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SSCT Score for Malware Detection

A Project

Presented to

The Faculty of the Department of Computer Science

San Jose State University

In Partial Fulfillment

of the Requirements for the Degree

Master of Science

by

Srividhya Srinivasan

December 2015

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The Designated Project Committee Approves the Project Titled

SSCT Score for Malware Detection

by

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APPROVED FOR THE DEPARTMENTS OF COMPUTER SCIENCE

SAN JOSE STATE UNIVERSITY

December 2015

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ABSTRACT

SSCT Score for Malware Detection

by Srividhya Srinivasan

Metamorphic malware transforms its internal structure when it propagates, making detection of such malware a challenging research problem. Previous research considered a score based on simple substitution cryptanalysis, which was applied to the metamorphic detection problem. In this research, we analyze a new score based on a combined simple substitution and column transposition (SSCT) cryptanalysis. We show that this SSCT score significantly outperforms the simple substitution score—and other malware detection scores—in many cases.

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CHAPTER 1

Introduction

Malware is a piece of software written with malicious intent. Over the years, malware have evolved to be more like benign software and hence it has become increasingly difficult to tell them apart from a normal harmless program [19]. The techniques used to detect malware files can be broadly classified under two categories - dynamic and static malware analysis. In dynamic analysis, the malware is allowed to be live in an emulated environment and its actions are observed. In static analysis, the information extracted from the malware file is used to analyze and decide whether the file is a malware or a benign file. Even from this high level definition, we can see that dynamic analysis techniques are, in most cases, more expensive in terms of running times than their static analysis counterparts.

Many malware detection techniques have been proposed and analyzed in the literature. Examples of such malware detection techniques include the Hidden Markov Model approach in [1, 2], as well as a score that relies on simple substitution cryptanalysis [8]. The Simple Substitution Distance (SSD) malware score in [8] is based on Jakobsen's algorithm [6], which is an extremely efficient attack on simple substitution ciphers. Consequently, the SSD score computation is fast and efficient, and in [8] it is shown to be very effective against some challenging classes of malware.

Signature-based virus detection systems search for a known pattern of bits or a signature in the body of the malware. If malwares had stopped evolving, all viruses could be detected by these systems. Unfortunately, that is not the case. Malware developers constantly look for techniques to break the performance of the virus de-

tection systems and sadly, keep succeeding in their attempts. Morphing the malware code is one such technique used to evade signature detections.

Polymorphic malware consists of the malware code, which is encrypted, and a module containing the decryption logic [13]. The decryption module is also morphed so that it does not adopt a common signature. Metamorphic virus follows a similar principle and mutates the virus body before infecting a system. There are several techniques available to achieve this including, but not limited to register renaming, renaming of subroutines and dead code insertion [13].

In both polymorphic and metamorphic viruses, each version of malware is different from the previous known version. Due to this, they are difficult to detect using the conventional signature based security systems. It is interesting to note that, through the evolution of different versions of these malware, the underlying functionality remains more or less the same. In such cases, it seems logical to view the known version of a malware as the "plaintext" and the newer, unknown version to be an encrypted cipher text. The unknown file or the ciphertext can be decrypted to see if it yields any of the known malware. If it cannot be decrypted successfully, we can assume that the unknown file is benign.

In this paper, we will discuss the use of an encryption technique called Simple Substitution Columnar Transposition as a way to distinguish a malware file from a benign file and compare the results obtained by this method with the existing techniques in static analysis. This paper is organized into the following sections. In this chapter, we have given a brief summary about polymorphic and metamorphic malware and how encryption techniques can be used as malware detection techniques. Chapter 2 talks about some existing implementation of this idea. In Chapter 3, we have an overview of the SSCT cryptanalysis technique followed by a detailed account

of our implementation. In Chapter 4, we present our experiments and the results obtained. We conclude with Chapter 5, which talks about the future work in this area.

CHAPTER 2

Previous Work

In this chapter, we will see some of the existing research that form the basis of our SSCT implementation. Since SSCT encryption is an extension of the Simple Substitution technique, a deeper understanding of both the simple substitution method and the Jakobsen's algorithm which helps in solving it, will help us in breaking the SSCT cipher.

2.1 Jakobsen's Algorithm

The naive approach to decrypt a simple substitution cipher is outlined below:

1. Guess an initial key K
2. Decrypt the cipher using K
3. If the decrypted message does not make sense, modify the key K
4. Go to step 2

Jakobsen's algorithm [6] provides a faster attack on the simple substitution cipher. This method makes use of digraph statistics of the plaintext and the ciphertext. Initially, the digraph frequencies of the plaintext letters are populated in the matrix E and the digraph frequencies for the ciphertext are filled in the matrix D. We compute the score for the initial D matrix using the formula

$$\text{Score} = \sum |e_{ij} - d_{ij}|$$

Table 1: Caesar Cipher with key = 2

A	B	C	D	E	F	G	H	I	J	K	L	...	S	T	U	V	W	X	Y	Z
C	D	E	F	G	H	I	J	K	L	M	N	...	U	V	W	X	Y	Z	A	B

An initial key K is guessed by comparing the individual letter frequencies in the plaintext and the ciphertext [4]. For every change in K, the D matrix changes as follows: if K_i and K_j are swapped, then we swap the ith and j^{th} columns and rows in the D matrix. We compute the score for the modified D matrix. If the score improves, we retain the changes, otherwise we swap the rows and columns again and continue with a different key.

2.2 Simple Substitution Distance

One of the earliest forms of encryption is the Caesar Cipher [13]. Here, the key is an integer indicating the shift in the alphabet position. For example, if the key is 2, every character in the alphabet maps to the character two units away from itself, as shown in Table 1. Simple Substitution is a modification of the Caesar Cipher where instead of a constant displacement, the key can be any permutation of the characters in the alphabet.

In static analysis, opcode sequences are often extracted from a known malware and compared to the opcode sequence from an unknown file [16]. By obtaining a similarity measure between the two sequences, the unknown file is classified either as a malware or a benign file. In these methods, opcodes are usually represented by characters from the English alphabet, making the extracted opcode sequence a string of letters from the English alphabet. Combining this representation and the opcode substitution that we saw in Chapter 1 to morph the malware, we can look at an unknown file as a cipher and try to decrypt it using the Simple Substitution method

to see if resembles any known version of the virus.

An effective implementation of the Simple Substitution method to detect malware is given in [8]. This implementation uses the Jakobsen's algorithm to avoid repeated decryption of the cipher or the unknown file.

Let us try to simulate the Jakobsen's algorithm on an example. Let us consider an alphabet with characters J,G,S,V and P in the decreasing order of their occurrence. Let the original digraph frequency in this alphabet be the matrix shown in Table 2. If our ciphertext is "GPSSPVJPSPSVJGSPJVJGSVSPVS", based on the frequency, we can come with the putative key shown in Table 3. The decrypted text using this putative key is "PGJJGSVGJGJSVPJGVSVPJSJGSJ". From this, we calculate the digraph frequencies and arrive at the matrix D given in Table 4. We calculate the score for this putative key using these two matrices E and D. As per Jakobsen's algorithm, the next step is two modify this putative key K and recompute the score. There are several ways to modify the key, but to maintain the simplicity of this example, we swap the first two elements. When we decrypt now, the text obtained is "PJGGJSVJGJGSVPGJVSVPGSGJSG". With this plaintext, the new digraph frequency matrix is given in Table 5. When we compare this with Table 4, we see that columns 1 and 2 and rows 1 and 2 are swapped. This means that we do not have to decrypt the ciphertext during every iteration in order to compute the score. Instead we can build the D matrix once, and swap its rows and columns based on the changes to the key K.

