocal fitness function converges much faster towards the global optimum as can be seen in Figure 6.4 than using a Hamming unweighted or weighted fitness functions, displayed in Figure 6.3.

The value of the elements of the array are changed in the second set of experiments so that the first array element varies between a numeric value of 1, 100, 127, 128, 256, 1024 and 10000 and all the other array elements have different values. The values 127, 128, 256, 1024 are chosen because of their characteristic bit patterns. The numeric value 127 has a bit pattern (111111100000_{binary}), 128 is in binary (000000010000_{binary}), 256 is (000000001000_{binary}) and 1024 is (000000000010_{binary}) in binary representation with the MSB on the right hand side. These patterns change completely if the numeric value is altered by only one unit, depending on the direction of change.

Thorough experiments are carried out and the results are displayed in appendix B. The experiments show the behaviour of different settings over a range of values for the first element of the array *A(1)*. The table in the Appendix B shows two main experiments using reciprocal and Hamming fitness functions with different selection and weighted mutation options as in Table 6.2.

Approaching the numeric value 128 from lower values may be difficult because many bit positions have to swap from a bit state 1 to 0 (e.g. the extreme case is 127 111111100_{binary}), whereas the approach from a higher value maybe easier. For example it needs more than 7240 tests (56% success) for the numeric value 127, and more than

8529 tests (47.6% success) for 128 and the success rate of full branch coverage is only achieved in about 50% of the test runs using reciprocal fitness function. Whereas it achieves one of the best results for small values, *A(1)* = 1, within only 256 tests. As soon as the values for *A(1)* increase the results become worse. Using these values, the GA with reciprocal fitness has great difficulty in generating the global optimum. This means it is quite difficult to approach these values from one side. If the numeric value is e.g. 1000 the success rate is higher at 88% and only 3967 tests are required and for a value of 100 the success rate is 99%. This is about half of the required tests which are needed for a numeric value of *A(1)* equal to 127 or 128 because the change of the pattern when approaching those values are not as drastic as for these data.

The option to increase the weighted mutation to '*10 bits*' is always better except for small values such as for *A(1)* = 1. If the values for *A(1)* are larger, the '*10 bits*' option increases the performance enormously, e.g. for *A(1)* = 128 the success rate is 99.8% success in >1743 tests, instead of only 47.6% in >8529 tests.

The option SELECTION_F, which selects the parents according to their fitness is only better for small values of *A(1)* and achieves the best result within only 212 tests, see Table 6.1. As soon as the value increases the performance decreases. The degradation in performance is explained by the tendency of the reciprocal fitness function to favour smaller values for *X*. This was realised previously when using the quadratic equation solver, where solutions with small values for the input variables are favoured over larger values. The option '*10 bits*' improves the results using SELECTION_F, because the chance is higher that several bit positions could change their state in only one reproduction cycle, but the improvement is higher using it in SELECTION_R.

Gray coding always gives higher success rates and requires fewer tests except for *A(1)* = 1 when more tests are needed but full branch coverage is achieved. Full branch coverage is always achieved with '*10 bits*'. However, for small values (*A(1)* = 1) '*5 bits*' is better. '*5 bits*' normally gives worse results in SELECTION_R than in SELECTION_F, but as soon as the weighted mutation is increased to '*10 bits*', SELECTION_F outperforms the option with '*5 bits*' by far especially for certain bit patterns, i.e. 100% success is always achieved and it is also better than using it in

SELECTION_R. The performance is influenced by the bit patterns of the numeric values 127, 128, 256 and 1024. Normally 100% success rate is achieved, but for these numeric values only about 96% success is achieved with '*5 bits*' ('*10 bits*' always achieved 100% success).

A fitness function based on the Hamming distance achieves the most consistent performance in all experiments with respect to success rate and required number of tests. It is not influenced by certain bit patterns as it is for the reciprocal fitness and it always achieves a 100% success rate. The number of tests are similar for all different values of *A(1)* and only slightly dependent on the setting of the GA with regard to selection and weighted mutation options. The option of '*10 bits*' always increases the number of required tests, no matter which select procedure is chosen. This is in contrast to the reciprocal fitness which improves the performance in most cases. SELECTION_F performs better than the random selection for all experiments by about 70 tests.

When using the Gray code representation of the bit pattern, the best results are obtained with the '*10 bits*' random selection option and the worst results are obtained when using the Hamming fitness function.

The best results are achieved with SELECTION_F and '*5 bits*' using binary coding which requires about 170 tests for the different *A(1)* values. In further experiments, the numeric value for *A(1)* are generated randomly in the range of ±20000 at the start of each test run. The results can be seen in Table 6.2.

	Reciprocal fitness				Hamming fitness			
	SELECTION_R		SELECTION_F		SELECTION_R		SELECTION_F	
random	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
Binary	84.6% 63.4 >4181 tests	98.4% 29.8 >1195 tests	85% 75.3 >4450 tests	97.4% 35.3 >1518 tests	100% 7.7 247 tests	100% 9.1 292 tests	100% 5.7 183 tests	100% 6.1 196 tests
Gray	96% 28.0 >1501 tests	100% 18.1 580 tests	99.8% 19.3 >648 tests	99.8% 13.8 >475 tests	96.4% 28.1 >1442 tests	99.6% 29.3 >997 tests	90.4% 29.2 >2379 tests	98.6% 22.3 >926 tests

Table 6.2: Results of generating *A(1)* randomly for each test run in the range ±20000.

These results confirm the findings of the previous set of experiments. Gray code is better than binary code for the reciprocal fitness and worse for the Hamming fitness. Hamming fitness achieves the best results as expected with 183 tests using

SELECTION_F and '*5 bits*'.

The next experiment investigates the case when the array elements *A(i)* are changed by the GA, hence both the key target *X* and the array elements *A(i)*, requires adjustment. In this case the array size is restricted to 5 elements, so that the total population is $P_{sz} = 6*32 = 192$. The results can be seen in Table 6.3. The maximum generation is restricted to 100 generations after which a test run terminates because of the amount of CPU time required.

Reciprocal fitness				Hamming fitness			
SELECTION_R		SELECTION_F		SELECTION_R		SELECTION_F	
5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
77.6%, 7.2 >3763 tests	90.8%, 8.2 >1711 tests	73.6%, 8.8 >4432 tests	76.8%, 12 >4007 tests	100%, 18.2 3495 tests	100%, 17.7 3399 tests	100% 5.6 1076 tests	100% 5.9 1133 tests

Table 6.3: Results of linear procedure for *zero* and *more than zero* iterations where the elements of the array are also changed by the GAs.

Selection of chromosomes according to their fitness values to become parents for the next generation is not as good as random selection using reciprocal fitness. This is due to the fact that there are too many optima which satisfy node 2 (*zero* iteration node). Global optima could be anywhere in the search space and not just at the predefined fixed numeric value of *A(1)* as in the previous experiments. The resulting disruption might therefore be too great, as observed when using the triangle and quadratic equation procedures.

The influence of different sizes of arrays is also investigated. The results of these experiments show that the outcome is similar to experiments where the population size is changed in proportion to the integer size for the quadratic equation in section 5. A set of experiments is carried out where the array consisted of 10 elements. In total $11*32 = 352$ chromosomes per generation are used (*key + array elements*). 1687 tests (4.8 generations) are required on average and full coverage is always obtained by using the Hamming distance fitness function. This test is repeated, but the number of chromosomes is reduced from 352 to 192. According to expectations the result of 1056 tests (5.5 generations) is similar with regard to the experiment where five array elements in Table 6.3 are used (1076 tests) within the same setting. Restricting the population

further to 96 chromosomes, full coverage is obtained after only 701 tests (7.3 generations), 64 chromosomes need 557 tests (8.7 generations) and restricting it to 32 chromosomes, branch coverage is achieved only in 378 tests (11.8 generations).

A comparison can be made between the above results and those of the quadratic problem experiments. The average number of generations required is usually similar. To achieve 100% success rate for all test runs the average number of generations varies only from 4.8 generations (352 chromosomes per population) to 11.8 generations (32 chromosomes per population) which is a factor of 3. However, the factor by which the population size changed is 11. The decisive factor is the number of chromosomes per generation which is the main element in determining the number of tests.

So far the investigation confirms that GAs are capable of generating and optimising test data in order to traverse and execute a predefined number of loop iterations. In the next section the testing strategy of loop conditions are extended to full loop, i.e. generating test data which makes the loop iterate *zero*, *once*, *twice* and *more*.

6.1.1.3 Experiments with full '*while ... loop*' testing

The experiments undertaken in this section, test the '*while ... loop*' conditions as mentioned in section 4. This means that a '*while ... loop*' condition has to be executed at least *zero* times, *once*, *twice* and *more than twice*. The nodes 3 and 4 (Figure 6.1) are now under consideration. These branches have to be traversed in order to perform full branch testing. As expected more tests are required to achieve full branch coverage for full loop testing because more branches need to be traversed, and hence maximum generation is set to 500. Table 6.4 shows the results of the experiments where the array consists of five default elements with the predefined fixed values of 1, 10000, 20000, 30000, 40000.

	Reciprocal fitness				Hamming fitness			
	SELECTION_R		SELECTION_F		SELECTION_R		SELECTION_F	
random	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
Binary	26% 144.5 > 13043 tes.	44% 191 > 11650 tes.	17.5% 139 > 13979 tes.	26.5%183 > 13312 tes.	100%, 35.1 1124 tests	100%, 32.9 1053 tests	100% 25.9 829 tests	100% 23.4 749 tests
Gray	100% 62.0 1985 tests	100% 53.3 1706 tests	100% 57.4 1837 tests	100% 45.6 1460 tests	84.5% 242 >9017 tests	96.5% 183 >6216 tests	56% 277 >11999 tes.	91% 217 >7773 tests

Table 6.4: Results of LINEAR_1 procedure for full loop testing.

The tendency of the results are similar to the previous ones, except that overall more generations are required to achieve full branch coverage. This is because of the increased number of branches, as can be observed in Figure 6.5.

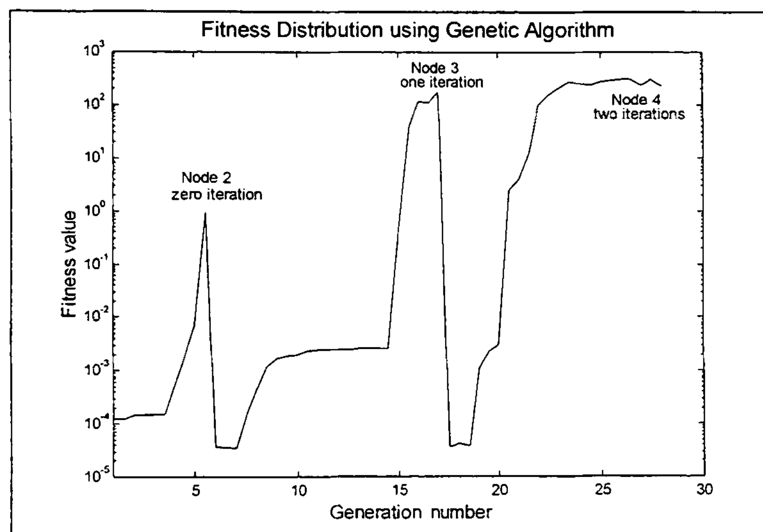


Figure 6.5: Typical fitness distribution of linear search with full loop testing.

Figure 6.5 shows that node 2 (*zero* iteration) is traversed after six generations, whereas node 3 (*one* iteration) is traversed after 14 and node 4 (two iterations) after 28 generations. The last two nodes need more tests than node 2 because the search space is initially well sampled by random numbers generated in the range ±20000. However, after optimising X towards its global optima of node 2, the population might lose some important information (genetic material) with regard to the other nodes. This means the genetic material has to be generated e.g. by mutation which can take some generations.

The Hamming fitness functions clearly achieve the best results and full branch coverage is accomplished. SELECTION_F requires fewer tests than SELECTION_R. It required only 23.4 generations (749 tests) with '*10 bits*' which is better by about 100 tests than

the '*5 bits*' option in this case because of the changing of the goal (branch) and the higher value of the third array element.

The results are worse when using the reciprocal fitness function for which the best result is achieved in 2544 tests by using '10 bits' and random selection.

This result is not unexpected being similar to the results of experiments for single loop testing where *A(1)* is a large value (e.g. 10000). Since the third element of the array is even larger (A(3) = 20000) it seems to be more difficult for the GA to adjust *X* towards the global optimum using SELECTION_F in combination with the reciprocal fitness function.

The survival probability is always set to $P_S = 0.5$. Experiments conducted with a reduced survival probability produced slightly worse results for the Hamming fitness (about 120 more tests) and even worse results using reciprocal fitness by up to about 650 tests.

Using Gray code with Hamming fitness, the results deteriorate whereas the performance of the reciprocal fitness function improve with branch coverage. The best result is achieved in 1460 tests which is double the number of tests using Hamming fitness with SELECTION_F and '*10 bits*' and binary sign format.

Choosing the array elements *A* randomly in the range of ±20000 at each start of a test run, no change in performance is observed using Hamming fitness. The performance of the reciprocal fitness degrades in the case of using '*5 bits*' and improves by about 100 tests using '*10 bits*'. This is due to the fact that the numeric difference of the array elements is higher than in the default predefined array and that difficult bit patterns of numeric values have to be generated.

6.1.1.4 Random testing of LINEAR_1

Random testing is carried out for the ranges ±20000, ±40000, ±80000 and ±100000. The array *A* is fixed to the predefined default values.

In the first set of experiments where the loop is tested for *zero* iterations and more

iterations, the random testing method used 40576 tests in order to generate the global optimum for *zero* iterations. The results correspond to the theoretical outcome of 40001 tests, because the range of random numbers is ±20000 and there is only one global optimum for *zero* iteration. In comparison, GA achieves the best result in 272 tests. GAs show a significant improvement in this case by a factor of approximately 150 according to the number of tests. Generating random numbers for the target key X and the array A requires 40032 tests which closely agrees with the theory.

The number of tests performed for the full loop using random numbers is 76733 tests which is close to the calculated number of tests of $NoRT$ = 73336, using equation (5.8). Only the nodes for *zero*, *one* and *two iterations* are taken into consideration for the calculation because these are the most difficult ones (with $L = 3$ and $k_L = 1$). Therefore random testing requires about 100 times more test executions than GAs (749 tests) in the range of ±20000 and increases with larger input ranges. A comparison of the CPU time required also favours GAs. Table 6.5 shows the different results for random and GA testing over different ranges of test data.

Range of input	Random testing with 100% success rate		GA using Hamming	
	Tests	CPU	Tests	CPU
±20000	76733	0.6s	762	0.12s
±40000	146637	1.12s	788	0.13s
±80000	298058	2.27s	813	0.13s
±100000	375661	2.86s	829	0.14s

Table 6.5: Results using random and GA testing for full loop testing.

The CPU time for both testing methods is displayed in Figure 6.6.

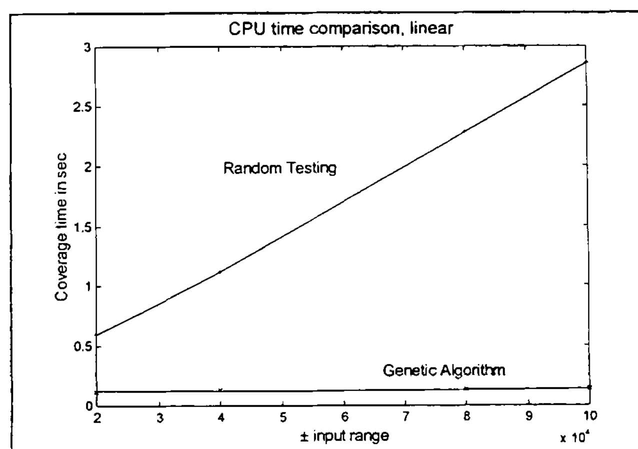


Figure 6.6: Comparison of random testing and Genetic Algorithm testing.

6.1.1.5 Interim conclusion of LINEAR_1

The LINEAR_1 search procedure is different from both previous test procedures, quadratic equation solver and triangle classifier procedures. In contrast the LINEAR_1 procedure has loop statements, arrays are used instead of single integer variables and in addition the loop branches (*zero, one* and *two* iterations) have only one global optima except the case when the array elements are also adjusted by the GA.

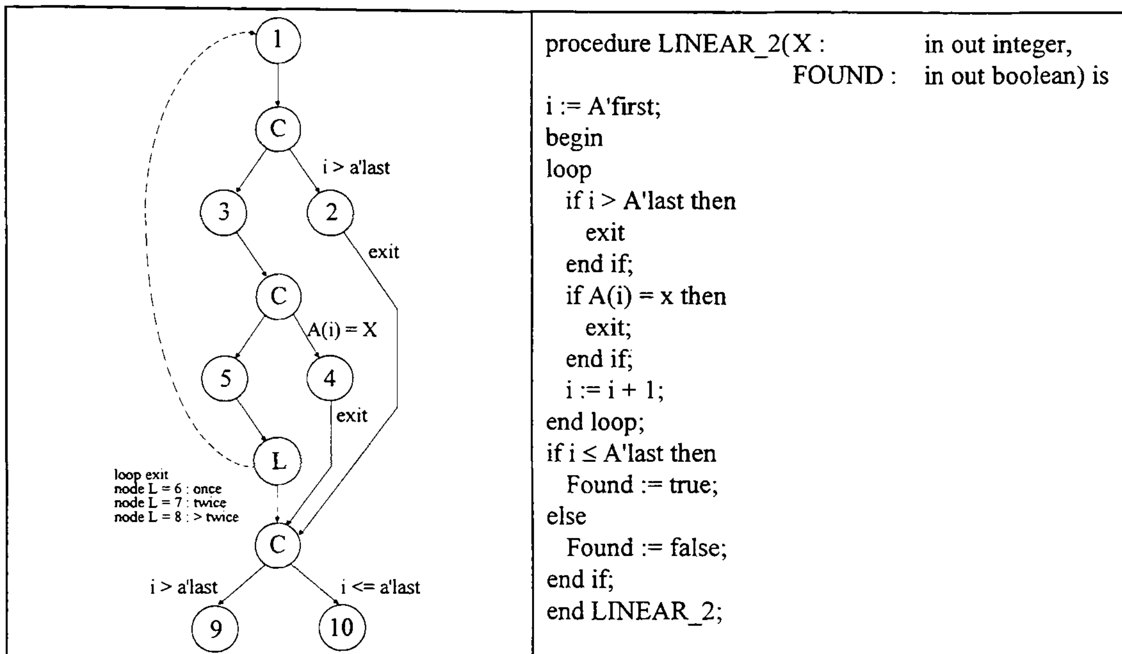
Testing only the loop for *zero* iterations, the Hamming fitness function achieves the better results according to test runs. In addition using the SELECTION_F procedure to select parents according their fitness improves the overall performance. When the first element of the array A has a large value (e.g. 10000), Hamming fitness achieves the better result whereas the reciprocal fitness deteriorates. This is especially true when certain bit pattern e.g. 127 or 128 have to be matched. Gray code decreases the performance of Hamming fitness whereas using SELECTION_F improves the performance by about 2 to 3 generations so that only about 160 tests are required.

The third part of these experiments is carried out with full testing of the loop condition. Gray code invariably performs better when it is used with the reciprocal fitness, as already stated in the earlier experiments. When using Gray code in conjunction with Hamming fitness, the results deteriorate strongly.

The selection of parents using the fitness value (SELECTION_F) always works very well for the Hamming fitness but slightly worse using the reciprocal fitness function. When tested in connection with Gray code and SELECTION_F the reciprocal fitness function achieves better results than without it. Overall the Hamming fitness function achieves the most consistent results over a large range of different values for the global optimum.

6.1.2 Linear Search 2

The control flow graph of LINEAR_2 procedure is given in Figure 6.7 and the code is shown in Listing 6.2. The LINEAR_2 procedure is similar to LINEAR_1, the only difference is that instead of a '*while ... loop*' a '*loop ... exit*' condition is used. In addition two '*if*' conditions are used in order to exit the loop. The testing goal is branch coverage. The first '*if*' condition node 2 terminates the loop when the index i is beyond the maximum index of the array A. When the second '*if*' condition is true (node 4), the loop is exited because the key element X matches one of the array elements $A(i)$.




```
procedure LINEAR_2(X :          in out integer,
                   FOUND :      in out boolean) is
i := A'first;
begin
loop
  if i > A'last then
    exit
  end if;
  if A(i) = x then
    exit;
  end if;
  i := i + 1;
end loop;
if i ≤ A'last then
  Found := true;
else
  Found := false;
end if;
end LINEAR_2;
```

Figure 6.7: Control flow graph of LINEAR_2 procedure.

