

# Mutation Clustering

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# Abstract

Mutation testing, a type of white box testing is one of the most important and powerful testing techniques, which guarantees to improve the software quality. This form of testing deals with mutating parts of the program intentionally and then detecting them. The purpose is not to find the faults but to generate an effective test suite, which can detect all the faults in the program.

Mutation testing, in spite of being effective and most powerful, is not widely used in software engineering. Basically because of high computational cost associated with it. The computational cost is due to too many mutants for even small programs. We have experimented with different programs of variable sizes, and was able to come up with the solution to the problem.

We have tried to reduce the computational cost of the mutation testing, reducing the number of the mutants by clustering.  $K$ -means clustering algorithm and agglomerative hierarchical clustering algorithm are implemented to cluster the mutants. Thereby, reducing the size of mutants by selecting one mutant from each cluster. The outcome of the results shows that the test set generated from the clusters are more efficient, having a mutation score of 100%, than the test set generated from the random mutants. This report elaborates the experimental steps and results.

Key words: *Mutation testing, clustering*

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# Abbreviations

LOC.... **L**ines **O**f **C**ode  
MS..... **M**utation **S**core

# Chapter 1

## Introduction

Software testing is one of the vital processes of the software development life cycle. It ensures that high quality systems reach the clients which are bug free and reliable. It is a process of finding faults in a software program, which consists of designing the test cases and executing the software with those test cases. Software testing, previously underestimated, is now given equal importance as software development. According to a research [5], 40-50% of the cost, effort and time is spent on testing and 50% on software development, it is said that this cost is even higher for critical software's like in avionics software's.

There are many techniques of testing software, classified as black box testing, white box testing and grey box testing, each one of these categories target different levels of complexity and coverage.

Mutation testing, a type of white box testing, is one of the most powerful testing techniques. The basic aim of this testing strategy is to generate effective test set, which can detect all the faults, by repeatedly improving the test cases. Mutation testing has two main problems: first, the large number of mutants; and second, the equivalent mutants. Our study focuses on the former problem of the mutation testing.

### 1.1 Project Aim

The main goal of this project is to overcome one of the problems of the mutation testing: computational cost incurred by large number of the mutants. For that, we cluster the similar mutants together, so that by selecting mutants from each cluster we can reduce the number of mutants required without reducing the power of the set of mutants. Mutant power will be measured in terms of the set of test cases required to kill the entire mutant set.

## 1.2 Objectives

Having clear, specific and realistic objectives improves the project a great deal. Very clear objectives were outlined for this project, which made it easy to present the deliverables in time throughout the project development.

The main objectives of this project are:

- To have a clear understanding of the mutation testing and clustering technique, and identifying the main issues and problems of mutation testing.
- To reduce the number of mutants by implementing different clustering techniques, in our case we have implemented the  $k$ -means clustering algorithm and the agglomerative clustering technique.
- To strive to get an efficient and mutation adequate test set generated from the mutants selected from the clusters.
- To write a detailed and comprehensive document.

## 1.3 Scope

The scope of this project is made limited in a number of ways. Mutation testing is a challenging strategy. It faces the problem of large number of mutants for even small programs. In addition to this, another problem is that most of these mutants are equivalent to original program. Firstly, we have chosen to deal with the former problem of mutation testing, i.e., large number of mutants. Secondly, it focuses on one of the many ways to deal with the computational cost incurred by large number of the mutants, i.e., by reducing the number of the mutants. Also, there are several different clustering algorithms which can be implemented, but for this project we have only chosen two such algorithms. These restrictions have allowed us to complete the work in the given time constraint.

## 1.4 Roadmap

The project is divided into phases of development. The first phase will deal with the implementation of the clustering algorithms, and clustering the mutants based on some similarity, to reduce the large number of the mutant's problem. In each cluster, the mutants will be killed by largely the same set of test cases and so we can choose to select only one member of each cluster. The project will start off with the implementation of the  $k$ -means clustering algorithm, different values of  $k$  will be experimented with, detail in chapter 4, and then the agglomerative clustering technique will be implemented. The experiment will be conducted on five C programs of different sizes and level of complexity. A mutation testing tool need not be implemented, as it is already implemented, all the data will be available from the CREST with the help of Yue Jia, which will help a great deal.

$P$	$x=y+z;$	Test Cases
m1	$x=y-z;$	$T1\{y=2, z=2\}$
m2	$x=y*z;$	$T2\{y=2, z=3\}$
m3	$x=y/z;$	$T1\{y=2, z=2\}$
m4	$x=y+z+1;$	$T1\{y=2, z=2\}$
m5	$x=y+z+0;$	$T2\{y=2, z=3\}$
m6	$x=y+z+y;$	$T1\{y=2, z=2\}$

Table 1.1: Original program  $P$ , associated mutants and test cases

The second stage of the project development, after the clustering of mutants, will be the evaluation as to whether by selecting mutants from clusters we can reduce the number of mutants without reducing the power of the set of mutants.

## 1.5 Simple Example

We can narrate the purpose of this project by a simple example. Consider a program  $P$  and some mutants of this simple program in table 1.1. Each one of these mutants are the faulty versions of  $P$ , which differ from  $P$  by a single error. These faulty versions or mutants represent the most likely faults made by the programmers. It is safe to say that these mutants can be innumerable for even simple statements like  $P$ . This forms the basis of the first phase of the project.

The idea behind mutation testing is to kill the mutants by the test cases, so if all the mutants are killed we are left with a good test set that is mutation adequate. The table 1.1 shows the test cases, T1 and T2, which can kill these mutants. But with so many mutants, executing each of the mutants against each test case leads to enormous computation. This computational cost makes mutation testing less feasible to be practised, therefore makes a good and interesting topic for research.

Considerable work is done in this area for reducing computational cost by reducing the number of mutants, discussed in chapter 3. The first phase of this study is based on the problem of tackling the large number of mutants formed. The second phase, however, is based on evaluating and analysing the results of clustering.

## 1.6 Organization Of Study

The remaining report is divided into following chapters. The chapter 2 gives an elaborated description of the problem statement. It starts off by outlining different problems of the domain, and then narrows off to selecting only one problem to tackle. The next chapter, chapter 3, describes the review from the literature, describing the current status of the research, explaining the key words of the project title and the work already done in this problem domain. The chapter 4 is about the methodology adapted for the project. The

chapter 5 deals with the evaluation part of the experiment. This is an important section of the report, as it explains in detail the results achieved. The chapter 6 provides a detailed conclusion of the thesis. Finally, chapter 7 ends the report by suggesting some future enhancements in the project.

## Chapter 2

# Problem Statement

Software testing has proven to maximize the reliability and quality of the software. Therefore, 50% of the cost and time is spent on testing the software thoroughly. For that purpose different testing techniques have been developed. Out of those, mutation testing has turned out to be most powerful in fault detection. Mutation testing, although being the most powerful testing technique, is not practised and widely used for testing. The major reason for this negligence is the computational cost that is associated with this technique.

### 2.1 Computational Cost

Let us analyse the cause of the huge computational cost associated with mutation testing, as discussed in [6, 7], which prevent the use of this technique. The main reason of this cost comes from the large number of generating and executing the mutants. A small program can have hundreds of mutants, for example a program less than 100K LOC will generate enormous number of mutants [10]. The C Triangle program used in the program is 50 LOC with 584 mutants. No doubt creating test cases and executing each one of these mutants can be computationally heavy. Each one of these generated mutants must be executed at least once by the test cases which leads to too much of computation. In [10], Wong says that the cost can be measured by two metrics, the size of the test set used to fulfil the criterion and the number of the mutants under observation.

#### 2.1.1 Possible ways to reduce Computational cost of Mutation Testing

There are different ways to reduce this computational cost [6]. The possible approaches are categorized into three different strategies: ‘do fewer’ approach, ‘do faster’ approach and ‘do smarter’ approach. The detail of these can be found in relevant literature.

1. **Do Fewer Approach [6, 9, 18]:** Reducing the number of the mutants without having critical information loss
2. **Do Smarter Approach [6]:** Distributing the computation of mutants over many

machines

**3. Do Faster Approach [6]:** Quick generation and running of the mutants

The limitation of this project is to focus on the ‘do fewer’ approach, and find a way to reduce the number of mutants leading to reduction in computational cost. Even the title of the project ‘Mutation Clustering’, further emphasizes the limited scope of the research; clustering the mutants to reduce the number of mutants.

## 2.2 Hypothesis

We hypothesize that by clustering the large number of the mutants we can considerably lower the computational cost. So that by selecting mutants from each cluster we reduce the size of the mutants. Furthermore, generating a test set that is mutation adequate for the mutants selected from the clusters. Thus, that test set will be efficient in killing all the actual number of mutants. We aim to investigate this hypothesis in this project.

## Chapter 3

# Literature Review

### 3.1 Overview

This section will elaborate the main keywords of the research topic, mutation testing and clustering. The first section of this chapter gives a detailed working of mutation testing. The second section explains the clustering technique and the techniques used in this project. The third section highlights the previous work done in this problem area, and the last section explains the validity of our research and how it differs from the current state of the art.

### 3.2 Mutation Testing

Mutation testing a type of white box unit testing is considered to be the most efficient in detecting faults [7]. This testing technique is based on an original program and numerous faulty versions of that program. These faulty versions are called as mutants. Each of these mutants is formed by mutating the program by one instruction only. See table 3.1 for some possible mutants of a program.

Original Program( $P$ )	Mutant1(m1)	Mutant2(m2)	Mutant3(m3)
a= b+c;	a= b*c;	a= b-c;	a= b+c+c;

Table 3.1: Some possible mutants of a program

The basic aim of the mutation testing is to iteratively produce a powerful test set [1]. This is achieved by intentionally adding faults into the original program and then generating the test cases that detect those faults. This process of generating test cases is continued until all the faults are detected (all the mutants are killed). Hence this is why we say mutation testing produces powerful test set, which detects all the faults.

Furthermore, the mutation operators are responsible in generating mutants of a program; they make syntactic changes to the original program. These syntactic changes



reflect the usual mistakes made by the programmers while coding. The mutation operators have two main goals to adhere; introduce typical mistakes the programmers make and enforce testing by executing each branch. The table 3.3, shows the 22 mutation operators of Mothra. The mutation operators are represented by their acronyms. For example, mutation operator ‘AAR’ is an acronym for ‘array reference for array reference replacement’, which replaces each array reference in a program by other distinct array reference in the program [9].

The process of mutation testing can be described with an example and a flow chart in figure 3.1, to fully understand the process behind this technique [1, 6]. We will carry on with the example described in the table 3.1.

First of all, the original program  $P$  is mutated by applying a single mutation operator. We have 3 syntactically correct mutants;  $m_1$ ,  $m_2$ ,  $m_3$  of  $P$ , table 3.1. The mutants are generated by applying a mutant operator. Next, test cases are generated. Each test case is run on  $P$ , if the output of the  $P$  is not correct then a bug is found and  $P$  is fixed before the test case can be executed on the mutants. If there are no errors in the  $P$  or the errors are fixed, the test cases are executed on each mutant.

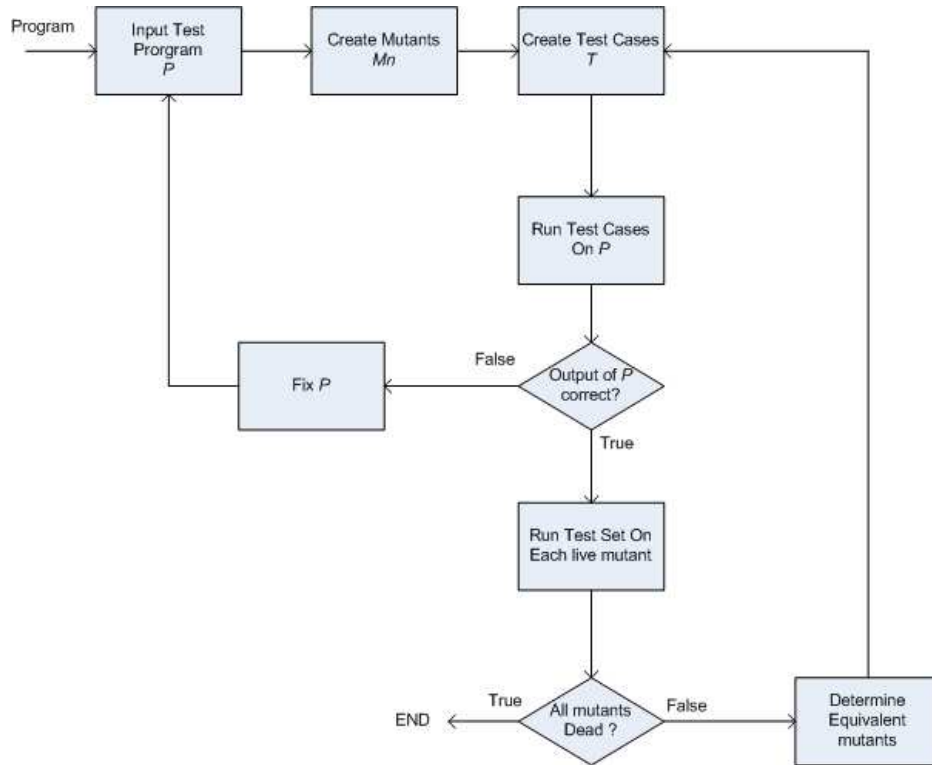


Figure 3.1: Flow chart representing typical process of mutation testing (Adapted from [6])

If the result is different, the fault is detected and the mutant is said to have been

killed, as in case of test case 1 in table 3.2. If the result of the test case is same for the original and the mutant program, as in case of test case 2 in table 3.2, then it suggests that either the mutant is an equivalent mutant (which cannot be killed) or the test case is not efficient and needs to be improved. An equivalent mutant is syntactically different but semantically same to the original program. They just increase the computational cost and do not help in determining the effectiveness of a test case; additionally they can never be killed by any test case.

	$P \ a=b+c$	$m1 \ a= b*c$
Test case 1 $b=4, c=2$	$a=6$	$a=2$
Test case 2 $b=2, c=2$	$a=4$	$a=4$

Table 3.2: Test cases generated to detect mutants

The test set achieved, after the killing of all the mutants, is checked for its goodness. The goodness of the test set is assessed by a test adequacy criterion. The metric used for the determination of the test adequacy is mutation score. Our aim is to achieve a high mutation score; a score close to 100% makes the test set mutation adequate. Mutation score is calculated by the formula 3.1.

$$MutationScore = \frac{Number\ of\ mutants\ killed}{Total\ number\ of\ non - equivalent\ mutants} \quad (3.1)$$

Where

$$0 \leq M.S. \leq 1 \text{ or } 0\% \leq M.S. \leq 100\%$$

If the test set does not satisfy the adequacy criteria, the test set is improved by adding new test cases until it satisfies the criteria [7]. Hence, the adequacy criterion improves the goodness of the test set and also helps in making new test cases [7].

### 3.2.1 Computational cost of Mutation Testing

According to Budd [11], number of mutants generated for a program is roughly proportional to the product of the number of data references times the number of data objects. This means that even small programs have large amount of mutants. The computational cost of mutation testing technique is associated with the execution of each and every mutant against the test cases.

### 3.2.2 Why mutation testing?

Coverage testing does not guarantee fault detection, so no full coverage of branches and statements is possible. However, mutation testing guarantees to detect the fault. This type of unit testing technique assures the improvement of the quality of the software [9],

	Mutation Operators	Description
1	AAR	array reference for array reference replacement
2	ABS	absolute value insertion
3	ACR	array reference for constant replacement
4	AOR	arithmetic operator replacement
5	ASR	array reference for scalar variable replacement
6	CAR	constant for array reference replacement
7	CNR	comparable array name replacement
8	CRP	constant replacement
9	CSR	constant for scalar variable replacement
10	DER	DOstatement end replacement
11	DSA	DATAstatement alterations
12	GLR	GOTO label replacement
13	LCR	logical connector replacement
14	ROR	relational operator replacement
15	RSR	RETURNstatement replacement
16	SAN	statement analysis
17	SAR	scalar variable for array reference replacement
18	SCR	scalar for constant replacement
19	SDL	statement deletion
20	SRC	source constant replacement
21	SVR	scalar variable replacement
22	UOI	unary operator insertion

Table 3.3: 22 Mutation operators of Mothra

and has been empirically proven to be the most efficient testing method to detect faults [11, 13].

### 3.3 Clustering

Machine learning deals with the extraction of information from the data by transformation, inference and conclusion from the data learning. Clustering falls in one of the sub fields of machine learning known as unsupervised learning [3, 4]. It is unsupervised learning because the algorithm is provided with only the data points and no labels, and the aim is to suitably group those data points [4].

Clustering is a technique used for the grouping of data, for pattern recognition and classification, based on some similar characteristics [2]. It is a form of unsupervised classification as described in [3]. It is defined as the members of a cluster being similar to the other members of that cluster, and dissimilar to members of other clusters [3]. The similarity of the cluster members is measured by some similarity measure. The similarity measure is important for cluster definition for most of the clustering algorithms [3]. The most common similarity or distance measures include Euclidean distance, Hamming dis-

tance, etc. The figure 3.2, shows the general idea of clusters. The members of each cluster are grouped because they had some common characteristics, this gives a boundary to each cluster so they can be differentiated from other clusters.

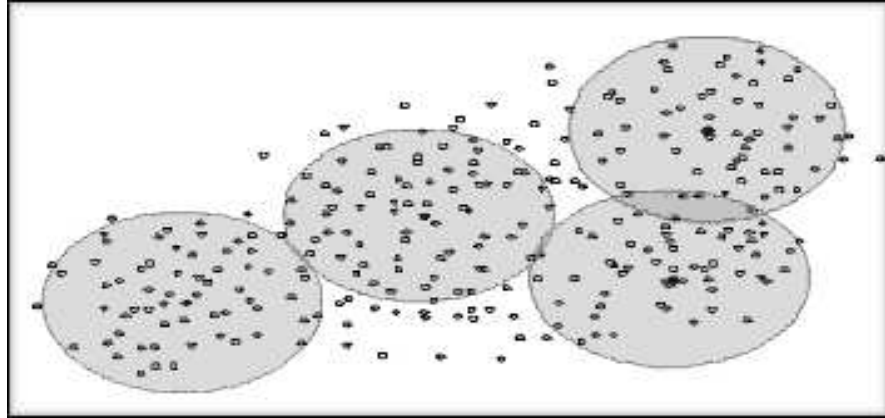


Figure 3.2: General cluster diagram, each one of the marked cluster is different from other clusters

There are different types of clustering algorithms, but the main classifications of clustering algorithms are:

1. Hierarchical clustering methods
  - Agglomerative algorithm
  - Divisive algorithm
2. Partitional clustering methods
  - $K$ -means algorithm
  - Fuzzy c-means algorithm

The  $k$ -means clustering algorithm and agglomerative clustering techniques from each classification, which are implemented in this project, are now discussed to give a clear understanding of these techniques and their purpose.

### 3.3.1 $K$ -means Clustering Algorithm

K-Means clustering algorithm is one of the first, simple and speedy clustering algorithms. The algorithm works as follows:

1. Select  $k$  initial clusters ( $k=1,2,3..$ ).

2. Then assign the data points to those  $k$  clusters with smallest distance based on some similarity measure (Euclidean distance, hamming distance).
3. The centroid of the clusters is calculated.
4. Repeat step 2 and 3 until convergence is achieved.

This algorithm depends heavily on the initial choice of clusters, the value of  $k$  [4]. The better and thoughtful choice of the initial  $k$  value leads to better cluster formation.

### 3.3.2 Agglomerative Clustering Technique

Agglomerative clustering algorithm is a hierarchical algorithm which goes from bottom to top. It starts off with each data object assigned a distinct cluster (singleton), and continues agglomerating the clusters until a stopping criterion is met [3]. It is represented with a dendrogram, which is a tree showing the merging of the clusters. This dendrogram can be broken at any point to get different clusters at different points. The merging of the clusters depends on the threshold value. If the distance of a cluster to another cluster is less than the threshold value then it is merged with it. Hence if the threshold is 0 then the number of clusters will be same as the data points, on the other hand if the threshold value is too big all the data points will fall into a single cluster.

#### 3.3.2.1 Example [14]

The figure 3.3 shows a dendrogram, abridged from [14]. Each one of the nodes merges two branches into one, which means merging two clusters into one larger cluster. The algorithm is applied to an example of 10 data points. Initially all the data points are single members of the clusters, so the clusters are equal to  $n$ . Then for each data point the average is calculated and is merged with minimum average. The dendrogram can be cut at any point to get the desired number of clusters. For example if cut at step 2, we get three clusters.

There are many options of distance measure in hierarchical clustering. The most common [4] are discussed briefly:

1. Average Linkage Clustering

It is the average distance of the data points in a cluster with all the data points in another cluster. Those two clusters are merged with the lowest average distance.

2. Centroid Linkage Clustering

The Centroid or mean of each cluster is calculated. Then the distance between the clusters is computed as the distance between their centroids, merging the two clusters with the smallest distance between the centroids.