Table 2: Expected digraph frequency E

	J	G	S	V	P
J	2	3	0	4	1
G	1	0	2	1	2
S	1	2	1	0	0
V	1	0	0	1	1
P	1	2	0	1	0

Table 3: Putative key

S	P	V	J	G
J	G	S	V	P

Table 4: Digraph frequency D

	J	G	S	V	P
J	1	4	2	0	0
G	3	0	2	1	0
S	2	0	0	3	0
V	0	1	1	0	2
P	2	1	0	0	0

Table 5: Digraph frequency D

	J	G	S	V	P
J	0	3	2	1	0
G	4	1	2	0	0
S	0	2	0	3	0
V	1	0	1	0	2
P	1	2	0	0	0

CHAPTER 3

Simple Substitution Columnar Transposition

We will first see how a piece of plaintext is encrypted using the simple substitution columnar transposition method. Once we have a clear understanding of the encryption, we can work backwards and come up with the steps to retrieve the plaintext from the ciphertext. This is crucial in implementing the scoring technique used in our project.

3.1 SSCT Encryption

Simple Substitution Columnar Transposition is a form of encryption that adds one more level of complexity to the simple substitution method. In this method, after the plaintext symbols are replaced with the ciphertext symbols, the text is written in the form of a matrix. The columns of this matrix are shuffled and the resulting text forms the ciphertext.

Let us encrypt the text "either the well was very deep or she fell very slowly" using SSCT, using the substitution key shown in Table 6. After substitution, the text now becomes "abcdaecdafaggfhijaeklaamneidaoaggjaekignfgk". We fill this intermediate ciphertext in a matrix as shown in Table 7. If the transposition key is (1,4,5,2,10,8,9,7,6,3), we get the final matrix as shown in Table 9. We obtain the ciphertext from this matrix, which in our case is "adabfdacecafhgkaejiglmnaodaieaa-

Table 6: Substitution Key

e	i	t	h	r	w	l	a	s	v	y	d	p	o	f
a	b	c	d	e	f	g	h	i	j	k	l	m	n	o

Table 7: Intermediate matrix

$$\begin{bmatrix} a & b & c & d & a & e & c & d & a & f \\ a & g & g & f & h & i & j & a & e & k \\ l & a & a & m & n & e & i & d & a & o \\ a & g & g & j & a & e & k & i & g & n \\ f & g & k & x & x & x & x & x & x & x \end{bmatrix}$$

Table 8: Ciphertext matrix

$$\begin{bmatrix} a & b & c & d & a & e & c & d & a & f \\ a & g & g & f & h & i & j & a & e & k \\ l & a & a & m & n & e & i & d & a & o \\ a & g & g & j & a & e & k & i & g & n \\ f & g & k & x & x & x & x & x & x & x \end{bmatrix}$$

jagnigkegfxxgxxxxxk”.

3.2 Attack on SSCT Using Jakobsen’s Algorithm

An approach to break the Zodiac-340 cipher using a combination of the Simple Substitutuion Columnar Transposition technique and the Jakobsen’s algorithm has been outlined in the research paper [20]. A major difference between the SSD and SSCT techniques is that in SSD, the plaintext and the ciphertext are a stream of characters, whereas in SSCT, they are represented as a matrix. If the initial ciphertext is represented as shown in Table 10, we need to store the digraph frequencies for every permutation of the columns. We should also note that when the matrix is flattened

Table 9: Final ciphertext matrix

$$\begin{bmatrix} a & d & a & b & f & d & a & c & e & c \\ a & f & h & g & k & a & e & j & i & g \\ l & m & n & a & o & d & a & i & e & a \\ a & j & a & g & n & i & g & k & e & g \\ f & x & x & g & x & x & x & x & x & k \end{bmatrix}$$

Table 10: Initial ciphertext matrix

$$\begin{bmatrix} c_{11} & c_{12} & c_{13} & \dots & c_{1n} \\ c_{21} & c_{22} & c_{23} & \dots & c_{2n} \\ \vdots & \vdots & \vdots & \dots & \vdots \\ c_{m1} & c_{m2} & c_{m3} & \dots & c_{mn} \end{bmatrix}$$

out, the last element of the ith row will be adjacent to the first element of the $i+1^{th}$ row. [20] describes a data structure to effectively store this information by parsing the ciphertext. Given a transposition key

$$K = (k_1, k_2, k_3, ...k_n)$$

the digraph matrix D is given by

$$D = D_{k1,k2} + D_{k2,k3} + \cdots + D_{kn-1,kn} + D_{kn,k1'}$$

where $D_{i,j}$ is the digraph frequencies matrix when column j is next to column i and $D_{i,j'}$ accounts for the digraph frequencies for the wrap around case

If we were to apply the Jakobsen's algorithm directly to this case, then, during every iteration, we would need to swap the rows and columns for each $D_{i,j}$ matrix. This would be time consuming. Instead, it is shown in [20] that swapping the rows and columns of the E matrix would yield the same score. Hence we avoid the cost of recomputing the D matrix during every iteration. With this modification, the steps to compute the score for each putative key is given by:

- Assemble the D matrix from the already computed $D_{i,j}$ matrices, based on the key K
- s $= \sum |e_{ij} - d_{ij}|$

3.3 SSCT for Malware Detection

In order to use SSCT as a scoring technique for malwares, we need to represent the data from the known virus files, which we will refer to as the model, as the plaintext and the data from the file to be scored, as the ciphertext. In both the model and the file to score, we take only the k top opcodes. All other opcodes are categorized as 'other'.

The E matrix should reflect the digraph statistics of all the files in the model. The algorithm to compute this matrix is given in Table 11. To build this matrix, we compute the normalized digraph frequencies for each file separately and sum up the individual matrices to get the final E matrix. It should be noted that in this approach, we have two keys—one corresponding to the opcode substitution and the other for the columns transposition in the matrix. We will denote the former as the substitutionKey and the latter as the transpositionKey.

Table 11: Compute E Matrix

```
Initialize E to 0
for each file in model
        Initialize digraph matrix m to 0
        opcodeCurrent = readOpcode from file
        opcodeNext = readOpcode from file
        total = 0
        while opcodeNext is not NULL
                m[opcodeCurrent][opcodeNext] + +
                opcodeCurrent = opcodeNext
                opcodeNext = readOpcode from file
                total + +
        end while
        m = m/total
        E = E + m
end for
```

The opcodes from the file to be scored are populated in a matrix. This would be our ciphertext matrix C. We use this to compute the $D_{i,j}$ matrices. We then guess an initial substitution key based on the opcode frequencies in the model and the file to score. The unknown file is scored using a nested hill climb approach against the model. The algorithm used to compute the score is outlined in Table 12. This function, in turn, calls the Jakobsen's algorithm explained in Table 13.

Table 12: Compute Score

```
Input: currentScore

Initialize transposition key K
tempKey = K
a = 0
b = 0
score = 0
while b < KEYSIZE
    temp = tempKey[a]
    tempKey[a] = tempKey[b]
    tempKey[b] = temp
    a++
    if a + b < KEYSIZE
        tempScore = Jakobsen(tempKey, currentScore)
        if tempScore < currentScore and tempScore! = 0
            currentScore = tempScore
            K = tempKey
            a = 0
            b = 1
        end if
    else
        a = 0
        b++
        tempKey = K
    end if
end while
return currentScore
```

Table 13: Jakobsen's Algorithm

Input: $tempKey$, $currentScore$

```
a = 0
b = 0
score = 0
while b < 26
    i = a
    j = a + b
    swap substitutionKey[a], substitutionKey[a + b]
    swap i^th and j^th rows and columns in E
    score = GetScoreForKey(tempKey)
    if score < currentScore
        currentScore = score
        a = 0
        b = 1
    else
        swap substitutionKey[a], substitutionKey[a + b]
        swap i^th and j^th rows and columns in E
        a++
        if a + b >= 26
            a = 0
            b++
        end if
    end if
end while
return currentScore
```

CHAPTER 4

Experiments and Results

Malware are categorized into several families based on their characteristics. As anyone would correctly assume, the response to any malware detection technique differs from one family to another. In this chapter, we will briefly describe the several malware families we have considered and present our experiments and their results.