Listing 6.2: Code of LINEAR_2 search procedure.

The method of testing a '*loop exit*' condition has to be changed because the loop has to be entered at least once, i.e. it is tested for *one*, *two* and *more than two* iterations where *one* iteration means $X = A(1)$. Because of the semantics of the 'loop...exit' construct, *zero* iterations cannot be tested. In addition the '*else*' branches of the '*if*' conditions inside the loop have both been tested to make sure that the '*if*' condition is not always being executed.

Since the two search procedures are very similar, LINEAR_2 is only tested for full loop testing. The array elements are fixed to the predefined default values of (1, 10000, 20000, 30000, 40000). The results are shown in Table 6.6.

	Reciprocal fitness				Hamming fitness			
	Random selection		SELECTION_F		Random selection		SELECTION_F	
random	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
Binary	24.5% 56.5 > 12524 tes.	75% 81.3 > 5952 tests	29.5% 64.8 > 11892 tes.	64.5% 97.4 > 7691 tests	100% 20.7 663 tests	100% 19.8 634 tests	100% 16.1 516 tests	100% 13.5 432 tests
Gray	100% 32.7 1047 tests	100% 30.5 976 tests	100% 31.8 1018 tests	100% 26.6 852 tests	96.5% 138 > 4823 tests	98.5% 113 > 3804 tests	86% 179 > 7175 tests	99.5% 125 > 4282 tests

Table 6.6: Results of LINEAR_2 procedure for full loop testing using binary coding.

The results in Table 6.6 show similarities to the results for LINEAR_1 procedure. The Hamming fitness achieves the best results of both fitness function. Using the SELECTION_F strategy for selecting parents the results improves with the Hamming fitness to 432 tests. In all cases full coverage is achieved. Gray code improves the performance considerably using the reciprocal fitness function for SELECTION_R as well as for SELECTION_F. The best result is accomplished in 852 tests using SELECTION_F. Gray code decreases the performance considerably when using Hamming fitness as previously observed.

6.1.2.1 Random testing of LINEAR_2

In order to test LINEAR_2 randomly, about 60928 tests have to be generated which agrees with the theoretical number of tests. The probability of generating the test data to traverse node 6 (*one* iteration) and node 7 (*two* iterations) can be described using equation (5.8). Therefore, $NoRT = 60001.5$ tests have to be theoretically generated.

6.1.2.2 Interim conclusion LINEAR_2

The GAs have no problem in generating test data to achieve branch coverage for full loop testing. The best result is achieved in only 432 tests using Hamming fitness and SELECTION_F option. This number of tests is about 140 times smaller than the number required for random testing. The results of these experiments are better than those from LINEAR_1, because LINEAR_2 has one branch of the loop iteration less to visit due to the semantics of the loop construct, but overall both sets of experiments achieve similar results.

6.1.3 Binary Search

Often the search of an array is required whose elements are already arranged in order by a key field. This fact can accelerate the search which is more efficient. This is an advantage in that an array A of (1 .. N) is ordered such as to eliminate half of the array elements with each probe into the array A. A suitable search algorithm is introduced which makes use of this arrangement. Thus:

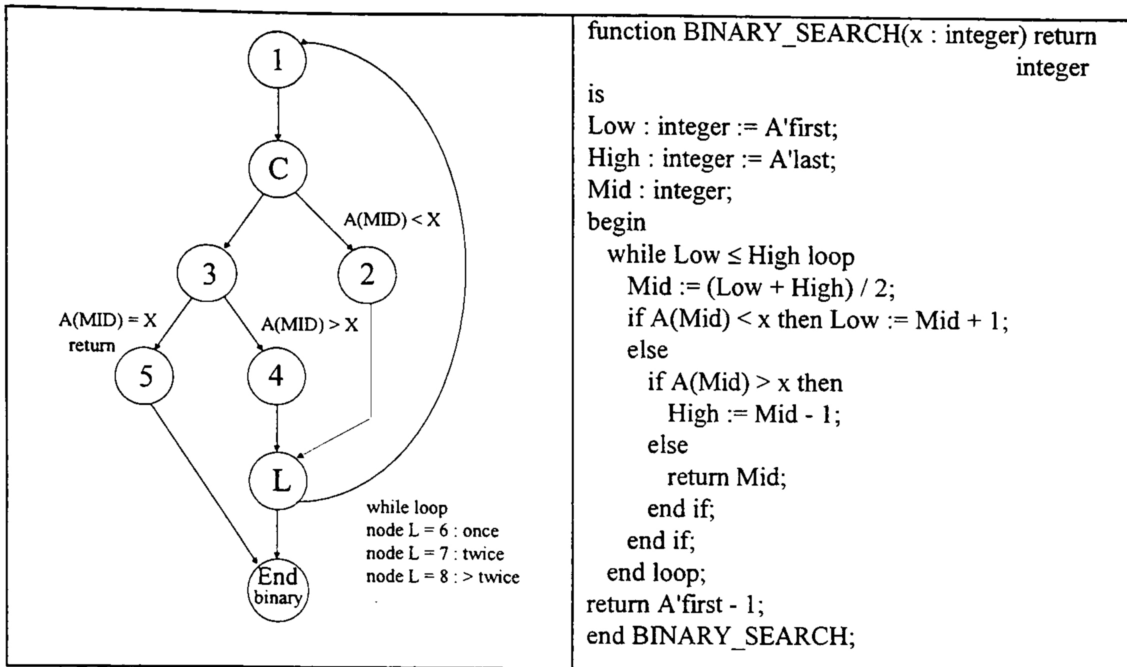
$$\forall k{:}\,Z \mid\ 2 \le k \le n \cdot A_{k-1} \le A_k \tag{6.1}$$

where Z is the set of all integers and k is a variable.

The basic idea of this algorithm, written as a function, is to check whether X (target key) is equal to the middle element of an array section $A(Mid)$. If so, X is found in the array A and the search function returns the index of the array element and terminates.

If X is larger than $A(Mid)$ it can be concluded that all elements with an index lower or equal to MID can be excluded. This method is called binary search, because it will eliminate, in each step, either the elements above or below the chosen try. If the key element X is absent, an index value is returned which is one unit smaller than the first index of the array in order to indicate that the key element is not present in the array.

Two index variables *LOW* and *HIGH* are used, which mark the left and the right end of an array section, in which the required element may be found. The number of tries which are necessary to search an array of the size N completely, directly depends on the number of array elements. Therefore, the maximum number of comparisons is $log_2(N)$ rounded to the next integer number. This algorithm is a huge improvement over the linear search algorithm, where the average expected number of comparisons is $N/2$. The control flow graph can be seen in Figure 6.8. The binary search function has 8 nodes 6 branches, two '*if*' conditions and one '*while ... loop*' statement. The peculiarity is the loop condition which has besides the '*while*' condition an extra second exit condition for the loop which is realised by a '*return*' statement in one of the '*if*' conditions. This will terminate and exit the loop when the target key matches one of the array elements.




```
function BINARY_SEARCH(x : integer) return
                                        integer
is
Low : integer := A'first;
High : integer := A'last;
Mid : integer;
begin
  while Low ≤ High loop
    Mid := (Low + High) / 2;
    if A(Mid) < x then Low := Mid + 1;
    else
      if A(Mid) > x then
        High := Mid - 1;
      else
        return Mid;
      end if;
    end if;
  end loop;
return A'first - 1;
end BINARY_SEARCH;
```

Figure 6.8: Control flow graph of the binary search function.

Listing 6.3: Code of the binary search function.

6.1.3.1 Results of binary search.

Since the array size *N* is predefined, it is not possible to test the loop for *zero* iterations. This is due to the fact that the array size is fixed so that the number of elements cannot be varied during a test run. At the start of the testing either the variable LOW (index of first element) is smaller or equal to HIGH (index of last element), i.e. the array consists of at least one element, or LOW is greater than HIGH which means the array is empty (e.g. array(1..0)). Both situations are not possible in one testing approach because the array is fixed to a certain size. An example of changing the array size without recompiling is described in chapter 7 where a generic sorting procedure is tested.

Experiments use either the reciprocal or Hamming fitness function and SELECTION_F, random selection, '*5 bits*' and '*10 bits*'. The maximum generation is set to 500.

The first experiments are carried out using a predefined number of iterations. The number of iterations (*NITS*) describes how many times the loop condition has to iterate to satisfy the global optimum, i.e. *NITS* defines the current goal. For example, when *NITS = 1* the '*while ... loop*' has to iterate only once with regard to the loop goal (*one*

iteration). This means that the target key has to match the middle element of the array ($X = A(MID_l)$, with $MID_l = (LOW_l + HIGH_l)/2$), so resulting in only one global optimum. Whereas $NITS = 2$ demands exactly two iterations before the match is realised. However, there are now two global optima which will satisfy this goal. Each of these solutions is either the middle element of the left subarray $MID_L = (LOW_l + (MID_l - 1))/2$ or the middle element of the right subarray $MID_R = ((MID_l + 1) + HIGH_l)/2$.

Obviously, if the number of iterations, *NITS*, increases, the number of global optima increases by $2^{(Nits-1)}$ in the domain. The more global optima that are present in the domain, the higher is the probability of generating one of these global solutions. This is observed in the results of Figure 6.9 which displays different settings using GAs. The graphs represent the required number of tests against the number of required iterations.

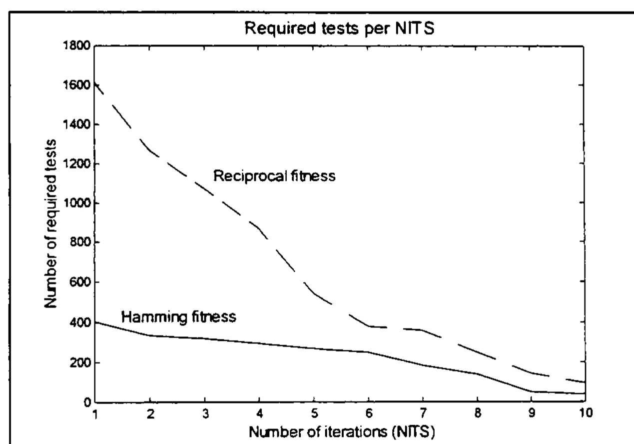


Figure 6.9: Required tests using reciprocal and Hamming fitness function.

As in the linear search procedures, the option '*10 bits*' performs better than the default value of '*5 bits*' with regard to the percentage of successful test runs. Hamming fitness always achieves 100% success in the test runs compared to the reciprocal fitness function. In order to test binary search for 10 iterations an array size of 1000 elements is chosen and filled with random numbers in the range of ±20000 which is then sorted using a quicksort algorithm.

The Hamming fitness optimising *X* to *A(MID)* works better, as shown in Figure 6.9, and always achieves full coverage in contrast to the reciprocal fitness function.

6.1.3.2 Full loop testing

Since the '*while ... loop*' condition depends on the array indexes, it cannot be tested for *zero* iterations unless the array's definition is also changeable. The testing strategy is to iterate the loop *once*, *twice* and *more than twice*. The results for these experiments are listed in Table 6.7.

	Reciprocal fitness				Hamming fitness			
	SELECTION_R		SELECTION_F		SELECTION_R		SELECTION_F	
Coding	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
binary	66.4%, 53.0 >6503 tests	98.8%, 45.4 >1628 tests	61.6%, 66.6 >7457 tests	95.6%, 45.7 >2103 tests	100%, 39.5 1264 tests	100%, 40.4 1293 tests	100% 27.2 871 tests	100% 29.1 932 tests
Gray	98.2% 32.9 >1322 tests	99.8% 45.4 >1482 tests	97.8% 35.4 >1460 tests	100% 28.7 919 tests	26% 75.7 >12470 tes.	37.4% 80.3 >10977 tes.	22.8% 78.4 >12925 tes.	31.6% 63.4 >11586 tes.

Table 6.7: Results of binary search procedure for full loop testing.

Table 6.7 shows that the Hamming fitness method of evaluating the fitness of the individuals is the best strategy with regard to success rate and speed. Using the SELECTION_F option increases the performance of the GA in conjunction with the Hamming fitness functions. Gray code representation only increases the performance of the GAs in combination with the reciprocal fitness.

6.1.3.3 Random testing of binary search

In order to receive an exact amount of test data which are required for random testing the number of maximum generation is increased to 300000 otherwise only 6.9% of all tests are successful. The results can be seen in Table 6.8.

Nits	Success rate	Tests
1	100% in 1261	40325
2	100% in 666	21312
5	100% in 83.0	2656
10	100% in 2.6	83

Table 6.8: Results of random testing with predefined number of iterations *NITS* = *1*.

The results for *NITS* = *1* using the random testing show that many tests are required, which is similar to the results obtained in the linear search procedures. The number of required tests using random testing is indirectly proportional to the number of global solutions and the range of randomly generated values. For *NITS* = *1*, *NoRT* = *40001*

(see equation (5.8) so that on average 40001 test data have to be generated in order to generate the global optimum. This figure agrees with the empirically determined results. As the number of iterations increases so the number of possible matches increases, and the performance of random testing, both in theory and in practice, approaches that of GAs. This is because the cardinality of the required sub-domain increases. When $NITS = 10$ there are 512 global solutions which require 79 tests, on average until one of the global solutions is generated. For full loop testing about 48640 tests are required compared to only 871 tests achieved with GA. The theoretical number of random tests using equation (5.8) is $NoRT = 50002$.

6.1.4 Using character in LINEAR_1 and BINARY_SEARCH

In all previous test procedures the global optima are based on integer array data types. In this section a character data type is used. The character data type is converted for the evaluation of the fitness either, into its corresponding ASCII value (if the reciprocal fitness function is used) or immediately into a binary string in the case of using Hamming fitness function.

The GAs have no problems in generating test data to traverse all nodes. For the linear search and the binary search, the GA performed better than in pure random testing. The LINEAR_1 search procedure achieves 100% success in only 7.0 generations for *one* iteration (binary search required 7.1 generations). This corresponds to 56 tests, since a character consists of eight bits, so the population size P_{SZ} has correspondingly only 8 individuals. For the full loop testing about 8.7 generations are required. Using the LINEAR_1 procedure, random testing achieves 100% in 83 tests for *zero* iterations and for full testing criteria the number of required generations increases to 198 tests.

The last experiment using the search procedure LINEAR_1 is carried out with a new data type. A string of four characters (array of four characters) is used in order to generate test data for full loop testing. The string of characters is handled as a one bit string. Considerably more test data are required in order to satisfy all branch conditions for full iteration testing since the input domain has a size of 127^4 and only three solutions exist (global optima) to iterate the loop *zero*, *one* and *two times*. About 93.2 generations are needed to generate test data (100% success rate) which execute all

branches, where the number of individuals per generation has increased from 8 (character size) to 32 bits (P_{SZ} = four times the character size). Random testing is not feasible for all available characters (ASCII code from 1 to 127) because of the amount of test data which have to be produced. Theoretically 127^4 possible combinations exist, i.e. for *one* iteration $X = A(1)$. This means on average 127^4 test data have to be generated in order to traverse the iterations once. This would take too long a period of time.

6.1.4.1 Conclusion of search procedures

One of the problems which occurs during the use of the reciprocal fitness function is that it is difficult for the GA to optimise towards large values. This is observed in the first and second set of experiments using LINEAR_1 where a value of 10000 or random numbers are used for the first element of the array *A*, whereas it achieves good results when global optima represent small values. The reason for this lies in the nature of the reciprocal fitness function which favours smaller values. This is reflected in the results of the quadratic and triangle procedures, which favours smaller values for their input variables to generate global solutions. This is expressed by the increased number of zero solutions generated in the quadratic equation solver program.

Although the GA rapidly finds an area with a global optimum, the GA will not locate the global optimum with the same kind of speed, DeJong [1993] and Figure 6.2 and Figure 6.4. Therefore, the idea of the weighted mutation is to undertake a local search to speed up the finding of the global optimum, when the population seems not to improve anymore, and thereby endeavouring to overcome local optima. If the GA tries to optimise towards the value of 10000, a possible local optimum could be 9983 which is in binary code 11111111011100100. Just by changing only one bit of the bit string, the quality of the test data will diminish because the test data moves further away from the optimum. If *bits* is restricted to the last five bits of the bit string, the weighted mutation operator cannot do anything to improve the fitness (using reciprocal fitness function) of the test data because the last 8 significant bits are already set to 1 and changing them to 0 decreases the numeric value and so the fitness. Increasing the parameter value *bits* to '*10 bits*', or using Gray code in the case of the reciprocal fitness function could reduce

this trap as shown in the results of the search procedures. The advantage of the Hamming fitness function is that it compares the bit pattern and not the numeric values.

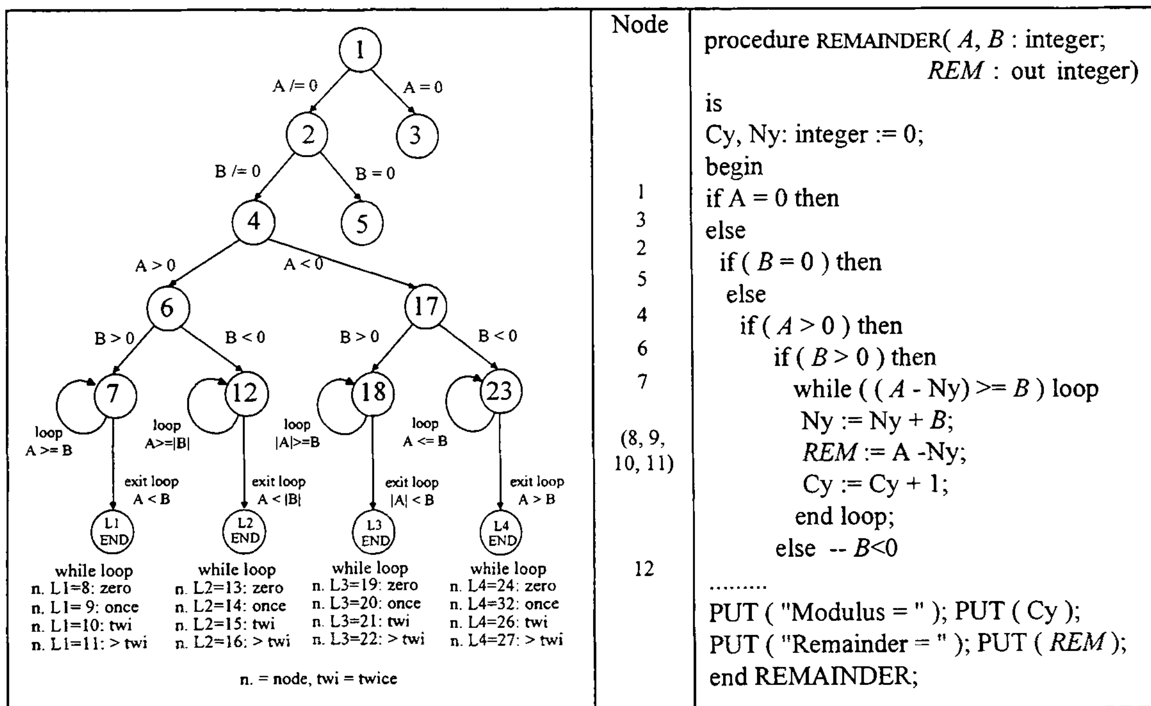
If the loop conditions are thoroughly tested, the testing for more than two iterations is usually done instantly which means the GA or the random testing do not have to spend much time on that special branch in order to execute it. Using Hamming fitness is more consistent than the reciprocal fitness function. In conjunction with SELECTION_F it is always faster in generating global solutions.

6.2 Remainder procedure

The remainder procedure accepts two input variables *A* and *B* of type integer and returns the remainder as an output variable REM (of integer type) when *A* (dividend) is divided by *B* (divisor). The remainder is evaluated by repeatedly subtracting *B* from *A* within a loop until the result becomes less than *B*.

6.2.1 Description

Six cases arise from all possible combinations of zero, positive and negative values for *A* and *B*. Two out of these six cases originate from the event when either *A* or *B* are zero in which case a remainder of 0 is returned. The other four cases arise from the combination of $A \neq 0$ and $B \neq 0$ being positive and negative, for which the remainder is evaluated. These are treated separately by using the relational operator '<' or '>'. Therefore, the remainder procedure has four different loop conditions. The iterations of the loops will be assigned to a node number, as can be seen in the control flow tree of Figure 6.10 and their fitness function will be based only on the number of iterations, see chapter 4.




```
Node
            procedure REMAINDER( A, B : integer;
                                 REM : out integer)
            is
            Cy, Ny: integer := 0;
            begin
1           if A = 0 then
3           else
2             if ( B = 0 ) then
5             else
4               if ( A > 0 ) then
6                  if ( B > 0 ) then
7                    while ( ( A - Ny) >= B ) loop
(8, 9,                 Ny := Ny + B;
10, 11)                REM := A -Ny;
                       Cy := Cy + 1;
                     end loop;
                  else -- B<0
12
            .........
            PUT ( "Modulus = " ); PUT ( Cy );
            PUT ( "Remainder = " ); PUT ( REM );
            end REMAINDER;
```

Figure 6.10: Control flow tree of the REMAINDER.