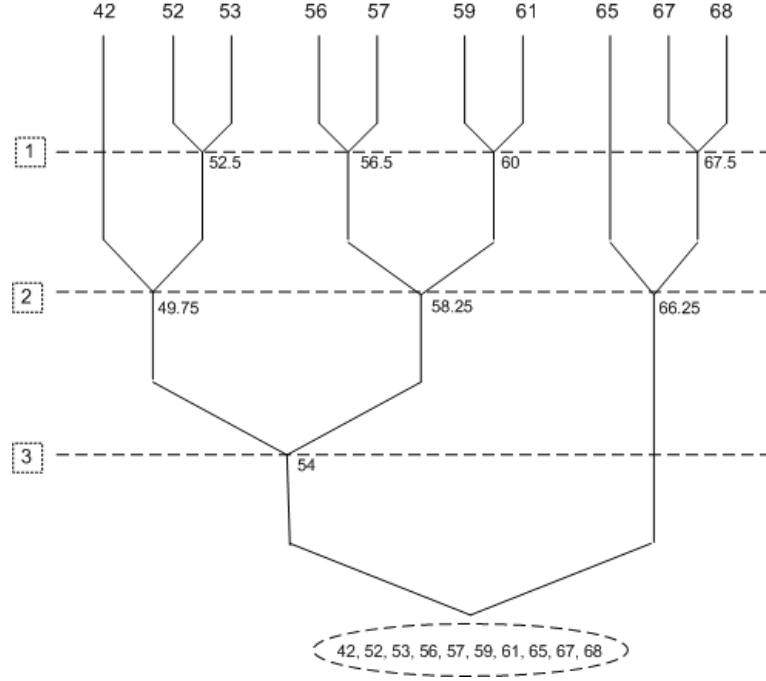


Figure 3.3: Agglomerative dendrogram/tree, showing pair wise merging of clusters at each step (Adapted and abridged from [14])

### 3. Complete Linkage Clustering

This is the distance between the farthest data points in two clusters. The two clusters with the minimum farthest distance are merged.

### 4. Single Linkage Clustering

It is the opposite of the complete linkage clustering. It is the distance between the nearest data points in two clusters. The clusters with the minimum nearest distance are merged.

## 3.4 Previous Work

In order to tackle the computational problem of mutation testing, researchers have proposed a number of strategies. Wong and Mathur in [7] proposed a way to reduce the computational cost, by reducing the number of mutants. Mathur suggested using the approximation technique to reduce the number of the mutants and another technique of random mutant selection. These two approaches are referred as ‘do fewer’ approaches in [6] or alternate mutation. There are other approaches as well. For example, ‘do smarter’ approach, this emphasises on dividing the computational cost on several machines. Another approach called as ‘do fewer’ approach is based on generating and running each mutant as quickly as possible.

All these are the approaches to minimize the computational cost, but we will only address the ‘do fewer’ approach, describing other approaches in detail is out of the scope of this project and report.

### 3.4.1 Selective/ Constrained Mutation Criterion

The idea of this approach is to select only those mutants which are different from other mutants in the true meaning. It is also called as constrained mutation, as it deals with specific types of mutants. For example, considering only ABS mutants and ignoring the remaining mutants [10]. This idea was first conceived by Wong et al. [8]; they suggested mutating with only critical mutation operators.

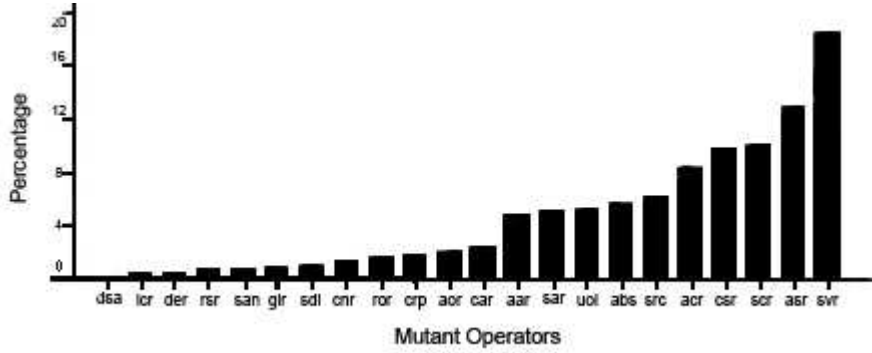


Figure 3.4: Number of mutants produced by the 22 mutation operator (Adapted from [9])

The application of all the mutation operators leads to the generation of large number of mutants. This strategy works by minimizing the number of mutation operators, and getting testing strength with fewer mutants [6]. Figure 3.4 shows the percentage of the mutants formed by the 22 mutation operators for a set of 28 programs. The scalar variable replacement operator (SVR) is evidently the most dominant operator. There are different variations of the selective or constrained mutation; we will discuss them briefly in the following paragraphs.

Mathur suggested not using the operators which produce the most mutants, hence the name selective mutation [12]. Mathur excluded the operators like, scalar variable replacement (SVR) and the array reference for scalar variable replacement (ASR) operators.

This approach was later extended by Offutt. Experimental results shown by Offutt in [9] described that application of only 5 mutant operators provided the same coverage as non-selective mutation, this approach is called as the sufficient mutation. This significantly reduced the cost to 50 times with large programs and 4 times with small programs. It reduced the number of mutants to 60%. According to the work in [9] the key critical operators are ABS, AOR, LCR, ROR and UOI. This subset of mutation operators is sufficient, if they produce fewer mutants and their strength is same as all the mutation operators. Offutt’s strategy also ignored the mutation operators that generate large number

of mutants like SVR and ASR. This study showed that, a maximum of 99.99% mutation score was achieved with two selective mutation adequate test sets of ten subject programs with a 24% saving in the number of mutants [18].

Wong in [10], emphasised on selecting mutant operators based on their significance in fault detection, operators like ABS and ROR. Wong, by selecting these operators, was able to reduce the number of mutants by 80% and the test cases by 40% to 58%.

Offutt in [9] says that the selective mutation is as powerful as the non-selective mutation and results in less computational cost by reducing the number of mutants. Also, it was aimed that the mutation score be over 95% with selective mutation, since test set with mutation score over this percentage are considered to be effective.

### 3.4.2 Random Mutant Sampling

This strategy selects random mutants from the large set of mutants. It examines a small subset of randomly selected mutants, ignoring the others. This subset is then tested against the test set and its sufficiency is determined. In case not satisfied, a new sample is selected randomly, and this process is continued until the test set is efficient.

Budd in [11] experimented by selecting only 10% of the mutant samples found that the test cases generated from this sample overlooked only 1% of the non equivalent mutants.

## 3.5 Justification of the undertaken research

Although researchers have proposed several strategies to control the number of mutants, still they are not very precise. It is still an open research area, and therefore attracts and invites more research to handle the problem.

The two approaches of the ‘do fewer’ strategy are not very optimal. According to [17], the selective mutation ignores some critical mutation operators. The selective mutation by Offutt [9], may lead to possible elimination of some critical mutation operators since it was proposed using only 5 operators out of 22. It is difficult to find a good sufficient subset of mutation operators. This strategy depends heavily on the efficient selection of the mutation operators [10]. Similarly, the random mutant sampling, works better with small randomly selected subset of mutants [17]. This technique is not very precise and efficient, as it is just a random selection of mutants from a large number of mutants, which clearly ignores some critical mutants altogether.

The motivation behind this project was to come up with an optimal way of dealing with the number of mutants.



## Chapter 4

# Experimental Methodology

### 4.1 Introduction

This chapter explains the methodology and the strategy used in the under taken project: mutation clustering. We have divided the methodology in specific steps:

**Step1:** Clustering of the mutants of five different programs.

**Step2:** Evaluating the effectiveness of the test set generated from the clustered mutants.

### 4.2 Experiment Setup

In order to evaluate the clustering of mutants, we conducted experiments on five different C programs. Each one of these programs has different number of mutants and varying test cases. The size of the programs varies from 50 to 750 lines of code, table 4.2. To proceed with the experiment we eliminated all the pseudo-equivalent mutants. We call those mutants pseudo-equivalent which are not killed by any test case. These mutants are represented as either all 1s or all 0s.

	tc1	tc2	tc3	tc4	tc5	tc6	tc7	tc8
m1	1	0	0	0	1	0	1	0
m2	1	0	1	1	1	0	1	1
m3	0	1	0	0	0	1	1	0
m4	0	1	1	0	1	0	1	0
m5	0	0	0	0	1	0	0	0
.....	.....	.....	.....	.....	.....	.....	.....	.....

Table 4.1: Data strucure representing mutants m1, m2, etc. in terms of test cases tc1, tc2, etc that kill them

The data that we worked on consisted of mutants. These mutants were generated by a C mutation testing tool MILU [21]. Each mutant was represented by the test cases that



equivalent mutants left us with 827 mutants.

#### 4.2.4 Totinfo Program

Totinfo of 500 LOC was the fourth program that we experimented with, it is a program that is used to calculate statistics from the input data [19]. There were 1879 mutants of this program and a test suite of 1052 test cases, mutants reduced to 1794 after the deletion of pseudo equivalent mutants.

	Program	LOC	Number of mutants	Number of test cases
1	Triangle	50	584	34
2	TCAS	150	856	1608
3	Schedule2	350	972	1399
4	Totinfo	500	1879	1052
5	Printtokens	750	506	2021

Table 4.2: Specifications of five experimental Programs [19]

#### 4.2.5 Printtokens Program

The last program that was clustered and evaluated was Printtokens of 750 LOC, which is a lexical analyser [19]. The program had 506 mutants and 2021 test cases associated with it. The 506 mutants were reduced to 345 after the removal of pseudo-equivalent mutants.

### 4.3 Clustering Methodology

Clustering is one of the major implementation parts of the project. We aim to reduce the number of mutants by clustering or grouping together the similar mutants. Those mutants are clustered together which are largely killed by the same set of test cases, this will allow us to choose only one mutant from each cluster, subsequently reducing the number of the mutants.

The chosen clustering algorithms are  $k$ -means clustering algorithm and the agglomerative clustering algorithm. We will outline these algorithms with respect to their working in the project.

#### 4.3.1 $K$ -means Clustering Algorithm

The general  $k$ -means clustering algorithm is described in chapter 3. This algorithm is sensitive to the initial selection of clusters and the value of  $k$ .  $K$ -means algorithm has many variations [15]. One of these variations is to select good initial values as the  $k$ -means clustering depends heavily on the initial selection of the  $k$  values. Wrong selection of  $k$  values leads to wrong formation of clusters. Hence, in this project we have carefully

selected the initial  $k$  mutants. Although the initial mutants are selected randomly, but they are truly distinct, this leads to the formation of truly distinct clusters. Also, the initial value of  $k$  is determined from the agglomerative algorithm, discussed in subsection 4.3.4..

1. Decide upon an initial  $k$  cluster value, the value of  $k$  must be less than the number of distinct mutants (value of  $k$  is determined from agglomerative algorithm).
2. Randomly select  $k$  distinct mutants.
3. Calculate the centroid of the cluster.
4. Calculate the distance, using the hamming distance, of each of the mutants to the centroid.
5. Group the mutants with the clusters with the minimum distance.
6. Recompute the centroid of the gaining cluster (and the losing cluster).
7. Repeat the steps 4-5 until convergence is achieved and the mutants do not move.

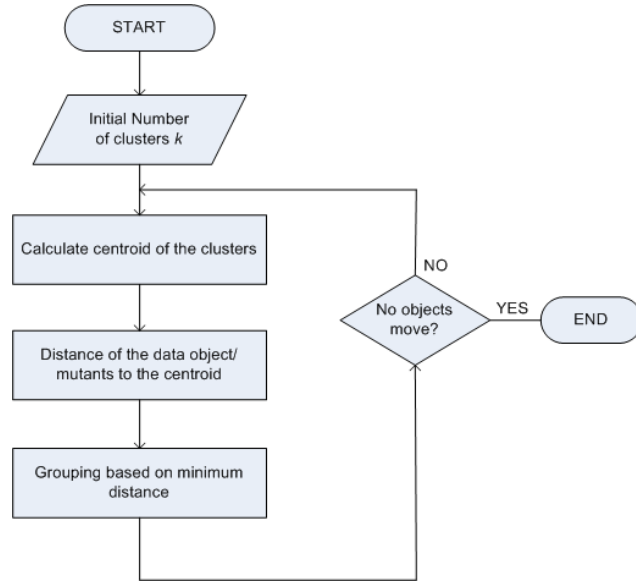


Figure 4.2: Flow chart of  $k$ -means clustering algorithm (Adapted from [22])

### 4.3.2 Agglomerative Clustering Algorithm

The agglomerative algorithm does not require any prior specification of number of clusters unlike  $k$ -means clustering algorithm. However, this algorithm depends on a threshold value  $T$  [16]. The data objects are merged pair wise if the distance between them is below the threshold value. The clustering stops when the distance between the clusters exceed the

threshold value. This gives us the distinct number of clusters, and this is the number that we use as  $k$  in k-means clustering algorithm.

We have done a bit of variation by merging two techniques of agglomerative clustering. Firstly, we start off by merging clusters based on distance lower than  $T$ . Afterwards, when the merging of clusters stops due to distance becoming greater than  $T$ ; the clusters are merged based on minimum distance.

The clustering of the mutants with the agglomerative algorithm followed the following algorithmic steps:

1. Initially numbers of clusters are equal to the number of mutant's  $n$ .
2. Then calculate the distance of each cluster to the other cluster, distance measure used is the average linkage.
3. Decide upon a threshold value  $T$ , we have set  $T=2$ .
4. Merge the two clusters pairs having the distance lower than the threshold value.
5. Repeat steps 2-4, this process continues until the distance becomes greater than the value of  $T$ .
6. Now here we start merging the clusters not based on the threshold value but on the minimum distance value.
7. Calculate the average linkage and merge the two clusters with minimum average distance.
8. Repeat step 6-7, this pair wise merging continues until all the mutants are agglomerated into one big cluster of size  $n$ .

### 4.3.3 Similarity Measure

Similarity measures are essential in clustering of the objects as they determine the similarity between two clusters or data objects, or dissimilarity of two clusters. The similarity measure used is the hamming distance. Hamming distance is the number of substitutions needed to change from one string into another. For example consider three mutants  $m1$ ,  $m2$  and  $m3$ , in table 4.3:

m1	1	1	0	0	1	0	1
m2	1	1	1	1	1	0	0
m3	0	1	1	1	1	0	0

Table 4.3: Three mutants  $m1$ ,  $m2$ ,  $m3$

	m1	m2	m3
m1	0	3	4
m2	3	0	1
m3	4	1	0

Table 4.4: Distance matrix representing distance between mutants

The Hamming distance between the two mutant strings m1 and m2 is 3, as the two strings differ from one another by 3 digits. It is the XOR between the bits.

We calculate the distance between three mutants m1, m2 and m3. We represent the pair wise distances between mutants with a distance matrix, table 4.4. This  $n \times n$  matrix is updated after new clusters are formed. Distance between m1 and m2 is 3, whereas, distance between m1 and m3 is 4. On the other hand distance between m2 and m3 is 1. Those mutants are clustered with the smallest distance, because smaller the value of dissimilarity, the more similar are the two clusters. If based on this distance, generally speaking, m2 and m3 will be clustered together and m1 will remain un-clustered.

Why we did not use Euclidean distance, is because Euclidean distance is the distance between two points which is measured using the Pythagoras Theorem. This leads us to say that with mutants being our central data, we can have no such parameters. On the other hand, Hamming distance suits our needs.

#### 4.3.4 Deciding value of $k$ for $k$ -means Clustering Algorithm

The first time selection of  $k$  for the mutants of a particular program is not straight forward as it may seem. The results will not be good if the value of  $k$  is unrealistic. Since our implemented algorithm carefully chooses distinct random mutants, so the initial  $k$  may not always be the half of the total number of the mutants for the first time. We have used the agglomerative algorithm to determine value of  $k$ . Agglomerative algorithm, merges two clusters based on the distance lower than the threshold value, it stops merging the clusters when the distance start becoming more than the threshold. The threshold value was 2, so the point where the algorithm stopped gave us the number of clusters which were very distinct. Subsequently, the first initial  $k$  value achieved gives us smaller intra-cluster distance and larger inter-cluster distance.

Furthermore, the later selections of the value of initial  $k$ , are half of the first selection. For example, we had 512 mutants from the Triangle program. The first run of  $k$ -means clustering algorithm was based on  $k=64$ . For the second run, we chose  $k=31$  and the next run was experimented with  $k=15$ .

The largest of these values of  $k$ , is considered to be optimal. The reason is that the clusters formed based on this value have very less intra-cluster dissimilarity, since mutants in each cluster are killed by same set of test cases. In addition to that, an optimal value will result in a mutation adequate test set.

## 4.4 Evaluation Methodology

Once the mutants are clustered by the chosen clustering algorithms, the evaluation of the clusters is done in order to support our results. Before we describe the evaluation approach, we mention the notations we will be using in this section and onwards.

- $Sc$  is selection of one mutant from each cluster.
- $Tc$  is the test set selected from the  $Sc$ .
- $Sr$  is the actual size of all the un-clustered random mutants.
- $Tr$  is the test set selected from  $Sr$ .

### 4.4.1 Evaluation approach

In order to do the evaluation the following approach is followed, this approach is also depicted in figure 4.3.

1. Firstly one mutant from each cluster is selected randomly for each of the clustering algorithms ( $K$ -means and Agglomerative), this selection is called  $Sc$ .
2. Now the test set  $Tc$  is generated for the mutant selection.
3. The test set is generated by using the greedy approach, which only selects those test cases which kills the most mutants in  $Sc$ . This way we have a very strong set of test cases,  $Tc$ .  $Tc$  is mutation adequate for  $Sc$ .
4.  $Tc$  is kept fixed and test set is generated from the random mutants  $Sr$ ,  $Tr$  is of the same size as the  $Tc$ .
5.  $Tr$  is generated 30 times for the fixed number of  $Tc$ .
6. Both  $Tc$  and  $Tr$  are observed to kill the total mutants  $Sr$  and the efficiency for each set is analyzed based on the mutation score.

### 4.4.2 Greedy strategy for adequate test set generation $Tc$

We began by experimenting with the selection of  $Tc$  from the clusters, in the hope to achieve 100% Mutation score for  $Tc$ . One of the selections of  $Tc$  was based on selecting test set  $Tc$  randomly from the mutants without any greedy selection. However, we noticed that this strategy does not provide a good efficient and mutation adequate test set. Eventually, this led us to follow the greedy approach in the selection of test set  $Tc$  from the clusters.

Now we explain how the greedy approach works and how it helped us to achieve a highly efficient test set  $Tc$ . According to this strategy, we achieve local optimum at each

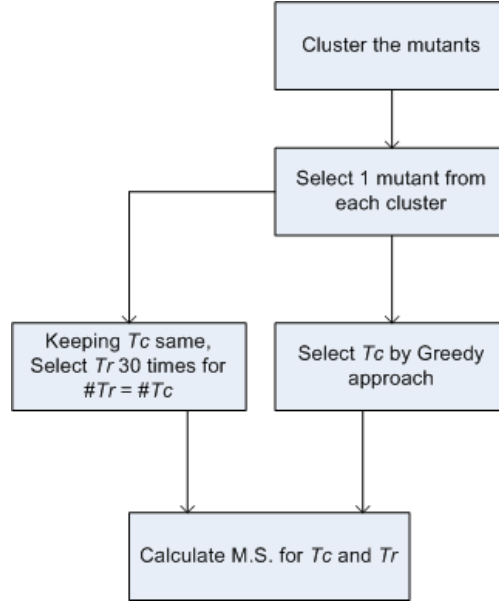


Figure 4.3: Flow Chart of the methodology

step in the hope to achieve global optimum [20]. It makes decisions based on the current information without worrying about the effects of the decisions in the future.

How this strategy works in our evaluation is, that mutants are selected from different clusters then for each step that test case is chosen which kills the most mutants. The mutants killed by that test case are removed and the test cases that kill the remaining mutants are calculated. Then again that test case is selected that kills the most mutants. This process of selecting test cases continues until all the selected mutants are killed. This results in a test set  $T_c$  that is mutation adequate for the selected mutants, see the flow chart in figure 4.3.



## Chapter 5

# Experimental Results and Analysis

### 5.1 Aim

The aim of this section is to describe the evaluation to investigate our hypothesis. The mutants are clustered and the clusters are evaluated to find that the test cases selected from the clusters are better and efficient in killing the mutants than the test set selected randomly. This is done by calculating how many percentages of the mutants are killed by the test set from clusters and how many by the test set from the random mutants, or in simpler words, by calculating the mutation score for each test set.

### 5.2 Clustering Results

We cluster the mutants based on the similarity. For each of the clustering algorithms we have repeatedly experimented with different values of the number of clusters to come up with an optimal value for each program under test. The clustering results in figures 5.1, 5.2, 5.3, 5.4, 5.5 are just for the  $k$ -means clustering algorithm, to give an idea of the clustering results.

The highest values of  $k$  used for the programs under test are, for Triangle program  $k=64$ , for TCAS program  $k=200$ , for Schedule2 program  $k=83$ , for Totinfo program  $k=173$  and for Printtokens  $k=68$ . For all these values of  $k$ , the intra-cluster distance among the mutants is as less as 0, 1 3, 4. This shows that all those mutants are clustered together which are killed by the same test cases. However, if we start reducing the number of clusters or the value of  $k$ , the intra-cluster distance starts increasing, such that for some clusters the intra-cluster distance reaches to 300. This is because the initial selection of the number of clusters are less and this forces the not so similar mutants to be merged in that cluster.

1. **Triangle Program:** The clustering of the 512 mutants from triangle program considerably reduced the number of the mutants. With  $k$ -mean algorithm 512 mutants were reduced to 64 clusters for the first run of the algorithm,  $k=64$  being an optimal value, figure 5.1. With Agglomerative clustering technique the 512 mutants were re-

duced to 62 clusters. Subsequently, the clusters were further reduced to  $k=31$  and  $k=15$  with  $k$ -means, whereas, 30 and 16 with agglomerative algorithm

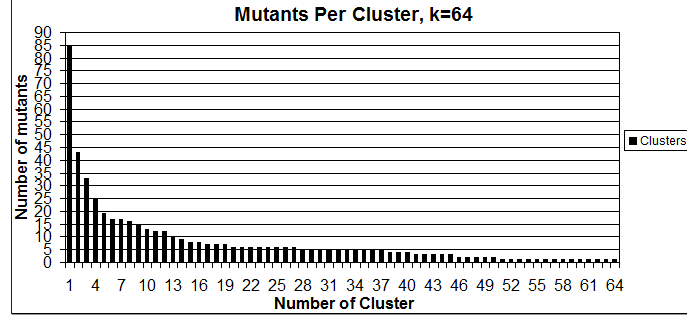


Figure 5.1:  $K$ -means clustering algorithm clusters of Triangle program mutants

2. **TCAS Program:**  $K$ -mean clustering algorithm reduced the 585 mutants to 200.  $K=200$  is an optimal choice since the mutation score is close to 100%, discussed in section 5.3. With the agglomerative clustering algorithm, the 585 mutants are reduced to 212 mutants, figure 5.2. Additionally, the further reductions with  $k$ -means, resulted in 100 and 50 clusters and with agglomerative 73 and 48 clusters.