4.1 Dataset

The SSCT implementation described in this project has been run on several malware families like Metamorphic Worm (MWOR), Next Generation Virus Creation Kit (NGVCK), Cridex, Security Shield, ZBOT, Smart HDD, Harebot and Winwebsec. A brief description of these families is given below.

- MWOR [12] is a type of worm that includes a metamorphic engine. This metamorphic engine is responsible in mutating the worm across generations, helping it to evade detection by security systems

- NGVCK is a self replicating, metamorphic virus. The NGVCK morphing engine uses techniques like function ordering and dead code insertion to morph the virus [18]

- Cridex is a Trojan that spreads by infecting removable disk drives. It infects the system by creating a backdoor entry point [9]

- Security Shield is a variant of the winwebsec family. It is a malicious software that displays fake alerts in the system [10]

Table 14: Dataset

Family	Number of files
MWOR	100
NGVCK	50
Cridex	74
Security Shield	58
ZBOT	2136
Smart HDD	68
Harebot	53
Winwebsec	4360
Benign set	214

- ZBOT or Zeus is a trojan horse that steals information from infected systems by techniques like form grabbing [17]
- Smart HDD is a virus that disables the security softwares in the infected systems [7]
- Harebot is a rootkit that uses keystroke logging to get unauthorized information from the infected system
- Winwebsec is a malicious software that displays fake warning messages and popups in the infected system [11]

Benign files used in the experiments for Linux malware were taken from several Linux utility programs like mv, cp, mkdir etc., Several Cygwin utility files were used as the benign files to score the malware files for Windows platform. The number of virus files in each family can be found in Table 14. All the files in each family were grouped into five sets and a five fold cross validation was done in order to obtain the malware and the benign scores.

4.2 Parameters

When we disassemble both the malware and the benign files, we find that they contain a large number of distinct opcodes. Of these opcodes, only a certain number of them appear consistently and contribute to the inherent malicious or benign nature of these files. All other opcodes occur quite infrequently and can collectively be categorized as the 'other' category. Hence, the opcode sequence of the files now contain the top K frequently occurring opcodes and the 'other' opcodes. In the previous research involving Simple Substitution Distance [8], it has been shown that taking the top 25 distinct opcodes yields the best results. Hence, in our experiments, we adopt the same value.

We have tried out three different approaches for our implementation. In the first approach, we use the same number of columns for all the test files and compute their scores. This is repeated for various column configurations, that is, all test files are scored by arranging them in a two column matrix first, then 5, 10 and so on. In the second approach, each file is scored using various number of columns and then the scores are collected for all test files. Since the scores did not differ from each other by a large margin, and since the first approach is faster, we have continued all further experiments using the first approach. The third approach uses Index Coincidence scores to find the correct column permutation and then uses a hill climb approach to arrive at the best possible substitution key. The difference between this and the first two approaches is that, in this approach, we separate the transposition and the substitution layers in our problem. We have tested this approach on a subset of Winwebsec files. Figure A.24 and Figure A.23 represent the ROC curve and the scatter plots for this approach.

In this project, we have also experimented with different number of columns for

the ciphertext matrix shown in Table 10. The number of columns taken were 2, 5, 10, 15, 20 and 25. Since the score obtained was the same in all these cases and since the running time is lesser when the number of columns is 2, we have continued all our experiments using that value.

4.3 Results

We obtained the malware and benign scores for the test data from the experiments we carried out on the different malware families. Using this data, we calculate the false positive and the false negative rates for each of the families and use them to plot Receiver Operating Characteristics curve (ROC curve) [5]. The area under the ROC curve (AUC value) is a value between 0 and 1, inclusive. This value gives the probability with which our system will correctly classify any random file as a malware or a benign file [3]. Table 15 gives a comparison of the AUC values for the different malware families obtained by using the SSCT, SSD and HMM techniques [1, 2, 16, 15, 14]. The visualization of the results in this table are provided through scatterplots and ROC curves for each of the families and are included in the Appendix A.

As we see from Table 15, for some families, the AUC value obtained using the SSCT technique is 1, which is the ideal value we strive for, and for a few others, the value drops. The AUC value of 1 is obtained when there is a clear demarcation between the malware and the benign scores. For example, from the scatterplot of these values for the family NGVCK given in Figure 1, we see that the range of values for the malware and benign scores do not overlap. As, a result, we have a perfect ROC curve with an AUC value of 1, as shown in Figure 2. On the other hand, in the case of the Cridex family of malware, there is some overlapping of the malware

Table 15: AUC values

Malware Family	AUC using SSCT	AUC using SSD	AUC using HMM
MWOR0.5	0.51	1	1
MWOR1	0.58	1	0.99
MWOR1.5	0.70	0.9921	0.9625
MWOR4	0.80	0.9933	0.8225
NGVCK	1	1	1
Cridex	0.96288	0.58306	0.596
SecurityShield	1	0.62902	0.994
ZBOT	0.867	0.8664	0.9874
Smart HDD	1	0.8855	0.99875
Harebot	1	0.5606	1
Winwebsec	0.7328	0.8374	1

and the benign scores, as shown in Figure 3. This results in the ROC curve shown in Figure 4. The scatterplot and the corresponding ROC curves for the remaining families are included in the Appendix A.