Listing 6.4: Code of a part of the REMAINDER.

The remainder program is divided into 27 nodes and 18 different branches where the

longest path consisted of 8 nodes (path to node 11, 16, 22 and 27). The entire code of the remainder procedure is listed in Appendix C. Listing 6.4 shows an excerpt of the code of the REMAINDER procedure covering the path to the first loop conditions (path: 1, 2, 4, 6, 7, 8 or 9 or 10 or 11), i.e. A positive and B negative.

6.2.2 Results of Remainder

In these experiments, the two variables A and B are to be optimised by the GA, therefore the population has $P_{sz} = 64$ members and the mutation probability is $P_m = 0.016$, since $P_m = 1/P_{SC}$.

Two of the branches (node 3 and node 5 seen in Figure 6.10) have the lowest probability of being traversed because these branches filter the cases when $A = 0$ or $B = 0$. This means that there is only one global solution for each of these nodes. These branches are only traversed if test data are generated for A and B which have the value of 0. Assuming that the input range is between ± 20000, the probability for each branch having been traversed is $P_{3,5} = \frac{1}{40001} = 2.5 \cdot 10^{-5}$. This reflects the high number of tests required to be performed for random testing to achieve full branch coverage. The test data are checked using a post condition which is the Ada function REM.

Results of the experiments are shown in Table 6.9 where MAX_GENERATION is set to 200.

	Reciprocal fitness				Hamming fitness			
	SELECTION_R		SELECTION_F		SELECTION_R		SELECTION_F	
Coding	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
binary	100% 15.2 973 tests	100% 14.7 944 tests	86% 12.9 2502 tests	95.5% 11.4 1273 tests	100% 15.2 974 tests	100% 15.5 959 tests	98% 10.9 937 tests	100% 10.1 644 tests
Gray	100% 22.9 1463 tests	100% 20.3 1297 tests	87.5% 22.6 2863 tests	97% 19.8 1616 tests	72% 39.3 5416 tests	92% 33.7 3010 tests	49% 38.7 7741 tests	84% 38.4 4115 tests

Table 6.9: Results for full loop testing using REMAINDER.

Reciprocal and Hamming fitness functions achieves similar results when random selection is chosen. However, SELECTION_F improves the performance using Hamming fitness by about 5 generations and full branch coverage is nearly always

achieved. The reciprocal fitness results deteriorate to about only 86% to 95% success rate. The nodes 3 and 5 are not responsible for the decrease in performance, as expected. The problem nodes are the iteration nodes which have many global optima, so that the SELECTION_F option does not always work very well; similar results are obtained for the quadratic and triangle procedures in chapter 5.

Using the Gray coded representation achieves 100% branch coverage for the reciprocal fitness function, but it needs about 9 generations (about 580 tests) more than binary representation and is worse in combination with SELECTION_F.

The weighted mutation works very well with the default value of '*5 bits*', but it makes only a slight improvement using '*10 bits*' because all nodes can be traversed with small numeric values, especially nodes 3 and 5. These experiments are compared using single and double crossover operators and the results are shown in Table 6.10.

Reciprocal fitness		**Hamming fitness**	
SELECTION_R	**SELECTION_F**	**SELECTION_R**	**SELECTION_F**
Single crossover			
100% in 21.4 1367 tests	85.5% in 17.5 2816 tests	99% in 22.2 1533 tests	96.5% in 15.2 1390 tests
Double crossover			
98% in 20.7 gen. 1556 tests	81% in 17.1 3320 tests	99% in 21.8 1511 tests	94.5% in 15.4 1634 tests

Table 6.10: Results of remainder procedure using different crossover operator.

The results of the experiments shown in Table 6.10 are carried out with the option '*5 bits*' and binary representation. Comparing the results given in Table 6.10 with those in Table 6.9 shows that uniform crossover achieves a better performance than single or double crossover by about 5 to 6 generations.

Figure 6.11 displays a fitness distribution over a test run. It can clearly be seen that for example after node 3 has been executed the fitness functions switch over to the next fitness function. All other branches are already covered after 3 generations.

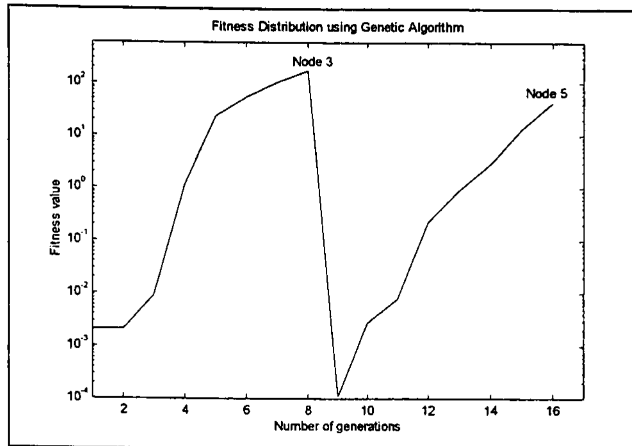


Figure 6.11: Distribution of off-line performance for the remainder procedure using GA.

As shown in Figure 6.11 after node 3 is executed the fitness function automatically changed in order to evaluate the fitness for the next untraversed node. After node 3 has been executed the fitness falls to a lower value than that at the start at the run. This is because *B* is not part at the fitness function for node 3, and the GA has found no advantage for all values of *B*. *B* can be larger than the initial ±20000 input range because of mutation and crossover operators, i.e. the fitness value for node 5 (based only on *B*) is at the beginning smaller than for the node 3.

6.2.3 Random testing using REMAINDER procedure

Assuming that the input range is between ± 20000, the average theoretical number of randomly generated test data required, is $NoRT = \frac{1}{P} = \frac{40001}{1} + \frac{40001}{2} = 60001.5$ tests, using equation (5.8). This is the reciprocal of the probability that nodes 3 and 5 are traversed. This reflects the high number of tests required by random testing in order to achieve full branch coverage.

The maximum number of tests is increased to 500,000 tests before the test run is abandoned, so that the success rate of full branch coverage is always 100% which is achieved in 63,568 tests for random testing. This number of tests is slightly higher than the theoretical number calculated, because all other probabilities for traversing the nodes are neglected. Comparing random testing with GA testing, GA is clearly better in respect of the number of tests required and CPU time which can be seen in Table 6.11. The improvement over random testing is a factor of about 90 for an input range of

±20000 for the number of tests and increases for larger ranges up to 130 for an input range of ±100,000.

Range of input	Random testing with 100% success rate		GA using Hamming	
	Tests	CPU	Tests	CPU
±20000	63260	0.94s	680	0.21s
±40000	119597	1.77s	1002	0.32s
±80000	238080	3.52s	2131	0.67s
±100000	317773	4.71s	2476	0.78s

Table 6.11: Results of random and GA testing.

As can be seen, GA uses much less CPU time and the factor of the gap between random and GA testing grows with increasing input range (from 4.5 to 6.0).

6.2.4 Interim Conclusion

As can be seen from Table 6.11, GAs are a powerful method of generating test data for '*if* condition and loop predicates where the fitness of the loop nodes are only based on the number of iterations. The remainder test procedure is similar when compared to the previous procedures, in that it has only one global optimum for each of the nodes 3 and 5, which are the most difficult branches to traverse. Therefore, the selection procedure which selects the parents for the next reproduction phase by their fitness, is superior to a random selection strategy. Binary representation produced more favourable results then Gray coded representation which confirms the experimental results of the previous section.

6.3 Conclusion of procedures with loop conditions

Throughout the experiments, the number of purely random tests predicted to obtain full branch coverage of the software agreed with the experimental findings.

In all cases, full branch coverage is achieved by GA with less effort than random testing when measured in terms of the number of tests required and the CPU time. The improvement factor varies from problem to problem up to two orders of magnitude (150). This improvement does not take into account the important issue of computation effort per test which is considerably greater for GAs than for random testing. However, the total CPU time for branch coverage using GA is less than using random testing.

Furthermore, GAs are able to closely control the number of iterations used in the remainder procedure. This is apparent when using random numbers for *A* and *B* because if these input variables have very different values, the loop will iterate many times which costs a lot of CPU time, whereas GAs try to control these variables so that the number of iterations are reduced.

In this instance, the SELECTION_F option of selecting parents for reproduction by their fitness values is better than random selection. The reason for this result is that in all search procedures, specially in the linear search procedures, there is only one global optimum per node so that there is no confusion regarding different goals per node. In the remainder procedure, the fitness for executing the loops is based solely on the number of iterations required. This provides a straight forward way of controlling the loops. However, in linear and binary search procedures, this approach causes problems, since the array element values are not continuous, especially in the case of the linear search where the values of the array elements are not sorted. Therefore, the array elements, which are used as the predicate condition in the '*while ... loop*' (LINEAR_1), '*loop ... exit*' (LINEAR_2) and in the '*while ... loop ... return*' (binary search) are needed as the base for the fitness functions. The binary search procedure is in one sense an exception because of the construction of the loop condition which has one condition in the '*while ...*' statement and a second condition is involved in nested '*if*' condition with a 'return' command which terminates the loop as soon it is executed.

The results of these experiments confirm several hypotheses and clarify them in more detail. Hypothesis 1 is confirmed by the much more efficient behaviour of GAs. The standard setting (hypothesis 2) has been made more precise for different features. Gray code is normally better with a reciprocal fitness function than using binary code (hypothesis 2_1) which is better in combination with Hamming fitness function. If only few global optima exists, it is better to use selection according to fitness, if there are several, use random selection (hypothesis 2_2). Hypothesis 2_3 is confirmed again that uniform crossover is superior. Hypothesis 2_4 is justified by using different population sizes and the best is found as stated in the hypothesis. The hypothesis 3 which is under close investigation in this chapter is confirmed by generating test data for the different number of loop iterations.

In the next chapter commercially available software is used as the procedure under test, which has more complex data types.

CHAPTER 7

Testing generic procedure

In previous chapters, test data have been generated automatically for various procedures. These include a quadratic equation solver, a system of five procedures for classifying triangles, remainder calculation procedure and linear and binary search procedures. The quadratic equation solver and the triangle procedures contain '*if*' conditions and the other procedures in addition have various loop conditions. The performance of the GAs with regard to these procedures is undoubtedly better than pure random testing which need up to more than two orders of magnitude more tests to achieve full branch coverage.

The aim of this chapter is to investigate and characterise the behaviour of a generic procedure and its implementation and effect. A generic sorting procedure is used which has more complicated data structure such as records.

7.1 Generic Sorting Procedure: Direct Sort

The procedure DIRECT_SORT is commercially available and is tested as supplied. The purpose of the procedure is to sort an array of elements in the main memory into ascending order; it is based on the quicksort algorithm which partitions the array and swaps low values in the upper partition with high values in the lower partition. The out-of-order values move large distances which leads to efficient sorting under favourable circumstances. It is considerably more complicated than many of the other procedures because:

- it is generic,
- it contains two local procedures (INSERT and PARTITION), and
- procedure PARTITION has its own local procedure SWAP.

Overall, DIRECT_SORT consist of six loops and eight selections several of which are nested. The control flow graphs of the procedures MAIN, PARTITION, INSERT and SWAP are shown in Figure 7.1, Figure 7.2, Figure 7.3 and Figure 7.4 respectively and the Ada code for these procedures is in Appendix D.

The symbol C in a node means that this is a decision node with no extra node number

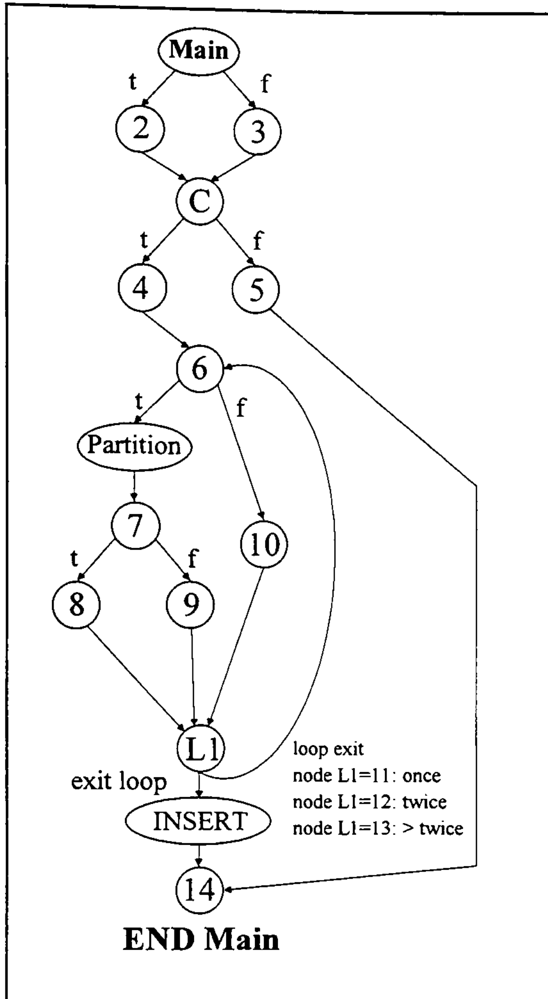


Figure 7.1: Control flow graph of DIRECT_SORT.

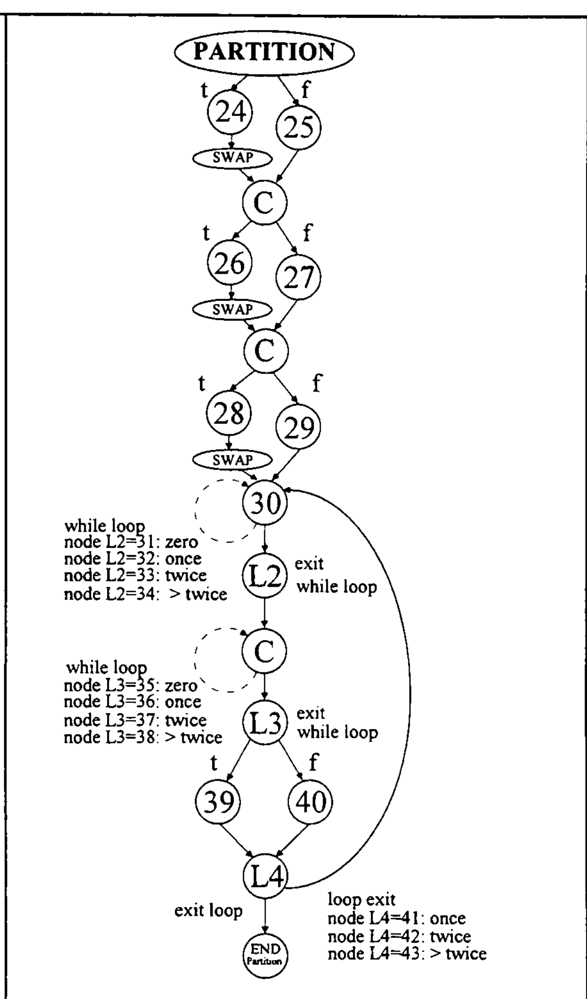


Figure 7.2: Control flow graph of procedure PARTITION.

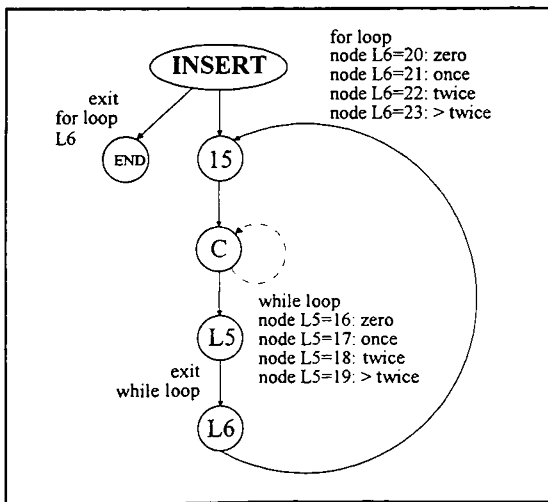


Figure 7.3: Control flow graph of procedure INSERT.

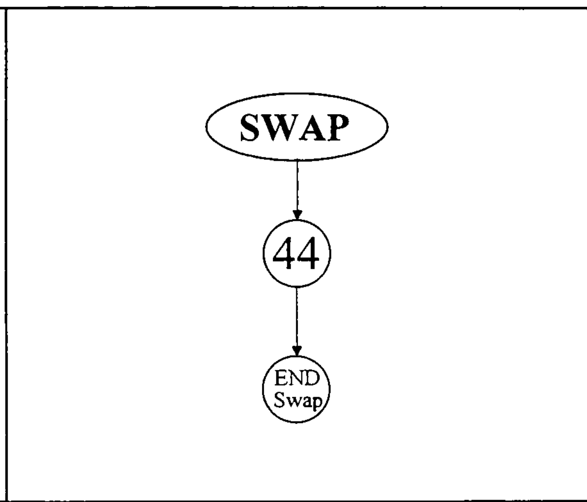


Figure 7.4: Control flow graph of procedure SWAP.

7.2 Generic feature

Since DIRECT_SORT is written as a generic package (see chapter 5), it has to be instantiated in the main program. The generic package header of the sorting procedure is:

1. *type index_type is (<>);*
2. *type scalar_type is private;*
3. *type vector_type is array(index_type range <>) of scalar_type;*
4. *with function LT (a, b: in scalar_type) return boolean;*

This generic section at the head of the DIRECT_SORT package allows different data types to be sorted by instantiation of those generic types, Barnes [1984], without recompiling the source code. The first statement of the generic section defined the *index_type* to be any discrete type, (<>), which could declare the indices of an array to be sorted. The array type elements can be defined as being of any type and is instantiated into the *scalar_type*. The third statement declares the array type to be sorted in terms of a limited range of *index_type* and *scalar_type*. In order to define the ordering of the elements in a sorting procedure, it is essential that the user defines a '*L*ess-*T*han' function (*LT*) for variables of *scalar_type* (fourth statement). This has to be done because the *'Less-Than'* operators, i.e. '<' or '>' are only defined for primitive data types. The program which calls the generic DIRECT_SORT has, therefore, to declare appropriate types for *index_type*, *scalar_type* and *vector_type* as well as an appropriate function definition for *LT*. These are then used to instantiate the sort package.

Due to the increased complexity and expected usage, (valid for all possible data types), of DIRECT_SORT, and the combined instantiation of the package, the testing of such generic procedure needs to be more thorough than normal, even though the Ada compiler is very precise in type checking.

Generic procedures may contain more complex '*if*' and '*loop*' conditions than encountered previously, and this is reflected in an increased complexity of testing. This is due to the fact that some conditions relate to the definition of the discrete types which are instantiated into the generic package. One example of this is the condition for checking the indexes of the array where *top* is equivalent to *UPPER* and *bottom* to *LOWER*:

if (index_type'pos(top) < index_type'pos(bottom)) then...

This tests the *index_type* to see whether the top array index is smaller than the bottom index, as allowed by the Ada compiler. If this is the case, the array is empty (Ada83 LRM, 3.6.1 [1983]) and DIRECT_SORT returns an error flag and terminates the sorting.

Another test case checks the size of *index_type* (number of elements to be sorted) in order to ascertain whether the array section is of sufficient length to make partitioning worth while. The condition is of the form:

if index_type'pos(right) - index_type'pos(left) > 10 then...

If the condition is true, the array will be partitioned and sorted by the procedure PARTITION and the local procedure SWAP. In the case of an array size smaller than 10 elements the array is sorted by the procedure INSERT. Such conditions have to be tested and can be difficult to check manually, because of the complexity of the conditions.

The size of the array has to vary in order to test the second condition. This can make things difficult since the GAs normally use a fixed length number of bits for the chromosomes. A strategy, therefore, has to be found to compensate for this phenomenon as described in the next section, Sthamer [1994].

7.3 Test strategy and data structure

The first experiments are carried out using the normal method of implementing the instrumentation procedures (see chapter 3), into the procedure under test. On feeding test data, in this case arrays, into the DIRECT_SORT procedure, the array elements should be sorted into ascending order on completion of the procedure. The original test data is then fed into a different quicksort procedure to verify the functionality of DIRECT_SORT.