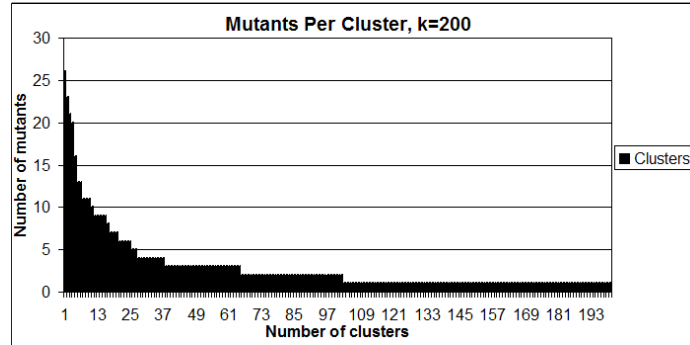


Figure 5.2:  $K$ -means clustering algorithm result on TCAS program

3. **Schedule2:** The  $k$ -mean algorithm clustered the 827 mutants of Schedule2 program into 83 clusters, figure 5.3. Similarly the agglomerative algorithm reduces the 827 mutants to 83 clusters. Further reduction in the number of mutants by  $k$ -means algorithm, led to 40 and 20 clusters. On the other hand, using the agglomerative algorithm, the mutants were reduced to further 32 and 24 clusters.
4. **Totinfo:** The  $k$ -means algorithm reduced the 1879 mutants to 173 clusters, figure 5.4, further reduction in the number of mutants led to the formation of 85, 40 and 20 clusters. However, with agglomerative algorithm, the optimal size of the cluster was 173 like  $k$ -means. Similarly, it also formed clusters of sizes 84, 45 and 19.

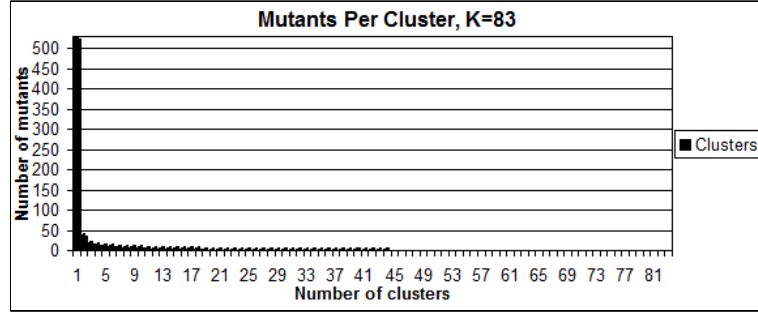


Figure 5.3:  $K$ -means clustering algorithm result on Schedule2 program

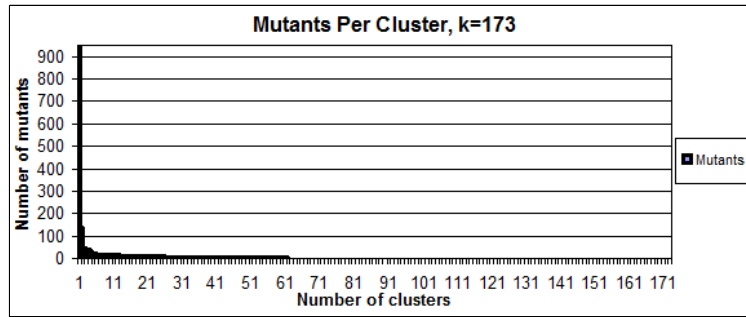


Figure 5.4:  $K$ -means clustering algorithm result on Totinfo program

5. **Printtokens:** The 506 mutants of Printtokens program was reduced to 68 clusters with both the  $k$ -means and agglomerative algorithm, figure 5.5. Reducing the size of the mutants further, formed 35 and 15 clusters with  $k$ -means algorithm and 31 and 16 clusters with agglomerative algorithm.

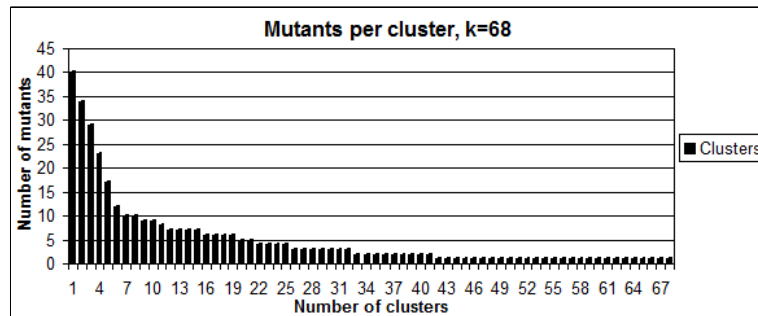


Figure 5.5:  $K$ -means clustering algorithm result on Printtoken program

### 5.3 Experimental Results

This section explains the efficiency of test set for each program under evaluation. Each graph represents the 30 different selections of  $Tr$  with a fixed number of  $Tc$  and their corresponding mutation scores. Only two graphs for each algorithm are shown, for complete results refer to Appendix B.

#### 5.3.1 Results for the Triangle Program

Each run of  $k$ -means clustering algorithm has a fixed same cluster test set  $Tc$ , and 30 different random test set  $Tr$ . In figure 5.6 the graph *a* shows the three runs of the  $k$ -means clustering algorithm for different samples of the same number of  $Tc$ , i.e., 13. Figure 5.6 graph *b* shows the four runs of  $k$ -means algorithm on different selection of mutants from each cluster for same value of  $Tc=9$ . In the graph *a*, the mutation score of  $Tc$  is closer to 100 %. The mutation score of  $Tr$  start off at 85% and gradually increases, although at one point it become closer to  $Tc$ .

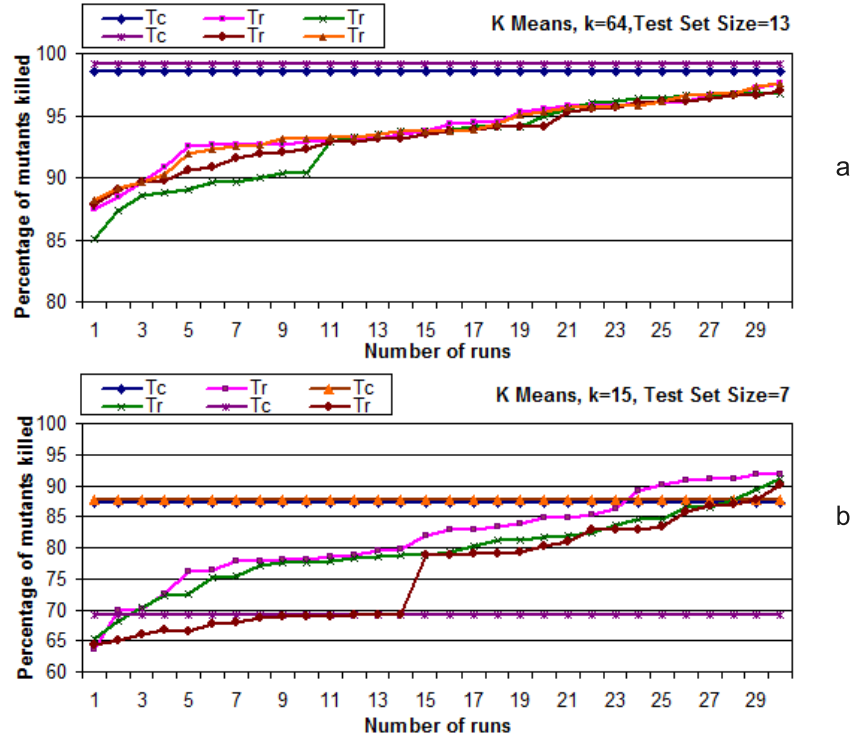


Figure 5.6:  $K$ -means clustering algorithm result on triangle program for  $k=64$  and  $k=15$

Applying the agglomerative clustering algorithm on triangle program of 512 mutants, yields 62 clusters. Figure 5.7 shows, the efficiency of  $Tc$  and  $Tr$  for three samples of 62 clusters and 16 clusters respectively. The graph with greater number of clusters, i.e. 62, shows that the MS of closer and below 95% is achieved for  $Tc$ , which is not very good It

is also worth mentioning, that the test set size 34 is reduced to 13 and 12 with  $k$ -means and agglomerative algorithms respectively.

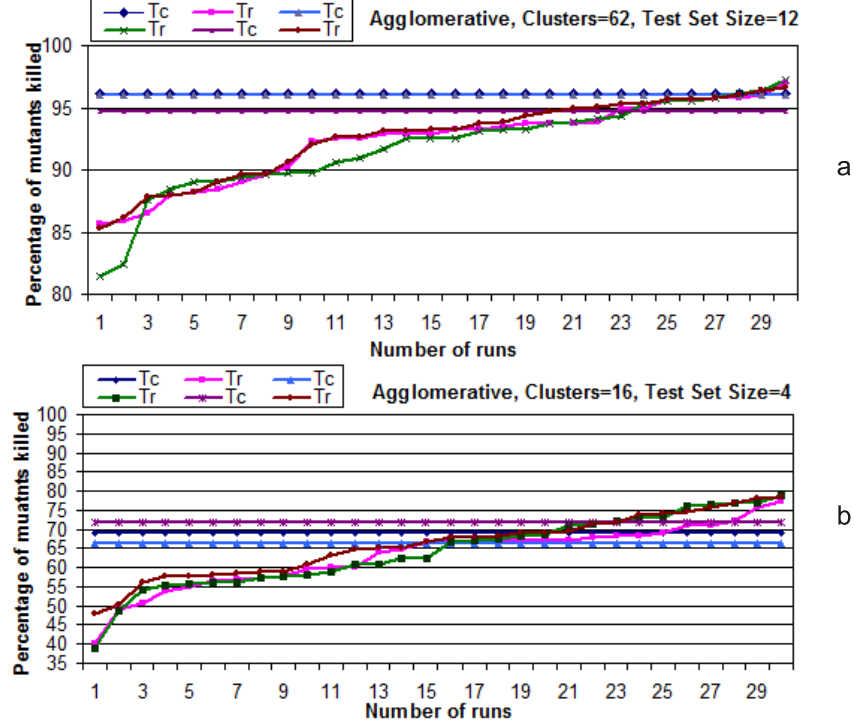


Figure 5.7: Agglomerative clustering result on triangle program for clusters=62 and clusters=16

### 5.3.2 Results for the TCAS Program

Figure 5.8 graph *a* shows the three runs of the  $k$ -means algorithm having the test set size 19 and  $k=200$ . The mutation score of  $T_c$  for the three samples is 99.3%. Whereas, the mutation score for the three samples of  $T_r$  is less than 95%. Similarly, the graph *b* in figure 5.8 shows the three runs of  $k$ -means algorithm of the same test set size of  $T_c=8$  and  $k=50$ . Evidently the mutation score of  $T_c$  has decreased in  $k=50$  than in  $k=200$ .

On the other hand, the agglomerative clustering algorithm, resulting in 212 clusters, achieved a mutation score of 100% for  $T_c$  with the test set size being 21. The graph *a* in figure 5.9 shows the efficiency of  $T_c$  and  $T_r$  of five different samples of  $Sc$ , and same test size. The mutation score of  $T_r$  for the five samples is less than 95%. Also the graph *b* of figure 5.9 shows the mutation score of  $T_c$  and  $T_r$  for 48 clusters. The MS for  $T_c$  has decreased considerably well below 95%.

The optimal number of clusters is 200 and 212 resulting from  $k$ -means and agglomerative algorithm. Furthermore, these algorithms result in the reduction of test cases to 19 and 21 from a total of 1608 test cases, this reduced test set is strong enough to achieve a mutation score of 100% or above 99% in case of  $k$ -means algorithm.

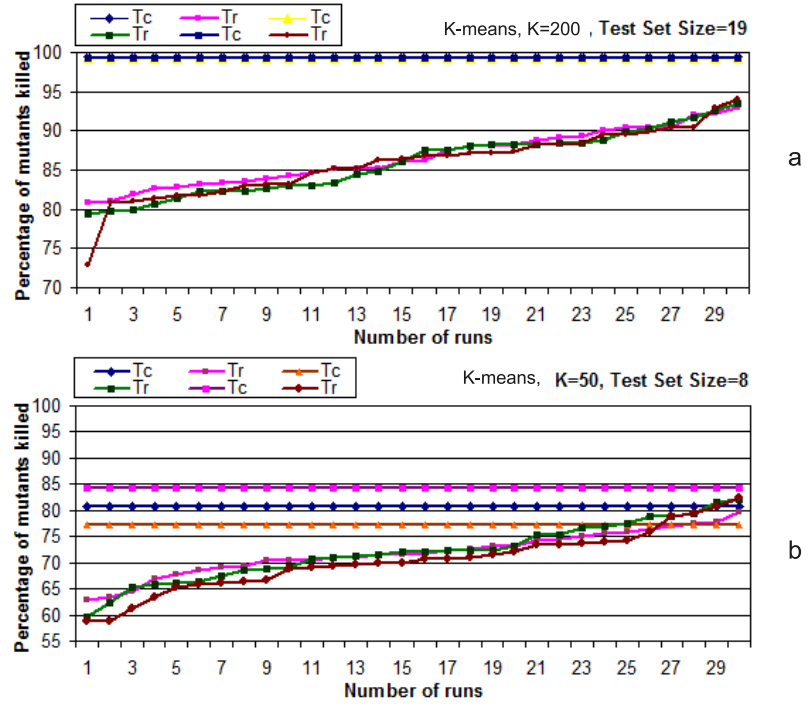
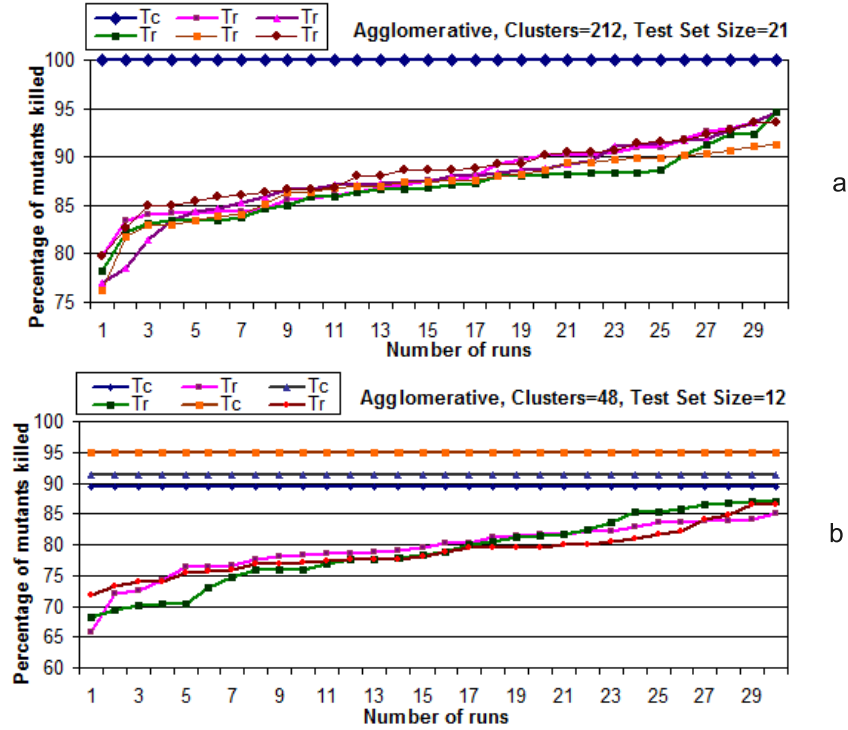

 Figure 5.8: K-means clustering algorithm result on TCAS program for  $k=200$  and  $k=50$ 


Figure 5.9: Agglomerative clustering algorithm result on TCAS program for clusters=212 and clusters=48

### 5.3.3 Results for the Schedule2 Program

The efficiency for  $k$ -means algorithm on the schedule2 program is shown in figure 5.10. The graph *a* for  $k=83$ , shows the MS of 100% for  $Tc$ . However, the MS for  $Tr$  reaches 99.5% at one point. It is also noteworthy that the MS of  $Tr$  starts off at 79.4% in this case. Similarly the graph *b* of figure 5.10 reveals the MS for  $Tc$  and  $Tr$  for  $k=20$ . The MS for  $Tc$  has decreased. Also the MS for  $Tr$ , starting off at 76.5% crosses the MS of  $Tc$  at one point.

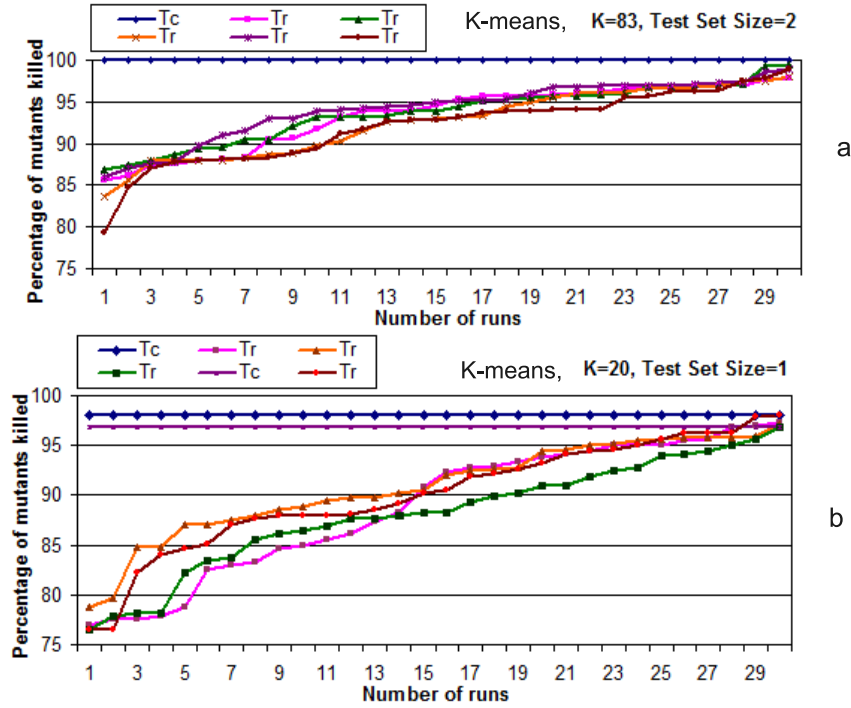


Figure 5.10:  $K$ -means clustering algorithm result on Schedule2 program for  $k=83$  and  $k=20$

The figure 5.11 shows the efficiency results of agglomerative algorithm for 83 and 24 clusters. The MS of  $Tc$  for 83 clusters is 100%, whereas for  $Tr$  it starts off at 79.9% and maximum MS achieved is 99.5%. On the other hand, lowering the cluster value in graph *b*, reveals a MS of maximum 99% and minimum 97.8% for  $Tc$ . However, the MS of  $Tr$  crosses the efficiency of  $Tc$  at one point. Again, the test suite size is reduced to 2 from a total of 1399 test cases.

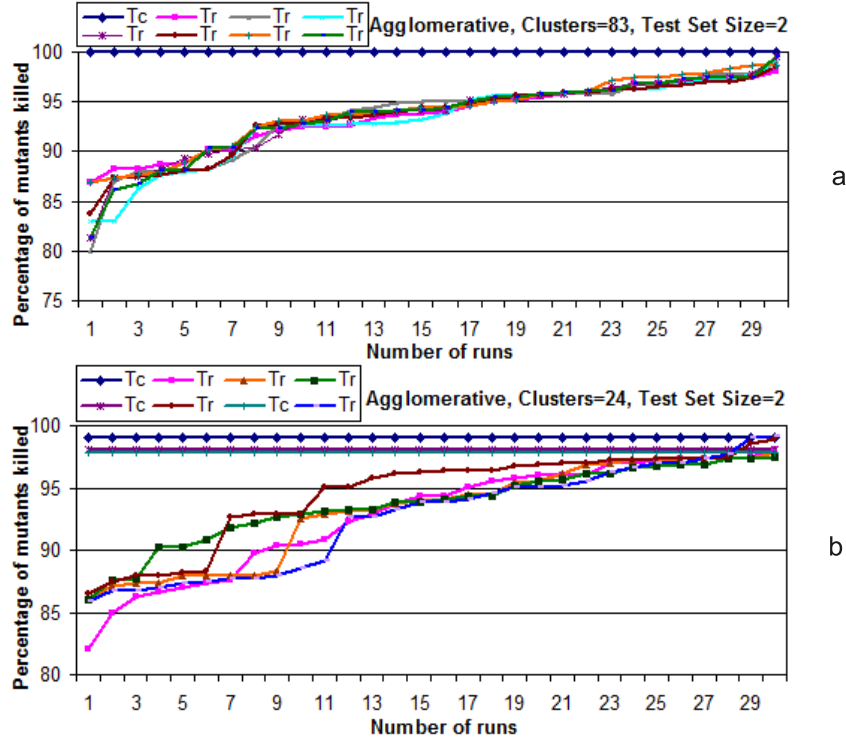


Figure 5.11: Agglomerative clustering algorithm result on Schedule2 program for  $k=83$  and  $k=24$

### 5.3.4 Results for the Totinfo Program

The efficiency results of  $Tc$  for both  $k$ -means algorithm and agglomerative algorithm are given in figures 5.12 and 5.13. The optimal value of the number of clusters is 173 for both of the algorithms. The MS of  $Tc$  in figure 5.12 *a* and figure 5.13 *a* is 100%. It is also evident from the graphs *b* of the figures 5.12 and 5.13 that the MS of the test set  $Tc$  has reduced with reducing the number of mutants.

