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Function Call Graph Score for Malware Detection

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Function Call Graph 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

Deebiga Rajeswaran

Dec 2015

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The Designated Project Committee Approves the Project Titled

Function Call Graph Score for Malware Detection

by

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Dec 2015

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ABSTRACT

Function Call Graph Score for Malware Detection

by Deebiga Rajeswaran

Metamorphic malware changes its internal structure with each infection, while maintaining its core functionality. Detecting such malware is a challenging research problem. Function call graph analysis has previously shown promise in detecting such malware. In this research, we analyze the robustness of a function call graph score with respect to various code morphing strategies. We also consider modifications of the score that make it more robust in the face of such morphing.

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CHAPTER 1

Introduction

Today, computer systems are a basic necessity and malware has become a common problem faced by users of such systems. Cryptolocker [7] is a well-known example of a class of malware known as ransomware [5]. As another example, it is claimed that the Carberp banking trojan [7] looted approximately \$250 million from banks and financial institutions. When the hacker who created Carberp was arrested, the source code was leaked and the code served as a resource for other aspiring hackers.

With the increase in the number of networked devices, there has been a rapid growth in the malware population, which has led to an arms race between anti-virus developers and malware writers [2, 18]. Anti-virus vendors have to be equally competitive and try to stay one step ahead of the malware developer. McAfee labs claim that some of their predictions for 2015 like the master boot record getting wiped, rapid growth in malvertising like the came true within a span of two months [16].

The most common malware detection method is signature based detection [6]. In this method, malware is matched with a database of known patterns. To evade signature detections, malware writers may obfuscate their code. Metamorphic malware morphs its code structure at each infection, without changing its essential functionality [13, 21]. A variety of code obfuscation techniques have been used to generate metamorphic code. Metamorphic detection is a challenging research problem. Among the techniques previously analyzed for metamorphic detection [13, 9], function call graph analysis has been among the most successful [6, 17, 21].

The function call graph in [6, 17] is constructed by forming a graph with vertices

representing subroutines and edges corresponding to control flow between the functions. This score is based on these graphs, where we distinguish between external functions and internal functions, and the score also uses opcode statistics and cosine similarity.

In this research, we first implement the function call graph score as described in [17, 21]. We then score several challenging malware families and we analyze the effect of various code obfuscations [14, 15, 28] on the score. The goal is to determine an effective and practical means of defeating this function call graph score. Based on these results, we then consider ways to construct an improved function call graph score.

This paper is structured as the follows. Chapter 2 provides details on types of malware and malware detection techniques. Chapter 3 outlines the construction of the function call graph and the similarity score based on these graphs. Chapter 4 covers code obfuscation techniques and the impact of such techniques on function call graph analysis. In Chapter 5, we present experimental results for related to our function call graph analysis. Finally, Chapter 6 concludes the paper, and we also discuss future work.

CHAPTER 2

Types of malware and Detection Techniques

The term "malware" means a malicious software [2] that causes undesired outcome and effects in the system either without user's command or misusing the user's command indirectly. It comprises of different types like virus, worm, trojan horse, backdoor bot, spam, spyware, adware and ransomware [11]. In this chapter, we will look into different types of malware based on action and concealment strategy and malware detection techniques.

2.1 Types of malware

The malwares can be broadly classified based on their infection strategy as: Viruses, Worms and Trojans

Virus is a self-replicating malware which attaches itself to other programs and manifests its existence. On being triggered by a specific event or file execution, the virus infects the target and conceals itself. Viruses are parasitic by nature and hence reside in boot sector, executables or in data files.

Worms are spread through networks and generally aim at attacking the bandwidth of the system. Unlike viruses, worms can execute standalone without depending on a host. The worms can be further sub-classified into Email worms, Instant Messaging worms, Internet worms, IRC worms, File-sharing network worms.

Trojan horse deceives the user by representing itself as a useful application but executes malicious code and harms the system. They can infect the system through remote access, data destruction, down loader, server Trojan, anti-virus

software dialog box or as a Denial of Service(DoS) attack. `Trojan.Zbot` [23] and `Trojan.ZeroAccess` [24] used in our experiments are examples of Trojan virus.