For the first experiments the array size is restricted and fixed to 10 elements and the data type is an array of integers. The result is unsatisfactory although the testing tool traversed all possible branches within this set-up. The problem is identified as the

definition of the array's set-up. Since the array is fixed in this first experiment and the size is limited to 10 elements, it is not possible to execute those branches which involved the size of the array. In total only twelve nodes are executed. These are nodes 3, 4, 6, 10, 11, 14, 15, 16, 17, 18, 19 and 23. All other branches could not be executed. Branches 3 and 4 are executed because the top index of the array (*index_type*) is always larger than the bottom index (10 > 1), therefore nodes 2 and 5 could not have been executed. Since the array is fixed to ten elements, node 10 can only be executed which is directly related to the size of the array. Node 11 is executed which is a loop condition for one iteration. The loop can only be executed once as long as the array consists of less than 11 elements. Nodes 15, 16, 17, 18 and 19 are executed because they do not relate to the array size or the values of the array indices. They belong to a loop condition in the procedure INSERT. Node 23 belong to a *'for ... loop'* condition with more than two iterations. *Zero*, *one* and *two* iterations (node 20, 21 and 22) are not traversed because they relate directly to various sizes of the array. Zero iterations could only be fulfilled when top index minus bottom index is zero (one array element), one iteration is performed if the difference is one, etc.

The next experiment carried out, uses an array size of 12 elements. Compared to the previous experiment more nodes are executed in total, but full branch coverage is not achieved. Node 2 is not executed because the size of the array is still fixed at 12 elements since upper'*index_type* (12) is always larger than lower'*index_type* (1). In order to traverse nodes 20, 21 and 22, the *index_type* ought to be variable as explained above.

All those untraversed nodes relate to the main condition that the *index_type* (array size) is fixed and not a variable. The structure of the testing tool requires altering so that the sizes of the array could change. This is achieved by varying the size of the actual chromosomes. Although the length of the active part of the chromosome of the array is altered, it is still fixed to a certain size. However, the size of the *index_type* which defines the array size to be sorted (test data) will be made variable within a certain range. In order to make the *index_type* variable two extra variables, (*LOWER* and *UPPER*) of type integer, are incorporated into the structure of the chromosome so that these two variables can also be influenced by the GA. It is decided that the maximum size of the array should be restricted to 16 array elements. The choice is now whether to

use the entire array or just a part of it. The maximum size of 16 elements is chosen because of the computational effort in the case of a larger array. The size of 16 elements is also convenient in that it can be represented with four bits between 0 and 15. The variables, *LOWER* and *UPPER*, are just four bits long and only positive values are allowed. These two variables restrict the size of the array by defining the *index_type* for each chromosome. Hence the entire size of the chromosome consists of 18 elements, as can be seen in Figure 7.5, which shows the new data structure.

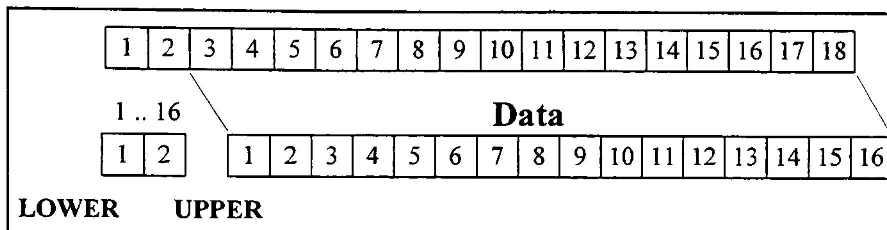


Figure 7.5: Data structure of the new chromosome.

The first row in Figure 7.5 shows the entire chromosome. The first two elements are the integer variables LOWER and UPPER. The remaining elements of *scalar_type* are the input which can be of any data type. The entire type structure of the chromosome is displayed in Listing 7.1

```
type data_record is record
        range_pointers : array(1..2) of integer;
        data : array(1..16) of scalar_type;
end record;
```

Listing 7.1: Type declaration of the chromosome.

The idea is to change and define *index_type* for each new test data. This result in the array size being variable. An example of how a chromosome could look is displayed in Figure 7.6.

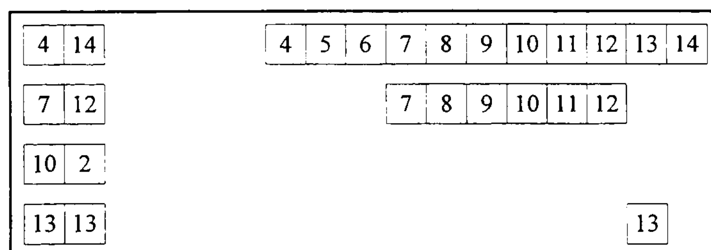


Figure 7.6: Usage of different array sizes as defined by *index_type*.

Referring to Figure 7.6, the first example shows the *index_type* between 4 and 14, which means that the variable *LOWER* is 4 and the variable *UPPER* is 14. The array section

used for DIRECT_SORT is, therefore, from the array element with the index 4 to the array element with the index 14. All the other elements of this chromosome are neglected. In the second case, the range of index_type is between 7 and 12, so that only the array section between array elements 7 and 12 is used. These variations in the size of the array are necessary in order to execute most of the untraversed nodes from the first two experiments. The third example describes the case when the top index (UPPER) is smaller than the bottom index (LOWER) of the array which will execute node 2 and then terminate the DIRECT_SORT procedure because the array is empty. The last example describes the case where the array consists of just one element.

Having developed the new structure, the GA testing tool should be able to generate and optimise the array so that full branch coverage may be achieved. In order to achieve this structure the generic types have to be declared as in Listing 7.2.

```
declare
type index_type is new integer range (LOWER) .. (UPPER);
subtype scalar_type is integer;
type vector_type is array (index_type range <>) of scalar_type;
```

Listing 7.2: Generic type declaration.

These three lines describe the array to be sorted or alternatively the test data. The first line after the 'declare' command defines *index_type* in the range of the LOWER and UPPER variables with maximum limits between 1 and 16. *Scalar_type* is defined for the first set of tests as integer type. The *vector_type* is an array of type *scalar_type* (here integer) in the range of *index_type* where the limits of *index_type* have not been constrained as yet. This is done later in the process, in the section of the procedure under test where the sort package is called and the variables defined, because *vector_type* in the generic sorting package is defined as an unconstrained array and therefore has to be defined in the main program. The declaration part of the array which required sorting can be seen below.

sorting_array : vector_type(index_type(LOWER)..index_type(UPPER));

The fitness functions has to be re-defined because of the different types declared for the sorting package. Since complicated data types could be used, the Hamming fitness function is chosen in order to make it as general as possible. However, due to the

generic types in the sorting procedure all arithmetic operations are not allowed because of the undefined types. In order to get around this problem for different data types, separate Hamming fitness functions are defined. Each fitness function has the same structure and deals with *index_types*, *scalar_types* or integer types.

7.4 Different Tests

Experiments are carried out with different *scalar_types*, such as integer, records with fields of type integer and character, and also where the fields are in reverse order. The key in each of these is the first data type. If the second data type is chosen as the key, the same results would have been produced.

Different experiments are carried out without changing the MSB in the weighted mutation operator when integers or records (of integer and character) are chosen as the *scalar_type*. Another set of experiments deals with disabling the CONTROL_PARENT procedure which converts the two's complement (produced by the conversion for negative numeric values) into a binary representation where the MSB is the sign bit. If a record is considered as a one bit string, no direct access to the MSB is possible in a single bit string which is explained in Figure 7.7.

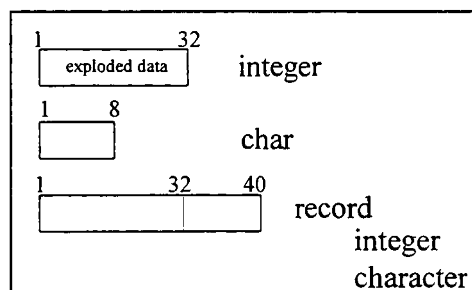


Figure 7.7: Example of a chromosome using different data types.

The records are defined for character and integer fields in two ways, with either the integer as the first variable of the record shown in Figure 7.7:

```
type scalar_type is record
        key : integer;
        data : character;
end record;
```

or vice versa the character type is the first variable.

Direct access of the MSB is only available if the testing tool takes advantage of the knowledge of the structure of the input data types (*scalar_type*). This means the testing tool can identify the beginning and end of the bit string of any variable, e.g. of an integer (32 bits long) or character (8 bits long) variable. This results in the MSB being directly accessible for using the weighted mutation operator and in using the CONTROL_PARENT procedure. If a record of different data types (here e.g. 40 bits long) is used as the *scalar_type* the position of one of the single data types (e.g. integer type) is not necessarily known unless the testing tool identifies those certain bit strings.

When two chromosomes have been selected for crossover, an additional option is to swap only the bits (using crossover and mutation operators) in the sections which are specified by the variables LOWER and UPPER in both chromosomes. However, using this method no improvement is noticed compared with when the entire chromosome is used for crossover and mutation.

The population size for all experiments is restricted to 45 chromosomes per population. Due to the number of variables, a square size of population would have resulted in a population size of 520 chromosomes. This would require a great deal of computational effort per generation and moreover the random search element would be stronger than the GA method so that a reduced population size is used. 45 chromosomes per population turns out to be sufficient, due to the fact that it requires fewer tests in order to generate full branch coverage when compared with other population sizes. With a population size of 15, 1800 tests have to be carried out before full branch coverage is achieved, whilst a population of 30 need 861 tests. 45 chromosomes per generation need only 738 tests and when the population size is increased to 60 chromosomes per generation, 838 tests are required. Therefore, the population size is set to 45 members per generation as default.

7.5 Results of DIRECT_SORT

The elements of the array (*vector_type*) are sorted using the DIRECT_SORT procedure. This is verified by putting the same test data through another independent quicksort procedure. This is used to check the functionality of the generic sorting procedure. Different results only occur when *scalar_type* is a record. This is because of the

different sorting algorithms. When a particular value for the key element occurs twice in the array, DIRECT_SORT does not swap the values, whereas the quicksort version does, thereby resulting in a different order of occurrence in the resulting array. This is apparent e.g. in the second data type of the record. This is called *stable* if two equal elements are not swapped after sorting occurred otherwise the sort is described as *unstable*.

The mutation probability is set to $P_m = 0.0015$ ($P_m = 1/(16*40+2*4)$) when using a record of integer and character and $P_m = 0.0019$ ($P_m = 1/(16*32+2*4)$) when using only integer types which corresponds to the reciprocal of the number of bits which *data_record* requires. The array elements of type integer are initialised at random to values which lie in the range from ±100 or between 0 to 200. The default range could turn out to be problematic for the experiments where the weighted mutation operator and CONTROL_PARENTS procedure are disabled due to the data structure. The second range randomly generates only positive values for the initial population, so that the sign bit (MSB) is always set to zero.

7.6 Test results

In each experiment the weighted reciprocal Hamming fitness is used. The experiments of DIRECT_SORT are terminated after 2000 generations (maximum generation) if full branch coverage is not achieved.

It is important to test a generic procedure using simple and complex data structures e.g. integers and records of various data types. In particular, if the record structure is converted to a bit pattern corresponding to the memory image, the integers are represented as two's complement rather than as sign and magnitude format.

The LT function is defined in terms of the key in each case on the first variable of the record. The second variable could also have been chosen, which would produce similar results. The records are manipulated in two ways. Firstly, only integers are used as the *scalar_type* to be sorted and the results are shown in Table 7.1. The second set of experiments used two's complement instead of binary sign and magnitude representation, the result can be seen in Table 7.2. Thirdly, a record is used and it is split

into its individual components (variables) and the crossovers and mutations are applied only to the key; The results are displayed in Table 7.3. In this case, the record is treated as a single bit string. For each set-up of the experiments two different initial random ranges are generated (from ±100 and from 0 to 200).

Experiment No.	**Set-up**	**Range: ±100**	**Range: 0 to 200**
1, 2	default	100% 19.9 898 tests	100% 19.3 870 tests
3, 4	default without MSB	86.4% 89.8 > 15730 tests	96.8% 109.5 > 7652 tests
5, 6	default, *10 bits*	100% 17.5 787 tests	100% 15.3 687 tests
7, 8	*10 bits*, without MSB	89% 90.1 > 13507 tests	100% 15.9 715 tests
9, 10	Default, Gray, 10 bits	100% 17.5 787 tests	100% 15.4 693 tests
11, 12	Gray, *10 bits*, without MSB	85.4% 96.7 > 16868 tests	100% 16.1 724 tests

Table 7.1: Results of testing DIRECT_SORT using integer data type.

The results of experiments 1 to 12 displayed in Table 7.1, apply to sorting a simple array of integers which are represented in the sign and magnitude format rather than two's complement. This avoids the problem associated with the gross change of pattern as the integer value passes from positive to negative, and vice versa. As expected, the results of the experiments where the array only contains integers compared to a record type of integer and character, Table 7.3, (variables handled separately), are similar with regard to the same set-up. This result is expected because the testing tool treats both experiments in a similar manner. As the results show, the set-up and the knowledge about the data structure are quite important in order to achieve full branch coverage in the least number of tests. The accessibility of the MSB for the weighted mutation and for the conversion of the two's complement into the binary plus sign bit format is important.

As a first result, it is found that when a range of ±100 is used for the first generation without the MSB in the weighted mutation operator, the results deteriorate quite badly (experiment 3) because the chance of changing the sign of a test data value is quite small and only relies on the normal mutation operator.

Confirmation that this causes the problem is obtained by repeating the experiment with

a positive (0 to +200) initial randomly generated population which means that negative integers are non existent (experiments 2, 4, 6, 8, 10, 12).

The best results are achieved using the MSB in weighted mutation and CONTROL_PARENTS with a high value for *bits* (experiment 5 and 6). There is clearly an improvement over the default set-up of experiment 1 and 2 ('*5 bits*'), in both the number of tests and in the percentage of the success rate. A distinct improvement is achieved for the experiments by ensuring that the initial randomly generated population range is positive e.g. between 0 and 200 (experiment 6). The number of tests are reduced by 183 compared to experiment 2 ('*5 bits*') and by 100 compared to experiment 5 (range ±100). In the range from ±100 the improvement is about 111 tests (experiment 5 compared with experiment 1) to get full branch coverage.

The results of the experiments which use the weighted mutation without MSB (experiments 3, 4 and 7, 8), deteriorate depending on its usage within the experiment. It can clearly be seen that the experiments in the range of 0 to 200 invariably achieved better results. Experiment 7 (range ± 100) needed more than 13507 tests, whereas, experiment 8 (range 0 to 200) need just 715 tests. This shows the importance and improvement of choosing the right initial range. Experiments with Gray code are conducted but the results do not improve. They achieve results which are similar to the default binary code.

Experiment No.	**Set-up**	**Range: ±100**	**Range: 0 to 200**
13, 14	Two's complement, default	100% 22.1 996 tests	100% 19.7 888 tests
15, 16	Two's complement, without MSB	68.4% 134.9 > 32591 tests	94.4% 173.6 > 12415 tests
17, 18	Two's complement, *10 bits*	100% 20.9 937 tests	100% 15.4 693 tests
19, 20	Two's complement, 10 bits, without MSB	67.6% 95.2 > 32056 tests	100% 15.6 710 tests

Table 7.2: Results using integer data type without CONTROL_PARENTS.

The second set of experiments, Table 7.2, are conducted without the conversion procedure CONTROL_PARENT, which converts negative values from two's complement into binary sign and magnitude code. The record is seen as a one bit string after converting it into a binary format. The bit string is then optimised rather than the single separate variables of the *scalar_type*.

Normally one could argue that the results using the two's complement should be worse than using binary and sign bit because of the different representations (for positive values binary code and for negative two's complement). In the case of using an initial range of ± 100 the statement is correct. On average about 3 more generations are needed to achieve full branch coverage using two's complement. The results deteriorated rapidly when the MSB for the weighted mutation is disabled. The percentage of full branch coverage is worse by up to 20% and about 17000 tests are needed in addition to experiment 3 to achieve full branch coverage in the other cases (experiment 3 compared to 15).

In the case where the initial population is in the range from 0 to 200, the results are also good (compared experiments 2 and 14, 6 and 18, 8 and 20) because only one representation of the data type is used namely the binary coded. When all values in a population are positive, they would remain so during the entire test run, because normally the only opportunity to change the sign of a value is by the mutation operator which has a very low probability of $P_m = 0.0016$.

The results deteriorate when the weighted mutation is performed without the MSB. This is especially the case in experiments 15 and 19. A positive initial range again gives much better results (experiments 14, 16 and 20) compared to the ±100 range (experiments 13, 15 and 19). A distinct improvement is apparent in experiment 20 when compared to experiment 19. An improvement by a factor of 45 is achieved when the least significant bits are increased to '*10 bits*'. The option '*10 bits*' improves the result by 195 tests in the case of experiment 18 as compared to experiment 14 ('*5 bits*').

Experiment No.	Set-up	Range: ±100	Range: 0 to 200
21, 22	Default	100% 20.1 905 tests	100% 19.4 873 tests
23, 24	Without MSB	87.3% 89.9 > 14962 tests	97.9% 109.9 > 6732 tests
25, 26	One bit string, two's complement, without MSB	55.5% 10.6 >40265 tests	96.4% 110.5 >8034 tests

Table 7.3: Results of testing DIRECT_SORT using record type of integer and character.

The results of the third set of experiments using records are shown in Table 7.3, and are only slightly different from those carried out in experiments 1 to 4. The use of a record

in this case does not affect the outcome of the results. When random testing is used to test DIRECT_SORT about 9100 tests have to be carried out to achieve 100% branch coverage. This means that for random testing more than 13 times more tests have to be carried out than using GAs to achieve full branch coverage.

An improvement is obtained by ensuring that the range of the initial integer values is positive i.e. 0 to 200, where the size of the range does not influence the result. When the records are manipulated as a single bit string, the success rate deteriorates; only 96.4% of all test runs achieve full branch coverage in more than 8034 tests (experiment 26 comparable to experiment 4 and 6). The case when the initial range lies between ±100 gives the worst results of all (experiment 25).

Experiments are carried out with a record as *scalar_type* which consists of a character and integer where the character type is the key element. The conversion procedure CONTROL_PARENT is not needed because the type character is used as the key element so that no two's complement is produced for it. The results can be seen in Table 7.4.

Experiment No.	Set-up	Range: 0 to 127
27	Default *3 bits*	100 % 21.4 961 tests
28	Default *5 bits*	100% 19.8 891 tests
29	Default *7 bits*	100% 17.2 774 tests
30	Random Testing	100% 199.4 8975 tests

Table 7.4: Results of DIRECT_SORT using record type of character and integer.

As can be seen from Table 7.4, the results are similar to the results of the experiments when integers are used as the *scalar_type*. The record is handled like a one bit string. The option *bits* define how many bits of the bit string should be used for the weighted mutation. In addition the MSB is not used.

7.7 Interim Conclusion

Like in all other procedures under test, it is only a few nodes for which it is difficult to find test data. In this case it is node 41. The condition for this node is that the number of the elements to be sorted should be at least 11. In addition the elements have to be

sorted in such a way that the element which is at the middle position of the array section, has a value, so that all elements with a lower array index have a smaller value and all elements with a higher array index have a bigger value. All other nodes are traversed with test data normally being generated in two generations.

The experiments and results have shown that the GAs achieved better results than random testing. This can be up to 13 times better with respect to the number of tests. However, when the set-up is not correctly chosen, it could mean that a lot more tests have to be performed before full branch coverage is achieved (e.g. experiment 25 with over 40000 tests). This is the case when a record is used as the *scalar_type* and the converted bit string is used as one single string for crossover and mutation because of the representation of the test data which is in the two's complement for negative values and for positive values in the ordinary binary code with sign and magnitude format. This happens because the conversion procedure CONTROL_PARENT and the weighted mutation cannot be used because the record is treated as a one bit string. This means that the binary and the two's complement coded bit strings are used in crossover which leads to completely different offspring so that the optimising process is slower and gives worse results. As soon as only a positive initial range is chosen (0 to 200) for the integer type (key element) the results improve and in addition by increasing to '*10 bits*' the results are similar to experiment 20 where only one integer type forms the *scalar_type*.

The easiest way would be when the testing tool automatically identifies the structure of the data type so that it determines where the single bit strings of each variable begin and end, so that all facilities of the testing tool can be used. This can be achieved by the attributes 'position, 'first_bit and 'last_bit.

In the next chapter the generated test sets and testing tool are under investigation to measure the test data adequacy.

CHAPTER 8

Adequate Test Data

The objective of this chapter is to portray the sets of experiments carried out to measure the adequacy of the test data generated by the testing tool with respect to error detection. In the previous chapter branch testing is used in order to satisfy the test criteria. This strategy proves to be especially difficult when the equality operator is used in the procedure under test.

The experiments described in this chapter demand that every branch is not only executed, but also that the test data sets are located close to the subdomain boundary, so called boundary test data. The advantage of boundary test data is that the test data should be as close as possible to the predicates (functions or conditions). Most software errors are at these boundaries, Clarke [1976] and White and Cohen [1980], which are also called domain errors.