The test cases are reduced to 6 and 7, by  $k$ -means and agglomerative algorithms respectively, from a total size of 1052. Even though the test cases are reduced, but these test cases achieve strength by achieving a mutation score of 100%.

### 5.3.5 Results for the Printtokens Program

The MS of  $Tc$  for  $k$ -means and agglomerative algorithm is shown in figures 5.14 and 5.15. The *a* graphs in both the figures represent a MS of 100% for  $Tc$ . However, the MS for  $Tc$  is reduced in graphs *b*, although the reduction is still above 95%. Additionally, the test set size of 2021 is reduced to 4.



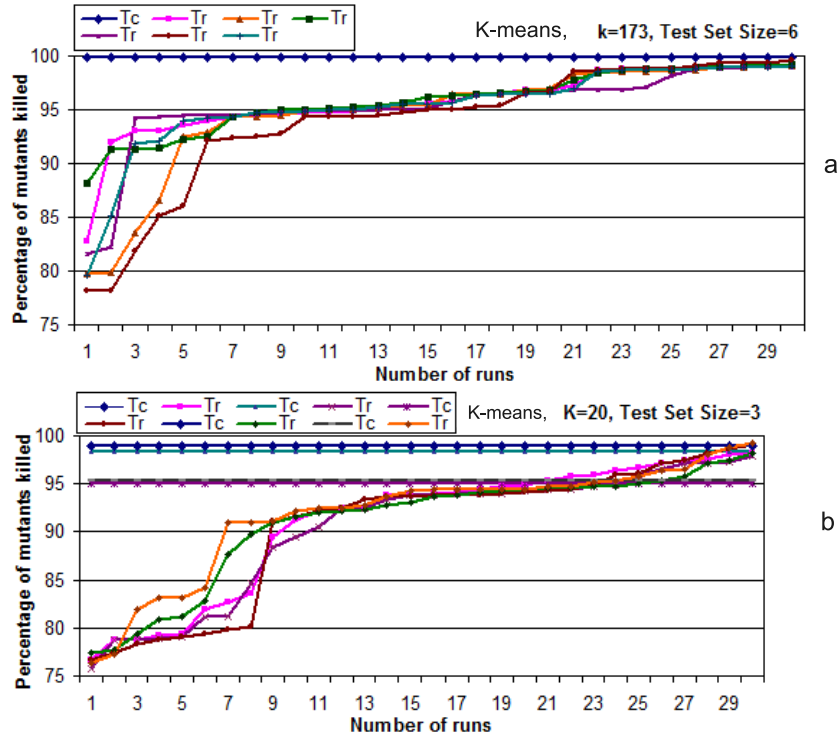


Figure 5.12: K-means clustering algorithm result on Totinfo program for k=173 and k=20

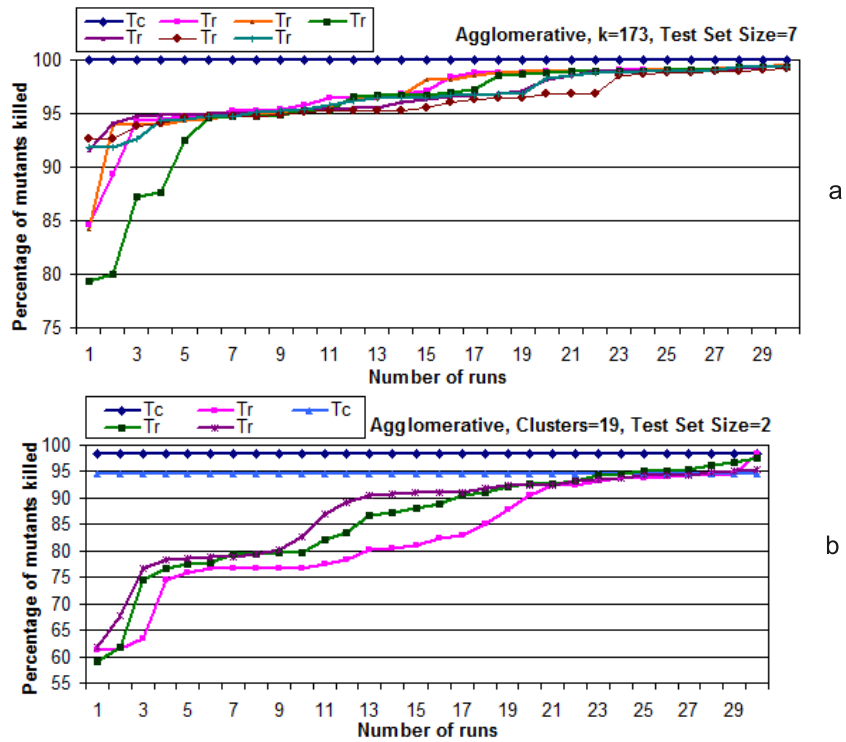


Figure 5.13: Agglomerative clustering algorithm result on Totinfo program for clusters=173 and 19

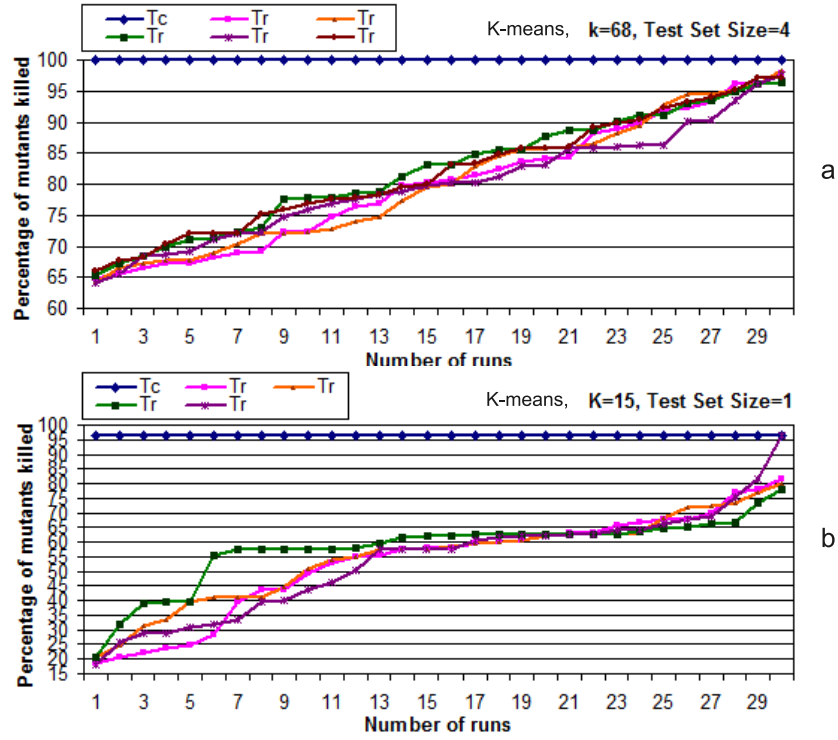
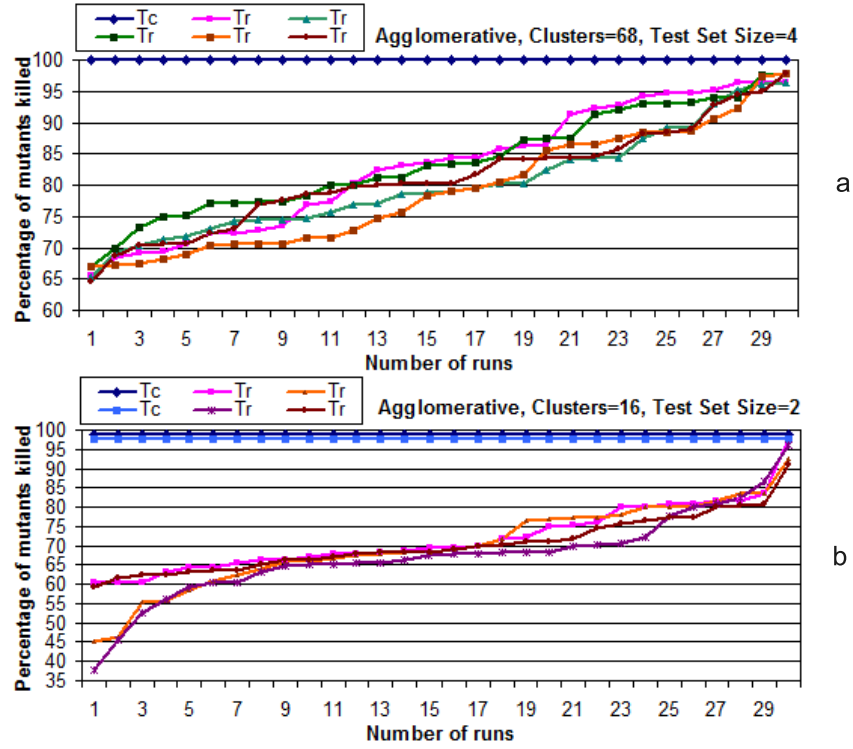

 Figure 5.14: *K*-means clustering algorithm result on Printtokens for  $k=68$  and  $k=15$ 


Figure 5.15: Agglomerative clustering algorithm result on Printtokens for clusters= 68 and 16

## 5.4 Results and Findings

The evaluation results shows that the test set from the clusters  $Tc$  are efficient in killing the mutants than the random test set  $Tr$ , this is particularly true for the TCAS, Schedule2, Totinfo and Printtokens. The  $Tc$  percentage of killing the mutant is always close to being 100% for the optimal cluster values of these programs, whereas the killing percentage of  $Tr$  starts off by killing somewhere around 80% of mutants. However, it is also significant to mention that by decreasing the number of the clusters, the efficiency of the  $Tc$  is greatly affected. Such that, in some cases it becomes below 95%. The MS below 95% is not desirable.

Program	Total # of mutants	Optimal # of clusters, reduced mutants	Total # of test cases	Reduced test cases	Average Mutation Score
Triangle	584	64	34	13	98.9%
TCAS	856	200	1608	19	99.3%
Schedule2	972	83	1399	2	100%
Totinfo	1879	173	1052	6	100%
Printtokens	506	68	2021	4	100%

Table 5.1: Summarized results of k-means algorithm on all five programs

Another important point worth mentioning is that the clustering works better on complex programs, as the evaluation shows that a MS of 100% is achieved in case of TCAS, Schedule2, Totinfo and Printtokens programs. With a considerably much smaller and less complex program like triangle program, the MS is never 100% for  $Tc$ .

Program	Total # of mutants	Optimal # of clusters, reduced mutants	Total # of test cases	Reduced test cases	Average Mutation Score
Triangle	584	62	34	12	95.6%
TCAS	856	212	1608	21	100%
Schedule2	972	83	1399	2	100%
Totinfo	1879	173	1052	7	100%
Printtokens	506	68	2021	4	100%

Table 5.2: Summarized results of agglomerative algorithm on all five programs

The evaluation results indicate that there are certain optimal values of the number of clusters, at which a mutation adequate test set is achieved. These values are optimal because of a number of reasons. Firstly, because these reduce the number of mutants, secondly a test set is produced with a 100% MS, thirdly, the size of this mutation adequate test set is less than the actual size of the test set. Hence, in addition to reducing the number of the clusters, the number of the test cases are also reduced. See tables 5.1 and 5.2, for a complete overview of the optimal values of the clusters and their effect on the mutants, test cases and their adequacy. The tables 5.1 and 5.2 summarizes our results and findings from the evaluation for both k-means and agglomerative algorithms.

## Chapter 6

# Conclusion

This section of the report elaborates the conclusion drawn from the empirical study conducted in this project.

This paper defines a novel approach to overcome one of the problems of mutation testing, i.e., large number of mutants. It is the originality of the research that makes it a significant contribution. Although work is done in this area previously, but that does not provide an overall optimal solution, as discussed in chapter 3.

Empirical results reveal that in spite of decreasing the large number of the mutants, the power of the set of the mutants is not reduced, which means the strength of the test set is not minimized. We get 100% mutation score for the test set generated from the clusters, this is what we hypothesized.

The empirical study was conducted on five different programs of different lengths and varying number of mutants and test cases. We have based our results and findings on the results of all the five programs. Here the size and complexity of the program is arguable. The test set  $T_c$  from large and complex programs, like TCAS, Schedule2, Totinfo and Printtokens, tend to do extremely well by achieving a mutation score of 100%, with an exception of TCAS clustered by  $k$ -means algorithm for which the MS is 99.3% Whereas, for small programs, like Triangle program of 50 LOC, the test set  $T_c$  never achieve a mutation score of 100% although it is close and below 95%. According to Offutt in [9], a test set with a mutation score below 95% is not effective. This leads us to say that this approach of mutation clustering, works extremely well for large and complex programs and better for small programs.

Another thing worth mentioning here is that by clustering the size of the mutants is reduced, but along with that the size of the test set is also minimized, see tables 5.1 and 5.2. Although the test set is minimized, yet it is strong and efficient enough to kill all the mutants, thereby achieving a mutation score of 100%. For example, in case of Schedule2 program, the  $k$ -means algorithm reduced the mutants to 83 from a total size of 972, consequently, the test cases are reduced to 2 from a test set of 1399.

We consider this project a great contribution in the particular research area. The reason for this is that it has provided a novel way to deal with the problem of mutation

testing. This claim is backed up by the positive results from the evaluation.

## Chapter 7

# Future Enhancement

Due to the time constraint, only five programs were used. Which were evaluated to backup our results. However, the empirical study can be broadened by including and evaluating more programs. It would be interesting to see the results based on larger set of programs.

Furthermore, this project can be extended by implementing some other clustering algorithms, apart from  $k$ -means and agglomerative clustering techniques. The other possible implementation of algorithms could be divisive clustering algorithm. This would be an interesting enhancement to see how this technique works with other algorithms.

# Bibliography

- [1] A. J. Offutt, A Practical System for Mutation Testing: Help for the Common Programmer, Proceedings of the IEEE International Test Conference on TEST: The Next 25 Years, Year of Publication: 1994, Pages: 824-830, ISBN: 0-7803-2103-0
- [2] T. Kanungo, D. M. Mount, N. S. Netanyahu, C. Piatko, R. Silverman, A. Y. Wu, An Efficient k-Means Clustering Algorithm: Analysis and Implementation, IEEE Transactions on Pattern Analysis and Machine Intelligence 24(7), 2002, Pages: 881-892.
- [3] A. K. Jain, M. N. Murty, P. J. Flynn, Data Clustering: A Review, ACM Computing Surveys (CSUR), Volume 31, Issue 3 (September 1999), Year of Publication: 1999, Pages: 264-323, ISSN: 0360-0300
- [4] G. Fung. A Comprehensive Overview of Basic Clustering Algorithms, June 22, 2001
- [5] M. J. Harrold. Testing: A Roadmap, College of Computing, In Future of Software Engineering, 22nd International Conference on Software Engineering, June 2000, Pages: 61-72.
- [6] A. J. Offutt, R. H. Untch. Mutation 2000: Uniting the Orthogonal, Kluwer International Series On Advances In Database Systems, Mutation testing for the new century, Section: Mutation: cost reduction, Year of Publication: 2001, Pages: 34-44
- [7] A. P. Mathur, W. E. Wong, Reducing the cost of mutation testing: an empirical study, Journal of Systems and Software, Volume 31, Issue 3 (December 1995), Pages: 185-196, Year of Publication: 1995, ISSN: 0164-1212
- [8] W. E. Wong, M. E. Delamaro, J. C. Maldonado, and A. P. Mathur, Constrained mutation in C programs, In Proceedings of VIII Symposium on Software Engineering, Oct 1994. in Curitiba, Brazil.
- [9] A. J. Offutt, G. Rothmel, C. Zapf, An experimental determination of sufficient mutation operators, ACM Transactions on Software Engineering and Methodology, vol. 5 (2), Pages: 99-118, 1996.
- [10] W. E. Wong. On mutation and data flow, Phd Thesis, 1993
- [11] T. A. Budd. Mutation analysis of program test data. Ph.D. thesis, Yale Univ., NewHaven CT, 1980.



- [12] A. P. Mathur. Performance, effectiveness, and reliability issues in software testing. In Proceedings of the 15th Annual International Computer Software and Applications Conference ,Tokyo, Japan, Sept. 1991, Pages: 604-605.
- [13] A. T. Acree. On mutation. Phd thesis, Georgia Institute of Technology, Atlanta Georgia 1980, Technical Report GIT ICS 80/12.
- [14] V. Faber. Clustering and the Continuous k-means Algorithm. Los Alamos Science, vol. 22, 1994, Pages: 138-144.
- [15] M. R. Anderberg. Cluster Analysis for Applications. Academic Press, Inc., New York, NY, 1973.
- [16] K. Daniels. Learning the Threshold in Hierarchical Agglomerative Clustering, Proceedings of the 5th International Conference on Machine Learning and Applications, Year of Publication:2006, Pages: 270-278, ISBN:0-7695-2735-3
- [17] K. Adamopoulos, M. Harman, R. M. Hierons. How to overcome the equivalent mutant problem and achieve tailored selective mutation using co-evolution. Proc. Genetic and Evolutionary Computation Conference (GECCO 2004), LNCS 3103, Springer, Berlin Heidelberg New York, Pages: 1338-1349.
- [18] A. J. Offutt, G. Rothermel, C. Zapf. An experimental evaluation of selective mutation. Proceedings of the Fifteenth International Conference on Software Engineering, IEEE Computer Society Press: Baltimore, Maryland, 1993; Pages: 100-107.
- [19] Y. Jia and M. Harman. Constructing Subtle Faults Using Higher Order Mutation Testing, 8th International Working Conference on Source Code Analysis and Manipulation (SCAM'08) Beijing, China, 28th-29th September 2008. To appear.
- [20] T.H. Cormen, C.E. Leiserson, R.L. Rivest, and C. Stein. Introduction to Algorithms, Second Edition. The MIT Press, September 2001.
- [21] Y. Jia and M. Harman. Milu: A Customizable, Runtime-Optimized Higher Order Mutation Testing Tool for the Full C Language, TAIC PART'08, Windsor, UK, 29th-31st August 2008.
- [22] K. Teknomo. Similarity Measurement, <http://people.revoledu.com/kardi/tutorial/Similarity>

# Appendix A

## Mutants data for Triangle program

- 584 mutants and a test set of 34 test cases.

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3 11111111111111111111111111111111	33 0100111000101100000000001111100000	63 00000000000000000000000000000000
4 11111111111111111111111111111111	34 0100111000101100000000001111100000	64 0100111000101100000000001111100000
5 0100111000101100000000001111100010	35 00000000000000000000000000000000	65 0100111000101100000000001111100000
6 00000000000000000000000000000000	36 011111111110110000111111111111101	66 0100111000101100000000001111100000
7 0100111000101100000000001111100010	37 011111111110110000111111111111101	67 0100111000101100000000001111100000
8 0100111000101100000000001111100010	38 0100111000101100000000001111100000	68 00000000000000000000000000000000
9 00000000000000000000000000000000	39 00000000000000000000000000000000	69 010111111110110000001111111111101
10 0100111000101100000000001111100010	40 0100111000101100000000001111100000	70 010111111110110000001111111111101
11 0100111000101100000000001111100000	41 0100111000101100000000001111100000	71 0100111000101100000000001111100000
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13 0100111000101100000000001111100010	43 0100111000101100000000001111100000	73 0100111000101100000000001111100000
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15 0100111000101100000000001111100010	45 00000000000000000000000000000000	75 00000000000000000000000000000000
16 000010000000100000000000001000010	46 0100111000101100000000001111100000	76 0100111000101100000000001111100000
17 0100111000101100000000001111100000	47 0100111000101100000000001111100000	77 0100111000101100000000001111100000
18 0100111000101100000000001111100010	48 0100111000101100000000001111100000	78 00000000000000000000000000000000
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20 0100111000101100000000001111100010	50 0100111000101100000000001111100000	80 0100111000101100000000001111100000
21 00000000000000000000000000000000	51 0100111000101100000000001111100000	81 0100111000101100000000001111100000
22 00000000000000000000000000000000	52 0100111000101100000000001111100000	82 010011111001100000001111011111101
23 00000000000000000000000000000000	53 0100111000101100000000001111100000	83 010011111001100000001111011111101
24 00000000000000000000000000000000	54 00000000000000000000000000000000	84 00000000000000000000000000000000
25 00000000000000000000000000000000	55 00000000000000000000000000000000	85 010011111110110000001111111111101
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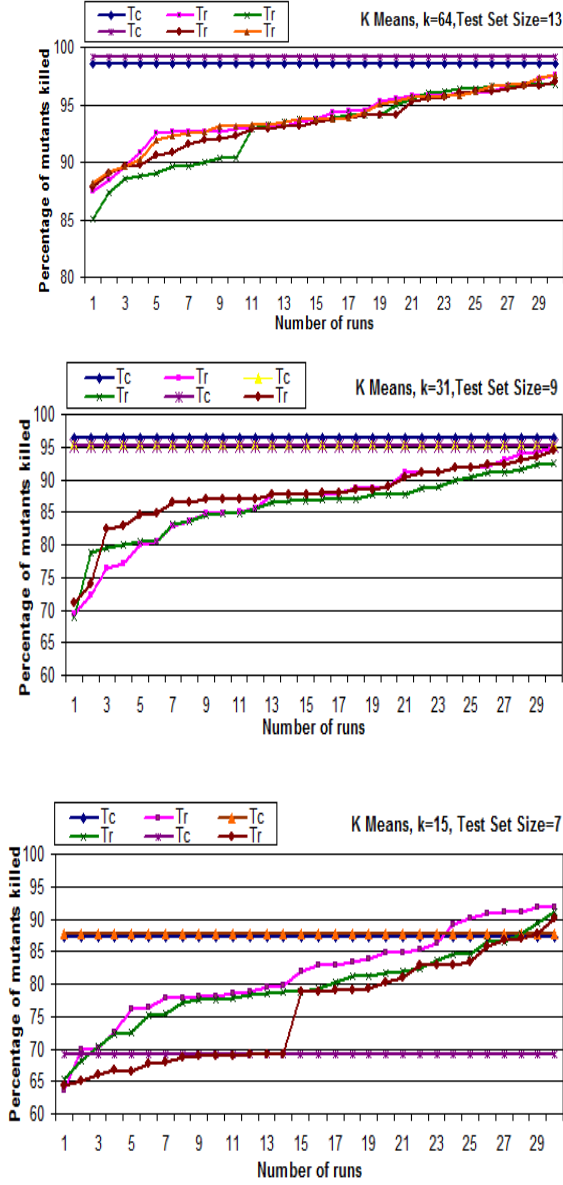
# Appendix B