Backdoor: Backdoor [2] is another notable malware that bypasses authentication, obtains remote access to the infected system and uses stealth techniques to lock the resources of the system. It does not execute standalone but waits for orders from the remote system. `Harebot.M` [8] is an example of the backdoor and has been used in our research.

Few other notable types of malware are:

Bots: The bot is a malware that is vulnerable and lets the attacker or botmaster to control it [19]. Once infected, the bot operates and obeys commands issued by the botmaster without the system owner's knowledge.

Spam: Spam are not malware by themselves but a medium for spreading malware files. Bulk messages are sent through the electronic messaging system with malware attachments to random users.

Spyware: Spyware mainly aim at spying on the host system and stealing data like user keystrokes.

Adware: Adware are the annoying pop up ads that we encounter. They display ads without any user input or misleads a genuine user interaction.

Ransomware: Ransomware has been the worst form of malware [11]. It encrypts data in infected system or alters its access privileges and demands ransom from the user to retrieve data. It not just fools people into paying ransom to save data but most are not even ethical enough to provide data in return to the ransom [11].

In recent times, viruses are designed by malware writers such that they are

undetected by the traditional signature based detection used by most of the anti-virus softwares. With respect to the strategies used to conceal the signature of the virus, they are classified into encrypted virus, oligomorphic virus, polymorphic virus and metamorphic virus [22, 26].

2.1.1 Encrypted virus

In an encrypted virus, the malicious part of the code is encrypted by performing a simple XOR operation with a key or a constant. The encryption is kept simple as complicating it will affect the performance efficiency of the virus. Though not detected initially [22], once a malware is identified, the decryption code in the malware is not encrypted and hence it can be used as a signature and easily detected.

2.1.2 Oligomorphic virus

Oligomorphic virus is a slightly sophisticated version of the encrypted virus. The only difference is that there are several copies of the decryption code that are used at random. But again as discussed in encrypted virus, it will not take long for the anti-virus software to add all the copies of decryptor code to the signature database.

2.1.3 Polymorphic virus

Polymorphic virus is a form of encrypted virus that posed a serious threat to malware detection techniques [22]. The malware is encapsulated in a layer of encryption, the decryption code is programmed in such a way that it changes its form and hence makes it difficult for the signature detection method. On every infection, the decryption code restructures itself to evade signature check. These viruses can be detected by executing the virus in an emulator where the decryption code decrypts

and the actual malware code is exposed which can be checked for a signature match.

2.1.4 Metamorphic virus

Metamorphic virus are more advanced than the previous attempts by malware writers. They are a challenging problem for the virus scanners [22, 26]. As the name suggests, the virus changes the form of the whole code. The metamorphic virus has a mutation engine which uses several obfuscation techniques [15] to tamper the signature with no damage to the actual functionality of the malware. [22, 26] The code has no encryption but the whole structure and pattern of the malware is modified and hence detection by signature is almost impossible. The mutation engine may be carried along by the virus or standalone generating multiple copies of the same malware. The former may have limitations in the amount of metamorphism that can be achieved as the mutation engine has to morph itself to stay undetected in signature detection, but the latter is hard to be detected by signature detection.

2.2 Malware detection techniques

The malware detection techniques can be broadly classified as signature based, heuristics based and statistics based of the malware.

2.2.1 Signature based detection

The signature based detection is the simplest and most effective detection means for scanning known malwares. After a malware is identified, a unique string of the malware is labeled as the signature of the malware and stored in the database of identified malwares by the anti-virus softwares. After the initial identification phase, when the system is scanned the bytecodes of the files are compared with the signatures in

the database. When any of the file matches the signature, it is considered as a malware and notified to the user. [26] The only limitation in the signature based detection is that it fails to identify new malwares and advanced malwares like polymorphic or metamorphic malwares.

2.2.2 Heuristics based detection

The heuristics based detection has a more practical approach towards detecting malware. The executable is tested in a simulated environment [22] which strips out a layer of obfuscation. The actual execution of the code in a safe environment exposes the true intent of the file. Any suspicious file can be isolated from the rest of the files and prevent the spread of the malware. This method effectively identifies new viruses whose signature may not be in the database of the anti-virus software.