The technique used to measure if the test data is adequate is based on mutation analysis. Mutation analysis is a fault based testing method which derives test cases (mutants) and is devised to find particular types of errors. This section describes problems that have been solved developing the implementation of the technique and the success rate of producing the boundary test data.

8.1 Adequacy of Test Data

Test adequacy refers to the ability of the test data to ensure that certain errors are not present in the program under test, i.e. that the program runs successfully on the data set and all incorrect programs run incorrectly, DeMillo [1987]. However, by showing that these errors do not occur, does not guarantee the absence of all errors, Weyuker [1983].

The definition of adequacy in relation to test data can be defined as the close proximity of the data to a subdomain boundary, see chapters 2 and 4. Boundary test data has a better likelihood of revealing and detecting errors, in contrast to test data which are far from the boundary, as it was observed by Clarke [1976].

8.1.1 Subdomain boundary test data

Subdomains have previously been explained in chapter 2. A subdomain boundary is the border between subdomains which is determined by the predicates of the path. There are different kinds of subdomain boundaries, such as *open* and *closed borders*, described by White and Cohen [1980]. Which kind depends on the relational operator in the predicate. Although an open border forms a part of the boundary domain, it does not, however, belong to it and it is achieved by ' < ', '>' or '≠' operators. A closed border is actually part of the domain and is created with ' ≤' , ' ≥ ' or ' = ' operators. Figure 8.1 displays such a change from an open boundary (' > ') to an closed boundary (' ≥ '). The change of the operator results in a boundary shifting effect being produced.

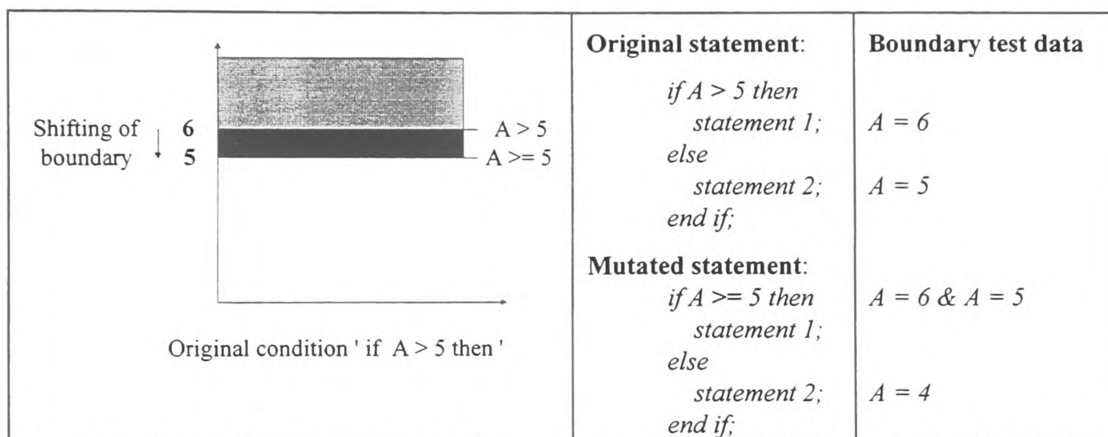


Figure 8.1: Original and mutated statement causing shifting of subdomain boundary.

This shifting of the boundary might not be revealed with normal branch test data, which could be anywhere in the subdomain. When test data are close to the subdomain boundary of both border segments and executed correctly, it can be concluded that the relational operator and the position of the border are correct. Only this kind of test data can reveal incorrect shifting of the boundary. In the case of the original condition (if $D > 5$ then) a test data of A = 6 would traverse the true branch (statement 1) and a test data of A = 5 the false branch (statement 2). Putting this test data into the mutant, would result in both cases the true branch being executed. The second set of test data, i.e. A = 6, would reveal the error because, corresponding to the original condition, it would take the wrong branch (else branch) and so execute statement 1. These values (5 and 6) are the boundary test data and are most likely to reveal errors.

8.2 Mutation Testing and analysis

In this section a mutation testing strategy is used as a measurement and for evaluation of the level of adequacy of the test data that can be achieved by the testing tool, using GA and the random method. It can be said that a test set is adequate if it can distinguish between the original test program and the set of incorrect mutated programs which are represented by faults. The goal of mutation testing is to generate test data which reveals or kills the mutants which simulate typical program errors, Burns [1978].

8.2.1 Overview of mutation analysis

Mutation analysis is a fault-based analysis and is a testing method that measures the adequacy of a set of independently created test data. Mutation testing tests for specific and particular types of faults and have been made to the original program by simple syntactic changes. These mutants reflect common mistakes which are generally introduced by competent programmers. The set of faults is commonly restricted by two principles; the *competent programmer hypothesis* and the *coupling effect.*

The competent programmer assumption states that competent programmers tend to write programs that are *close* to being correct. The restriction of the mutants to single errors is justified by the principle of the coupling effect which states that simple types of faults are sensitive enough to detect more complex types of faults. Both assumptions are experimentally confirmed, Budd *et al.* [1980] and Offutt [1989, 1992].

8.2.2 Detection of mutants

To detect a mutant, it is obvious that the mutated statement must be executed. Furthermore, the test data has to cause the mutant to produce an incorrect status after execution of the mutated statement with respect to the original program. Although the status after execution of the mutated statement is different compared to the original statement, it is not sufficient to kill the mutant. The status has to propagate through to an output, to reveal the fault, in order to kill the mutant. If the status of both versions, the mutated and original program, after the last executed statement is unchanged, then the mutant is still alive. The essential condition to kill a mutant is, therefore, the request that the status of the mutated program is incorrect after some execution of the mutated

statement. The status does not have to be specifically incorrect after either the first, or last execution, but it should be incorrect after some execution, DeMillo [1993].

Mutation testing can show two things. The percentage of dead mutants reveals how well the program has been tested. On the other hand, the live mutants reveal either inadequacies in the used test data set, which reflects on the test data generator (testing system) or that the original program is incorrect. The presence of live mutants have thus revealed these faults. If there are live mutants present, then new test data has to be added until the program tester is satisfied with the proportion of dead mutants.

For example, looking at the quadratic equation solver problem which is correct to the best of our knowledge, node 1 (see page 5-1) mutated from $A = 0$ to $A = 1$, produces for the test data $A = 1$, $B = 1$ and $C = 1$ the following output 'Error_not_a_quadratic' (node 2). This test data is then put through and compared to the original program where the output produces: 'Roots_are_real_and_unequal' (node 4) and the mutant is, therefore, revealed.

In practice it is impossible to reveal and kill all mutants of a program especially when the changes have no functional effect. These mutants are called *equivalent mutants*. This occurs when the outputs of both programs are always the same. These mutants have to be detected manually and this is one of the most expensive of all current mutation systems as stated by Offutt [1992]. For example, if the condition in node 6 is mutated from $D = 0$ to $D \geq 0$, no difference can ever be found, because only zero and negative values for D can go this way due to the fact that the condition in node 5 filters out all positive values for D ($D \leq 0$). The same output will invariably be produced as in the original program.

If test data can reveal a high percentage of mutants, it can be said the test data is of high adequacy (near to the sub domain boundary) and that its likely that the original program is correct, Budd *et al.* [1980]. The detection rate, mutation score (MS), of a set of test data using non-equivalent mutants can be expressed by the definition;

$$MS(T) = \frac{K}{M - E} \tag{8.1}$$

where M is the number of mutants

E is the number of equivalent mutants

K is the number of mutants which are killed by the test data set T.

An adequate mutation score for a test data set achieves 100%, which means that all non-equivalent mutants are killed. Offutt [1992] suggested that a mutation score of 95% is sufficient to be effective for findings errors, i.e. the program has been thoroughly tested and that most of the errors are revealed, which fulfils the mutation adequacy criteria.

Mutants are an expression of programmer's faults, DeMillo [1978]. If it is possible to generate every possible error a programmer can make and to create mutated programs for all these errors, then passing them through the mutation testing would be enough to ensure the correctness of the original program. With a few exceptions, it would be unrealistic to assume that it is possible to construct all possible errors. Therefore, a small sub set of mutants are chosen, which can then be used to measure the sensitivity of the test data to small changes in the original program. These mutants are not just randomly generated, they are carefully chosen to evaluate the quality of test data.

8.2.3 Construction of mutants

Mutants are constructed by various methods, e.g. replacing an operator by all other operators of the same type (relational (e.g. <, >, =), logical (e.g. and, or, xor), arithmetic (+, -, *, /)) which creates a syntactically correct program. Furthermore, relational and logical conditions can be replaced by the constants '*true*' and '*false*'. Using arithmetic and relational conditions, the sub-expression can be substituted by exchange, e.g.:

'$A > B$' for '$B > A$'.

After testing the software with a large number of well generated test data and when no error is detected during extensive executing of the program, then it is reasonable to believe that the program is correct. However, there may still be a chance that the program is incorrect. Budd [1981] mentioned that the programmer has to live with less assurances of total correctness. Budd categorised the different mutants into 4 different levels in terms of levels of analysis.

The first level describes *statement analysis* which ensures that every branch is traversed

and that all statements are doing a useful and necessary task. This is achieved by deleting or replacing a condition, (e.g. *'if A = 0'* becomes *'if TRUE'*). In order to check whether all statements in the software are essential and performing a useful task, each statement is systematically deleted and replaced with a *null* statement in Ada. If the deletion of a statement has no effect on the output of the program, either it is unnecessary, which means a waste of computational effort, or worse it could indicate a much more serious error.

The second level deals with *predicate analysis* which exercises the predicate boundaries by altering the predicate and sub-expressions by a small amount e.g. *'if D = 0'* becomes *'if D = 1'*. Absolute value operators are inserted, e.g. *'if D > 0'* becomes *'if abs(D) > 0'*, and relational operators are altered, e.g. *'if A = 0'* becomes *'if A /= 0'*. Level three describes *domain analysis* which exercises different data domains. This is achieved by changing constants and sub-expressions by a small amount and inserting absolute value operators wherever syntactically correct. An example of this is altering line 9 of the QUADRATIC procedure from '$D = B^2 - 4AC$' to '$D = abs(B^2 - 4AC)$'. The fourth and last level deals with coincidental correctness analysis, which guards against coincidental correctness and is accomplished by changing data references and operators to other syntactically correct alternatives. An example of this is altering line 6 from '*if* $A = 0$ *then*' to '*if* $B = 0$ *then*'.

8.3 Application of mutation testing to measure test data efficiency

Mutation testing is used in this investigation to measure the efficiency and adequacy of the test data generated for the procedure under test. The original program, e.g. the quadratic equation solver, is manually mutated in several ways, according to the mutation levels introduced by Budd [1981], and then re-compiled. The method of application of mutation testing differed slightly from the method described above. The intention is not to reveal errors in the original procedure, since to the best of our knowledge it is correct but to classify the effectiveness of the testing tool.

Test data are generated for the mutated program until all branches are executed with boundary test data. These branch test data are then put through the original program, one

at a time. When the output of this test data gives a different result, or a different branch of the original program is executed compared to the mutant, it is concluded that the mutant has been killed and the test data is of a high quality and efficiency.

The test data sets that are generated and found to reveal a mutant, are not re-used, Holmes [1993]. The reason for reusing of test data is that the test data will be tied very closely to the boundaries of the predicates and functions in the original procedure. The non re-use option is chosen in order to make it more difficult for the test data generation method with each and every mutant. This provides us with the necessary opportunity to measure the adequacy of the test data generated. Thus, the strengths and weaknesses of the test data generating method can be explored.

8.3.1.1 Different mutants

The first 14 mutants are of the form of statement analysis which is the first level of analysis in the proposed mutation testing system of Budd [1981]. They can be seen in Table 8.1 where the *Line No*, the *Original statement* and the *Mutated statement* are shown. Eight out of these 14 mutants delete some statements. The other six mutants replace relational operator with '*true*' and '*false*'.

Mutant No.	Line No.	Original statement	Mutated statement
1	7	Quad := Error_not_a_quadratic;	null;
2	11	Quad := Roots_are_real_and_unequal;	null;
3	14	Quad := Roots_are_real_and_equal;	null;
4	16	Quad := Roots_are_complex;	null;
5	9	$D = B^2 - 4AC$;	null;
6	6 - 19	if ... end if;	null;
7	10 - 18	if ... end if;	null;
8	13 - 17	if ... end if;	null;
9	6	if A = 0 then	if true then
10	6	if A = 0 then	if false then
11	10	if D > 0 then	if true then
12	10	if D > 0 then	if false then
13	13	if D = 0 then	if true then
14	13	if D = 0 then	if false then

Table 8.1: First level of mutation analysis: Statement Analysis.

In the predicate analysis a total number of 24 mutants are created which can be seen in Table 8.2. Six mutants alter the predicate by a small amount (for the variables A and D). Three mutants describe the insertion of absolute value operators (abs) into the predicate

sub-expressions. The remaining 15 mutants display the alteration of relational operators.

Mutant No.	Line No.	Original statement	Description of mutant
15	3	A = 0	A = 1
16	3	A = 0	A = -1
17	7	D > 0	D > 1
18	7	D > 0	D > -1
19	14	D = 0	D = 1
20	14	D = 0	D = -1
21	3	A = 0	abs(A) = 0
22	7	D > 0	abs(D) > 0
23	14	D = 0	abs(D) = 0
24	3	A = 0	A /= 0
25	3	"	A > 0
26	3	"	A >= 0
27	3	"	A < 0
28	3	"	A <= 0
29	7	D > 0	D <= 0
30	7	"	D < 0
31	7	"	D /= 0
32	7	"	D = 0
33	7	"	D >= 0
34	14	D = 0	D /= 0
35	14	"	D > 0
36	14	"	D >= 0
37	14	"	D < 0
38	14	"	D <= 0

Table 8.2: Second level of mutation analysis: Predicate Analysis.

Table 8.3 shows 13 mutants that are created from the third level of mutation testing, i.e. the domain analysis. These mutants are produced by inserting the absolute value operator (abs) into the equation where D is evaluated (line 9; $D := B^2 - 4AC$) and by changing the sub-expressions by small amounts.

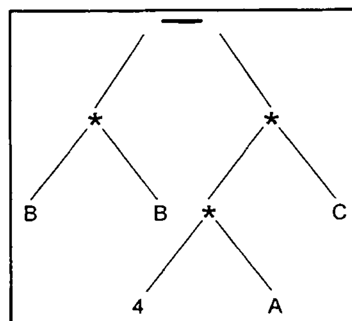


Figure 8.2: Definition of sub-expression for the quadratic equation solver problem.

Figure 8.2 shows the definition of sub-expressions. The variables are connected by the arithmetic operators, in these cases by '-' and '*'. The sub-expressions 'B' are not taken

for creating mutants in order to restrict the number of mutants.

Mutant No.	Line No.	Original statement	Description of mutant
39	9	$D = B^2 - 4AC$	D = abs(B^2) - 4AC
40	9	"	$D = B^2$ - abs(4AC)
41	9	"	D = abs(B^2 - 4AC)
42	9	"	$D = B^2$ - abs(4A)C
43	9	"	$D = B^2$ - 4A abs(C)
44	9	"	$D = B^2 - 4AC - 1$
45	9	"	$D = B^2 - 4AC + 1$
46	9	"	$D = B^2 - (4 - 1)AC$
47	9	"	$D = B^2 - (4 + 1)AC$
48	9	"	$D = B^2 - (4A - 1)C$
49	9	"	$D = B^2 - (4A + 1)C$
50	9	"	$D = B^2 - 4A(C - 1)$
51	9	"	$D = B^2 - 4A(C +1)$

Table 8.3: Third level of mutation testing: Domain Analysis.

The fourth level of mutation analysis deals with coincidental correctness analysis. Table 8.4 refers to these mutants. The mutants are made by changing the data references (e.g. exchange the variable A for variable B) and by changing an operator (e.g. '-' to '+'), which counts for 15% of all non-syntax errors in software, DeMillo [1989].

Mutant No.	Line No.	Original statement	Description of mutant
52	6	if A = 0 then	if B = 0 then
53	6	"	if C = 0 then
54	6	"	if D = 0 then
55	10	if D > 0 then	if A > 0 then
56	10	"	if B > 0 then
57	10	"	if C > 0 then
58	13	if D = 0 then	if A = 0 then
59	13	"	if B = 0 then
60	13	"	if C = 0 then
61	9	$D = B^2 - 4AC$	$D = A^2 - 4BC$
62	9	"	$D = C^2 - 4AB$
63	9	"	$D = B^2 + 4AC$
64	9	"	$D = B^2 \times 4AC$
65	9	"	$D = B^2 - 4A - C$
66	9	"	$D = B^2 - 4A + C$
67	9	"	$D = B^2 - 4 - AC$
68	9	"	$D = B^2 - 4 + AC$
69	9	"	$D = (B - B) - 4AC$
70	9	"	$D = (B + B) - 4AC$

Table 8.4: Fourth level of mutation testing: Coincidental Correctness Analysis.

All 70 mutants are compiled and test data are generated in order to execute every branch in the mutated program. The results and outputs are then compared with the original results and outputs.

Since the GA and random tool box are only generating test data in order to traverse each branch, they would not be suitable for mutation testing. There may be many test data in a subdomain which could prove to be satisfactory in traversing branches, but only a limited amount of boundary test data can reveal shifting of boundaries. For this reason the program testing tool is expanded, and altered in the sense that boundary test data have to be generated. The advantage of using boundary test data is that there is a higher chance of revealing errors, the disadvantage being that the search procedure for boundary test data may be longer.

Boundary test data generation is achieved by looking at one node until the predicate of the node is traversed as closely as possible. This means that the node is not set to be traversed with any possible test data set from the sub domain. It is only set to be traversed when the boundary test data of a predicate is generated or a certain number of attempts (generations) are completed. For each node the fittest test data is stored in the database.

The criterion for this new method is that the branch is only set to be traversed when the highest possible fitness (boundary test data) is achieved, where the fitness values are directly evaluated by the predicate conditions. To traverse a node with boundary test data, a certain number of generations (tests) can be pre-defined (similar to a threshold) for the node. The pre-defined generations can be used just for observing this node in order to get closer to the boundary of the predicate. If no boundary test data are produced, after using the certain number of pre-defined generations (this can vary from node to node), the test data with the highest fitness will be taken instead which is automatically stored in the data base.

The counting of the pre-defined generations only starts when the testing tool is actually searching and trying to traverse that particular node. If the test data traverses a node which is not under investigation, then the test data is stored if it has a higher fitness than the data already in the database.

8.3.1.2 First mutation results

In the initial experiment of mutation testing, boundary test data are generated in order to

traverse all branches of the mutated procedure under test. After test data are generated for all the branches and stored, they are put through the original procedure. Any difference in the expected and actual output from the mutant kills that mutant.

The first test runs show that no test data are generated for node 7 (D < 0) with $D = -1$. Since no integer combination of A, B and C exist to give a value of $D = -1$ or $D = -2$ the boundary test data is $D = -3$; the testing tool always exceeds the pre-defined number of generations for node 7 and abandoned the run for this node because the system does not look for a $D = -3$. A new stopping condition is introduced in order to avoid many unnecessary tests. This is due to the fact that the boundary test data of $D = -3$ could have been already generated without realisation, thereby resulting in the testing tool still performing a search for the value of $D = -1$. This new condition stops the specific search of a test data for a certain node if the fitness reaches a certain threshold. Therefore, after a certain number of generations, it is assumed that the test data are close enough to the boundary of the subdomain. This means a decrease in the number of generations and a better comparison between the use of random and GA methods of generating of test data.

Two strategies are adopted using mutation testing. In order to perform mutation analysis two procedures of the same kind are used; the original procedure and the mutated procedure. Test data are always generated for the procedure under test. In one case, the data are produced for the mutated procedure and then in the next experiment for the original procedure. The answer to the question here is to find out how robust are GAs to reveal the mutants, in other words can GAs generate adequate test data (hypothesis 4) and for which, the original or the mutant, the test data should be generated for. As it can be seen later generating test data for the original program is better than for the mutant.

From all 70 mutants, 6 mutants could not be revealed at all and 14 mutants are only partly revealed (success rate between 42% and 99%) when test data are generated for the mutant. On taking a closer look at the six unrevealed mutants, the result is that four of them (mutants 21, 23, 36 and 39) are *equivalent mutants* which means that they always produced the same output as the original procedure. That means they could not be distinguished by their functionality. Thus only two mutants are not revealed at all

(mutants 26 and 28).