## Experiment Results

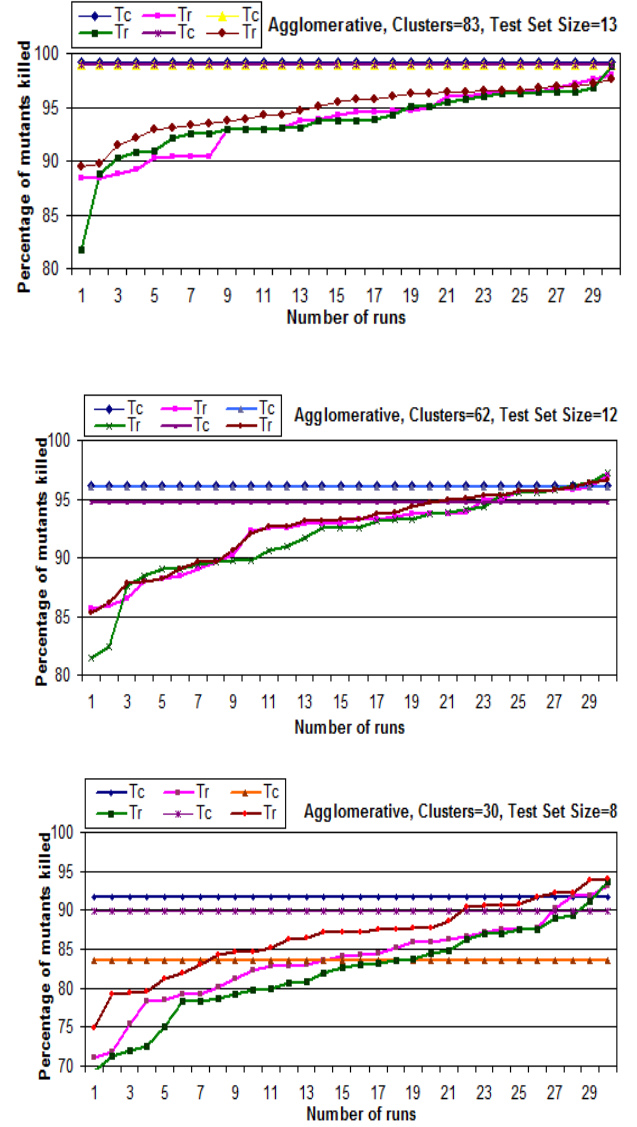
Results of Triangle program.....	IX
Results of TCAS program.....	X
Results of Schedule2 program.....	XI
Results of Totinfo Program.....	XII
Results of Printtokens program.....	XIII