2.2.3 Statistics based detection

Statistics based detection is a detection technique in which in recent times more research are done and there has been promising advancements. Machine learning has been used to classify malware from benign files on many aspects as API calls, opcode sequences, function calls, value set analysis etc. Hidden Markov Model (HMM) has been a very effect means of static analysis that classifies malware but since it does not store the position information of the hidden states it may not classify metamorphic malware that effectively. But the Profile Hidden Markov Model (PHMM) solves the limitation and has been found successful in classifying the metamorphic malwares [25].

CHAPTER 3

Function call graph implementation

We will be discussing about the previous work done in functionality based analysis of viruses, the construction of the function call graph and the similarity detection between the malwares in this chapter.

3.1 Previous work

The detection of metamorphic malware by searching for a unique string is almost impossible [13]. The code obfuscation layer has to be removed as part of the detection and the score must be based only on the functional part of the malware or the behavior of the malware.

Christodorescu and Jha [4] were the first to implement a static analysis based on a control flow graph to eliminate code obfuscation techniques. Since then, there has been many researches in the detection of metamorphic malware based on static analysis like external functions [29] and cosine similarity between the functions [10]. Ming et al. [17] explains a similarity metric based on the function calls in the malware and Shang et al. [21] details the time and space complexities involved in control flow graphs and proposes a function call graph based detection method.

Shahid and Ibrahim [1] have proposed an annotated control flow graph in which the instructions are grouped into 21 patterns and they have also parallelized the process to boost the performance of the detection technique. Prasad [6] has proposed a function call graph analysis in which a graph coloring technique is used to eliminate several other obfuscation layers.

3.2 Construction of the function call graph

This section details the pre-processing involved before constructing the function call graph and construction.

3.2.1 Defining function boundaries

The executables are disassembled using IDA Pro disassembler. The functions in the malware can be classified as local functions and external functions. The start of the local functions are of format `sub_xxxxxx proc near` and ends with `sub_xxxxxx endp`. The external functions comprises of the system functions and the library routines. The local functions are labeled differently in each malware but the external functions are consistently named the same across all malwares. Our detection technique only considers the functions or sub-routines and the instruction sequences that they execute. This defeats code transposition or sub-routine ordering obfuscations in the code.

3.2.2 Building the Function call graph

Function call graph $G = (V, E)$ are composed of vertices V and edges E in which the vertices denote the functions and the edges denote the function calls between them [17, 21]. The functions and the corresponding instruction sequences are parsed to identify the entry point in the program. We have used Breadth First Search (BFS) [12] technique in the graph construction. We identify the entry point functions in the code. The non-entry point functions are added in the graph based on their function call relationship with the entry point functions. So, the entry point functions are in the first level and the non-entry point functions are mapped in the subsequent levels, thus demonstrating breadth first search. The function that calls

another function is called the "caller", the function that is being called is called the "callee" and the relationship is called a "caller-callee" relationship [6].

All the sub-routines in the program are stored in `FuncSet`. The entry point sub-routine are identified and saved in `EntryFuncSet`. The `FuncQ` is the function queue in which the `EntryFuncSet` is initialized and until empty, the function dequeued from the front of the queue is saved as `baseVertex`. The `baseVertex` is then added to the graph and the `enQ` flag is set true to avoid duplicate additions to the graph. The `baseVertex` is then scanned for its callee set and stored in `VerSet`. Each function in `VerSet` is inserted in `FuncSet` if it is not present already and assigned as the `headVertex`. If not added to the graph it is added with an edge to the `baseVertex`, if else it just increments the `outDeg` of the caller and the `inDeg` of the callee by one. If `enQ` flag of the `headVertex` is not set true yet, it is set true and enqueued to the `FuncQ`. On building the vertices in the graph, the sub-routine name, type, callee list, indegree, outdegree, `EnQ` flag status and opcode sequences are stored as shown in Figure 1. The time complexity of this algorithm is $O(|V| * |E|)$ where V is the total number of vertices and E is the total number of edges [21].