Therefore, the mutation score is $MS = 0.97$ (97%) when including the partly revealed mutants. This is in excess of Offutt's stated sufficient mutation score threshold of 95%. The reason why the two mutants could not be revealed is because the predicate for node 2 is changed from $A = 0$ to $A \geq 0$ (mutant 26) and $A \leq 0$ (mutant 28). Since boundary test data are generated, the testing tool would generate the value $A = 0$ for node 2 in the mutant and the original program. The only difference at this point is that only negative values are used for the rest of the program to traverse the remaining nodes. The boundary does not shift. This kind of error could not be revealed with the current method.

However, generating test data for the original procedure, only mutant 40 could not be exposed besides the four equivalent mutants and 13 mutants are only partly revealed with variations of 33% to 97% success of the test runs.

8.3.1.3 Improving the testing tool with regard to mutation testing

In order to achieve a better mutation score (which means to kill the unrevealed and partly unrevealed mutants) more boundary test data have to be generated. Where '=' (equal) or '/=' (unequal) operators are used, two sets of boundary test will be generated on both sides of the subdomain boundary, see chapter 4. For all other predicates only one boundary test has to be produced. That means, for node 3, two boundary test data has to be generated and stored for each side of the border in order to traverse this node successfully. In addition the strategy of the mutation testing is changed in the sense that every test data which is put through the procedure under test and produced an output, has to be entered straight away into the original procedure in order to compare the output. If any difference in the output is noticed, the mutant would be instantly killed and the test run stops in order to start the next test run. This should give information of how many generations are actually needed in order to reveal the mutants and to compare the results with a random testing.

Four different sets of mutation testing experiments have been conducted. In the first set of experiments test data are generated for the mutated procedure. Therefore, the fitness

functions are adapted for the mutant. The second column of the results tables (*GA mutant in test procedure*, e.g. Table 8.5) refers to the results of this experiment. The second experiment (third column: *Random mutant in test procedure*) uses a random number generator in order to generate the test data. Columns four (using GA), and five (using random), display the results of a different approach. This time, boundary test data sets are generated for the original procedure, and then these are put into the mutant. This should show whether boundary test data are important, what kind of influences these have regarding the software, and for which procedure, mutant or original, it is better to adapt the generation of test data. The results are displayed as the percentage of successful test runs and number of required tests.

8.3.1.4 Test results

Using this new method, all non-equivalent mutants are revealed in less than or about 1344 tests using both GA approaches, which corresponds to a mutation score of 100%. Each mutant runs 1000 times in order to get a good statistical result of how many generations are needed. Table 8.5 displays the results for the statement analysis, Table 8.6 refers to predicate analysis, Table 8.7 shows the results of domain analysis and Table 8.8 shows the results of the coincidental correctness analysis. Displayed in the tables below are the percentage of revealed mutants in test runs and the required number of tests.

In the first set of experiments in the statement analysis all mutants are revealed by using GAs. Only two of the mutants (3 and 14) required about 1340 tests. The other non-equivalent mutants are revealed in the first or second generation. These mutants are also easily revealed by random testing, where boundary test data are not necessarily needed. However, random testing achieves much worse results for mutants 3 and 14 (about 7060 tests) which is shown in Table 8.5.

Mutant No.	GA mutant in test procedure	Random mutant in test procedure	GA mutant in original proc.	Random mutant in original proc.
1	100% in 144	100% in 202	100% in 142	100% in 194
2	100% in 3	100% in 3	100% in 3	100% in 3
3	100% in 1320	99.4% in 7536	100% in 1373	99.6% in 6874
4	100% in 4	100% in 4	100% in 4	100% in 4
5	100% in 3	100% in 3	100% in 3	100% in 3
6	100% in 10	100% in 10	100% in 3	100% in 3
7	100% in 3	100% in 3	100% in 3	100% in 3
8	100% in 4	100% in 4	100% in 4	100% in 4
9	100% in 3	100% in 3	100% in 3	100% in 3
10	100% in 138	100% in 203	100% in 140	100% in 204
11	100% in 4	100% in 4	100% in 4	100% in 4
12	100% in 3	100% in 3	100% in 3	100% in 3
13	100% in 4	100% in 4	100% in 4	100% in 4
14	100% in 1309	99.7% in 7076	100% in 1297	99.0% in 7152

Table 8.5: Results of statement analysis.

For each of these two mutants, the mutant can only be revealed by generating a test data which will result in $D = 0$ and traverse node 6, that explains the high number of required tests. Table 8.6 shows the results of predicate analysis.

Mutant No.	GA mutant in test procedure	Random mutant in test procedure	GA mutant in original proc.	Random mutant in original proc.
15	100% in 88	100% in 99	100% 95	100% 102
16	100% in 90	100% in 102	100% 96	100% 99
17	100% in 1133	99.1% in 4445	100% 1066	97.9% 4109
18	100% in 1354	99.2% in 7412	100% 1335	99.2% 6884
19	100% in 1334	99.8% in 7152	100% 1373	99.5 6893
20	100% in 1311	99.0% in 6989	100% 1364	99.3% 6788
21	0% in 4407 not detectable	0% in 19508 not detectable	0% 4445 not detectable	0% 19652 not detectable
22	100% in 4	100% in 4	100% 4	100% 4
23	0% in 4503 not detectable	0% in 19392 not detectable	0% 4359 not detectable	0% 19690 not detectable
24	100% in 3	100% in 3	100% in 3	100% in 4
25	100% in 3	100% in 4	100% in 3	100% in 4
26	100% in 4	100% in 4	100% in 4	100% in 3
27	100% in 4	100% in 4	100% in 3	100% in 3
28	100% in 4	100% in 4	100% in 3	100% in 4
29	100% in 3	100% in 3	100% in 3	100% in 3
30	100% in 3	100% in 3	100% in 3	100% in 3
31	100% in 4	100% in 4	100% in 4	100% in 4
32	100% in 3	100% in 3	100% in 3	100% in 3
33	100% in 1364	99.2% in 7103	100% in 1392	99.7% in 6807
34	100% in 4	100% in 4	100% in 4	100% in 4
35	100% in 1277	99.3% in 7162	100% in 1325	99.6% in 7383
36	0% in 4359 not detectable	0% in 18759 not detectable	0% in 4368 not detectable	0% in 19671 not detectable
37	100% in 4	100% in 4	100% in 4	100% in 4
38	100% in 4	100% in 4	100% in 4	100% in 4

Table 8.6: Results of predicate analysis.

In the predicate analysis three out of 24 mutants have been detected as equivalent mutants (mutants 21, 23 and 36). GAs require about 4370 tests to produce boundary test data for these mutants whereas random testing always needs over 19200 tests until it terminates the search. But the mutants are not revealed in either case. The number of tests required is in agreement with an experiment of just producing boundary test data using GA or random testing.

Six additional mutants (17, 18, 19, 20, 33 and 35) need several tests in order to be detected, the GA requires about 1050 - 1400 tests and random testing needs between 4000 - 7400 tests. In all except one of these cases the mutants are revealed as soon as a test data of $D = 0$ ($D = 1$ in the case of mutant 17) is generated.

Only in one case, mutant 17, less generations are needed for GAs and random testing with regard to the number of required tests. The mutant is revealed by inputs resulting in $D = 1$ while traversing node 5 in the mutated program, but node 4 in the original procedure. The generation of a combination of A, B and C giving $D = 1$ is more likely than D = 0 because there are about 1.7 times more solutions in the search domain in the range of ±100. All other 6 mutants are revealed when a test data set of $D = 0$ is generated. Table 8.7 displays the results of domain analysis.

Mutant No.	GA mutant in test procedure	Random mutant in test procedure	GA mutant in original proc.	Random mutant in original proc.
39	0% 4301 not detectable	0% 19373 not detectable	0% 4253 not detectable	0% 19230 not detectable
40	100% in 4	100% in 4	100% in 4	100% in 4
41	100% in 4	100% in 4	100% in 4	100% in 4
42	100% in 4	100% in 4	100% in 4	100% in 4
43	100% in 4	100% in 4	100% in 4	100% in 4
44	100% in 911	100% in 2546	100% in 864	100% in 2629
45	100% in 1207	99.1% in 7178	100% in 1361	99.5% in 7408
46	100% in 38	100% in 39	100% in 39	100% in 40
47	100% in 58	100% in 56	100% in 59	100% in 55
48	98.3% in 656	100% in 862	98.7% in 692	100% in 907
49	99.3% in 672	100% in 870	98.5% in 695	100% in 874
50	100% in 212	100% in 202	100% in 215	100% in 204
51	100% in 213	100% in 224	100% in 214	100% in 220

Table 8.7: Results of domain analysis.

One equivalent mutant is detected in mutant 39 out of 13 mutants of the domain analysis. An interesting point is noted in the results from the mutants 44 and 45 which

need a different number of generations. The mutants are created by changing D in small amounts i.e. by adding and subtracting the value 1 from D. By changing the function D, the subdomains for the different paths changes as well. That means that for traversing node 4 the new subdomain is $B^2 - 4AC > -1$ and for node 6, $B^2 - 4AC = -1$ in mutant 45. The latter corresponds to an unfeasible path because there is no combination that could match $D = -1$. The only test data which could reveal this mutant is a test data of $D = 0$ which causes node 4 to be traversed in the mutant, and node 6 in the original procedure. However, it appeared that mutant 44 can be killed with two different solutions, which result in fewer required generations. For node 4 the actual condition in the mutant is $B^2 - 4AC > 1$ ($D > 1$) and for node 6, $B^2 - 4AC = 1$ ($D = 1$) which would result in different nodes being traversed in both cases compared to the original procedure. Both paths are feasible, therefore, the probability of generating one of these solutions in order to reveal the error is higher than in mutant 45.

Mutants 48 and 49, which are created by changing the sub-expression '*4A*' by a small amount (-1 and +1), cannot always be revealed in all test runs. The reason for this event is that if the variable $C = 0$ the mutant cannot be killed. This leads to a zero solution ($B = C = 0$).

In the last set of mutation results, the coincidental correctness analysis, in Table 8.8, only three results are interesting enough to mention in more detail. These are the results of mutants 58, 59 and 61. These mutants originated by exchanging variable names with existing ones, (i.e. $D = 0$ into $A = 0$, $B = 0$ and $C = 0$).

By creating mutant 58, an unfeasible path is produced in node 6. The condition in node 6 of '*if* $A = 0$' cannot become true because zero values for A are not allowed after node 2 since they have already been filtered out. Only a test data of $D = 0$ which traverses the mutant node 7 is able to reveal the error, by traversing node 6 in the original procedure. This is reflected in the number of required tests (1340 tests).

Mutant No.	GA mutant in test procedure	Random mutant in test procedure	GA mutant in original proc.	Random mutant in original proc.
52	100% in 84	100% in 97	100% in 88	100% in 104
53	100% in 85	100% in 97	100% in 83	100% in 102
54	100% in 3	100% in 3	100% in 3	100% in 3
55	100% in 3	100% in 4	100% in 3	100% in 4
56	100% in 3	100% in 3	100% in 3	100% in 3
57	100% in 3	100% in 4	100% in 4	100% in 4
58	100% in 1344	99.4% in 7147	100% in 1388	99.6% in 6589
59	99.8% in 273	100% in 384	100% in 285	100% in 363
60	42.4% in 1360	86.4% in 7278	72.2% in 2228	92.4% in 7883
61	100% in 4	100% in 4	100% in 4	100% in 4
62	100% in 4	100% in 4	100% in 4	100% in 4
63	100% in 3	100% in 3	100% in 3	100% in 3
64	100% in 3	100% in 3	100% in 3	100% in 3
65	100% in 4	100% in 4	100% in 4	100% in 4
66	100% in 3	100% in 4	100% in 4	100% in 4
67	100% in 8	100% in 9	100% in 8	100% in 8
68	100% in 3	100% in 3	100% in 3	100% in 3
69	100% in 9	100% in 9	100% in 10	100% in 10
70	100% in 9	100% in 9	100% in 9	100% in 9

Table 8.8: Results of coincidental correctness analysis.

Mutant 59 is revealed very quickly by generating negative values for D with the condition $B = 0$ which executes node 6 in the mutant. However, 2 out of 1000 test runs could not reveal the error in the mutant whereas 100% mutation detection rate is achieved by generating test data for the original.

Mutant 60 is by far the most difficult mutant to reveal compared to the other ones. In order to traverse node 6 of the mutant, a certain value of test data have to be found in order to fulfil the criteria of $D \leq 0$ (node 5) and $C = 0$. This only happens when $B = 0$, because of the condition $D = B^2 - 4AC$. This has the effect that a test data of $D = 0$ is produced which also traverses node 6 in the original procedure. Since many zero solutions are generated, the mutant could not always be revealed because the testing tool tries to generate and prefer those test data where C is tending towards zero. Since the fitness of the test data in order to traverse node 6 is calculated in node 7, the premier task, therefore, is to optimise C to become 0. This results in high fitness values for small abs(C), but B has to decrease as well, because in order to execute node 7, D has to be at least or less than 0 ($D \leq 0$). Therefore, only one solution fulfils all of these requirements. This is when $C = 0$ with $D = 0$ and $B = 0$ which executes node 6 of the mutant and original procedure. The only test data which could reveal the mutant is a test

data which causes $D = 0$ with $C \neq 0$ and, therefore, $B \neq 0$, this causing node 7 to be traversed in the mutant and node 6 in the original. Mutant 60 is revealed in only 42.4% in all test runs. The mutant detection rate improves when the test data are generated for the original procedure (72.2%) because the target is then to generate *any* test data which cause $D = 0$ and not in addition $C = 0$. The results for the random testing method also improved by about 11% when test data is generated for the correct procedure and not for the mutant. Moreover, in both cases random testing have a higher detection rate, but it has to be paid for in the higher number of tests required. This is due to the fact that random testing has a better chance of producing a non zero solution since many more test data are generated until all branches are tested with boundary test data.

8.4 Interim conclusion

The results for the first set of experiments, where only the final boundary test data are used to put through the original procedure, turns out to be different depending on which procedure (mutant or original) the test data are generated for. In the first case two and 14 non-equivalent mutants have only partly been revealed (success under 100%), whereas, using the original as the procedure under test, one non-equivalent mutant is not revealed and 13 mutants are not always revealed. Thus, these results show that adaptive boundary test data generation for the original procedure is slightly better than for the mutant.

In the improved version of mutation testing every single test data is put through both procedures (mutant and original) and two boundary data have to be produced depending on the relational operator per node, resulting in all mutants being revealed except for four. These four mutants 48, 49, 59 and 60 are only partly revealed when the test data are generated for the mutated procedure. Only three mutants, mutant 48, 49 and 60, are only partly revealed when generating test data for the original procedure. The GA always requires fewer tests than random testing in order to complete the task of generating boundary test data and revealing the mutants.

All partly revealed mutants are revealed in at least 98% of all test runs except mutant 60. Including the partly revealed mutants a mutation score of 100% has been achieved, leaving aside mutant 60, a mutation score of about 99% is achieved. 62 out of 66 non-equivalent mutants are always killed in every test run which means strictly a mutation

score of 94% for generating test data for the mutant and 63 out of 66 (96%) for the original procedure being the procedure under test. This indicates again that generating test data for the original program is slightly better than for the mutant. This and the fact that GAs can generate adequate test data, confirms hypothesis 4.

When observing the results of these experiments, it can be seen that there is not much difference in these for the GA experiments (see columns 2 and 4). The same situation applies for random testing (see columns 3 and 5). For each procedure under test the boundary test data are generated separately (either for the mutant or original) and GAs have a better mutation detection rate in all cases except one, mutant 60. For this single mutant random testing proves to be better.

A way of increasing the detection rate is to compare in the mutant and the original other kinds of computational effects, e.g. intermediate calculations, which means monitoring statement executions during program testing. In this case, it means trying to monitor D for each calculation. This kind of analysis will lead to weak mutation analysis, derived by Foster [1980] and is related to ideas on circuit testing where the most widely studied physical faults of digital circuits errors are '*stuck at*' line faults. In the single fault model for circuits, test data are derived to reveal the presence or absence of gates which are stuck at 0 or 1.

Some of the mutant's effect is that they produce an overflow error because the integer value calculation of D is greater than the highest possible (2^{32}). This is due to the change of the function of D in some mutants, e.g. mutant 64 ($D = B^2 \times 4AC$). Thus the overflow error occurs just in the mutant and not in the original in this case. It can also be the other way round, e.g. mutant 69 ($D = (B - B) - 4AC$). The best example is mutant 5, where the calculation of D is replaced by a null statement, so that a calculation could not cause an overflow error in the mutant at all.

The results have shown that the attempt to generate test data automatically to satisfy the mutation adequacy criteria by revealing mutants can be achieved by using GA in most cases. They also show that the testing tool (GA) is suitable in producing boundary test data where it is necessary, in order to kill the mutants, whereas random testing needs many tests.

The most time consuming problem in these experiments is the generation of all these mutants since they are created and compiled manually. Howden [1982] mentioned that a software of m lines has an estimated m^2 mutants. This would imply about 400 mutants for the quadratic procedure. This would consume too much time for creating the mutants. Therefore, only a carefully selected number of mutants are tested.

In the next and last chapter the experiments and the testing tool are reviewed and conclusions are drawn from them.

CHAPTER 9

Review and Conclusion

In this chapter the thesis is summarised and conclusions are drawn from the results and analysis of the experiments.

9.1 Review of the project

The idea and objective of this research project was to investigate the effectiveness of test data generation using Genetic Algorithms. Therefore, a test harness was developed in order to apply branch, boundary and loop testing criteria which was to iterate a loop zero, one, two, and more than two times. Several experiments and test runs were carried out to measure the effectiveness of using GAs for generating test data and to verify hypotheses which have been listed in section 1_2. The effectiveness of the GA results were compared to the effectiveness of random testing with regard to the required number of tests and amount of CPU time used.

9.2 Summary

From the work reported in this thesis and from the results of the analysis of all experiments, a number of conclusions can be drawn. Hypothesis 2 was confirmed that there are standard sets of parameter settings for different features of the program under test. We have seen that the difficulty in choosing a good internal representation for the search space increases with its complexity. Similar care has to be taken to provide an effective feedback mechanism, called the fitness function. These and more issues are discussed in the following sections.

9.2.1 Operators

The idea of the various crossover operators is to try to achieve the recombination of above average genetic material from parents of above average fitness. All crossover operators share the same idea whereas they have considerably different mechanics. Experiments have shown that uniform crossover gave the best performance with regard

to the number of required tests and the success rate. Uniform crossover required up to 24% fewer tests for the QUADRATIC procedure, 32% fewer tests using the TRIANGLE classifier procedure and about 40% fewer tests for the REMAINDER procedure (confirming hypothesis 2_3). In general, the crossover operator was important for the optimisation process and combining good building blocks of parents. Experiments without the crossover operator showed for the QUADRATIC procedure a decrease in the GA's performance by requiring about 56% more tests which means that the building blocks are combining at a slower rate.

The mutation operators have a very important role. With a reduced or zero mutation rate the performance of test data generation decreased severely. For example for the QUADRATIC procedure, when the default P_m was reduced by a factor of 5, only 63% of all tests were successful in achieving full branch coverage instead of 100% with the default $P_m = \frac{1}{S}$ (confirming hypothesis 2_5). Disruption of the chromosomes plays an important role for the GA with the intention of creating better building blocks. In the right quantity, disruption prevents premature convergence and loss of genetic material and thus preventing being stuck at a local optimum. The weighted mutation operator which was involved when the population seemed to be stuck at a local optimum, plays a significant part in the optimisation process. In theory, as long as the mutation is active, it is guaranteed that every point in the space has a non-zero probability of being generated.

The selection and survival operators have shown how important they are. The survival of offspring into the next generation was always based upon their fitness value, whereas the selection for the crossover and mutation was performed either by corresponding to their fitness or randomly. This was dependent on the kind of search space (hypothesis 2_2). If there was only one global optimum to search for, the fitness based selection was superior, as for the linear and binary search, whereas the random selection performed better when many global optima were in the search space, e.g. for the quadratic and triangle classifier procedures.

9.2.2 Data types, fitness function and program structures

Several different data types were used for the various procedures under test such as integer, float and character variables and also in combinations with records and arrays. These different data types had no influence on the performance of the GA as long as the testing tool knew what kind of data structure and variables were used in order to utilise all its facilities. Two main fitness functions were used. The first is a simple numeric method which is based on a reciprocal function and which may be used only for simple data structures. Secondly a more general approach used a Hamming fitness function, weighted and unweighted, which had no problems in handling these data structures and types. Overall the Hamming fitness function turned out to be the most consistent and reliable fitness function in describing the fitness of the test data, whereas, the reciprocal fitness function favours too strongly smaller values of the test data.