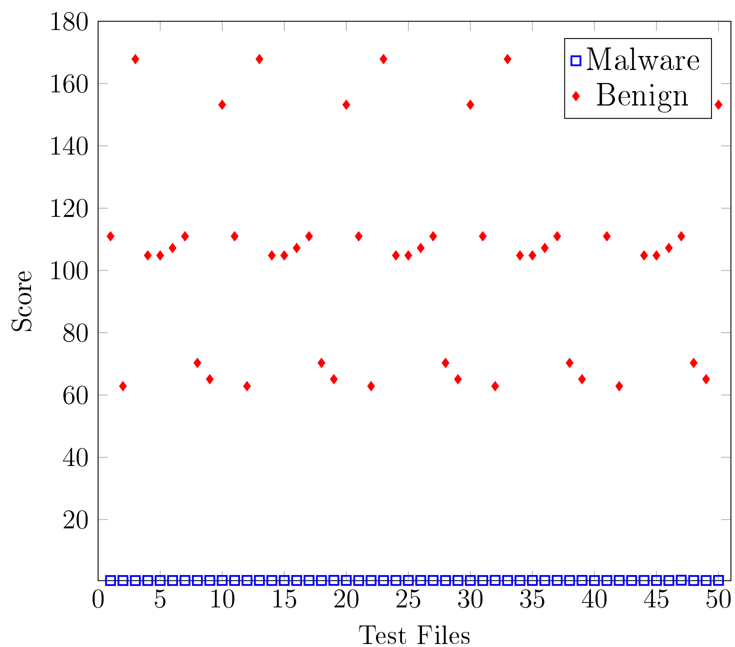

Figure 1: Scatter Plot NGVCK

We see from Table 15 that the SSCT scores give a better result compared to

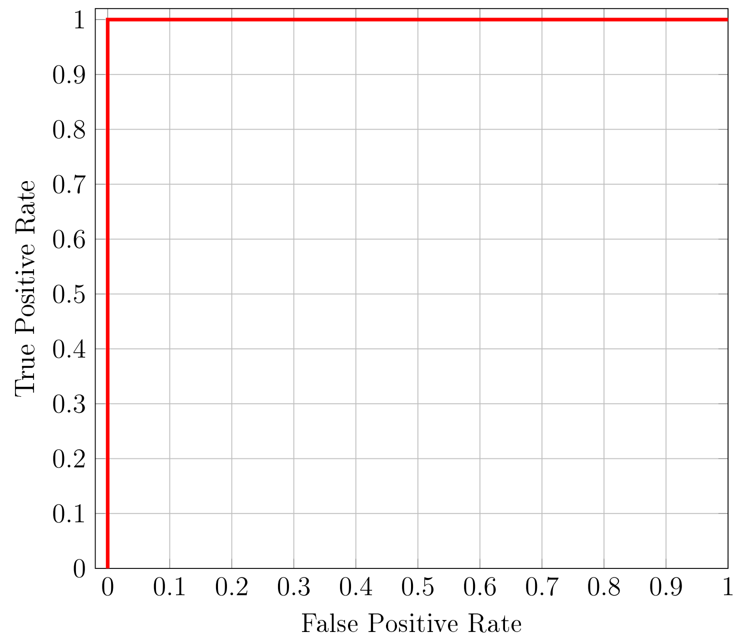

Figure 2: NGVCK ROC Curve

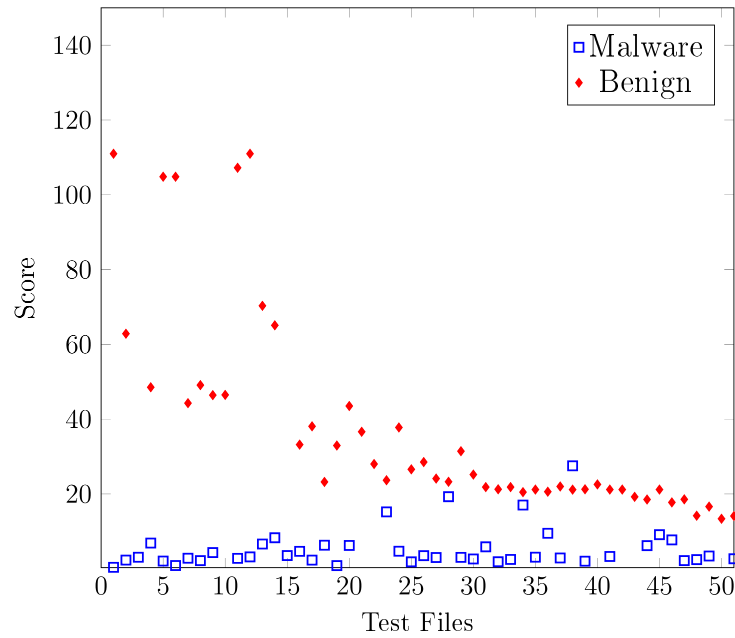

Figure 3: Scatter Plot Cridex

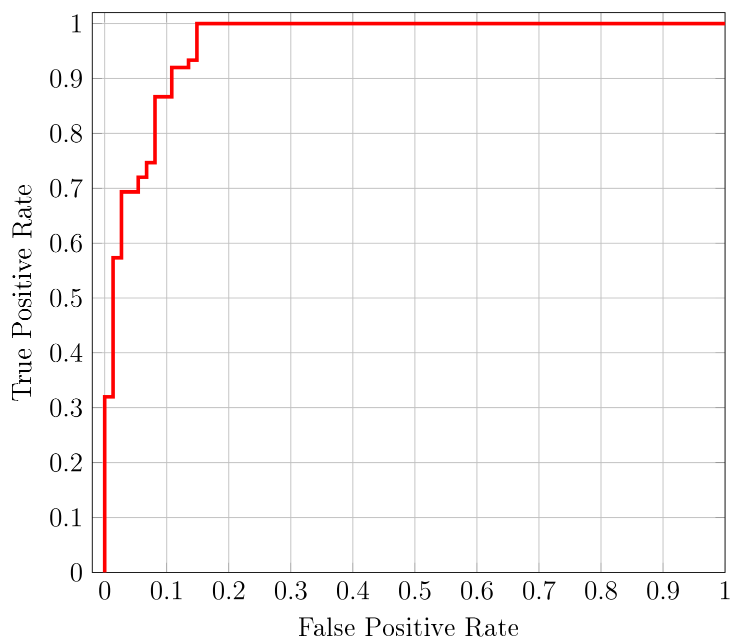

Figure 4: Cridex ROC Curve

the other techniques considered in the literature. We can attribute this performance improvement to two factors. First is the opcode substitution which is handled by the substitutionKey in our implementation. This addresses morphing techniques that replace opcodes with other interchangeable opcodes. It should be noted that the SSD technique also handles this case. The second, and the distinguishing factor, is the column transpositions in our ciphertext matrix, handled by the transpositionKey. Rearranging the columns in the matrix could account for morphing techniques that use sub-routine re-ordering and hence increase the detection rate in morphed malware. This might also be the reason causing this technique to not perform as well as the SSD method, in case of families like Winwebsec.

Another interesting fact to note from the results is that, when we observe the scatter plots in Figure A.5 to Figure A.8 in Appendix A for the different padding ratios in the MWOR family, the gap between the benign and the malware scores

seems to increase with the increase in the padding ratio. This can be due to the fact that as more and more dead code is inserted, the malware files become more similar to one another than to the benign files.

CHAPTER 5

Conclusion and Future Work

In this project we have implemented the SSCT algorithm to score several malware families. Our implementation takes a set of training files and builds a model out of those files. This model is then used to score a set of test files, which may be benign or malign. One of the challenging aspects of this project was to represent the information from all the files in the training set, in the model. We have used five fold cross validation to ensure that the results are unbiased. Our experiments were carried out on several hundreds of malware files across different families and this has given us a chance to observe how each of these families reacts to this scoring technique. In addition to the SSCT module, we have also implemented the SSD technique to compare our scores and to verify the correctness of our implementation.

On comparing the SSCT scores with the scores from previous researches like the Simple Substitution Distance for malware detection, we see that the SSCT technique gives better results in many families.

This project has sufficient scope for future research and optimization. Currently, we observe an increase in the running time of the module when the number of columns is increased. This aspect has definite room for improvement and any future work can attempt to optimize the running time of the algorithm. Another aspect that could be improved is the performance of the SSCT technique on families like Winwebsec and MWOR, where the detection rate is lower than that of the rate for the SSD method. We can try out different swapping techniques for the substitution key and the transposition key as discussed in [8] and compare the AUC values obtained in

each case. In this project, except for the MWOR family, we have not taken the padded variants of other families. It would be interesting to see if the SSCT method continues to detect these other families even with increased padding ratios.

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APPENDIX

Experiments

In this section, we provide the scatterplots and the ROC curves for all the families we have experimented on. When running the experiments on each of the families, we recorded the malware scores and the benign scores and used these to generate the scatterplots shown in figures A.5 to A.13. From these scores, we calculated the true positive and the false positive rates and used them to generate the ROC curves shown in figures A.14 to A.22. The ROC curves given here correspond to the AUC values displayed in Table 15.