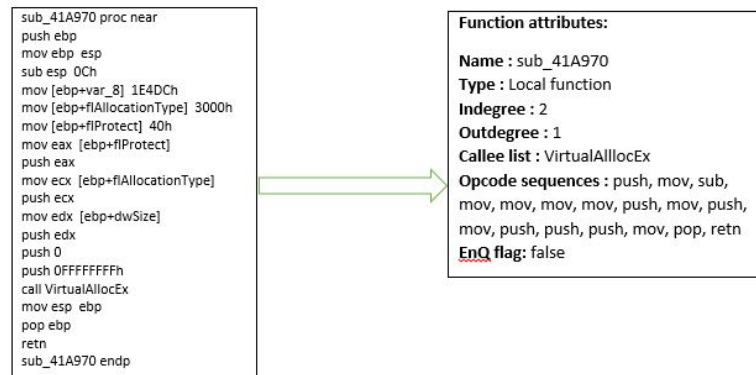


Figure 1: Function attributes stored in vertex for a Zbot file

Table 1: Building the Function call graph [17]

```

// Input: Functions in the malware  $F$ , Output: Function call graph  $G_F$ 
// Initializations
 $G_F.V = \phi$  and  $G_F.E = \phi$ 
EntryFuncSet =  $\phi$ , FuncSet =  $\phi$ , FuncQ =  $\phi$ , VerSet =  $\phi$ 
FuncSet = SplitFuncs( $F$ )
EntryFuncSet = IdentifyEntryPointFuncs( $M$ )
FuncQ = InitQ(EntryFuncSet)
while(FuncQ is not empty)
    baseVertex = Dequeue(FuncQ)
    Insert baseVertex in  $G_F$ 
    baseVertex.enQFlag = true
    VerSet = getCallee(baseVertex)
    for each vertex in VerSet
        if(vertex is not in FuncSet)
            continue
        endif
        headVertex = vertex
        // Construct an edge between tailVertex and headVertex
        if( $e \in G_F.E$ )
            baseVertex.outDeg++
            headVertex.inDeg++
        else
            Insert headVertex in  $G_F$ 
            Insert edge  $e$  in  $G_F$ 
        endif
        if(headVertex.enQFlag == false)
            Enqueue headVertex in FuncQ
            headVertex.enQFlag = true
        endif
    next vertex
end while
return  $G_F$ 
end

```

3.3 Function Call Graph Scoring

On building the function call graph, to find the similarity score between the two malware variants we need to compare the corresponding graphs. The similarity check between the graphs would imply finding common vertices which represents the functions or sub-routines. The functions cannot be identified based on specific string or pattern search as it can be easily defeated using several obfuscation techniques. The scoring of the similarity is calculated by matching external and internal functions. The system or library functions have common function names which are of the same naming convention in all files. So, the external functions are matched based on their function names. In the local functions, to overcome challenges set by code obfuscation techniques the instructions are color coded based on its type of action.

3.3.1 Common vertices based on External Functions

External functions generally refer to the system calls or library routine calls. The system functions are also called the atomic functions. Usually, the external functions form the leaf node in the graph with an indegree of 1 and outdegree of 0. They can be mapped using the symbolic names that are same across all executables. For example, `VirtualAllocA`, `GetWindowsDirectoryA`, `lstrcata`, `CreateFileA` are the external functions that forms the leaf nodes in the Zbot function call graph shown in Fig 2. Table 2 displays an algorithm that has been used to find common vertices based on external functions [17].