Xanthakis *et al.* [1992] and Watkins [1995] have recently applied GAs to the testing problem and using different approaches of applying fitness function. Watkins uses fitness functions based on the number of times a particular path is executed. This means that the more often the same path is taken the lower will be the fitness value. In comparison with Watkin's system using the triangle classifier procedure our testing system achieved full coverage in less than a fifth of the number of tests. This can be explained by the nature of Watkins fitness functions which can irritate the system because a test set can be of very low fitness while it is very close to execute an untraversed branch. M. Roper from the University of Strathclyde (by private communication) uses as a fitness for an individual the coverage it achieves of the software under test. Unfortunately, no results are yet published or what kind of software under test have been used.

Different program structures such as '*if*' and '*loop*' conditions have been tested. In chapter 6 special emphasise was put onto generating test data for different number of iterations that a loop will perform (*zero*, *once*, *twice* and *more than twice*). GAs had no problems in doing this, so confirming hypothesis 3.

9.2.3 Representation; Gray vs. binary

The easiest form of representation was the binary format which was then converted into a sign and magnitude representation where the MSB was the sign bit. The binary representation achieved better results in connection with the Hamming fitness function. Whereas Gray coded chromosomes with the numerical reciprocal fitness function required fewer tests than binary format in accordance with hypothesis 2_1. Using Gray code and Hamming fitness could mean that the GA is too disruptive. Changing the LSB of a Gray coded represented chromosome would not result in changing the data type by one unit. It could be a very large change. Those changes of the LSBs are made by using the weighted mutation. Using Hamming fitness to calculate the fitness, resulted in a total breakdown of the performance measurement.

9.2.4 Adequacy criteria and mutation testing

In chapter 8 the adequacy of the test data generated by the testing tools was under investigation. A set of test data is considered adequate if a program behaves correctly on the test data but on incorrect programs behave incorrectly.

It was shown that the GA produced test data to distinguish the mutant from the original, and a mutation score of 100% was achieved, including partly revealed mutants. GAs are highly effective at generating boundary value tests, which was confirmed by mutation testing which confirms hypothesis 4.

9.2.5 Random testing vs. GA testing

The results of random testing and GA testing have been compared. GAs always required fewer tests than random testing and needed less CPU time when the density of the solutions were quite small. GA testing needed up to two orders of magnitude fewer tests than randomly generated test sets. It was shown that using GAs was more efficient than random testing and more effective in the generating test data, which justifies hypothesis 1. Random testing had major problems with generating test data where the equality operator was used (small solution sub-domains). The recorded CPU time per test data set is also a good indicator of the complexity of the software under test.

A further disadvantage of random testing over using GA is the fact, that if the random generated input test data range is producing test sets which are located in a wrong area, e.g. for the triangle in the range from -100 to 0, not all branches of the software are able to be traversed. Whereas using GAs there is always the probability on generating the required test sets. The only disadvantage being that GA required more CPU time per test data generation.

9.3 Conclusion

The overall aim was to develop a self-learning algorithm that has the ability to process and incorporate new information as the work environment changes (changing from one predicate to the next). The GAs give good results and their power lies in the good adaptation to the various and fast changing environments.

The primary objective of this project was to propose a GA-based software test data generator and to demonstrate its feasibility. The experimental results show that this was achieved. The main advantage of the developed testing tool is the strength of GAs, in that the relationship between the predicate under investigation and the input variables may be complex and need not be known. Instrumentation capture the actual values of the predicates, so that the fitness can be based on these values.

Although some of the procedures under test are small, they contain complex non linear branch conditions with complex data types which use nested '*if*' and '*loop*' conditions. It is these non linear problems where the GAs develop their strengths.

The quadratic procedure (chapter 5) was used to establish the feasibility of using GAs to generate test sets and to determine the most appropriate parameters for the GAs. The GAs were then applied to various larger and more complex procedures with different characteristics. All tests clearly show that the GA generated test data are significantly better than randomly generated data.

An automated oracle, which can determine whether or not a program has been correctly executed on a given test case, is required to evaluate large numbers of automatically generated test data sets. An oracle is important because branch coverage does not imply that the executed branches are correct, Müllerburg [1995]. Such an oracle can be

realised by post condition or formal specification. This can be achieved by for example post conditions. If post conditions are not available, a subset of test sets were chosen, which had the highest fitness value (close to the boundary) of each branch to reduce the number of test data to check.

The results using GAs can be improved by more research into the performance of the various operators and testing harness strategy in order to guide the test data generation process to the required branches and nodes to traverse. However, the results of using random testing cannot be changed, since the test data generation process does not depend on heuristics or algorithms. An advantage of this approach is that the test harness can easily be changed depending on the testing criteria without influencing the GAs.

The previous problems regarding software testing, mentioned in chapter 2, contrast with our GA testing tool which does not require any analysis or interpretation of the code so that in addition the form of the predicate need not be known, thus avoiding the problems with e.g. symbolic execution. Functions or procedures calls and dynamic data types are no problems for our system. The GA testing tool gets the predicate function value by suitable code instrumentation. These instrumentation statements keep a record of branches and statements that are executed during the testing of a program which do not affect the functional behaviour. Each time the program under test performs a significant event, the occurrence of that event is recorded in order to measure test coverage, Ince [1989].

GAs show good results in searching the input domain for the required test sets, however, other methods like simulated annealing or tabu search may be an effective testing tool, too. GAs may not be the answer to the approach of software testing, but do provide an effective strategy.

9.4 Contribution to published Literature

During the period of the research, details and results of this investigation have been reported and published in various conferences and journals. These are as follows:

I. Sthamer, H. - H., Jones, B. F. and Eyres, D. E., *Generating test data for ADA generic procedures using Genetic Algorithms,* Proceedings of ACEDC '94, PEDC, University of Plymouth, UK., pp. 134-140, 1995;

II. Jones, B. F., Sthamer, H. - H., Yang, X. and Eyres, D. E., *The automatic generation of software test data using adaptive search techniques*, Proceedings of third Int. Conf. on Software Quality Management SQM '95, Seville, pp. 435 - 444, 1995;

III. Jones, B. F., Sthamer, H. - H. and Eyres, D. E., *Generating test data for ADA procedures using Genetic Algorithms*, GALESIA '95, IEE / IEEE International Conference on: Genetic Algorithms in Engineering Systems: Innovations and Applications; Sheffield University, September 1995, 65 - 70, 1995;

IV. Jones, B. F., Sthamer, H. H. and Eyres, D. E., *Genetic Algorithms : a new way of evolving test sets*, Eurostar '95, 27 - 30 November, Olympia Conference Centre, London, UK, 24/1 - 24/10, 1995;

V. Jones, B. F., Sthamer, H. H. and Eyres, D. E., *Use of genetic algorithms to generate test data automatically*, Software Engineering Journal, accepted;

9.5 Further studies

One major aspect of future work is to develop new operators which make the search and optimisation process easier and faster. New crossover and mutation operators are under investigation. Operators such as crossover, mutation, selection and survive procedures have to evolve or adapt their probability with the search space (fixed parameters should be avoided). This would improve and automate the parameter settings for the GAs which makes it easier to run.

Although the instrumentation of the procedures under test is straight forward and corresponds to fixed rules, an automated tool to insert those procedure calls would considerably simplify the entire process.

Although the instrumentation of the procedures under test is straight forward and corresponds to fixed rules, an automated tool to insert those procedure calls would considerably simplify the entire process.

A new approach to using GA is using them in parallel such as it is in nature, Hesser and Männer [1990], Cohoon *et al.* [1987] and Prettey *et al.* [1987] who mentioned that they have a distinctive advantage because for example the population is split into several smaller sub populations. Depending on the method these sub populations can then exchange genetic material or entire chromosomes to form a new population. The parallel GAs are distinguished by their faster searching because now these sub populations can explore the search space more thoroughly.

Data flow analysis may be used to identify those variables which are involved in the search process, so that only those will be used in order to cut down the CPU time as is the case in the triangle classifier and the remainder procedure. Some branches of these procedures need only one input variable out of several to traverse them.

An automated module for identifying the test data type may be introduced in order to distinguish different types. This will automatically identify the bit strings belonging to one data type so that the CONTROL_PARENT and W_MUTATE can work properly.

REFERENCES

'ADA Language Reference Manual, ANSI/MIL-STD-1815A-1983', 1983

Ablay P.: 'Optimieren mit Evolutionsstrategien', Spektrum der Wissenschaft, July 1987

Allen P. M. and Lesser M. J.: 'Evolution: Traveling in an Imaginary Landscape', Parallelism, Learning Workshop on Evolution and Evolution Models and Strategies;Neubiberg, Germany, pp. 419-441, March 1989

Baker J. E.: 'Adaptive Selection Methods for Genetic Algorithms', Proccedings of the first international Conf. on Genetic Algorithm and their Applications, pp. 101-111, 1985

Barnes, J. G. P.: 'Programming in ADA', Second Edition, London: Addison-Wesley, 1984

Bayer S. E. and Wang L.: 'A genetic Agorithm programming environment: Splicer', 3rd Intern. Conference on Tools for Artificial Intelligent [Cat.No.: 31ch30544] USA 1991; ISBN 0818623004, Part Nov, pp. 138-44, November 1991

Bayliss, D. and Taleb-Bendiab, A.: 'A global optimisation technique for concurrent conceptual design', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 179-184, 1994

BCS SIGIST (British Computer Society, Specialist Interest Group in Software Testing): 'Glossary of terms used in software testing, 1995

Beizer, B.: 'Software Testing Techniques', Second Edition, New York: van Nostrand Rheinhold, ISBN 0442206720, 1990

Bertolino, A.: 'An overview of automated software testing', Journal Systems Software, Vol. 15, pp. 133-138, 1991

Box, M. J.: 'A new method of constrained optimisation and a comparison with other methods', The Computer Journal, No. 8, pp. 42-52, 1965

Budd T. A., DeMillo R. A., Lipton R. J. and Sayward F. G.: 'Theoretical and empirical studies on using program mutation to test the functional correctness of programs', Proc of 7th Conf. on Principles of Programming Languages, pp. 220-233, 1980

Budd T. A.: 'Mutation Analysis: Ideas, Examples, Problems and Prospects', Computer Program Testing, SOGESTA 1981, pp. 129-148, 1981

Burns J. E.: 'Stability of test data from program mutation', In digest for the workshop on Software Testing and test Documentation, Fort Lauderdale, pp. 324-334, 1978

Caruana R. and Schaffer J. D.: 'Representation and Hidden Bias: Gray vs. Binary Coding for Genetic Algorithms', Proceedings of the 5th Int. Conf. on Machine Learning, pp. 153-161, 1988

Clarke L. A.: 'A system to generate test data and symbolically execute programs', IEEE Trans. on Software Engineering, Vol. SE-2, No. 3, pp. 215-222, September 1976

Clarke L. A. and Richardson D. J.: 'The application of error-sensitive testing strategies to debugging', ACM SIGSOFT/SIGPLAN, Vol. 8, No. 4, pp. 45-52, 1983

Cohoon J. P., Hegde S. U., Martin W. N. and Richards D.: 'Punctated Equilibria: A parallel Genetic Algorithm classifier system', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 148-154, 1987

Coward, P. D.: 'Symbolic execution systems - a review' Software Engineering Journal, pp. 229 - 239, November 1988

Dahl, O. J., Dijkstra, E. W. and Hoare, C. A. R.: 'Structured programming', Academic Press., 1972

Deason W. H., Brown D. B., Chang K.H.and Cross J. H.: 'A rule-based software test data generator', IEEE Transactions on Knowledge and Data Engineering, Vol. 3, No. 1, pp. 108-117, March 1991

DeJong, K. A.: 'Analysis of the behaviour of a class of genetic adaptive systems', Dept. Computer and Communication Sciences, Uni of Michigan, 1975

DeJong K. A.: 'Learning with Genetic Algorithms: An overview', Machine Learning 3, Vol. 3, pp. 121-138, 1988

DeJong K. A. and Spears W. M.: 'An Analysis of the Interacting Roles of poplation size and crossover in Genetic Algorithms', Internat. Workshop parallel problem solving from nature, Uni. of Dortmund, pp. 38-47, 1990

DeJong K. A. and Spears W. M.: 'A formal analysis of the role of multi-point crossover in genetic algorithms', Annals of Mathematics and Artificial Intelligence, Vol. 5, Part 1, pp. 1-26, 1992

DeJong K. A.: 'Genetic Algorithms are not function optimizers', Foundations of Genetic Algorthms, Whitley L, California, pp. 5-17, 1993

DeMillo R. A., Lipton R. J. and Sayward F. G.: 'Hints on test data selection: Help for the practicing programmer', IEEE Trans. on Computer, Vol. 11, Part 4, pp. 34-41, April 1978

DeMillo R. A., McCracken W. M., Martin R. J. and Passafiume J. F.: 'Software testing and evaluation', 1987

DeMillo, R. A.,: 'Test adequacy and program mutation', ACM, Vol. May, pp. 355-56, 1989

DeMillo R. A. and Offutt A. J.: 'Constraint-based automatic test data generation', IEEE Transactions on Software Engineering, Vol. 17, No. 9, pp. 900-910, September 1991

DeMillo R. A. and Offutt A. J.: 'Experimental results from an automatic test case generator', ACM Transactions on Software Engineering and Methodology, Vol. 2, No. 2, pp. 109-127, April 1993

Donatas K. and DeJong K. A.: 'Discovery of maximal distance codes using Genetic Algorithms', IEEE 2nd International Conf. on Tools for Artificial Intelligence [Cat. No.: 90CH2915-7], pp. 805-811, 1990

Donne, M. S., Tilley, D. G. and Richards, C. W.: 'Adaptive search and optimisation technique in fluid power system design', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 67-76, 1994

Duran, J. W. and Ntafos S., 'A report on random testing', Proceedings 5th Int. Conf. on Software Engineering held in San Diego C.A., pp. 179-83, March 1981

Duran J. W. and Ntafos S. C.: 'An Evaluation of Random Testing', IEEE Transactions on Software Engineering, Vol. SE-10, No. 4, pp. 438-444, July 1984

Eshelmann L. J., Caruana R. A. and Schaffer J. D.: 'Biases in the crossover landscape', Proceedings of the third International Conference on Genetic Algorithms, pp. 10-19, June 1989

Falkenauer E. and Bouffouix S.: 'A Genetic Algorithm for Job Shop', Proceedings of the 1991 IEEE International Conference on Robotics and Automation, Sacramento, Carlifornia - April 1991 [Cat. No.: 91CH29694], Vol. 1, pp. 824-9, 1991

Feldman, M. B. and Koffman, E. B.: 'ADA, problem solving and program design', Addison-Wesley Publishing Company, 1993

Foster K. A.: 'Error sensitive test cases analysis (ESTCA)', IEEE Transactions on Software Engineering, Vol. SE - 6, No. 3, pp. 258-264, May 1980

Frankl P. G. and Weiss S. N.: 'An experimental Comparison of the effectiveness of branch testing and Data Flow Testing', IEEE Transactions on Software Enginneering, Vol. 19, No. 8, pp. 774-787, August 1993

Fujiki C. and Dickinson J.: 'Using the Genetic Algorithm to generate lisp sopurce code to solve the prisoner's dilemma', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 236-240, 1987

Gallagher M. J. and Narasimhan V. L.: 'A software system for the generation of test data for ADA programs', Microprocessing and Microprogramming, Vol. 38, pp. 637-644, 1993

Geoges-Schleuter M.: 'ASPARAGOS: A parallel Genetic Algorithm and population genetics', Parallelism, Learning Workshop on Evolution and Evolution Models and Strategies;Neubiberg, Germany, pp. 407-419, March 1989

Girard, E. and Rault, F. C.: 'A programming technique for software reliability', IEEE Symp. Computer Software Reliability, pp. 44-50, 1973

Glover, F.: 'Tabu search - part I', ORSA Journal on Computing, Vol. 1, No. 3, pp. 190-206, 1989

Goldberg D. E.: 'Sizing populations for serial and parallel Genetic Algorithms', Proceedings of the 3rd Int. Conf. Genetic Algorithms, pp. 70-79, 1989

Goldberg, D. E.: 'Genetic algorithms in search, optimization and machine learning', Addison-Wesley Publishing Company, INC, 1989

Goldberg D. E. and Samtani M. P.: 'Enginnering optimization via Genetic Algorithm', Proceedings of the 9th Conference on Electronic Computation, pp. 471-82, Feb 1986

Graham, D. R.: 'Software testing tools: A new classification scheme', Journal of Software Testing, Verification and Reliability, Vol. 1, No. 2, pp. 18-34, 1992

Grefenstette J. J.: 'Optimazation of control parameters for Genetic Algorithms', IEEE Trans. on Systems, Man and Cybernetics, Vol. SMC-16,1, No. 1, pp. 122-128, February 1986

Grefenstette J. J. and Fitzpatrick J. M.: 'Genetic Search with approximate function evaluation', Proccedings of the first international Conf. on Genetic Algorithm and their Applications, pp. 112-120, 1985a

Grefenstette J .J., Gopal R., Rosmaita B. and Van Gucht V.: 'Genetic Algorithms for the Traveling Salesman Problem', Proccedings of the first international Conf. on Genetic Algorithm and their Applications, pp. 160-168, 1985b

Gutjahr W.: 'Automatische Testdatengenerierung zur Unterstuetzung des Softwaretests', Informatik Forschung und Entwicklung, Vol. 8, Part 3, pp. 128-136, 1993

Hamlet D. and Taylor R.: 'Partition testing does not inspire Confidence', IEEE Trans. on Software Engineering, Vol. 16, No. 12, pp. 1402-1411, December 1990

Hamlet, R. G.: 'Probable correctness theory', Information Processing Letters, Vol. 25, pp. 17-25, 1987

Hesser J. and Männer R.: 'An alternative Genetic Algorithm', Parallel Problem Solving from Nature: Proceedings of the first Workshop, PPSNI Dortmund, FRG, pp. 33-37, October 1990

Hills, W. and Barlow, M. I.: 'The application of simulated annealing within a knowledge-based layout design system', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 122-127, 1994

Hoffmann, K. H., M Christoph and M Hanf: 'Optimizing Simulated Annealing', pp. 221-225, 1991

Holland J.: 'Adaptation in natural and artificial systems', 1975

Holland, J. H.: 'Genetische Algorithmen', Spektrum der Wissenschaft, pp. 44-51, Sept 1992

Holmes, S. T., Jones, B. F. and Eyres, D. E: 'An improved strategy for automatic generation of test data', Proc. of Software Quality Management '93, pp. 565-77, 1993

Hooke, R. and Jeeves, T. A.: 'Direct search solution of numerical and statistical problems', JNL Assoc. Comp. Mach., Part 8, pp. 212-229, 1961

Howden W. E.: 'Methodology for the generation of program test data', IEEE Transactions on Computer, Vol. c-24, No. 5, pp. 554-559, May 1975

Howden W. E.: 'Reliability of the path analysis testing strategy', IEEE Transactions on Software Engineering, Vol. SE-2, No. 3, pp. 208-214, September 1976

Howden W. E.: 'Symbolic testing and the dissect symbolic evaluation system', IEEE Transactions on Software Engineering, Vol. SE-3, No. 4, pp. 266-278, July 1977

Howden W. E.: 'Weak mutation testing and completeness of test sets', IEEE Trans. on Software Engineering, Vol. SE-8, No. 4, pp. 371-379, July 1982

Huang J. C.: 'An approach to program testing', ACM Computer Surveys, Vol. 7, Part 3, pp. 113-128, 1975

Ince, D. C. and Hekmatpour, S.: 'An empirical evaluation of random testing', The Computer Journal, Vol. 29, No. 4, pp. 380, 1986

Ince, D. C.: 'The automatic generation of test data', The Computer Journal, Vol. 30, No. 1, pp. 63-69, 1987

Ince D. C.: 'Testing times for software', Computer Systems Europe, pp. 31-33, May 1989

Int Def ence Standard 00-55, Ministry of Defence, Directorate of Standardization, Kentigern House, Glasgow G2 8EX, 1991

Jin L., Zhu H. and Hall P.: 'Testing for quality assurance of hypertext applications', Proceedings of the third Int. Conf. on Software Quality Management SQM 95, Vol. 2, pp. 379-390, April 1995

Jog P., Suh J. Y. and Van Gucht D.: 'The effects of population size, heuristic crossover and local improvement on a Genetic Algorithm for the Traveling Salesman Problem', Proc. of the third Int. Con. on Genetic Algorithms, pp. 110-115, June 1989

King J. C.: 'Symbolic execution and program testing', Communication of the ACM, Vol. 19, No. 7, pp. 385-394, 1976

Korel B.: 'Automated software test data generation', IEEE Transactions on Software Engineering, Vol. 16, No. 8, pp. 870-879, August 1990

Korel B.: 'Dynamic method for software test data generation', Software Testing, Verification and Releliability, Vol. 2, pp. 203-213, 1992