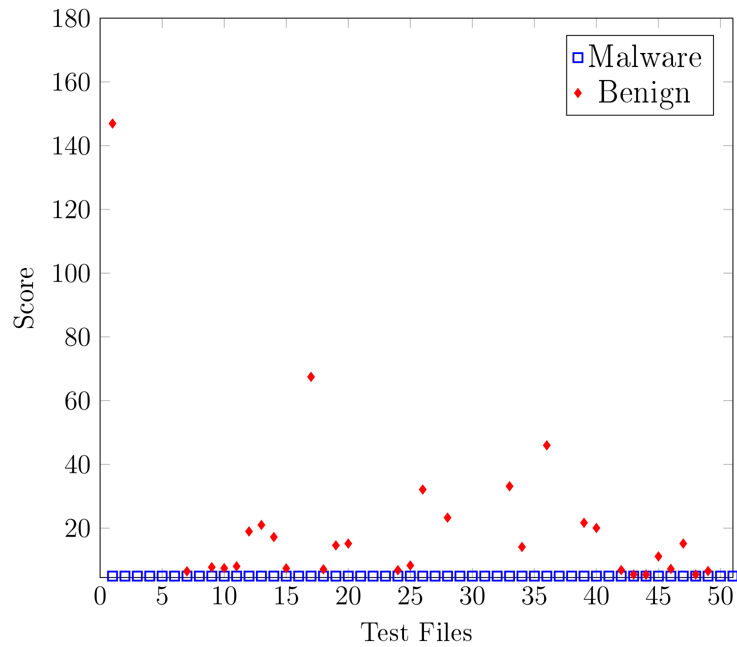

Figure A.5: Scatter Plot MWOR 0.5

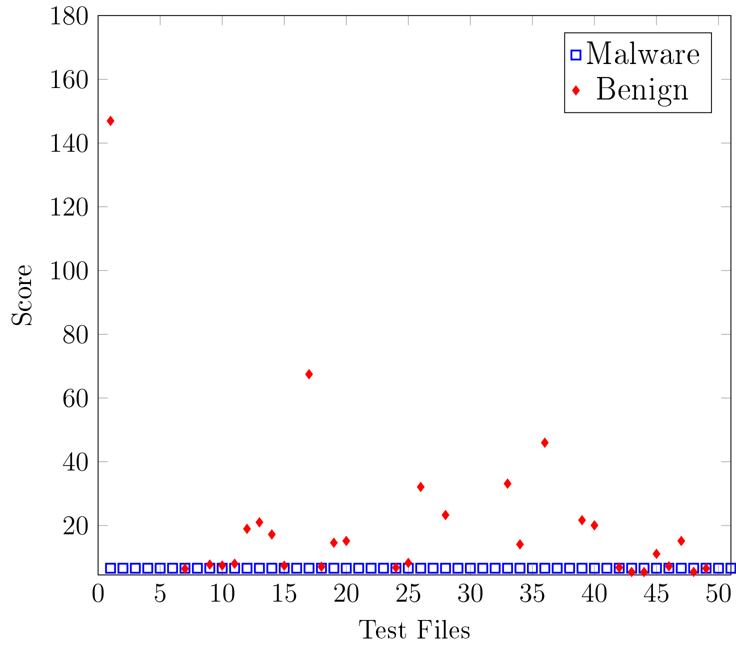

Figure A.6: Scatter Plot MWOR 1

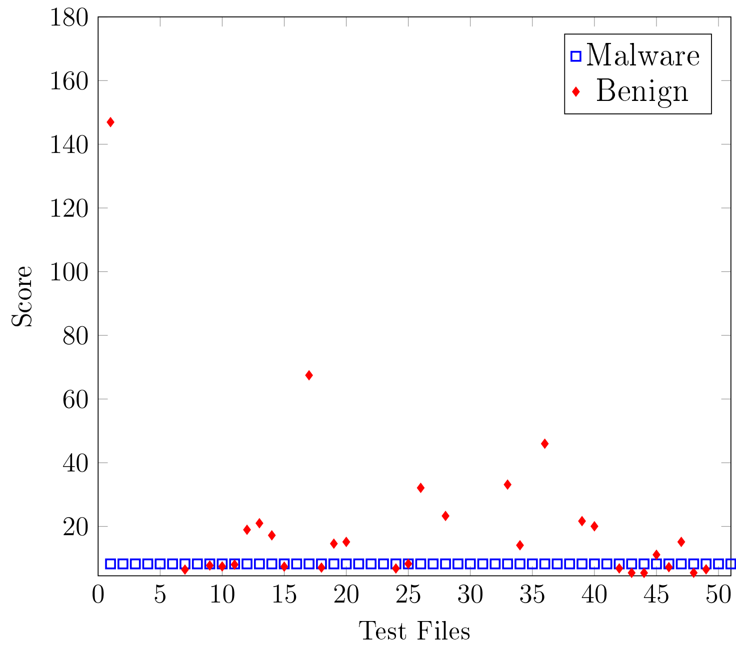

Figure A.7: Scatter Plot MWOR 1.5

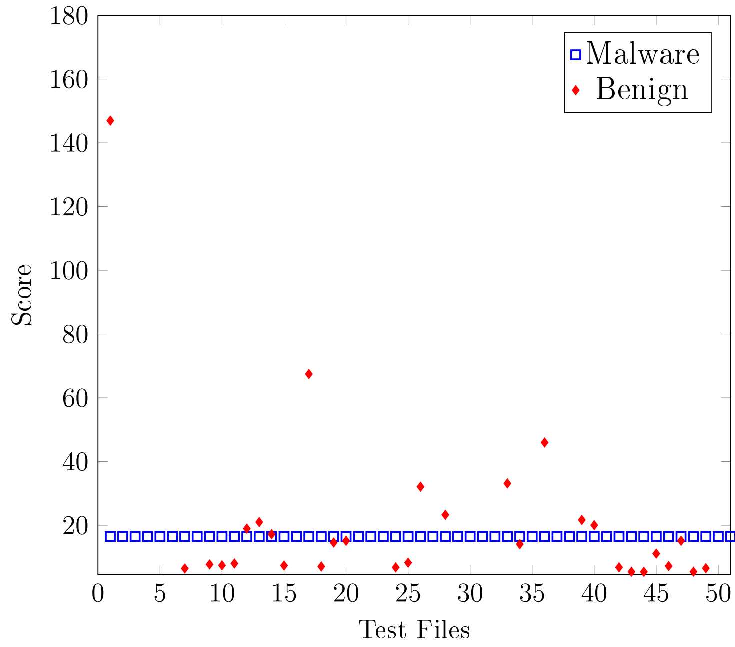

Figure A.8: Scatter Plot MWOR 4

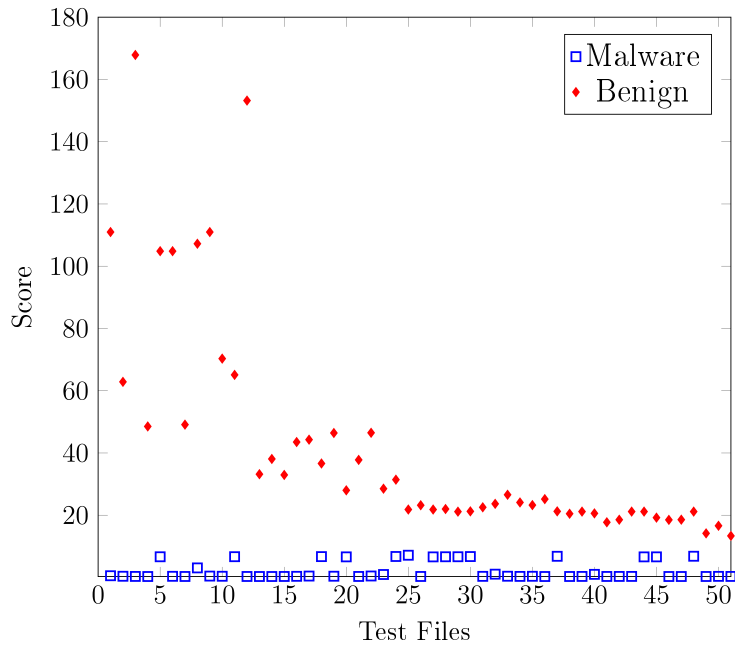

Figure A.9: Scatter Plot SecurityShield