The external functions are taken from function call graphs of the two malware variants that are being scored for similarity G_1 , G_2 and stored in `ExtFuncSet1` and `ExtFuncSet2` respectively. The instructions in the vertices of both sets are analysed. Each of the i vertices in `ExtFuncSet1` are assigned to U_s and checked with

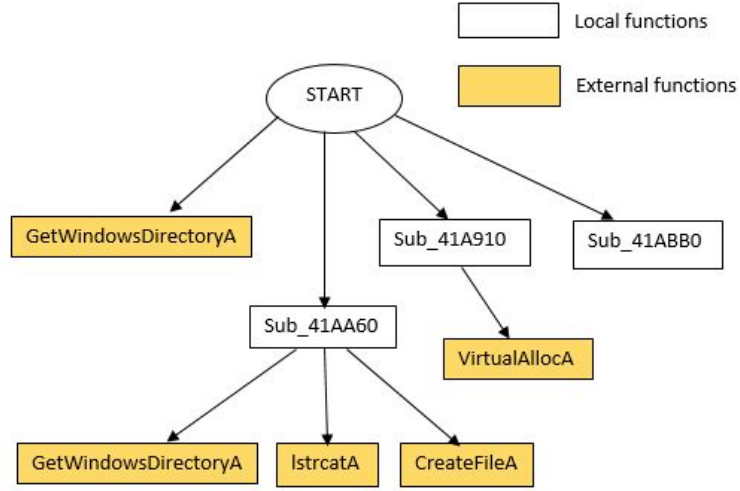


Figure 2: Function call graph with external functions

Table 2: Pseudocode to find common vertices using external functions [17]

```

// Input: Function call graph of two malware variants  $G_1$  and  $G_2$ 
// Output:  $\text{common\_vertex}(G_1, G_2)$ 
ExtFuncSet1  $\leftarrow$  External function from  $G_1$ 
ExtFuncSet2  $\leftarrow$  External function from  $G_2$ 
Copy vertices from  $G_1$  into  $U_s$ 
Copy vertices from  $G_2$  into  $V_s$ 
foreach vertex  $U_{si} \in \text{ExtFuncSet1}$  do
  foreach vertex  $V_{sj} \in \text{ExtFuncSet2}$  do
    if( $U_{si}.\text{name} = V_{sj}.\text{name}$ )
       $\text{common\_vertex}(G_1, G_2) \leftarrow \text{common\_vertex}(G_1, G_2) \cup (U_{si}, V_{sj})$ 
      Remove  $U_{si}$  from  $U_s$ 
      Remove  $V_{sj}$  from  $V_s$ 
    end
  end
end
end
end

```

all j vertices in ExtFuncSet2 assigned to V_s and finds if both graphs have any vertices that call the same external function. If such a vertex is found it is stored in

`common_vertex(G1, G2)`.

3.3.2 Match local functions based on external functions similarity

If two or more external functions are found matching in a vertex, then it is considered as a similarity between the local functions that make the call to external functions. Table 3 is the pseudocode that was used to find matching local functions pair [17, 21].

Table 3: Pseudocode to find similar local functions based on external functions [17]

```
// Input: Function call graph G1 and G2, Us, Vs, common_vertex(G1, G2)
// Output: common_vertex(G1, G2)
foreach vertex Usi ∈ Us do
  foreach vertex Vsj ∈ Vs do
    if(ExtFunc(Usi) ∩ ExtFunc(Vsj) ≥ 2) then
      common_vertex(G1, G2) ← common_vertex(G1, G2) ∪ (Usi, Vsj)
      Remove Usi from Us
      Remove Vsj from Vs
    end
  end
end
end
```

each of the local functions in the function call graphs G_1 , G_2 are matched to see if they call the same external functions. If the external functions count exceeds 2, then the function pair is considered as common vertices and added to the `common_vertex(G1, G2)`.

3.3.3 Similarity between local functions based on opcode sequence

Finding the similarity between the local functions based on a specific pattern or signature will not be effective as it can be defeated on using simple dead code insertion itself. So, we use a unique graph coloring technique. Every vertex is vectorized based

on the occurrence and frequency of the opcodes which are classified into 15 types as shown in Table 4.