Lucasius C. B. and Kateman G.: 'Understanding and using genetic algorithms; Part 1. Concepts, properties and context', Chemometrics and Intelligent Laboratory Systems, Vol. 19, Part 1, pp. 1-33, 1993

McMorran, A. and Nicholls, J. E.: 'Z User Manual', IBM UK Lab. Technical Report, 1989

Miller E.: 'Progrm Testing', IEEE computer, pp. 10-12, April 1978

Morell L. J.: 'A theory of fault-based testing', IEEE Transactions on Software Engineering, Vol. 16, No. 8, pp. 844-857, August 1990

Mühlenbein H.: 'Darwin's continent cycle theory and its simulation by the Prisoner's Dilemma', Complex Systems 5, Vol. 5, Part 5, pp. 459-78, 1991a

Mühlenbein H.: 'Parallel Genetic Algorithms, Population Genetics and Combinational Optimization', Parallelism, Learning Workshop on Evolution and Evolution Models and Strategies;Neubiberg, Germany, pp. 398-407, March 1989

Mühlenbein H., Schomisch M., Born J.: 'The parallel genetic algorithm as function optimizer', Parallel Computing (Netherlands), Vol. 17, Part 6-7, pp. 619-32, 1991b

Müllerburg, M.: 'Systematic stepwise testing: a method for testing large complex systems', Proceedings of the third Int. Conf. on Software Quality Management SQM 95, Vol. 2, pp. 391-402, April 1995

Myers: 'The Art of Software Testing', 1979

O'Dare, M. J. and Arslan, T.: ' Generating test patterns for VLSI circuits using a genetic algorithm', Electronics Letters, Vol. 30, No. 10, pp. 778-779, February 1994

Offutt A. J.: 'The coupling effect: Fact or Fiction?', ACM Sigsoft, pp. 131-140, December 1989

Offutt A. J.: 'Investigations of the software testing coupling effect', ACM Transactions on Software Engineering and Methodology, Vol. 1, No. 1, pp. 5-20, January 1992

Oliver I. M., Smith D. J. and Hollandt J. R. C.: 'A study of permutation crossover operatord on the Traveling Salesman Problem', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 224-230, 1987

Osborne, L. J. and Gillett, B. E.: 'A comparision of two simulated annealing algorithms applied to the direct steiner problem on networks', ORsa Journal on Computing, Vol. 3, No. 3, pp. 213-225, 1991

Ould, M. A.: 'Testing - a challenge to method and tool developers', Software Engieering Journal, pp. 59-64, March 1991

Parmee I. C. and Bullock G. N.: 'Evolutionary techniques and their application to engineering design', Plymouth, pp. 1-, 1993

Parmee, I . C. and Denham, M. J.: 'The integration of adaptive search techniques with current engineering design practice', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 1-13, 1994

Parmee I. C., Denham M. J. and Roberts A.: 'evolutionary engineering design using the Genetic Algorithm', International Conference on Design ICED'93 The Hague 17-19, August 1993

Parmee, I. C. and Purchase, G.: 'The development of a directed genetic search technique for heavily constrained design spaces', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 97-102, 1991

Pettey C. B., Leuze M. R. and Grefenstette J. J.: 'A parallel Genetic Algorithm classifier system', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 155-161, 1987

Ramamoorthy C. V., Ho S. F. and Chen W. T.: 'On the automated generation of program test data', IEEE Transactions on Software Engineering, Vol. 2, No. 4, pp. 293-300, December 1976

Rayward-Smith, V. J. and Debuse, J. C. W.: 'Generalized adaptive search techniques', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 141-145, 1994

Rechenberg, I.: 'Cybernetic solution path of an experimental problem', Royal Aircraft Establishment, Ministery of Aviation, Farnborough, Hants, Library Translation No. 1122, pp. 1-14, 1965

Reeves, C., Steele, N. and Liu, J.: 'Tabu search and genetic algorithms for filter design', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 117-120, 1994

Roberts, A. and Wade, G.: 'Optimisation of finite wordlength Filters using a genetic algorithm', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 37-43, 1994

Robertson G. G.: 'Parallel Implementation of Genetic Algorithms in a classifier system', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 140-147, 1987

Roper, M.: 'Software testing', International software quality assurance Series, 1994

Schaffer J. D.: 'Multiple objective optimization with vector evaluated Genetic Algorithms', Proccedings of the first international Conf. on Genetic Algorithm and their Applications, pp. 93-100, 1985

Schaffer J. D.: 'An adaptive crossover distribution mechanism for Genetic Algorithms', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 36-40, 1987

Schaffer J. D., Caruana R., Eshelman L. and Das R.: 'A study of control parameters affecting online performance of Genetic Algorithms for function optimization', Proceedings of the 3rd Int. Conf. of Genetic Algorithms, pp. 51-60, 1989

Schaffer J. D. and Eshelman L. J.: 'On crossover as an evolutionarily viable strategy', Proceedings of the fourth International Conference on Genetic Algorithms, pp. 61-68, July 1991

Schultz A. C., Grefenstette J. J. and DeJong K. A.: 'Adaptive testing of controllers for autonomous vehicles', Proceedings of the 1992 Sympo. on Auto. underwater veh. Technique, pp. 158-64, 1992

Schultz A. C., Grefenstette J. J. and DeJong K. A.: 'Test and evaluation by Genetic Algorithms', U.S. Naval Res. Lab. Washington D.C. USA, IEEE Expert, Vol. 8, Part 5, pp. 9-14, 1993

Schwefel H. P.: 'Understanding evolution as a collective strategy for groping in the dark', Parallelism, Learning Workshop on Evolution and Evolution Models and Strategies; Neubiberg, Germany, pp. 338-398, March 1989

Spears W. M. and Anand V.: 'A study of crossover operators in genetic programming', Methodologies for Intelligent Systems, 6th Intern. Symposium ISMIS'91, Charlotte,N.C. USA October 91, pp. 409-418, 1991

Spears W. M. and DeJong K. A.: 'On the virtues of parameterized uniform crossover', Proceedings of the fourth International Conference on Genetic Algorithms, La Jolla, Carlifornia, pp. 230-236, July 1991

Staknis, M. E.: 'Software quality assurance through prototyping and automated testing', Inf. Software Technol., Vol. 32, pp. 26-33, 1990

Sthamer, H.-H., Jones, B. F. nd Eryes, D. E.: 'Generating test data for ADA generic Procedures using Genetic Algorithms', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 134-140, 1994

Suckley D.: 'Genetic algorithm in the design of FIR filters', IEE Proceedings-G, Vol. 138, No. 2, pp. 234-238, April 1991

Syswerda G.: 'Uniform Crossover in Genetic Algorithms', Proceedings of the third International Conference on Genetic Algorithms, pp. 2-9, June 1989

Tai K. - C.: 'Program testing complexity and test criteria', IEEE Transactions on Software Engineering, Vol. SE - 6, No. 6, pp. 531-538, November 1980

Taylor R.: 'An example of large scale random testing', Proc. 7th annual Pacific North West Software Quality Conference, Portland, OR, pp. 339-48, 1989

Tennant A. and Chambers, B.: 'Adaptive optimisation techniques for the design of microwave absorbers', Proc. of ACEDC'94, PEDC, University of Plymouth, UK., pp. 44-49, 1994

Tsai, W. T., Volovik, D. and Keefe, T. F.: 'Automated test case generation for Program specified by relational algebra queries', IEEE Transactions on Software Engineering, Vol. 16, No. 3, pp. 316-324, March 1990

Tsoukalas M. Z., Duran J. W. and Ntafos S. C.: 'On some reliability estimation problems in random and partition testing', IEEE Transactions on Software Engineering, Vol. 19, No. 7, pp. 687-697, July 1993

Watkins, A. L.: 'The automatic Generation of Test Data using Genetic Algorithms', Conference proceedings Dundee, 1995

Watt D. A., Wichman B. A. and Findlay W.: 'ADA language and methodology', 1987

Weyuker E. J.: 'Assessing test data adequacy through program inference', ACM Transaction on Programming Languages and Systems, Vol. 5, No. 4, pp. 641-655, October 1983

White L. J. and Cohen E. I.: 'A domain strategy for computer program testing', In digest for the workshop on Software Testing and test Documentation, Fort Lauderdale, pp. 335-354, 1978

White L. J. and Cohen E. I.: 'A domain strategy for computer program testing', IEEE Transactions on Software Engineering, Vol. SE-6, No. 3, pp. 247-257, May 1980

Whitley D.: 'The GENITOR algorithm and selection pressure: Why rank-based allocation of reproductive trials is best', Proceedings of the third International Conference on Genetic Algorithms, pp. 116-121, June 1989

Wilson S. W.: 'The Genetic Algorithm and biological developmenturce code to solve the Prisoner's Dilemma', Proceedings of the second International Conf. on Genetic Algorithms and their Applications, pp. 247-251, 1987

Woodward M. R., Hedley D. and Hennell M. A.: 'Experience with path analysis and testing of programs', IEEE Transactions on Software Engineering, Vol. SE-6, No. 6, pp. 278-286, May 1980

Wright A. H.: 'Genetic Algorithms for real parameter optimization', Foundations of genetic algorithms: G J E Rawlins, pp. 205-218, 1991

Xanthakis S., Ellis C., Skourlas C., Le Gall A. and Katsikas S.: 'Application of Genetic Algorithms to Software Testing', 5th International Conference on Software Engineering, Toulouse, France, December 1992

Yang, X., Jones, B. F. and Eyres, D.: 'The automatic generation of software test data from Z specifications', Research Project Report III, CS-95-2, February 1995

Zeil, S. J., Afifi, F. H. and White, L. J.: 'Detection of linear errors via domain testing', ACM Transactions on Software Engineering and Methodology, Vol. 1, No. 4, pp. 422-451, 1992

Zhigljavsky, A.: 'Theory of Global Random Search', Kluwer Academic Publishers, The Netherlands, 1991

Appendix A

Software Listing of TRIANGLE classifier function

```
function TRIANGLE ( a,b,c : integer )
        return TRI_KIND
is
    procedure TRIANGLE_2(A, B, C:in integer)
    is
        procedure RIGHT_ANGLE_CHECK (A, B, C:in integer) is
        begin
        if ( ( ( A*A ) + ( B*B ) ) = ( C*C ) ) then
            TRI_KIND := RIGHT_ANGLE_TRIANGLE;
        else
            if ( ( ( B*B ) + ( C*C ) ) = ( A*A ) ) then
                TRI_KIND := RIGHT_ANGLE_TRIANGLE;
            else
                if ( ( ( A*A ) + ( C*C ) ) = ( B*B ) ) then
                    TRI_KIND := RIGHT_ANGLE_TRIANGLE;
                else
                    TRI_KIND := TRIANGLE;
                end if;
            end if;
        end if;
        end RIGHT_ANGLE_CHECK;
    begin  -- Triangle_2
    if ( A = B ) then
        if ( B = C ) then
            TRI_KIND := EQUILATERAL_TRIANGLE;
        else
            TRI_KIND := ISOSCELE_TRIANGLE;
        end if;
    else
        if ( A = C ) then
            TRI_KIND := ISOSCELE_TRIANGLE;
        else
            if ( B = C ) then
            TRI_KIND := ISOSCELE_TRIANGLE;
            else
                RIGHT_ANGLE_CHECK ( A, B, C );
            end if;
        end if;
    end if;
    end TRIANGLE_2;
begin  --Triangle_full
if ( A > 0 ) then
    if ( B > 0 ) then
        if ( C > 0 ) then
            PERIM := ( A + B + C );
            if ( ( 2 * A ) < PERIM ) then
                if ( ( 2 * B ) < PERIM ) then
                    if ( ( 2 * C ) < PERIM ) then
                        TRIANGLE_2 ( A, B, C );
                    else
                        TRI_KIND := NOT_A_TRIANGLE;
```

```
                end if;
            else
                TRI_KIND := NOT_A_TRIANGLE;
            end if;
        else
            TRI_KIND := NOT_A_TRIANGLE;
        end if;
    else
        TRI_KIND := NOT_A_TRIANGLE;
    end if;
else
    TRI_KIND := NOT_A_TRIANGLE;
end if;
end TRIANGLE;
```

Appendix B

Results of varying A(i) for LINEAR SEARCH procedure.

A(1) & code	Reciprocal fitness				Hamming fitness			
	Random selection		SELECTION_F		Random selection		SELECTION_F	
	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits	5 bits	10 bits
100								
binary	99.0% 38.5 >1380 tests	100% 20.2 647 tests	97.6% 47.2 1859 tests	100% 18.8 602 tests	100% 7.5 242 tests	100% 8.8 283 tests	100% 5.4 173 tests	100% 6.0 192 tests
Gray	100% 12.7 407 tests	100% 12.7 407 tests	100% 17.2 551 tests	100% 13.6 436 tests	98.5% 49.9 >1814 tests	100%% 19.3 617 tests	94% 67.2 >2983 tests	100% 26.8 857 tests
127								
binary	56% 11.1 >7240 tests	99.8% 49.1 >1602 tests	55.2% 9.4 >7335 tests	84% 81.6 >4755 tests	100% 7.2 232 tests	100% 8.5 273 tests	100% 4.9 159 tests	100% 5.7 184 tests
Gray	97% 30.5 >1426 tests	100% 18.0 577 tests	95.8% 80.8 >3151 tests	100% 13.6 435 tests	99% 35.7 >1293 tests	100% 21.0 672 tests	91.5% 79.5 >3688 tests	99% 24.6 >941 tests
128								
binary	47.6% 9.5 >8529 tests	99.8% 53.6 >1743 tests	45.2% 9.6 >8908 tests	81.2% 91.1 >5374 tests	100% 7.8 250 tests	100% 8.6 276 tests	100% 5.4 173 tests	100% 5.7 181 tests
Gray	97.7% 29.8 >1299 tests	100% 18.2 581 tests	96.8% 75.9 >2863 tests	100% 13.9 445 tests	99.5% 47.0 >1577 tests	100% 16.9 542 tests	93% 71.0 >3234 tests	99.5% 21.2 >756 tests
256								
binary	49.2% 11.4 >8308 tests	97.8% 76.2 >2737 tests	47.2% 12.8 >8642 tests	65.8% 66.8 >6879 tests	100% 7.5 240 tests	100% 8.5 273 tests	100% 5.0 161 tests	100% 5.8 186 tests
Gray	96.4% 69.5 >2720 tests	100% 17.7 567 tests	96.4% 83.0 >3137 tests	100% 13.7 440 tests	97.5% 47.0 >1865 tests	100% 21.3 683 tests	92.5% 70.2 >3278 tests	100% 23.4 750 tests
1000								
binary	88.0% 72.7 >3967 tests	100% 28.3 906 tests	88.0% 74.1 >4008 tests	100% 36.6 1173 tests	100% 7.4 237 tests	100% 8.6 275 tests	100% 5.2 168 tests	100% 6.0 194 tests
Gray	100% 13.9 446 tests	100% 18.3 578 tests	100% 14.5 464 tests	100% 14.5 462 tests	99.5% 48.4 >1621 tests	100% 19.6 627 tests	94% 65.9 >2941 tests	100% 21.2 680 tests
1024								
binary	49.9% 10.0 >8176 tests	86.3% 86.8 >6296 tests	49.0% 9.5 >8310 tests	55.8% 35.7 >7709 tests	100% 7.9 252 tests	100% 8.6 278 tests	100% 4.9 155 tests	100% 11.9 380 tests
Gray	73.0% 73.5 >2843 tests	100% 19.0 608 tests	96.2% 83.4 >3176 tests	100% 13.9 444 tests	100% 51.4 1645 tests	100% 18.4 590 tests	91% 79.2 >3746 tests	100% 21.2 680 tests
10000								
binary	68.8% 18.2 >1399 tests	99% 26.4 >868 tests	61.8% 19.5 >1610	93% 29.2 >1094	100% 7.8 250 tests	100% 9.3 299 tests	100% 5.3 170 tests	100% 6.3 201 tests
Gray	96% 24.2 >877 tests	100% 18.5 593 tests	100% 14.5 464 tests	100% 14.4 462 tests	99.5% 42.6 >1436 tests	100% 17.5 559 tests	96% 81.9 >3156 tests	100% 17.8 570 tests

Appendix C

Software listing of REMAINDER procedure

```
procedure REMAINDER(A, B : integer) is
R : integer := -1;
Cy,
Ny: integer := 0;
begin --test_procedure
if A = 0 then
else
  if ( B = 0 ) then
  else
      if ( A > 0 ) then
          if ( B > 0 ) then
              while ( ( A - Ny) >= B ) loop
                  Ny:= Ny+ B;
                  R := A -Ny;
                  Cy := Cy + 1;
              end loop;
          else  --B<0
              while ( ( A + Ny) >= abs ( B ) ) loop
                  Ny:= Ny+ B;
                  R := A + Ny;
                  Cy := Cy - 1;
              end loop;
          end if;
      else  --A<0 --11
          if ( B > 0 ) then
              while ( abs(A + Ny) >= B ) loop
                  Ny:= Ny+ B;
                  R := A +Ny;
                  Cy := Cy - 1;
              end loop;
          else
              while ( ( A - Ny) <= B ) loop
                  Ny:= Ny+ B;
                  R := abs ( A - Ny);
                  Cy := Cy + 1;
              end loop;
          end if;
      end if;
  end if;
end if;
PUT ( "Cy = " ); PUT ( Cy );
new_line;
PUT ( "R = " ); PUT ( R );
end REMAINDER;
```

Appendix D

Software listing of DIRECT_SORT procedure

```
with text_io;
use text_io;

generic
    type index_type is (<>);
    type scalar_type is private;
    type vector_type is array(index_type range <>) of scalar_type;
    with function lt (a,b:in scalar_type) return boolean;
package dk_generic_m01aa is
    procedure direct_sort(a:in out vector_type;
    error: in out integer);
end dk_generic_m01aa;

package body dk_generic_m01aa is
procedure direct_sort(a:in out vector_type;error :in out integer) is
    stack:array(0..50) of index_type;-- := (others => a'first);
    j,i,left,right:index_type;
    p:integer;
    bottom:index_type :=a'first;
    top:index_type:=a'last;
    procedure insert(a :in out vector_type; bottom,top: in index_type) is
        x:scalar_type;
        j:index_type;
    begin
    for k in index_type'succ(bottom)..top loop
        x:=a(k);
        j:=k;
        while (j > bottom) and then
            lt(x , a(index_type'pred(j))) loop
            a(j):=a(index_type'pred(j));
            j:=index_type'pred(j);
        end loop;
        a(j):= x;
        end loop;
    end insert;

    procedure partition(a : in out vector_type;
        bottom,top :in index_type;p,q :out index_type) is
        mid,i,j:index_type;
        x:scalar_type;
        hh:integer;
        procedure swap(e1,e2 :in out scalar_type) is
            t:scalar_type;
            begin
            t:=e1;
            e1:=e2;
            e2:=t;
        end swap;
    begin
    hh:= (index_type'pos(bottom) + index_type'pos(top));
    hh:=hh / 2;
```

```
    mid:= index_type'val(hh);
    if lt(a(mid), a(bottom)) then
        swap(a(bottom),a(mid));
    end if;
    if lt(a(top), a(bottom)) then
        swap(a(bottom),a(top));
    end if;
    if lt(a(top), a(mid)) then
        swap(a(mid),a(top));
    end if;
    i:=index_type'succ(bottom);
    j:=index_type'pred(top);
    x:=a(mid);
    loop
        while lt(a(i) , x) loop
            i:=index_type'succ(i);
        end loop;
        while  lt(x , a(j)) loop
            j:= index_type'pred(j);
        end loop;
        if i<= j then
            swap(a(i),a(j));
            i:=index_type'succ(i);
            j:=index_type'pred(j);
        end if;
    exit when  i > j;
    end loop;
    p:=j;q:=i;
    end partition;
begin
if (index_type'pos(top) < index_type'pos(bottom) ) then
    error :=1;
else
    error :=0;
end if;
if error = 0 then
    left:=bottom; right:=top; p:=2;
    loop
        if index_type'pos(right) - index_type'pos(left) > 10 then
            partition (a,left,right,i,j);
            if (index_type'pos(i)-index_type'pos(left)) > (index_type'pos(right) - index_type'pos(i)) then
                stack(p):=left;
                stack(p+1) :=i;
                left:= j;
            else
                stack(p):=j;
                stack(p+1):=right;
                right:=i;
            end if;
            p:=p+2;
        else
            p:=p-2;
            left:=stack(p);
            right:=stack(p+1);
        end if;
        exit when p = 0;
    end loop;
    insert(a,bottom,top);
```

```
end if;
end direct_sort;
end dk_generic_m01aa;
```