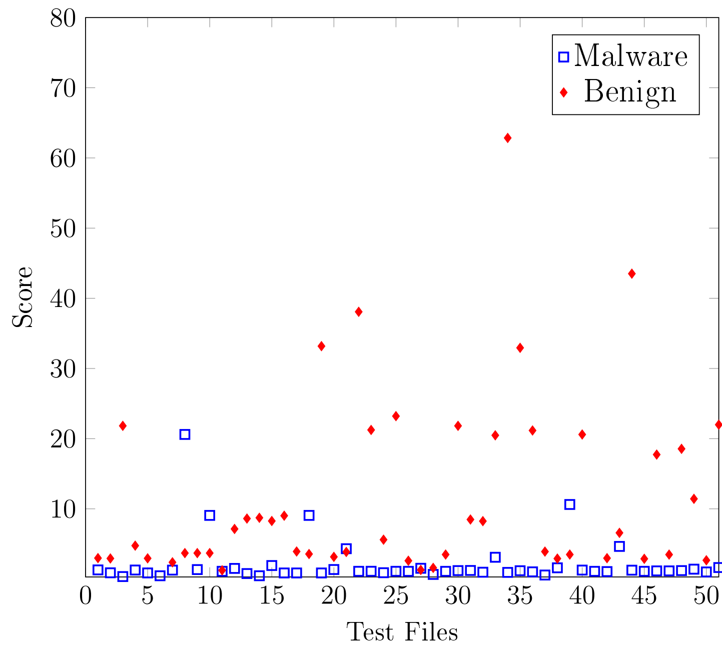

Figure A.10: Scatter Plot ZBOT

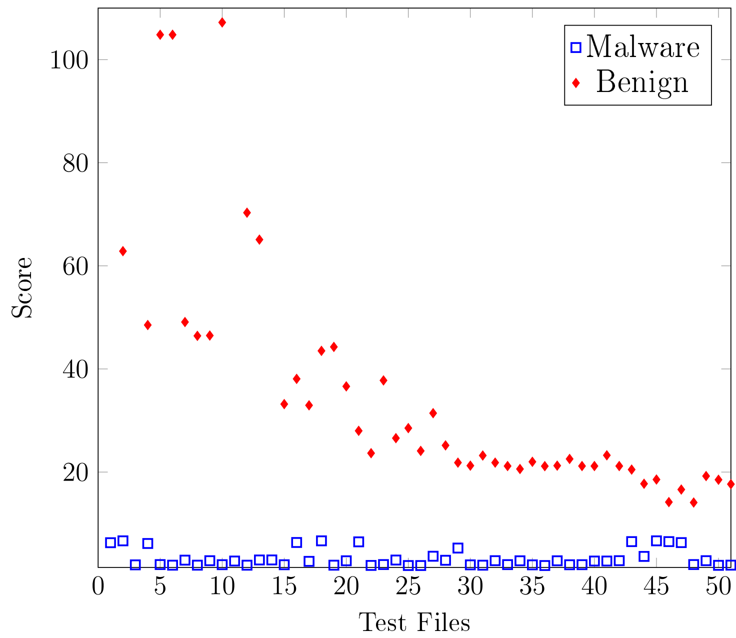

Figure A.11: Scatter Plot SmartHDD

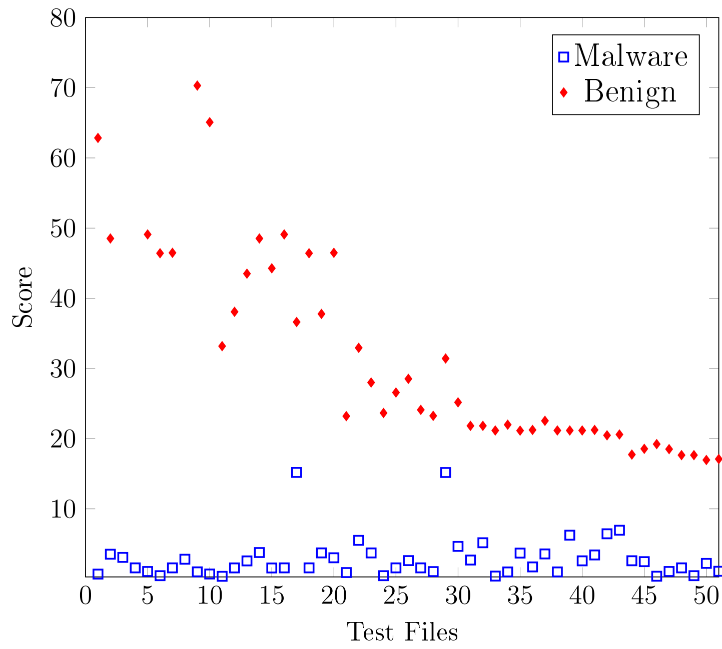

Figure A.12: Scatter Plot Harebot

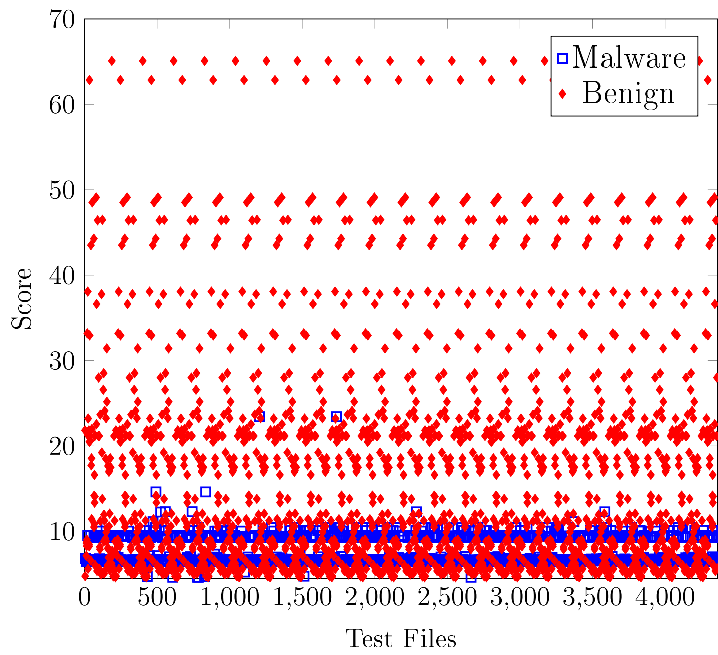

Figure A.13: Scatter Plot Winwebsec

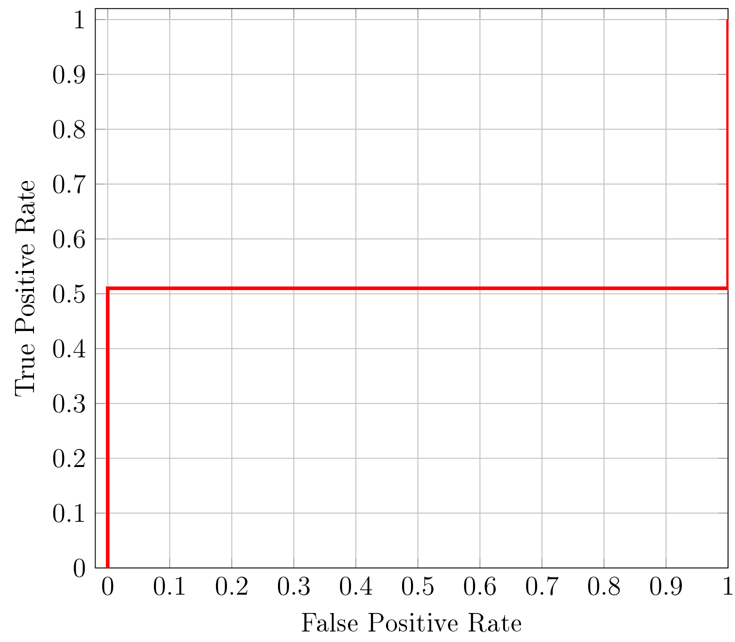

Figure A.14: MWOR0.5 ROC Curve