Table 4: x86 instruction classification [17]

Code	Instruction Type	Description
C_1	Data	Data Transfer as mov stmt
C_2	Stack	Stack Operations
C_3	Port	In and out
C_4	Lea	Destination address transmit
C_5	Flag	Flag transmit
C_6	Arithmetic	Shift, Rotate etc.
C_7	Logic	Bitbyte operation
C_8	String	String operation
C_9	Jump	Unconditional transfer
C_{10}	Branch	Conditional transfer
C_{11}	Loop	Loop control
C_{12}	Halt	Stop instruction execution
C_{13}	Bit	Bit test and bit scan
C_{14}	Processor	Processor control
C_{15}	Float	Floating point operation

All vertices in the graph are colored based on a 15-bit variable which marks the occurrence of instructions in each color code. The variable is initialized to 0. On reading an instruction, the color code that it belongs to based on its operation is marked 1 in the corresponding bit. Another 15-bit vector stores the frequency of the corresponding color codes. Table 5 shows a sub-routine from Zbot virus and Table 6 displays the corresponding color codes and frequency vector.

Table 5: A sub-routine in Zbot virus

```

sub_401000 proc near
push ebp
mov ebp, esp
mov esp, 0Ch
mov [ebp+var_8], 1E4DCh
mov [ebp+flAllocationType], 3000h
mov [ebp+flProtect], 40h
mov eax, [ebp+flProtect]
push eax
mov ecx, [ebp+flAllocationType]
push ecx
mov edx, [ebp+dwSize]
push edx
push 0
push 0FFFFFFFh
call VirtualAllocA
mov esp, ebp
pop ebp
retn
sub_401000 endp

```

Table 6: Occurrence and Frequency color coded vector of the above Zbot sub-routine

Opcode's	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁	C ₁₂	C ₁₃	C ₁₄	C ₁₅
Occurrence	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0
Frequency	9	7	0	0	0	0	0	0	2	0	0	0	0	0	0

The frequency vector of the two graphs are stored as $X = (x_1, x_2, \dots, x_{15})$ and $Y = (y_1, y_2, \dots, y_{15})$ and the cosine similarity of them are computed as shown in formula (1) [17]:

$$\text{sim}(X, Y) = \frac{\sum_{i=1}^{15} x_i \cdot y_i}{\sqrt{\sum_{i=1}^{15} x_i^2} \cdot \sqrt{\sum_{i=1}^{15} y_i^2}} \quad (1)$$

The calculated cosine similarity is checked for whether it is greater than or equal to a threshold value of α and we also compare the color codes of the two vertices and if found the same the local functions are found as a common vertex match. Table 7 shows a pseudocode that is used to compute the color similarity between the vertices [17, 21].

Table 7: Pseudocode to find color similarity between two functions [17]

```

// Input: Functions  $f_1$  and  $f_2$ 
// Output: color similarity between  $f_1$  and  $f_2$ 
colorCode1 ← getColorSequence from  $f_1$ 
colorCode2 ← getColorSequence from  $f_2$ 
if(color1=color2)
    freqVector1 ← getVector from  $f_1$ 
    freqVector2 ← getVector from  $f_2$ 
    color_sim ← compute cosine similarity between vector1 and vector2
end
return color_sim

```

In the pseudocode, the computation of color similarity between two functions is described. Similarly, all the functions in the malware variants are computed. The functions f_1 and f_2 are provided as input to calculate the cosine similarity between the functions. The functions are first assigned a color based on the occurrence of the instructions which are stored as `colorCode1` and `colorCode2` from f_1 and f_2 . If the color code of the two functions are found similar, then the frequency of the corresponding instructions are stored in vectors `freqVector1` and `freqVector2`. The cosine similarity between the frequency vectors are computed using the formula(1) mentioned above. Aiming for perfection, two more criteria as the length of the opcode

sequences which refers to the number of bytes in the function and the total degree of the function which is calculated by adding the indegree (total number of times the function is called) and the outdegree (total number of times the function is called by other functions) are used for scoring. If the cosine similarity of the two frequency vectors is greater than or equal to α and the length similarity (`len_sim`) is greater than or equal to β and degree similarity(`degree_sim`) is greater than or equal to γ .