## Triangle Program

### K-means clustering Algorithm



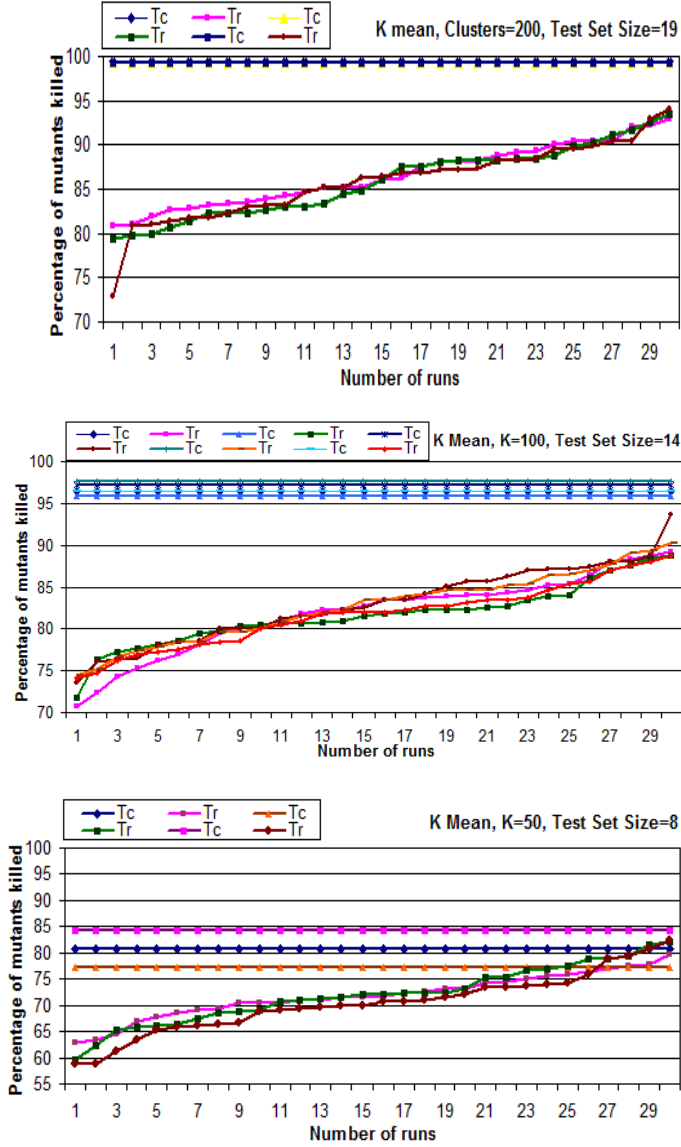
### Agglomerative clustering algorithm



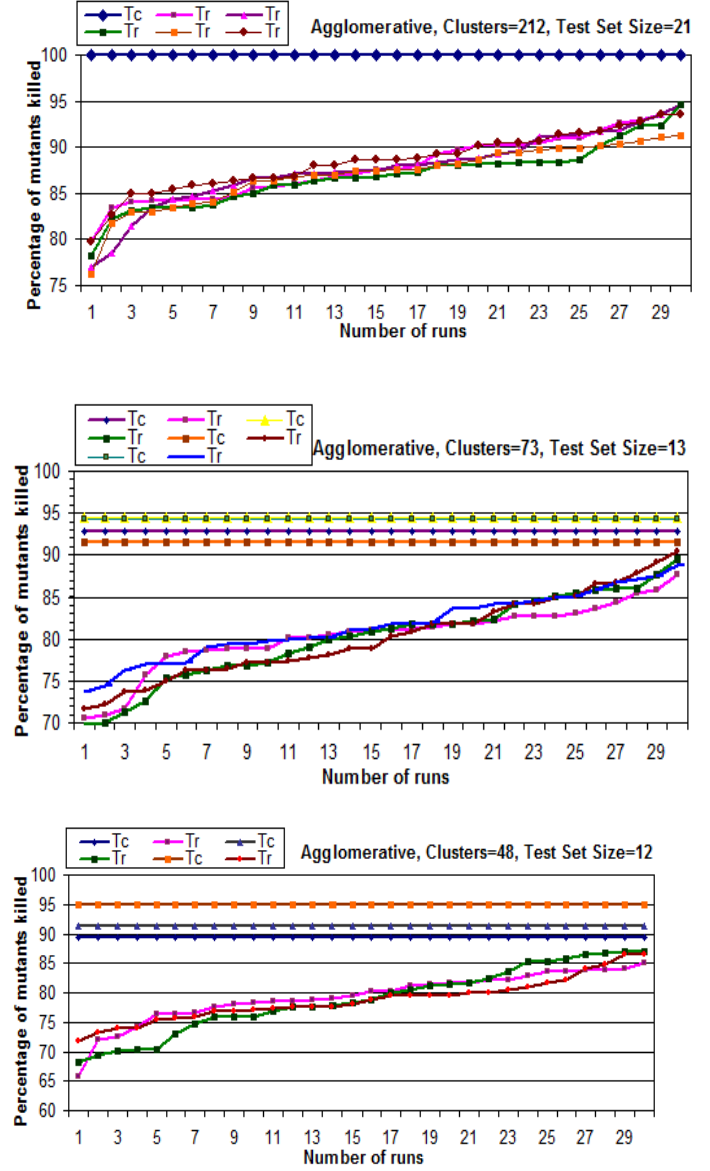


## TCAS program

### K-Means Clustering algorithm

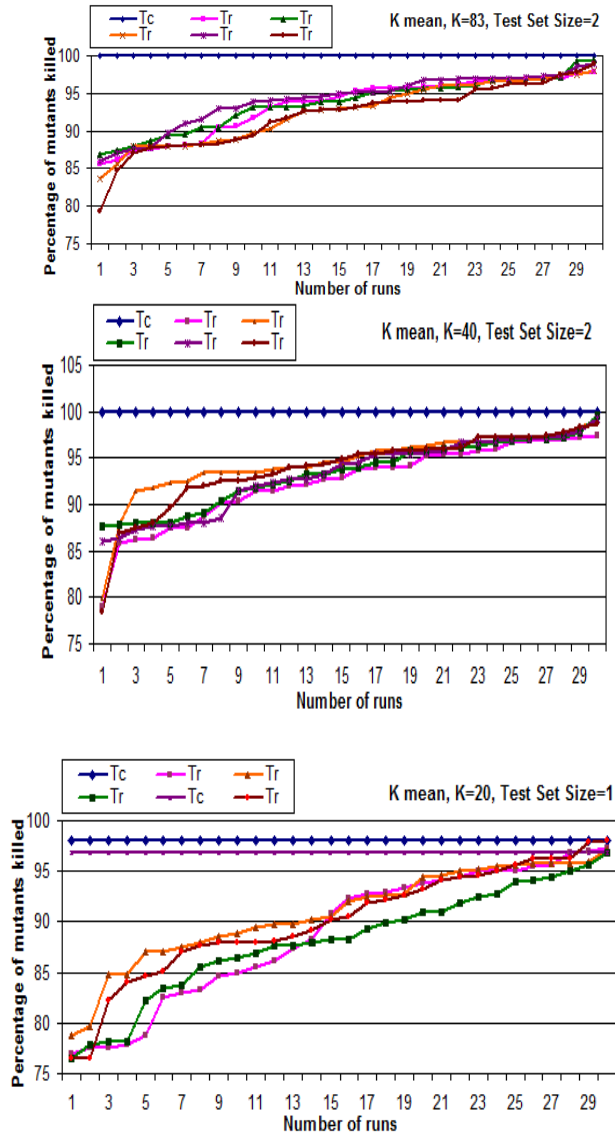


### Agglomerative clustering algorithm

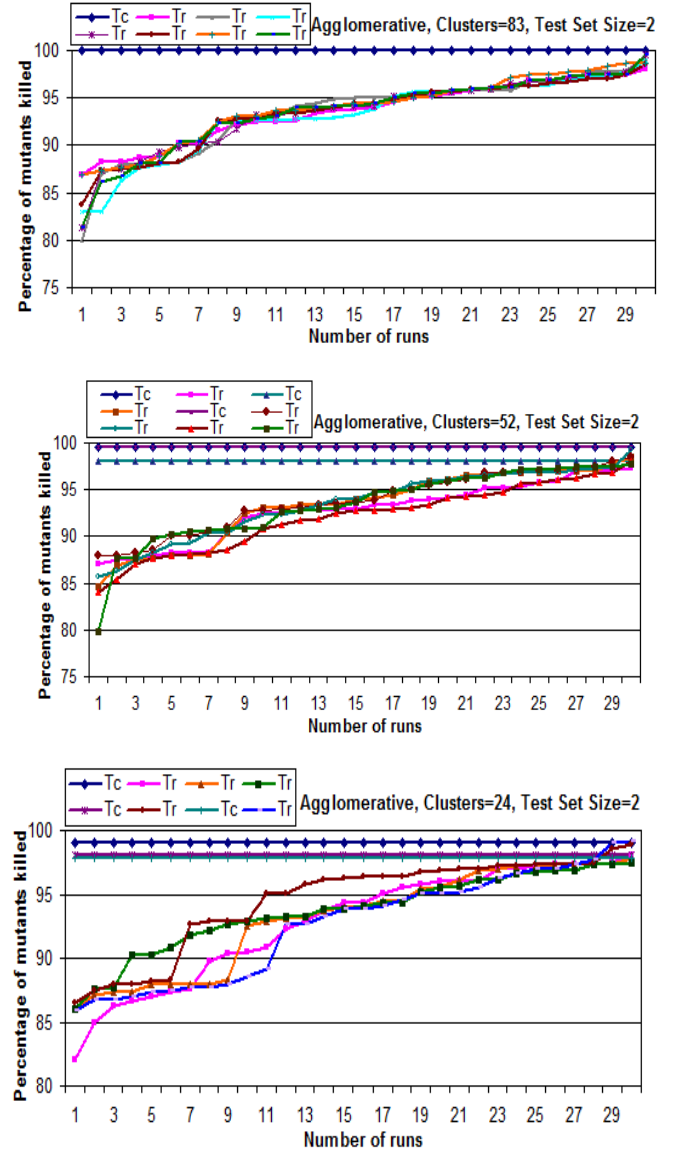


## Schedule2 Program

K-means clustering Algorithm

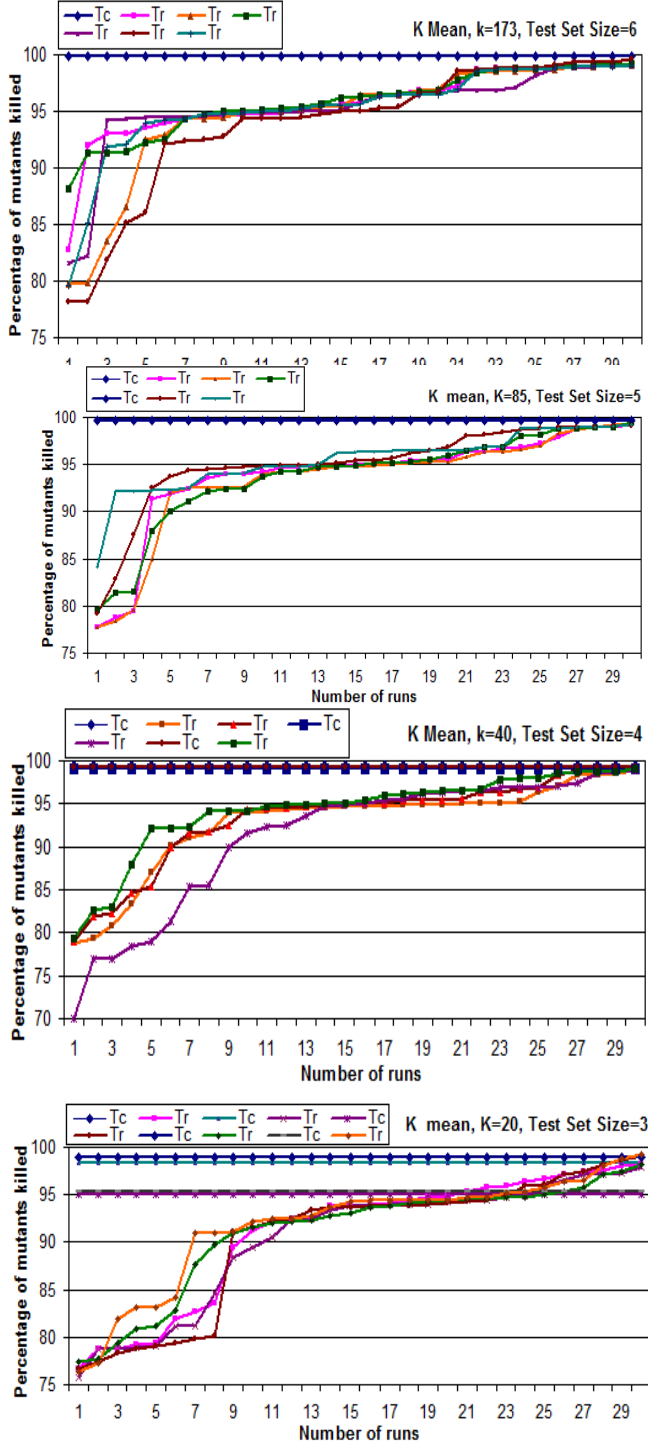


Agglomerative clustering algorithm

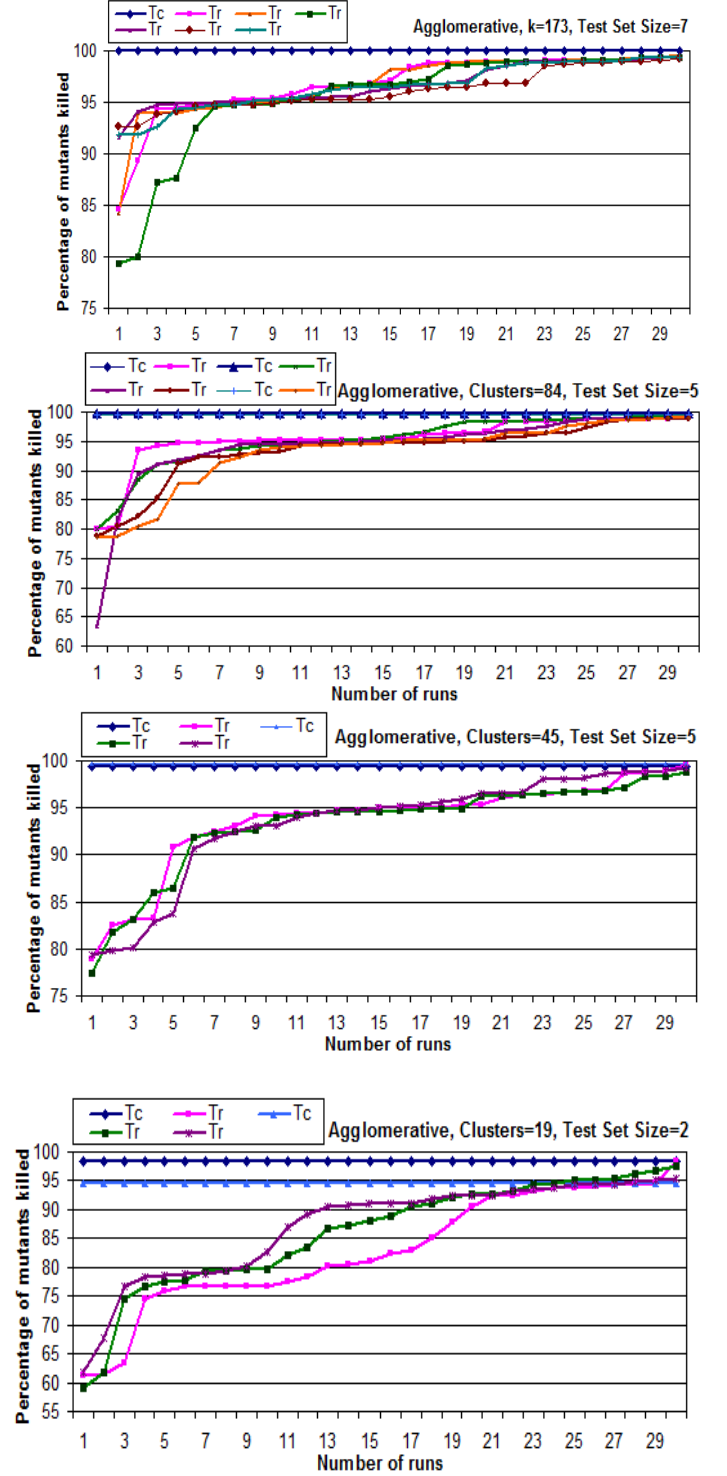


# Totinfo Program

## K-means clustering Algorithm

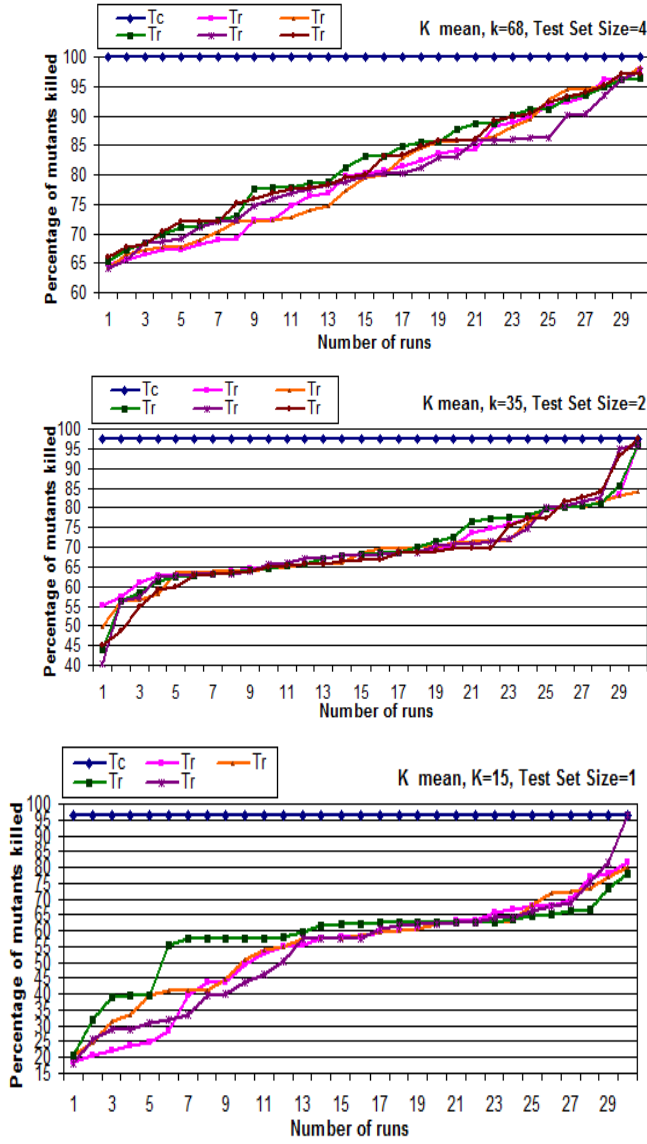


## Agglomerative clustering algorithm

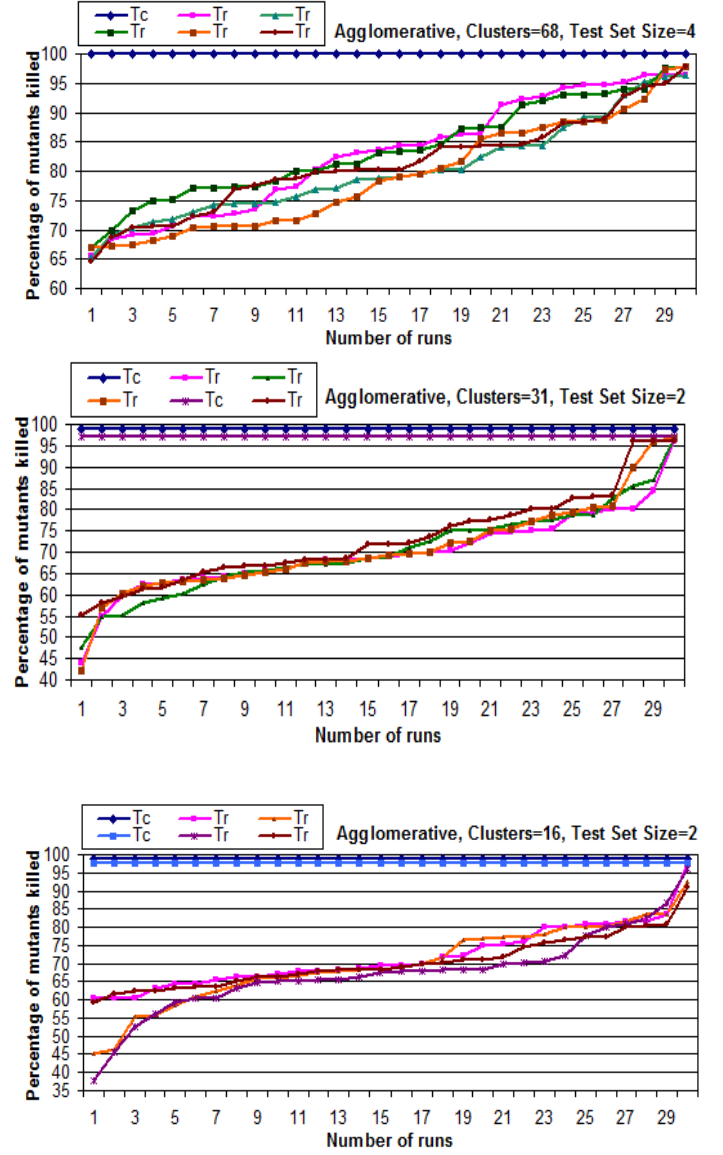


## Printtokens Program

K-means clustering Algorithm



Agglomerative clustering algorithm



# Appendix C

## *K*-mean Clustering Class

The project is implemented in Visual Studio 2005 C#.Net.

This class has the following functions:

- ReadMutants(): Gets the list of the entire size of mutants.
- CalculateCentroid(): To calculate the centroids
- CalculateDistance(): To calculate the distance of each mutant to the centroid
- UpdateClusters(): Updates the clusters based on minimum distance
- WriteToFile(): Writes to file the clustered mutants

```
using System;
using System.Collections.Generic;
using System.Text;
using System.Collections;
using System.IO;

////////// K Mean Clustering Algorithm..//////////
////////// based on careful selection of initial k points //////////

namespace GUI
{
    class KMeanAlgo
    {
        int NumberOfAlgoRuns=0;// specifies how many times we need to run the algo
        string[,] mutantsArray;
        int BitSize = 0;
        int NumberOfClusters; // number of k
        int[,] newDistanceMatrix;
        int[,] oldDistanceMatrix;
        int[,] InitialDistance;
        float[,] HammingDistanceArray;
        float[,] Centroids;
        int CentroidIteration = 0;
        int NotEqualFlag = 0;
        int[] AddBitsArray; // used for calculating the centroid
        int[,] AllMutants;// this is the array that copies all the mutant bit by bit
        Random rand = new Random(); // function for random numbers
        // to avoid selecting same indexes for initial k values
        ArrayList NoRepetitionIndex = new ArrayList();
        // saves different mutants for the initial K
        ArrayList NoRepetitionMutant = new ArrayList();

        ////////////
        ///// function that gets the mutants //////////

        public void ReadMutants(string[,] mutantsArray1, int ClusterNumber, int NumberOfAlgoRuns1)
        {
            NumberOfAlgoRuns = NumberOfAlgoRuns1;

            while (NumberOfAlgoRuns != 0) // runs the algorithm for specified number of times
            {
                NumberOfAlgoRuns = NumberOfAlgoRuns - 1;
```

```

        mutantsArray = new string[mutantsArray1.GetLength(0), mutantsArray1.GetLength(1)];
        Array.Copy(mutantsArray1, mutantsArray, mutantsArray1.Length);

        string mutantString = mutantsArray[1, 1];
// gives the length or number of bits of the mutant
        BitSize = mutantString.Length;

        // to get the size of the number of clusters by a loop
        NumberOfClusters = 0;
        for (int kNumber = 0; kNumber < ClusterNumber; kNumber++)
        {
            NumberOfClusters = NumberOfClusters + 1;
        }
// saves the smallest distance as 1's and rest as 0's
        newDistanceMatrix = new int[mutantsArray.GetLength(0), NumberOfClusters];
        oldDistanceMatrix = new int[mutantsArray.GetLength(0), NumberOfClusters];
        InitialDistance = new int[NumberOfClusters, mutantsArray.GetLength(0)];

        HammingDistanceArray = new float[ mutantsArray.GetLength(0), NumberOfClusters];
// 2-d array to, for k number of clusters and for the size of the mutant bits
        Centroids = new float[ClusterNumber, BitSize];

        AllMutants= new int[mutantsArray.GetLength(0), BitSize];

////////////////////////////////////
///////// saves all the mutants bit by bit in the array AllMutants////////

        for (int rows = 0; rows < mutantsArray.GetLength(0); rows++)
        {
            mutantString= mutantsArray[rows,1];

            for (int col = 0; col < mutantString.Length; col++)
            {
                if (System.Convert.ToInt32(mutantString[col]) == 49)
                {
                    AllMutants[rows, col] = 1;
                }

                else if (System.Convert.ToInt32(mutantString[col]) == 48)
                {
                    AllMutants[rows, col] = 0;
                }
            }
            Calculate_Centroid();
        } // ends while of the number of runs
    }

////////////////////////////////////
///////// FUNCTION TO CALCULATE THE CENTROID //////////
////////////////////////////////////

public void Calculate_Centroid()
{
    int CentroidsSelected=0;
    CentroidIteration = CentroidIteration + 1;
    string MutantString;
    if (CentroidIteration == 1)    //initial K selection
    {
        int selectInitialCentroids;
        int select = 0;

        while (CentroidsSelected<NumberOfClusters)
        {
            selectInitialCentroids= rand.Next(mutantsArray.GetLength(0)-1);
            if (NoRepetitionIndex.Count > 0)
            {
                MutantString= mutantsArray[selectInitialCentroids,1];

                // this loop iterates and checks that the mutant has not already been selected of initial K
                // it prevents repetition of mutant selection
                for (int check = 0; check < NoRepetitionIndex.Count; check++)
                {
                    if (System.Convert.ToInt32(NoRepetitionIndex[check]) != selectInitialCentroids &
                        System.Convert.ToString(NoRepetitionMutant[check]) != MutantString)
                    {
                        select = 1;
                    }
                    else
                    {
                        select = 0;
                        break;
                    }
                }
            }
            else
            {
                select = 1;
            }
        }
    }
}

```

```

    }

    if (select == 1)
    {
        NoRepetitionIndex.Add(selectInitialCentroids);
        MutantString= mutantsArray[selectInitialCentroids,1];
        NoRepetitionMutant.Add( MutantString);
        for (int loop = 0; loop < MutantString.Length; loop++)
        {
            if (System.Convert.ToInt32(MutantString[loop]) == 49)
            {
                Centroids[CentroidsSelected, loop] = 1;
            }
            else if (System.Convert.ToInt32(MutantString[loop]) == 48)
            {
                Centroids[CentroidsSelected, loop] = 0;
            }
        }

        CentroidsSelected = CentroidsSelected + 1;
        select = 0;
    }
} // ends while
} // ends if

else if (CentroidIteration > 1) // more than 1 iteration
{
    int countOnes = 0;
    // iterates the columns, (cluster by cluster)
    for (int distCol = 0; distCol < newDistanceMatrix.GetLength(1); distCol++)
    {
        countOnes = 0;
        AddBitsArray = new int[BitSize];
        // iterates the rows to find 1
        for (int distRow = 0; distRow < newDistanceMatrix.GetLength(0); distRow++)
        {
            if (newDistanceMatrix[distRow, distCol] == 1)
            {
                countOnes = countOnes + 1;
                // now iterate the columns of ALLMUTANTS array at that row where it is 1
                for (int AllMutantIndex = 0; AllMutantIndex < AllMutants.GetLength(1); AllMutantIndex++)
                {
                    AddBitsArray[AllMutantIndex] =
                    AddBitsArray[AllMutantIndex] + AllMutants[distRow, AllMutantIndex];
                }
            }
        } // ends for loop for distRow

        //////////////// now here calculate the centroid by dividing by the CountOnes and save in
        ////////////////the array Centroid for each cluster
        for (int loop = 0; loop < AddBitsArray.Length; loop++)
        {
            float CentroidValue = (float)AddBitsArray[loop] / (float)countOnes;
            CentroidValue = (float)(Math.Truncate(CentroidValue * 10) / 10);

            //***** saves the calculated centroid column by column
            Centroids[distCol,loop]= CentroidValue;
        }

    } // ends distCol

} // ends else if (CentroidIteration > 1)

Calculate_Distance();
}

//////////////////////////////////////
////////////////////////////////////// CALCULATE DISTANCE//////////////////////////////////////
//////////////////////////////////////

public void Calculate_Distance()
{
    float Difference = 0;
    float AddedValues = 0;
    int col;
    newDistanceMatrix= new int[mutantsArray.GetLength(0), NumberOfClusters];

    //////////////////////////////////// CALCULATE HAMMING DISTANCE//////////////////////////////////////

    for (int rows = 0; rows < AllMutants.GetLength(0); rows++) // rows of the all mutants array
    {
        // rows of the Centroids Array
        for (int CentroidRow = 0; CentroidRow < Centroids.GetLength(0); CentroidRow++)
        {
            // iterates columns of both arrays(AllMutants and Centroids)
            for (col = 0; col < Centroids.GetLength(1); col++)
            {

```

```

        if ((float)AllMutants[rows, col] > Centroids[CentroidRow, col])
        {
            Difference = (float)AllMutants[rows, col] - Centroids[CentroidRow, col];
        }

        else
        {
            Difference = Centroids[CentroidRow, col] - (float)AllMutants[rows, col];
        }

        AddedValues = Difference + AddedValues;
    } // ends for loop of col
    HammingDistanceArray[rows, CentroidRow] = AddedValues;
    AddedValues = 0;
    Difference = 0;
} //ends for loop of centroidRow

} // ends the for loop for row

////////// ASSIGN 0'S AND 1'S TO THE DISTANCE MATRIX //////////

float SmallestValue = 0;
int SaveColumn = 0;

for (int DistanceRow = 0; DistanceRow < HammingDistanceArray.GetLength(0); DistanceRow++)
{
    for (int DistanceCol = 0; DistanceCol < HammingDistanceArray.GetLength(1); DistanceCol++)
    {
        if (DistanceCol == 0)
        {
            SmallestValue = HammingDistanceArray[DistanceRow, DistanceCol];
            SaveColumn = DistanceCol;
        }
        else
        {
            if (SmallestValue < HammingDistanceArray[DistanceRow, DistanceCol])
            {
            }
            else if (SmallestValue > HammingDistanceArray[DistanceRow, DistanceCol])
            {
                SmallestValue = HammingDistanceArray[DistanceRow, DistanceCol];
                SaveColumn = DistanceCol;
            }
        }
    }
    // ends loop DistanceCol

    newDistanceMatrix[DistanceRow, SaveColumn]=1;

} // ends loop DistanceRow

////////// NOW COPY THE NEWDISTANCEMATRIX INTO THE OLD DISTANCE MATRIX //////////

// first check rhat the two matrix are not equal
NotEqualFlag=0;
for (int row = 0; row < newDistanceMatrix.GetLength(0); row++)
{
    for (int coll = 0; coll < newDistanceMatrix.GetLength(1); coll++)
    {
        if (oldDistanceMatrix[row, coll] == newDistanceMatrix[row, coll])
        {
            NotEqualFlag=0;    // EQUALLLLLL
        }
        else if (oldDistanceMatrix[row, coll] != newDistanceMatrix[row, coll])
        {
            NotEqualFlag=1;
            break;
        }
    }
    if (NotEqualFlag == 1)
    {
        break; // breaks from the row loop
    }
} // ends row

if (NotEqualFlag==1)
{
    // copy 2D Arrays
    Array.Copy(newDistanceMatrix, oldDistanceMatrix, oldDistanceMatrix.Length);
    // here update the cluster values and assign the cluster values to the mutants they belong to
    Update_Clusters();
}
else if (NotEqualFlag==0)
{
    // means the distances has become same and now thet mutants willnot converge or move
    // write to file here
    //KMeanSecondMethod file

```



```

    Update_Clusters();    // update before writing to file
}

} // ends the function Calculate_distance

////////////////////////////////////
//////////////////////////////////// FUNCTION TO UPDATE THE CLUSTER VALUES AND ASSIGN CLUSTER ///////////////////////////////////
////////////////////////////////////VALUES TO THE MUTANTS THEY BELONG TO////////////////////////////////////
////////////////////////////////////

public void Update_Clusters()
{
    // means which cluster it belongs to... 1, 2, 3 ,... so on
    int ClusterValue = 0;
    // iterates the columns, (cluster by cluster)
    for (int distCol = 0; distCol < newDistanceMatrix.GetLength(1); distCol++)
    {
        ClusterValue = ClusterValue+1;
        for (int distRow = 0; distRow < newDistanceMatrix.GetLength(0); distRow++)
        {
            if (newDistanceMatrix[distRow, distCol] == 1)
            {
                mutantsArray[distRow, 0] = System.Convert.ToString(ClusterValue);
            }
        }
    }
    // ends distCol

    if (NotEqualFlag == 1)
    {
        Calculate_Centroid();
    }
    else if (NotEqualFlag == 0)    // if the oldDistanceMatrix and newDistanceMatrix are same
    {
        WriteToFile();
        SanityFileWrite();
    }
}

////////////////////////////////////
//////////////////////////////////// WRITE THE CLUSTERED MUTANTS TO FILE ///////////////////////////////////
////////////////////////////////////

public void WriteToFile()
{
    // Specify file, instructions, and privileges
    FileStream file = new FileStream("KMeanSecondMethod.txt", FileMode.OpenOrCreate, FileAccess.ReadWrite);
    int ClusterValues=1;
    StreamWriter sw = new StreamWriter(file);
    string line;

    if (file.Length == 0)    // if file is initially empty then write on it
    {
        sw.WriteLine("*****Initial K values *****");
        for (int ind = 0; ind < NoRepetitionMutant.Count; ind++)
        {
            sw.WriteLine(NoRepetitionMutant[ind]);    // write all the initially selected k mutants
        }
        sw.WriteLine("Clustered mutants");
        while (ClusterValues <= NumberOfClusters)
        {
            sw.WriteLine(ClusterValues);
            for (int rows = 0; rows < mutantsArray.GetLength(0); rows++)
            {
                if (mutantsArray[rows, 0] == System.Convert.ToString(ClusterValues))
                {
                    sw.WriteLine(mutantsArray[rows, 1]);
                }
            }
            ClusterValues = ClusterValues + 1;
        }
    }
    // ends if (file.length ==0)

    else
    {
        StreamReader sr = new StreamReader(file);
        line = sr.ReadLine();
        while (line != null)    // read the file until blank line is read
        {
            line = sr.ReadLine();
        }
        sw.WriteLine("*****Initial K values *****");
        for (int ind = 0; ind < NoRepetitionMutant.Count; ind++)
        {
            sw.WriteLine(NoRepetitionMutant[ind]);
        }
    }
}

```

```

    }
    sw.WriteLine("Clustered mutants");
    while (ClusterValues <= NumberOfClusters)
    {
        sw.WriteLine(ClusterValues);
        for (int rows = 0; rows < mutantsArray.GetLength(0); rows++)
        {
            if (mutantsArray[rows, 0] == System.Convert.ToString(ClusterValues))
            {
                sw.WriteLine(mutantsArray[rows, 1]);
            }
        }
        ClusterValues = ClusterValues + 1;
    }
    sw.WriteLine("*****");
} // ends else
sw.Close();
}

////////////////////////////////////
//////////////////////////////////// FUNCTION TO COUNT THE NUMBER
//////////////////////////////////// OF MUTANTS IN EACH CLUSTER////////////////////////////////////
////////////////////////////////////

public void SanityFileWrite()
{
    // Specify file, instructions, and privileges
    FileStream filee = new FileStream("Sanity_Check.txt", FileMode.OpenOrCreate, FileAccess.ReadWrite);
    string linee;
    StreamWriter Sww = new StreamWriter(filee);
    int pass_Mutants_Length;
    pass_Mutants_Length = newDistanceMatrix.GetLength(0);
    int TotalClusters = newDistanceMatrix.GetLength(1);

    //***** Write to file *****//
    if (filee.Length == 0) // if file is initially empty them write on it
    {
        Sww.WriteLine(TotalClusters);
        for (int col = 0; col < TotalClusters; col++)
        {
            for (int row = 0; row < newDistanceMatrix.GetLength(0); row++)
            {
                Sww.WriteLine(newDistanceMatrix[row, col]);
            }
        }
        Sww.WriteLine("***"); // used for seperation
        Sww.Close();
    }
    else // if file is not empty then look for a blank line and then write after that
    {
        StreamReader srr = new StreamReader(filee);
        linee = srr.ReadLine();
        while (linee != null) // read the file until blank line is read
        {
            linee = srr.ReadLine();
        }

        Sww.WriteLine(TotalClusters);
        for (int col = 0; col < TotalClusters; col++)
        {
            for (int row = 0; row < newDistanceMatrix.GetLength(0); row++)
            {
                Sww.WriteLine(newDistanceMatrix[row, col]);
            }
        }
        Sww.WriteLine("***"); // used for seperation
        Sww.Close(); // this closes the file
    }
}
}
}
}

```

## Agglomerative Clustering Algorithm Class

Has the following functions:

- ReadMutants(); Gets the list of the entire size of mutants.
- CalculateCentroid(): To calculate the centroids
- CalculateDistance(): To calculate the distance of each mutant to the centroid
- Agglomerate(): To merge the two clusters based on min value.
- WriteToFile(): Writes to file the clustered mutants

```
using System;
using System.Collections.Generic;
using System.Text;
using System.Collections;
using System.IO;

////////////////////////////////////
//////////Agglomerative Threshold/ Minimum Value//////////
////////// This algorithm first agglomerate based on a //////////
//////////threshold value 1 then it agglomerate based //////
//////////on minimum value until all are merged into one cluster//

namespace GUI
{
    class AggloThresholdPLUSmin
    {
        // all the variables of the classs
        int ClusterNumber = 1;
        /// saves how many total clusters are there
        int TotalClusters;
        string[,] mutantsArray;
        int BitSize = 0;
        int CentroidIteration = 0;
        int ClusterIteration = 1;
        /// clustering is done based on this threshold
        int Threshold = 2;
        // this will have the cluster numbers against eash mutant
        int[] Clusters;
        int[] OldClusters;
        int checkClusterValue = 0;
        int MinValueCriteria = 0;
        int FinallySame = 0;
        float[,] Distance; // saves the actual distance
        int[,] DistanceMatrix; // saves the 0's and 1's
        float[,] Centroids; // saves the Centroid of the clusters
        int WithoutThreshold = 0;

        //////////////////////////////////
        ////////// gets the total mutants of a particular program
        //////////////////////////////////

        public void ReadMutants(string[,] mutantsArray1)
        {
            mutantsArray = mutantsArray1;
            string MutantString = mutantsArray[0, 1];
            BitSize = MutantString.Length; // gives the length of bits or mutants

            OldClusters = new int[mutantsArray.GetLength(0)];

            Centroids = new float[mutantsArray.GetLength(0), BitSize];

            Calculate_Centroid(); // call the method to calculate centroids
        }

        //////////////////////////////////
        ////////// CALCULATE THE CENTROID OF THE CLUSTERS//////////
        //////////////////////////////////

        public void Calculate_Centroid()
        {
            CentroidIteration = CentroidIteration + 1;
            // first iteration of calculating the centroid
            if (CentroidIteration == 1)
            {
```

```

        for (int rows = 0; rows < mutantsArray.GetLength(0); rows++)
        {
            string mutant = mutantsArray[rows, 1];

            for (int cols = 0; cols < BitSize; cols++)
            {
                if (System.Convert.ToInt32(mutant[cols]) == 49)
                {
                    Centroids[rows, cols] = 1;
                }
                else if (System.Convert.ToInt32(mutant[cols]) == 48)
                {
                    Centroids[rows, cols] = 0;
                }
            }
        }
    }
    else /// for second time iteration
    {
        // this saves the indexes of the mutants with same cluster numbers
        ArrayList SameClusters = new ArrayList();
        TotalClusters = ClusterNumber - 1;
        Centroids = new float[TotalClusters, BitSize];
        int StartClusters = 1;
        int calculated_cent_of_all = 0;
        int CentRow = 0; // row index of the array centroids[]
        while (calculated_cent_of_all != TotalClusters)
        {
            for (int Xindex = 0; Xindex < Clusters.Length; Xindex++)
            {
                if (Clusters[Xindex] == StartClusters)
                {
                    SameClusters.Add(Xindex);
                }
            }
            //ends for loop

            StartClusters = StartClusters + 1;
            //// now calculate the centroid of a particular cluster////
            string SameClusterMutantString;
            int AddBits = 0;
            for (int cols = 0; cols < BitSize; cols++) // traverse the columns
            {
                for (int rowss = 0; rowss < SameClusters.Count; rowss++)
                {
                    int row = System.Convert.ToInt32(SameClusters[rowss]);
                    SameClusterMutantString = mutantsArray[row, 1];
                    if (System.Convert.ToInt32(SameClusterMutantString[cols]) == 49)
                    {
                        AddBits = 1 + AddBits;
                    }
                    else if (System.Convert.ToInt32(SameClusterMutantString[cols]) == 48)
                    {
                        AddBits = 0 + AddBits;
                    }
                }

                float CentroidValue = (float)AddBits / (float)SameClusters.Count;
                CentroidValue = (float)(Math.Truncate(CentroidValue * 10) / 10);
                Centroids[CentRow, cols] = CentroidValue;
                AddBits = 0;
            }
            CentRow++;
            SameClusters.Clear();
            calculated_cent_of_all = calculated_cent_of_all + 1;
        } // ends while

        int r = 0;
    } // ends else
    // call method to calculate the distance of clusters from other clusters
    Calculate_Distance();
}

////////////////////////////////////
////////// CALCULATE THE DISTANCE OF MUTANTS //////////
////////////////////////////////////

public void Calculate_Distance()
{
    /// this is the mutant with which we will calculate the distance with others
    float[] CalculateDistanceWith = new float[BitSize];
    float AddedDistance = 0;
    float Difference = 0;
    Distance = new float[Centroids.GetLength(0), Centroids.GetLength(0)];
    int AllCentroidsTraversedFlag = 0; // this keeps check that all the centroids have been traversed and calculated
    int row = 0;
    while (AllCentroidsTraversedFlag != Centroids.GetLength(0))
    {

```

```

    for (int coll = 0; coll < Centroids.GetLength(1); coll++)
    {
        CalculateDistanceWith[coll] = Centroids[row, coll];
    }
    row++; // moves onto next row for next iteration

    /// now using the CalculateDistanceWith Array, calculate
    ///the distance with other centroids///
    for (int IterateRows = 0; IterateRows < Centroids.GetLength(0); IterateRows++)
    {
        for (int IterateCol = 0; IterateCol < Centroids.GetLength(1); IterateCol++)
        {
            if (CalculateDistanceWith[IterateCol] > Centroids[IterateRows, IterateCol])
            {
                Difference = CalculateDistanceWith[IterateCol] - Centroids[IterateRows, IterateCol];
            }
            else
            {
                Difference = Centroids[IterateRows, IterateCol] - CalculateDistanceWith[IterateCol];
            }

            AddedDistance = AddedDistance + Difference; // adds the distance
        }

        Distance[AllCentroidsTraversedFlag, IterateRows] = AddedDistance;
        AddedDistance = 0;
    }
    AllCentroidsTraversedFlag = AllCentroidsTraversedFlag + 1;
    AddedDistance = 0;
} // ends while
Agglomerate();
}

////////////////////////////////////
//////////////// CKUSTER/ AGGLOMERATE BASED ON SOME THRESHOLD VALUE////////
////////////////////////////////////

public void Agglomerate()
{
    ClusterNumber = 1;
    DistanceMatrix = new int[Distance.GetLength(0), Distance.GetLength(1)];
    Clusters = new int[mutantsArray.GetLength(0)]; // saves the cluster numbers against the mutants
    int ClusterRow = 0;
    int ClusterCol = 0;
    int BothArraysSame = 0;
    ///*****/// first look for 2 0's ///*****///
    for (int row = 0; row < Distance.GetLength(0); row++)
    {
        for (int col = 0; col < Distance.GetLength(1); col++)
        {
            // if there is 0 at a location other then at row ==row
            if (Distance[row, col] == (float)0 & row != col)
            {
                if (DistanceMatrix[row, col] == 0 & DistanceMatrix[row, row] == 0 & DistanceMatrix[col, col] == 0)
                {
                    ClusterRow = row;
                    ClusterCol = col;
                    DistanceMatrix[row, col] = 1; // put 1 in place of the other 0
                    DistanceMatrix[row, row] = 1; // put 1 on place of the row==row
                    DistanceMatrix[col, row] = 1;
                    DistanceMatrix[col, col] = 1;
                    if (ClusterIteration == 1)
                    {
                        Clusters[row] = ClusterNumber;
                        Clusters[col] = ClusterNumber;
                    }
                    else if (ClusterIteration > 1)
                    {
                        for (int check = 0; check < Clusters.Length; check++)
                        {
                            if (OldClusters[check] == ClusterCol + 1)
                            {
                                Clusters[check] = ClusterNumber;
                            }
                            if (OldClusters[check] == ClusterRow + 1)
                            {
                                Clusters[check] = ClusterNumber;
                            }
                        }
                    }
                }
            }

            ClusterNumber = ClusterNumber + 1;
        }
    }
}
}
}

```

```

    } // ends for loop

    /// ****/// now look for smaller distances, other than 0, less than the threshold ****///

    int OneCluster = 0;

    float TemporaryClusterValue = 0;
    float SmallestValue = 0;
    int SaveCol = 0;
    int WentINTOLoop = 0;
    int OK1 = 0;
    int OK2 = 0;
    if (WithoutThreshold == 0)
    {
        for (int roww = 0; roww < Distance.GetLength(0); roww++)
        {
            OneCluster = 0;
            OK1 = 0;
            OK2 = 0;
            for (int coll = 0; coll < Distance.GetLength(1); coll++)
            {
                ClusterRow = roww;
                ClusterCol = coll;
                if (Distance[roww, coll] < Threshold & Distance[roww, coll] != 0)
                {
                    TemporaryClusterValue = Distance[roww, coll];
                    if (DistanceMatrix[roww, coll] == (float)0 & DistanceMatrix[roww, roww] ==
                        (float)0 & DistanceMatrix[coll, coll] == (float)0)
                    {
                        if (ClusterIteration == 1)
                        {
                            if (Clusters[coll] == 0)
                            {
                                WentINTOLoop = 1;
                                {
                                    SmallestValue = TemporaryClusterValue;
                                }
                                // saves the column where the value is the smallest
                                SaveCol = coll;
                            }
                        }
                        else
                        {
                            if (SmallestValue < TemporaryClusterValue)
                            {
                                {
                                    SmallestValue = TemporaryClusterValue;
                                }
                                // saves the column where the value is the smallest
                                SaveCol = coll;
                            }
                        }
                    }
                } // ends if (Clusters[coll] == 0 )
            }

            else if (ClusterIteration > 1)
            {
                for (int check = 0; check < OldClusters.Length; check++)
                {
                    if (OldClusters[check] == ClusterRow + 1)
                    {
                        if (Clusters[check] == 0) // checks if the value is 0
                            OK1 = OK1 + 1;
                    }
                    if (OldClusters[check] == ClusterCol + 1)
                    {
                        if (Clusters[check] == 0) // checks if the value is 0
                            OK2 = OK2 + 1;
                    }
                }
                if (OK1 > 0 & OK2 > 0) // means the values at particular indexes in Cluster array is 0
                {
                    WentINTOLoop = 1;
                    if (SmallestValue == (float)0)
                    {
                        SmallestValue = TemporaryClusterValue;
                        SaveCol = coll;
                    }
                    else
                    {
                        if (SmallestValue < TemporaryClusterValue)
                        {
                            {
                                SmallestValue = TemporaryClusterValue;
                            }
                        }
                        else if (SmallestValue > TemporaryClusterValue)
                    }
                }
            }
        }
    }

```

```

        {
            SmallestValue = TemporaryClusterValue;
            SaveCol = col1;
        }
    } // ends if (OK > 1)
}
}
} // ends for loop

if (WentINTOLoop == 1) // if the control went into the loop above
{
    DistanceMatrix[roww, SaveCol] = 1; // put 1 in place of the other 0
    DistanceMatrix[roww, roww] = 1; // put 1 on place of the row==row
    DistanceMatrix[SaveCol, roww] = 1;
    DistanceMatrix[SaveCol, SaveCol] = 1;
    ClusterRow = roww;
    ClusterCol = SaveCol;
    if (ClusterIteration == 1)
    {
        Clusters[roww] = ClusterNumber;
        Clusters[SaveCol] = ClusterNumber;
    }

    else if (ClusterIteration > 1)
    {
        for (int check = 0; check < Clusters.Length; check++)
        {
            if (OldClusters[check] == ClusterCol + 1)
            {
                Clusters[check] = ClusterNumber;
            }

            if (OldClusters[check] == ClusterRow + 1)
            {
                Clusters[check] = ClusterNumber;
            }
        }
    }

    ClusterNumber = ClusterNumber + 1;
    OneCluster = 1;
} // ends if (WentINTOLoop == 1)

if (OneCluster == 0 & DistanceMatrix[roww, roww] == 0)
{
    if (ClusterIteration == 1)
    {
        DistanceMatrix[roww, roww] = 1;
        Clusters[roww] = ClusterNumber;
    }
    else if (ClusterIteration > 1) // more than 1 iterations
    {
        DistanceMatrix[roww, roww] = 1;
        for (int find = 0; find < OldClusters.Length; find++)
        {
            if (OldClusters[find] == ClusterRow + 1)
            {
                Clusters[find] = ClusterNumber;
            }
        }
    }

    ClusterNumber = ClusterNumber + 1; // increments the cluster value
} // ends if (OneCluster==0 & DistanceMatrix[roww, roww]==0)

SaveCol = 0;
SmallestValue = 0;
TemporaryClusterValue = 0;
WentINTOLoop = 0;
} // ends for loop

} // end of WithoutThreshold

else if (WithoutThreshold == 1)
{
    int ColCheckk = 0;
    int findSomeOtherMinValue = 0;
    ArrayList NotThisCol = new ArrayList();
    int Other = 0;
    int NoSmallValue = 0;
    MinValueCriteria = 1;
    for (int roww = 0; roww < Distance.GetLength(0); roww++)
    {

```

```

OneCluster = 0;
OK1 = 0;
OK2 = 0;
findSomeOtherMinValue = 0;
// loops through the columns
for (int coll = 0; coll < Distance.GetLength(1); coll = coll + 1)
{
    ClusterRow = roww;
    ClusterCol = coll;
    Other = 0;
    ColCheckk = coll;
    if (Distance[roww, coll] != 0)
    {
        TemporaryClusterValue = Distance[roww, coll];

        if (DistanceMatrix[roww, coll] == (float)0 & DistanceMatrix[roww, roww]
            == (float)0 & DistanceMatrix[coll, coll] == (float)0)
        {
            for (int checkkk = 0; checkkk < NotThisCol.Count; checkkk++)
            {
                if (coll == System.Convert.ToInt32(NotThisCol[checkkk]))
                {
                    Other = 1;
                }
            }
            if (Other == 0)
            {
                if (ClusterIteration == 1)
                {
                    if (Clusters[coll] == 0)
                    {
                        WentINTOLoop = 1;
                        if (SmallestValue == (float)0)
                        {
                            SmallestValue = TemporaryClusterValue;
                            // saves the column where the value is the smallest
                            SaveCol = coll;
                        }
                        else
                        {
                            if (SmallestValue < TemporaryClusterValue)
                            {
                                SmallestValue = TemporaryClusterValue;
                                SaveCol = coll;
                            }
                            else if (SmallestValue > TemporaryClusterValue)
                            {
                                SmallestValue = TemporaryClusterValue;
                                // saves the column where the value is the smallest
                                SaveCol = coll;
                            }
                        }
                    } // ends if (Clusters[coll] == 0 )
                }
            }
            else if (ClusterIteration > 1)
            {
                for (int check = 0; check < OldClusters.Length; check++)
                {
                    if (OldClusters[check] == ClusterRow + 1)
                    {
                        if (Clusters[check] == 0) // checks if the value is 0
                        {
                            OK1 = OK1 + 1;
                        }
                        if (OldClusters[check] == ClusterCol + 1)
                        {
                            if (Clusters[check] == 0) // checks if the value is 0
                            {
                                OK2 = OK2 + 1;
                            }
                        }
                    }
                }
            }
            // means the values at particular indexes in Cluster array is 0
            if (OK1 > 0 & OK2 > 0)
            {
                WentINTOLoop = 1;
                if (SmallestValue == (float)0)
                {
                    SmallestValue = TemporaryClusterValue;
                    SaveCol = coll;
                }
                else
                {
                    if (SmallestValue < TemporaryClusterValue)
                    {
                        SmallestValue = TemporaryClusterValue;
                    }
                    else if (SmallestValue > TemporaryClusterValue)
                    {
                        SmallestValue = TemporaryClusterValue;
                    }
                }
            }
        }
    }
}

```



```

        SaveCol = coll;
    }
}

} // ends if (OK > 1)

}
} // ends "other" variable
}
}
coll++;

// now here check that the cminimum column value u have selected,
//does it also have some othet minimum value
if ((ColCheckk + 1) == Distance.GetLength(1)) // one before the length of column
{
    if (SmallestValue == 0)
    {
    }
    else
    {
        for (int iterateColl = 0; iterateColl < Distance.GetLength(1); iterateColl++)
        {
            if (SmallestValue < Distance[SaveCol, iterateColl])
            {
            }
            else if (SmallestValue > Distance[SaveCol, iterateColl] && SaveCol != iterateColl)
            {
                findSomeOtherMinValue = 1;
                NotThisCol.Add(SaveCol);
                SaveCol = 0;
                SmallestValue = 0;
                coll = 0;
                break;
            }
        }
    }
} //ends if

} // ends for loop for col

if (WentINTOLoop == 1) // if the control went into the loop above
{
    if (SmallestValue == 0)
    {
        DistanceMatrix[roww, roww] = 1; // put 1 on place of the row==row
    }
    else
    {
        DistanceMatrix[roww, SaveCol] = 1; // put 1 in place of the other 0
        DistanceMatrix[roww, roww] = 1; // put 1 on place of the row==row
        DistanceMatrix[SaveCol, roww] = 1;
        DistanceMatrix[SaveCol, SaveCol] = 1;
    }
    ClusterRow = roww;
    ClusterCol = SaveCol;
    if (ClusterIteration == 1)
    {
        Clusters[roww] = ClusterNumber;
        Clusters[SaveCol] = ClusterNumber;
    }
    else if (ClusterIteration > 1)
    {
        for (int check = 0; check < Clusters.Length; check++)
        {
            if (OldClusters[check] == ClusterCol + 1)
            {
                Clusters[check] = ClusterNumber;
            }

            if (OldClusters[check] == ClusterRow + 1)
            {
                Clusters[check] = ClusterNumber;
            }
        }
    }
    ClusterNumber = ClusterNumber + 1;
    OneCluster = 1;
} // ends if (WentINTOLoop == 1)

if (OneCluster == 0 & DistanceMatrix[roww, roww] == 0)
{
    if (ClusterIteration == 1)
    {
        DistanceMatrix[roww, roww] = 1;
        Clusters[roww] = ClusterNumber;
    }
}

```

```

    }
    else if (ClusterIteration > 1)    // more than 1 iterations
    {
        DistanceMatrix[roww, roww] = 1;
        for (int find = 0; find < OldClusters.Length; find++)
        {
            if (OldClusters[find] == ClusterRow + 1)
            {
                Clusters[find] = ClusterNumber;
            }
        }
    }
    checkClusterValue = ClusterNumber;
    ClusterNumber = ClusterNumber + 1;    // increments the cluster value
} // ends if(OneCluster==0 & DistanceMatrix[roww, roww]==0)

SaveCol = 0;
SmallestValue = 0;
TemporaryClusterValue = 0;
WentINTOLoop = 0;
NotThisCol.Clear();
} // ends for loop
}

ClusterIteration = ClusterIteration + 1;

TotalClusters = ClusterNumber - 1;
for (int check = 0; check < Clusters.Length; check++)    // loop to check the two cluster arrays
{
    if (OldClusters[check] == Clusters[check])    // if the content at a particular index are same
    {
        BothArraysSame = 1;    // both cluster arrays are same
    }
    else
    {
        BothArraysSame = 0;
        break;
    }
}

if (BothArraysSame == 0 && WithoutThreshold == 0)    // if the clusters has changed
{
    Clusters.CopyTo(OldClusters, 0);
    WriteToFile();
    Calculate_Centroid();
}
else if (BothArraysSame == 1 && WithoutThreshold == 0)
{
    WithoutThreshold = 1;
}
if (WithoutThreshold == 1 && checkClusterValue != 1 && FinallySame == 0)
{
    if (MinValueCriteria == 1 && checkClusterValue != 1)
    {
        WriteToFile();
    }

    if (checkClusterValue != 1)
    {
        Clusters.CopyTo(OldClusters, 0);
        Calculate_Centroid();
    }
}
}

//if both oldCluster and Cluster Arrays are same, means
// no new cluster has been formed
if (checkClusterValue == 1 && MinValueCriteria == 1 && FinallySame == 0)
{
    FinallySame = 1;
}
}

}

////////////////////////////////////
//////////////// WRITE THE CLUSTERED MUTANTS TO FILE //////////////////
////////////////////////////////////
public void WriteToFile()
{
    // Specify file, instructions, and privileges
    FileStream file = new FileStream("AggloClustersM1.txt", FileMode.OpenOrCreate, FileAccess.ReadWrite);
    int ClusterNum = 1;
    float dist = 0;
    StreamWriter sw = new StreamWriter(file);
    string line;
    if (file.Length == 0)    // if file is initially empty then write on it
    {

```

```

while (ClusterNumberr <= TotalClusters)
{
    sw.WriteLine(ClusterNumberr);
    for (int find = 0; find < Clusters.Length; find++)
    {
        if (Clusters[find] == ClusterNumberr)
        {
            sw.WriteLine(mutantsArray[find, 1]);
        }
    }

    ClusterNumberr = ClusterNumberr + 1; // increments the cluster to be assigned
}

sw.WriteLine("the distances*****");
for (int row = 0; row < Distance.GetLength(0); row++)
{
    for (int col = 0; col < Distance.GetLength(1); col++)
    {
        dist = Distance[row, col];
        dist = (float)(Math.Truncate(dist * 10) / 10);
        sw.Write(dist);
        sw.Write(" ");
    }
    sw.WriteLine("");
}

sw.WriteLine("");
sw.WriteLine("the distances matrix*****");
for (int row = 0; row < Distance.GetLength(0); row++)
{
    for (int col = 0; col < Distance.GetLength(1); col++)
    {
        dist = DistanceMatrix[row, col];
        dist = (float)(Math.Truncate(dist * 10) / 10);
        sw.Write(dist);
        sw.Write(" ");
    }
    sw.WriteLine("");
}
}
else
{
    StreamReader sr = new StreamReader(file);
    line = sr.ReadLine();
    while (line != null) // read the file until blank line is read
    {
        line = sr.ReadLine();
    }
    sw.WriteLine("*****");
    while (ClusterNumberr <= TotalClusters)
    {
        sw.WriteLine(ClusterNumberr);
        for (int find = 0; find < Clusters.Length; find++)
        {
            if (Clusters[find] == ClusterNumberr)
            {
                sw.WriteLine(mutantsArray[find, 1]);
            }
        }

        ClusterNumberr = ClusterNumberr + 1;
    }

    sw.WriteLine("the distances*****");
    for (int row = 0; row < Distance.GetLength(0); row++)
    {
        for (int col = 0; col < Distance.GetLength(1); col++)
        {
            dist = Distance[row, col];
            dist = (float)(Math.Truncate(dist * 10) / 10);
            sw.Write(dist);
            sw.Write(" ");
        }
        sw.WriteLine("");
    }
    sw.WriteLine("");
    sw.WriteLine("the distances matrix*****");
    for (int row = 0; row < Distance.GetLength(0); row++)
    {
        for (int col = 0; col < Distance.GetLength(1); col++)
        {
            dist = DistanceMatrix[row, col];
            dist = (float)(Math.Truncate(dist * 10) / 10);
            sw.Write(dist);
            sw.Write(" ");
        }
    }
}

```

```
        }
        sw.WriteLine("");
    }
}
sw.Close();
}
}
```

## Evaluation Class

Has the following functions:

- ReadFiles(): Reads all the mutants
- GreedyClusterTestSet(): Generates the test set Tc by greedy approach
- RandomTestSetFunction(): Generate test set Tr from random mutants of same size as Tc
- KillabilityEfficiency(): Calculates the mutation score of both test sets

```
using System;
using System.Collections.Generic;
using System.Text;
using System.Collections;
using System.IO;

////////////////////////////////////
// Evaluation using the greedy alorithm //
// Find the cluster test set Tc by greedy algo //
////////////////////////////////////

namespace GUI
{
    class GreedyEvaluation
    {
        ArrayList SelectFromClusters = new ArrayList(); // mutants selected from clusters
        ArrayList AllMutants4 = new ArrayList();
        ArrayList AllMutants = new ArrayList();
        int[] AllMutants1; // = new ArrayList(); // same as AllMutants saves all the 512 mutants
        int[] AllMutants2; // = new ArrayList(); // same as AllMutants saves all the 512 mutants
        Random rand = new Random();
        int HowManyMutants = 0;
        ArrayList MutantsPerCluster = new ArrayList();
        int MutantPerCluster = 2;
        int RandomNumber = 0;
        ArrayList ClusterTestSet = new ArrayList();
        ArrayList RandomTestSet = new ArrayList();
        // this will save the selected mutants from the clusters in the form of bits
        int[,] SelectFromClustersArray;
        // this saves all the mutants in the form of bits, o's and 1's
        int[,] AllMutantsArray;
        int[] ClusterKillability;
        int NumberOfRuns;
        int LengthOfMutant;
        // saves the test set generated form the clustered mutants
        ArrayList ClusterTestSet1 = new ArrayList();
        // saves teh test set generated from the random mutants
        ArrayList RandomTestSet2 = new ArrayList();
        ArrayList RandomEfficiency = new ArrayList();
        ArrayList ClusterEfficiency = new ArrayList();

        public void ReadFiles(int numberOfRuns1, int LengthOfMutant1, int MutantPerCluster1)
        {
            NumberOfRuns = numberOfRuns1;
            LengthOfMutant = LengthOfMutant1;
            MutantPerCluster = MutantPerCluster1;

            // agglomerative clustering with threshold
            //System.IO.StreamReader file = new System.IO.StreamReader("AggloEvaluationFileM1.txt");
            // agglomerative clustering with minimum value
            System.IO.StreamReader file = new System.IO.StreamReader("AggloEvaluationFileM2.txt");
            // k mean method 2, careful selection of initial k
            // System.IO.StreamReader file = new System.IO.StreamReader("EvaluationFileM2.txt");

            string line;

            // read and select 2 mutants from each cluster
            while ((line = file.ReadLine()) != null)
            {
                if (line.Length < LengthOfMutant) // means it is the cluster number like 1, 2, 3, 4...
                {
                    if (MutantsPerCluster.Count > 0 & MutantsPerCluster.Count >= MutantPerCluster)

```

```

    {
        // specifies the maximum value for the random function to generate
        int MaxValue = MutantsPerCluster.Count;
        // this loop is to select 2 random mutants from
        for (int select = 0; select < MutantPerCluster; select = select + 0) each cluster
        {
            RandomNumber = rand.Next(MaxValue);
        }
        // if the index does not have a 0 value instead of mutant
        if (System.Convert.ToString(MutantsPerCluster[RandomNumber]) != "48")
        {
            string SizeCheck = System.Convert.ToString(MutantsPerCluster[RandomNumber]);
            if (SizeCheck.Length < LengthOfMutant)
            {
                int t = 0;
            }
            else
            {
                SelectFromClusters.Add(MutantsPerCluster[RandomNumber]);
                MutantsPerCluster[RandomNumber] = 0; // once the mutant has been selected and
                //added to the arraylist , put a 0 in its place
                HowManyMutants = HowManyMutants + 1;
                select = select + 1;
            }
        }
        else // if 0 value then decrement and get another random integer.
        {
            select--;
        }
    }

    MutantsPerCluster.Clear();

} //ends if (MutantsPerCluster.Count > 0 & MutantsPerCluster.Count> MutantsPerCluster)

// if the number of mutants to select from each cluster is grater than the size of the array
// then select all the mutants from that cluster
else if (MutantsPerCluster.Count > 0 & MutantsPerCluster.Count < MutantPerCluster)
{
    for (int loopList = 0; loopList < MutantsPerCluster.Count; loopList++)
    {
        SelectFromClusters.Add(MutantsPerCluster[loopList]);
        HowManyMutants = HowManyMutants + 1;
    }
    MutantsPerCluster.Clear();
}

} // ends if (line.Length < LengthOfMutant)
else
{
    MutantsPerCluster.Add(line); // adds mutants of each cluster in array list
}

}

// this part is for the mutants just before the end
if (MutantsPerCluster.Count > 0 & MutantsPerCluster.Count >= MutantPerCluster) of file
{
    int MaxValue1 = MutantsPerCluster.Count; // specifies the maximum value for the random function to generate
    // this loop is to select 2 random mutants from each cluster
    for (int select = 0; select < MutantPerCluster; select = select + 0)
    {
        RandomNumber = rand.Next(MaxValue1);
    }
    // if the index does not have a 0 value instead of mutant
    if (System.Convert.ToString(MutantsPerCluster[RandomNumber]) != "48")
    {
        string SizeCheckk = System.Convert.ToString(MutantsPerCluster[RandomNumber]);
        if (SizeCheckk.Length < LengthOfMutant)
        {
        }
        else
        {
            SelectFromClusters.Add(MutantsPerCluster[RandomNumber]);
            // once the mutant has been selected and added to the arraylist , put a 0 in its
            MutantsPerCluster[RandomNumber] = 0; place
            HowManyMutants = HowManyMutants + 1;
            select = select + 1;
        }
    }
    else // if 0 value then decrement and get another random integer.
    {
        select--;
    }
}
} /// end for
}

```

```

else if (MutantsPerCluster.Count > 0 & MutantsPerCluster.Count < MutantPerCluster)
{
    for (int loopList = 0; loopList < MutantsPerCluster.Count; loopList++)
    {
        SelectFromClusters.Add(MutantsPerCluster[loopList]);
        HowManyMutants = HowManyMutants + 1;
    }

    MutantsPerCluster.Clear();
}

///// Read all the 512 mutants from the file and save in the AllMutants ArrayList  /////

System.IO.StreamReader file1 = new System.IO.StreamReader("Data.txt");
while ((line = file1.ReadLine()) != null)
{
    string[] splitData = line.Split(new Char[] { ' ' });
    AllMutants4.Add(splitData[1]); // all the 512 mutants added to the array list
}

// save the selected mutants from the clusters in the form
SelectFromClustersArray = new int[HowManyMutants, LengthOfMutant];    of bits

///// Copy mutants bit by bit in the array SelectFromClustersArray  /////

string mutant = System.Convert.ToString(SelectFromClusters[0]);
for (int row = 0; row < SelectFromClusters.Count; row++)
{
    mutant = System.Convert.ToString(SelectFromClusters[row]);

    for (int col = 0; col < LengthOfMutant; col++)
    {
        if (mutant[col] == 49)
        {
            SelectFromClustersArray[row, col] = 1;
        }
        else if (mutant[col] == 48)
        {
            SelectFromClustersArray[row, col] = 0;
        }
    }
}

///// copy all the mutants bit by bit in the AllMutantsArray  /////

AllMutantsArray = new int[AllMutants4.Count, LengthOfMutant];
string mutantt;
for (int Rowsss = 0; Rowsss < AllMutants4.Count; Rowsss++)
{
    mutantt = System.Convert.ToString(AllMutants4[Rowsss]);

    for (int Colll = 0; Colll < LengthOfMutant; Colll++)
    {
        if (mutantt[Colll] == 49)
        {
            AllMutantsArray[Rowsss, Colll] = 1;
        }
        else if (mutantt[Colll] == 48)
        {
            AllMutantsArray[Rowsss, Colll] = 0;
        }
    }
}

///// here write in file the selected mutants from the clusters  /////

// Specify file, instructions, and privileges
FileStream file22 = new FileStream("GreedyEfficiencyK0.txt", FileMode.OpenOrCreate, FileAccess.ReadWrite);

StreamWriter sw = new StreamWriter(file22);
string line1;
if (file22.Length == 0) // if file is initially empty them write on it
{
    //!!!!!!!!!!!!!!!!!!!! just checking!!!!!!!!!!!!!!!!!!!!
    for (int y = 0; y < SelectFromClusters.Count; y++)
    {
        sw.WriteLine(SelectFromClusters[y]); ;
    }
}
else
{
    StreamReader sr = new StreamReader(file22);
    line1 = sr.ReadLine();
    while (line1 != null) // read the file until blank line is read
    {
        line1 = sr.ReadLine();
    }
}

```

```

    }
    //***** writing the selected mutants onto the FILE *****
    for (int y = 0; y < SelectFromClusters.Count; y++)
    {
        sw.WriteLine(SelectFromClusters[y]); ;
    }

    //*****

}

sw.Close();
GreedyClusterTestSet();

} // ends the function readFile()

////////////////////////////////////
// Generate test set from clusters by greedy algorithm //
////////////////////////////////////

public void GreedyClusterTestSet()
{
    ArrayList ClusterTestSet = new ArrayList(); // saves the test set generated from the clustered mutants
    // this saves the total number of mutants killed by each test case
    int [] HowManyMutantsKilled = new int[LengthOfMutant];
    int MaxValue = 0; // saves the test set that kills the most

    /// ** */// get the CLUSTER TEST SET Greedily for the mutants from the clusters //****///

    int KillFlag = 0;
    int PreventTestCaseRepetition = 0;
    ClusterKillability = new int[HowManyMutants];
    int countZeros = 0;
    int TestCase = 0;

    while (KillFlag != 1)
    {
        // this loop counts all the mutants that can be killed by a particular test case
        for (int col = 0; col < SelectFromClustersArray.GetLength(1); col++) // iterates the column of the array
        {
            for (int row = 0; row < SelectFromClustersArray.GetLength(0); row++)
            {
                if (SelectFromClustersArray[row, col] == 0)
                {
                    countZeros = countZeros + 1;
                }
            } // end row for loop

            HowManyMutantsKilled[col] = countZeros;
            countZeros = 0;

        } // end col for loop

        // once all the data has been saved in the array HowManyMutantsKilled,
        // look for the test case that kills the most mutants
        // so now look for the maximum number
        for (int loop = 0; loop < HowManyMutantsKilled.Length; loop++)
        {
            if (MaxValue == 0)
            {
                MaxValue = HowManyMutantsKilled[loop];
                TestCase = loop; // saves the index of the test case
            }
            else if (MaxValue < HowManyMutantsKilled[loop])
            {
                MaxValue = HowManyMutantsKilled[loop];
                TestCase = loop; // saves the index of the test case
            }
        } // ends for loop

        MaxValue = 0;

        // now at the location of the maximum test case see which ones are killed by it
        // and put 1 at the place of killed mutants

        for (int rows = 0; rows < SelectFromClustersArray.GetLength(0); rows++) // iterates the rows
        {
            if (SelectFromClustersArray[rows, TestCase] == 0) // if the mutant is killed by the test case
            {
                ClusterKillability[rows] = 1;
            }
        }

        /// add the maximum value test case to the test set array
        ClusterTestSet.Add(TestCase);
        // now put all 0's in the rows where mutants are killed, in this array SelectFromClustersArray[]
        // this is done so that in next iteration when the max number of mutant killings are calculated, the

```



```

// ones that are already counted are excluded(by putting 0's)

for (int loopThrough = 0; loopThrough < ClusterKillability.Length; loopThrough++)
{
    if (ClusterKillability[loopThrough] == 1)
    {
        for (int coll = 0; coll < SelectFromClustersArray.GetLength(1); coll++)
        {
            SelectFromClustersArray[loopThrough, coll]=1;
        }
    }
}

// now iterate through ClusterKillability[] Array and see if all the mutants have been killed

for (int loopp = 0; loopp < ClusterKillability.Length; loopp++)
{
    if (ClusterKillability[loopp] == 1)
    {
        KillFlag = 1;
    }
    else if (ClusterKillability[loopp] == 0)
    {
        KillFlag = 0;
        break;
    }
}

} // while (KillFlag != 1)

int yy = 0;

ClusterTestSet1 = ClusterTestSet;
int u = 0;
while (NumberOfRuns != 0) // this is used to run the algorithm for specified number of runs
{
    NumberOfRuns = NumberOfRuns - 1;
    AllMutants = new ArrayList(AllMutants4); // this copies the array list AllMutants4 into AllMutants
    AllMutants1 = new int[AllMutants.Count];
    AllMutants2 = new int[AllMutants.Count];
    RandomTestSetFunction();
}
} // ends function ClusterTestSetFunction()

////////////////////////////////////
////////// Generate RANDOM TEST SET same number as generated by //////////
////////////////////////////////////greedy clusterTest SET////////////////////////////////////
////////////////////////////////////

public void RandomTestSetFunction()
{
    //***** here get the same number of RANDOM TEST SET as the CLUSTER TEST SET *****/
    int TotalNumberOfTestCases = ClusterTestSet1.Count; // we need same number of test cases from the RandomMutants
    int TestCaseCount = 0;
    int[] MutantBitRow = new int[LengthOfMutant];
    int NotAdded = 0;
    int killed = 0;
    ArrayList RandomTestSet = new ArrayList(); // saves teh test set generated from the random mutants
    // until the test cases are not equal to the cluster test set count
    while (TestCaseCount != TotalNumberOfTestCases)
    {
        int RandomRow = rand.Next(AllMutants.Count);
        string RandomMutant = System.Convert.ToString(AllMutants[RandomRow]);
        // the length of the selected random mutant should be equal to the length mutant bits
        if (RandomMutant.Length == LengthOfMutant)
        {
            // save this random mutant in the array bit by bit
            for (int index = 0; index < RandomMutant.Length; index++)
            {
                if (RandomMutant[index] == 49)
                {
                    MutantBitRow[index] = 1;
                }
                else if (RandomMutant[index] == 48)
                {
                    MutantBitRow[index] = 0;
                }
            }
        }
        while (killed != 1)
        {
            int KillingBit = rand.Next(RandomMutant.Length);
            NotAdded = 0;
            if (MutantBitRow[KillingBit] == 0)// if the test case kills it
            {
                for (int check = 0; check < RandomTestSet.Count; check++)

```

```

    {
// checks that the test case has not already been added to the test set
        if (System.Convert.ToInt32(RandomTestSet[check]) != KillingBit)
        {
            NotAdded = 0;
        }
        else
        {
            NotAdded = 1;
// put zero in its place if the row has been selected randomly
            AllMutants[RandomRow] = 0;
            killed = 1;
            break;
        }
    }

// only proceed if the test case has not already been added to the test set
    if (NotAdded == 0)
    {
        AllMutants[RandomRow] = 0; // put zero in its place if the row has been selected randomly
        RandomTestSet.Add(KillingBit);
        TestCaseCount = TestCaseCount + 1;
        killed = 1;
    }
    } // ends if
} // ends while, killed ==1

    killed = 0;
} // ends if (RandomMutant.Length > 0)
else
{
    int hello = 0; // length less then the length of the mutant bits
}

} // ends while(TestCaseCount != TotalNumberOfTestCases)

RandomTestSet2 = RandomTestSet;

KillabilityEfficiency();

} // ends the random test set function

////////////////////////////////////
//////////////// CALCULATES THE EFFICIENCY OF BOTH TEST SETS //////////////////
////////////////////////////////////

public void KillabilityEfficiency()
{
    //****//first see the killability of the CLUSTER TEST SET //****//
    int CTestCase;
    int KillCounts = 0;
    for (int Cloop = 0; Cloop < ClusterTestSet1.Count; Cloop++)
    {
        CTestCase = System.Convert.ToInt32(ClusterTestSet1[Cloop]);
        for (int row = 0; row < AllMutantsArray.GetLength(0); row++)
        {
            if (AllMutantsArray[row, CTestCase] == 0)
            {
                if (AllMutants1[row] != 1)
                {
                    AllMutants1[row] = 1;
                    KillCounts = KillCounts + 1;
                }
            }
        }
    }

    // calculate the killability percentage //

    int countZeros = 0;
    float CkillabilityPercentage;
    for (int looop = 0; looop < AllMutants1.Length; looop++)
    {
        if (AllMutants1[looop] == 1)
        {
            countZeros = countZeros + 1;
        }
    }

    CkillabilityPercentage = ((float)countZeros / (float)AllMutants1.Length) * 100;
// this is the percentage of killability
    KillabilityPercentage = (float)(Math.Truncate(CkillabilityPercentage * 10) / 10);
    ClusterEfficiency.Add(CkillabilityPercentage);

    //****//first see the killability of the RANDOM TEST SET //****//
    KillCounts = 0;
    int RTestCase = 0;
    for (int Rloop = 0; Rloop < RandomTestSet2.Count; Rloop++)

```

```

{
    RTestCase = System.Convert.ToInt32(RandomTestSet2[Rloop]);
    for (int roww = 0; roww < AllMutantsArray.GetLength(0); roww++)
    {
        if (AllMutantsArray[roww, RTestCase] == 0)
        {
            if (AllMutants2[roww] != 1)
            {
                AllMutants2[roww] = 1;
                KillCounts = KillCounts + 1;
            }
        }
    }
}

// now calculate the percentage killability of mutants by andom test set/////
int Ones = 0;
float RkillabilityPercentage;
for (int loop = 0; loop < AllMutants2.Length; loop++)
{
    if (AllMutants2[loop] == 1)
    {
        Ones = Ones + 1;
    }
}
RkillabilityPercentage = ((float)Ones / (float)AllMutants2.Length) * 100;
RkillabilityPercentage = (float)(Math.Truncate(RkillabilityPercentage * 10) / 10);
RandomEfficiency.Add(RkillabilityPercentage);

//////////***** //////////WRITE ON FILE //////////*****//////////

// Specify file, instructions, and privileges
FileStream file = new FileStream("GreedyEfficiencyK0.txt", FileMode.OpenOrCreate, FileAccess.ReadWrite);

StreamWriter sw = new StreamWriter(file);
string line;
if (file.Length == 0)    // if file is initially empty them write on it
{
    sw.WriteLine("TEST SET FROM CLUSTERS( Tc )");
    sw.WriteLine("{");
    for (int loop = 0; loop < ClusterTestSet1.Count; loop++)
    {
        sw.WriteLine(ClusterTestSet1[loop]);
        sw.WriteLine(",");
        sw.WriteLine(" ");
    }
    sw.WriteLine("}");
    sw.WriteLine("");
    sw.WriteLine("Killed mutants by Tc = ");
    sw.WriteLine(RkillabilityPercentage);
    sw.WriteLine(" %");

    sw.WriteLine("RANDOM TEST SET( Tr )");
    sw.WriteLine("{");
    for (int loop = 0; loop < RandomTestSet2.Count; loop++)
    {
        sw.WriteLine(RandomTestSet2[loop]);
        sw.WriteLine(",");
        sw.WriteLine(" ");
    }
    sw.WriteLine("}");

    sw.WriteLine("");
    sw.WriteLine("Killed mutants by Tr = ");
    sw.WriteLine(RkillabilityPercentage);
    sw.WriteLine(" %");
    sw.WriteLine("");
    sw.WriteLine(".....");
    sw.WriteLine("");
}
else
{
    StreamReader sr = new StreamReader(file);
    line = sr.ReadLine();

    while (line != null) // read the file until blank line is read
    {
        line = sr.ReadLine();
    }
    ///////////////////////////////////////////////////

    sw.WriteLine("TEST SET FROM CLUSTERS( Tc )");
    sw.WriteLine("{");
    for (int loop = 0; loop < ClusterTestSet1.Count; loop++)
    {
        sw.WriteLine(ClusterTestSet1[loop]);
        sw.WriteLine(",");
    }
}

```

```

        sw.Write(" ");
    }
    sw.Write("}");

    sw.WriteLine("");
    sw.Write("Killed mutants by Tc = ");
    sw.Write(KillabilityPercentage);
    sw.WriteLine(" %");

    sw.WriteLine("RANDOM TEST SET( Tr )");
    sw.Write("{");
    for (int loop = 0; loop < RandomTestSet2.Count; loop++)
    {
        sw.Write(RandomTestSet2[loop]);
        sw.Write(",");
        sw.Write(" ");
    }
    sw.Write("}");

    sw.WriteLine("");
    sw.Write("Killed mutants by Tr = ");
    sw.Write(RkillabilityPercentage);
    sw.WriteLine(" %");
    sw.WriteLine("");
    sw.WriteLine(".....");
    sw.WriteLine("");
}

sw.Close();
if (NumberOfRuns == 0)
{
    // Specify file, instructions, and privileges
    FileStream filee = new FileStream("SortedEfficiencyK0.txt", FileMode.OpenOrCreate, FileAccess.ReadWrite);

    StreamWriter sww = new StreamWriter(filee);
    string linee;
    if (filee.Length == 0)    // if file is initially empty then write on it
    {
        sww.WriteLine("Cluster Killability");

        for (int xx=0; xx< ClusterEfficiency.Count; xx++)
        {
            sww.WriteLine(ClusterEfficiency[xx]);
        }

        sww.WriteLine("Random Killability");
        RandomEfficiency.Sort(0, RandomEfficiency.Count, new Desc());

        for (int x=0; x< RandomEfficiency.Count; x++)
        {
            sww.WriteLine(RandomEfficiency[x]);
        }
    }
    else
    {
        StreamReader srr = new StreamReader(filee);
        linee = srr.ReadLine();

        while (linee != null)    // read the file until blank line is read
        {
            linee = srr.ReadLine();
        }
        sww.WriteLine("*****");
        sww.WriteLine("Cluster Killability");

        for (int xx=0; xx< ClusterEfficiency.Count; xx++)
        {
            sww.WriteLine(ClusterEfficiency[xx]);
        }

        sww.WriteLine("Random Killability");
        RandomEfficiency.Sort(0, RandomEfficiency.Count, new Desc());

        for (int x=0; x< RandomEfficiency.Count; x++)
        {
            sww.WriteLine(RandomEfficiency[x]);
        }
    }

    sww.Close();
}

}

public class Desc : IComparer
{
    public int Compare(object x, object y)

```

```
        {
            if ((float)x > (float)y) return 1;
            if ((float)x == (float)y) return 0;
            if ((float)x < (float)y) return -1;
            // MODIFY: Code below added to ensure all values returned.
            else
                return 0;
        }
    }
}
```