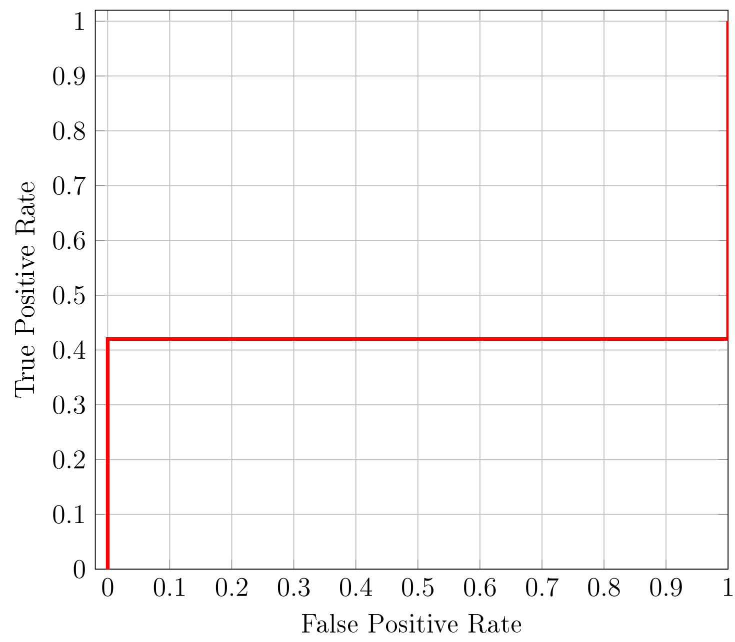

Figure A.15: MWOR1 ROC Curve

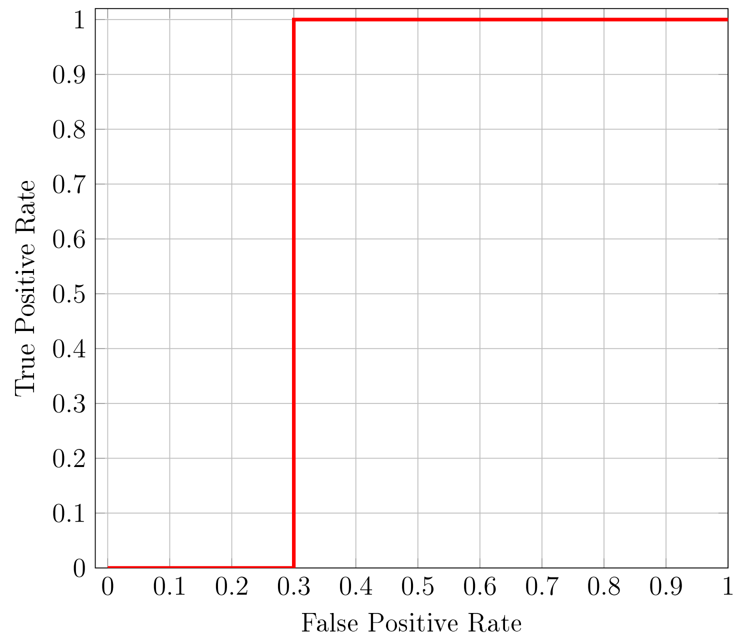

Figure A.16: MWOR1.5 ROC Curve

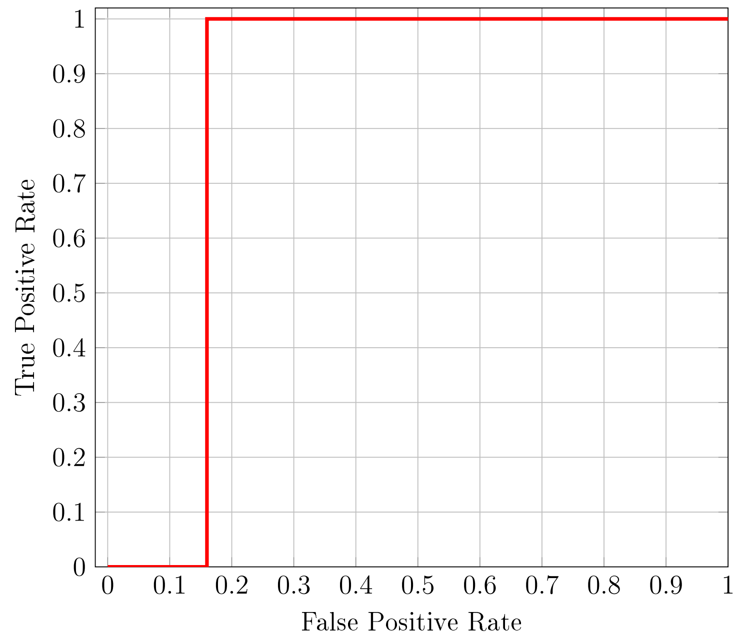

Figure A.17: MWOR4 ROC Curve

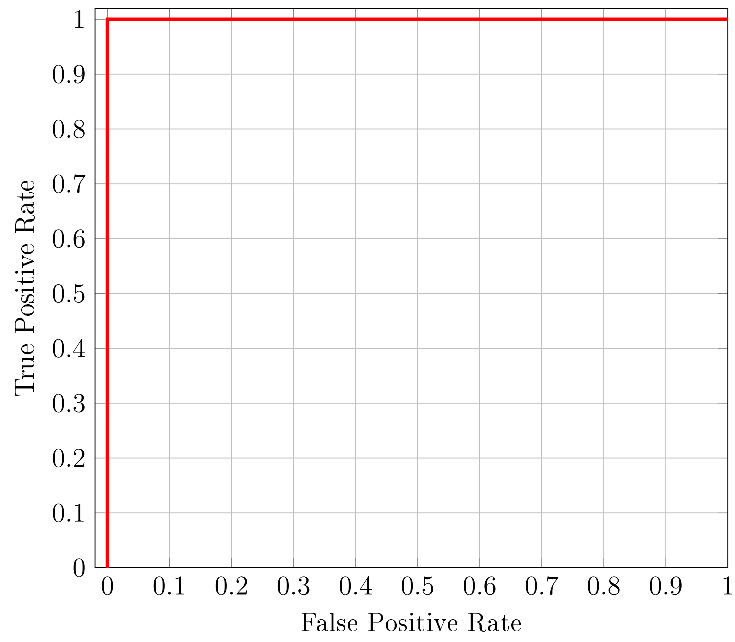

Figure A.18: SecurityShield ROC Curve

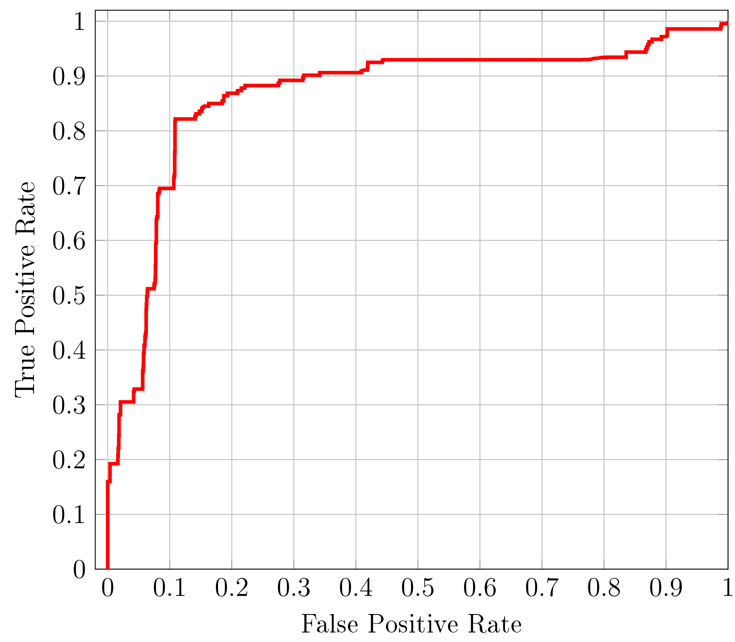

Figure A.19: ZBOT ROC Curve