The length similarity is computed based on the formula (2) as shown below. The `length(f_1)` is the number of bytes in function f_1 and `length(f_2)` is the number of bytes in function f_2 . The smaller value of the two is divided by the other to obtain a value between 0 and 1.

$$\text{length_sim}(f_1, f_2) = \begin{cases} \frac{\text{length}(f_1)}{\text{length}(f_2)} & \text{if } \text{length}(f_1) \leq \text{length}(f_2) \\ \frac{\text{length}(f_2)}{\text{length}(f_1)} & \text{otherwise.} \end{cases} \quad (2)$$

The degree similarity is computed using the formula (3) in which the `degree(f_1)` is the total degree of the function f_1 and `degree(f_2)` is the total degree of the function f_2 . The `degree_sim` is assigned 1 if the degrees of the two functions are equal, else the unsigned reciprocal of their differences is used.

$$\text{degree_sim}(f_1, f_2) = \begin{cases} 1 & \text{if } \text{deg}(f_1) = \text{deg}(f_2) \\ \frac{1}{|\text{deg}(f_1) - \text{deg}(f_2)|} & \text{otherwise.} \end{cases} \quad (3)$$

The threshold values of α , β and γ are set as 0.98, 0.83 and 0.5 respectively based on previous experiments [17, 21]. Table 8 details the pseudocode to find similar function pair using the color similarity [6].

Table 8: Pseudocode to find similar local functions using color similarity [17]

```

// Input: Function call graph  $G_1$  and  $G_2, U_s, V_s, \text{common\_vertex}(G_1, G_2)$ 
//Output:  $\text{common\_vertex}(G_1, G_2)$ 
foreach vertex  $U_{si} \in U_s$  do
    foreach vertex  $V_{sj} \in V_s$  do
        if( $\text{color\_sim}(U_{si}, V_{sj}) \geq \alpha \cap$ 
            $\text{length\_sim}(U_{si}, V_{sj}) \geq \beta \cap$ 
            $\text{degree\_sim}(U_{si}, V_{sj}) \geq \gamma$ ) then
             $\text{common\_vertex}(G_1, G_2) \leftarrow \text{common\_vertex}(G_1, G_2) \cup (U_{si}, V_{sj})$ 
            Remove  $U_{si}$  from  $U_s$ 
            Remove  $V_{sj}$  from  $V_s$ 
        end
    end
end
end

```

3.3.4 Similarity between local functions based on matched neighbors

Now that we have found common vertices between the two graphs based on the internal and external functions, we can further analyze based on the results. There is a high probability that two vertices are similar if their neighbors match in graph theory. So, if the predecessor or successor of a specific vertex is a common vertex then the vertex may also be a common vertex. In Figure 3 the vertices V_1 and V_2 are already identified as common vertices, then its neighbors A, B and C, D respectively are rechecked using a `color_relaxed_sim` to find whether they are similar. The `color_relaxed_sim` is computed same as the Table 7 except that the functions' color codes need not match and the cosine similarity can be computed from the frequency vectors directly. Table 9 presents the pseudocode used to find similar functions based on matched successors and the same pseudocode applies for predecessors too by replacing `successor(u)` and `successor(v)` by `predecessor(u)` and `predecessor(v)` respectively. [21].