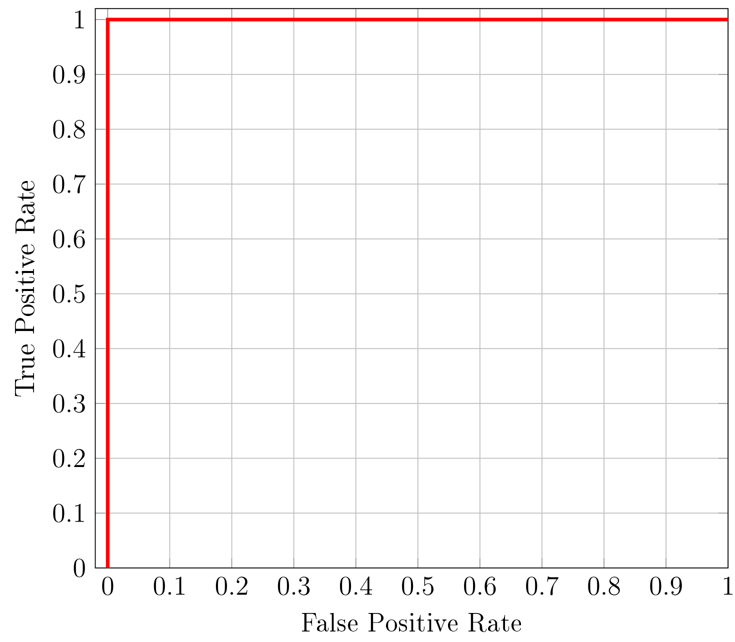

Figure A.20: SmartHDD ROC Curve

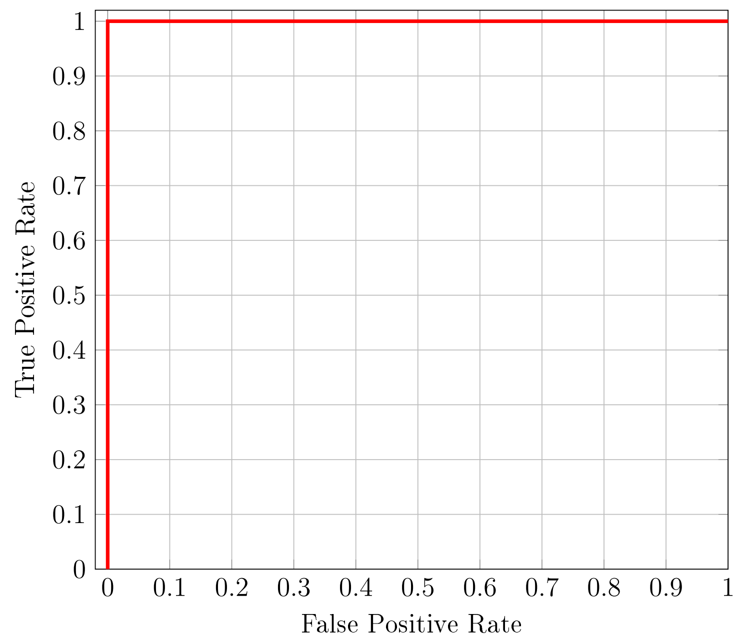

Figure A.21: Harebot ROC Curve

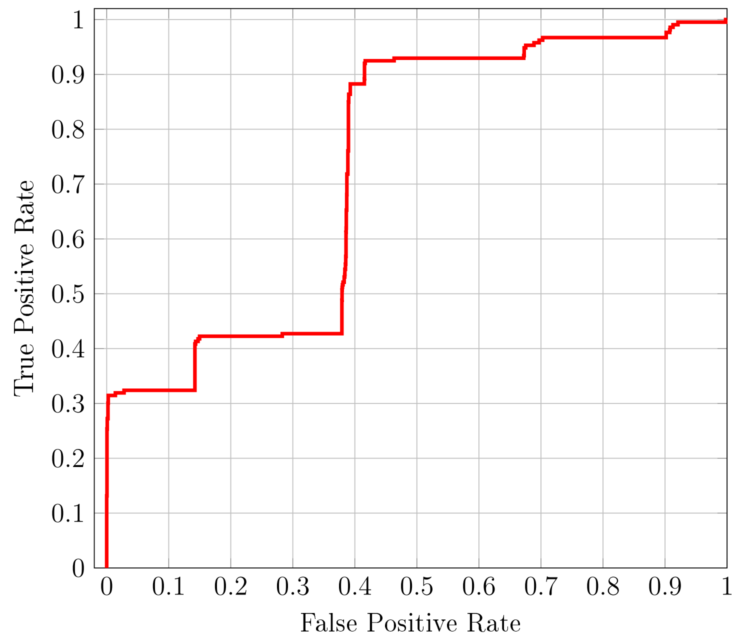

Figure A.22: Winwebsec ROC Curve

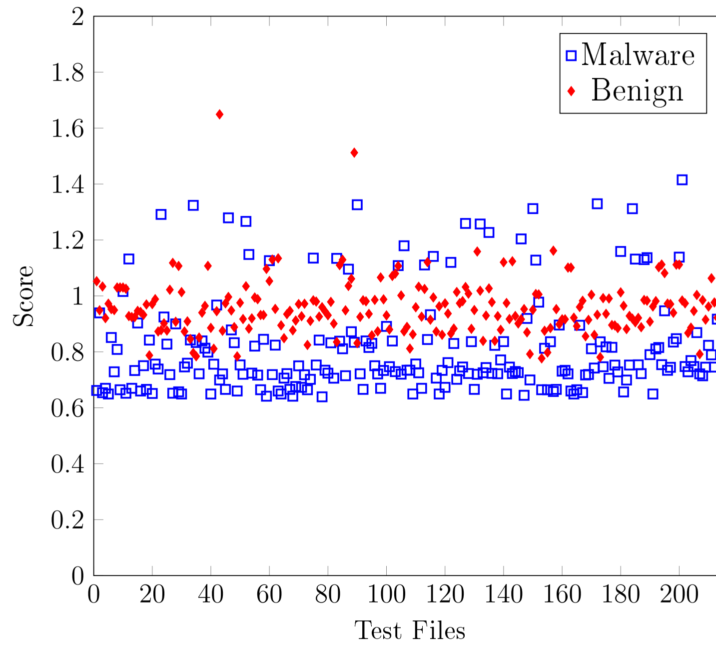

Figure A.23: Scatter Plot Winwebsec IC Scores

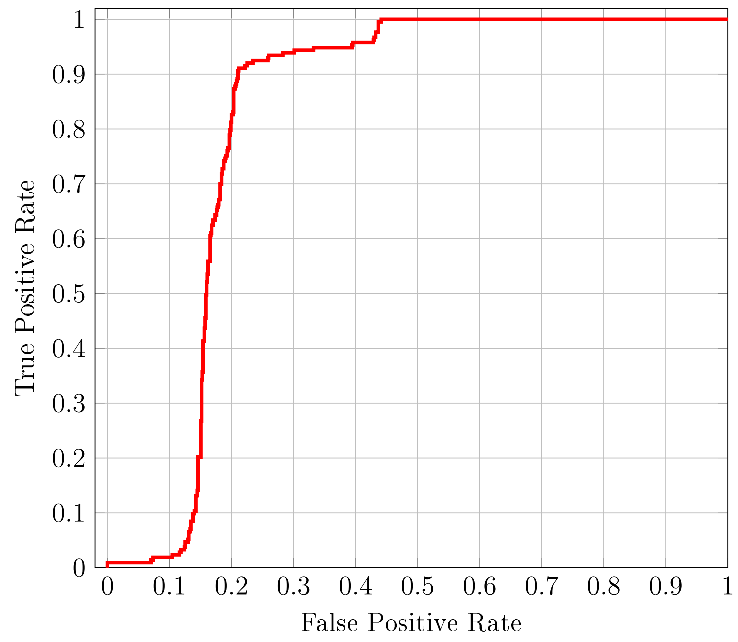

Figure A.24: Winwebsec ROC Curve(IC Scores)