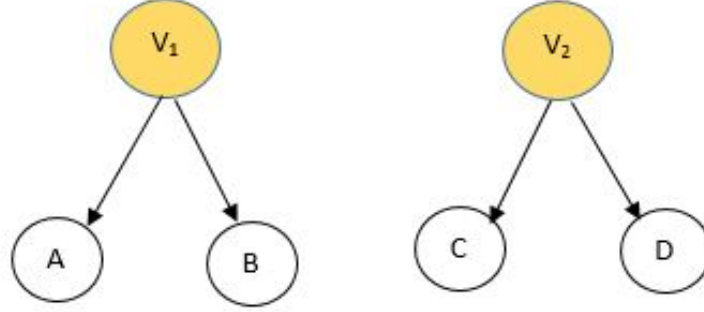


Figure 3: Successors of common vertices V_1 and V_2 are candidate vertices

Table 9: Pseudocode to find similar local functions based on matched successor [17]

```

// Input: Function call graph  $G_1$  and  $G_2, U_s, V_s, \text{common\_vertex}(G_1, G_2)$ 
// Output:  $\text{common\_vertex}(G_1, G_2)$ 
vertexQ  $\leftarrow$  InitvertexQ( $\text{common\_vertex}(G_1, G_2)$ )
while (vertexQ is not empty)
    (u,v)  $\leftarrow$  vertexQ.dequeue()
    foreach vertex  $U_{si} \in \text{successor}(u) \cap U_s$  do
        foreach vertex  $V_{sj} \in \text{successor}(v) \cap V_s$  do
            if( $\text{color\_relaxed\_sim}(U_{si}, V_{sj}) \geq \delta$ ) then
                 $\text{common\_vertex}(G_1, G_2) \leftarrow \text{common\_vertex}(G_1, G_2) \cup (U_{si}, V_{sj})$ 
                Remove  $U_{si}$  from  $U_s$ 
                Remove  $V_{sj}$  from  $V_s$ 
                vertexQ.enqueue( $U_{si}, V_{sj}$ )
            end
        end
    end
end
return  $\text{common\_vertex}(G_1, G_2)$ 

```

The `vertexQ` is initialized with the vertices in the $\text{common_vertex}(G_1, G_2)$. Each vertex in the queue are dequeued one by one and the successor or predecessor of the corresponding vertices. If the `color_relaxed_sim` of the successor or predecessor vertices are found to satisfy or exceed the threshold value set for δ then the vertices

are considered similar.

3.3.5 Similarity between function call graph

To compute the consolidated score of similarity between the function call graphs, the common edges are computed. The edge is the "caller-callee" relationship that was mentioned before. If common vertices W and X share an edge in graph G_1 and common vertices Y and Z share an edge in graph G_2 then it is called a common edge. The overall similarity between the two malware function call graphs are computed using Formula (4) [17, 6]:

$$\text{sim}(G_1, G_2) = \frac{2|\text{common_edge}(G_1, G_2)|}{|Edge(G_1)| + |Edge(G_2)|} * 100 \quad (4)$$

in which $|\text{common_edge}(G_1, G_2)|$ denotes all the common edges between the two function call graphs G_1 and G_2 and $|Edge(G_1)| + |Edge(G_2)|$ represents the total number of edges in graph G_1 and G_2 . Scoring the same file should give a value of 1 and scoring a malware variant should give a value between 0 and 1 based on the level of obfuscation in which the less obfuscated would be closer to 1.

CHAPTER 4

Types of obfuscation techniques

The metamorphic virus detection has been a tough task because the virus is capable of mutating its body to an extent that no two versions of the same malware can be assigned a common signature for detection and hence are undetectable by signature based detection [14]. This level of obfuscation in the code is achieved by one or a combination of multiple code obfuscation techniques which are detailed below:

4.1 Instruction substitution

The instruction substitution is a simple obfuscation technique in which the common instructions that have similar usage are replaced instead of the other. [15] By substituting the instruction with a similar one, the functionality of the code remains intact and the code also does not look the same as before. For example, the instructions JB (Jump if Below), JC (Jump if Carry), JNAE (Jump if Not above or Equal) all perform the same action of setting CF (Carry Flag) as 1. Using these instructions interchangeably will not affect the function of the code.

Considering this technique to impede the function call graph similarity it may not be effective, as in our detection technique, the opcodes are color coded based on functionality and used for computing the score. So, even if we substitute the instructions they will fall under the same group and will be no different from the previous code.

4.2 Register swap

Register swap is another simple technique in which the registers are swapped by not hindering the intended action of the part of the code; at the same time it forms another generation of the malware as it can evade signature based detection having altered registers all through the code. For example, the register `EAX`, `EBX`, `EDX` are swapped with `EBX`, `EDX`, `EAX` respectively. This small change is enough to fool the signature based detection. But if the detection method has wildcard search in place of registers it can be easily identified. [28]

Applying this technique to weaken our detection method will not fetch results as we only consider the opcodes for finding similarity and the registers are not considered for evaluation.

4.3 Subroutine ordering

In subroutine ordering, the order of the subroutines are altered in a random manner. [15, 14] Such an action will not change the effect of the code as the program with subroutines are not sequential, they call for the start address of the subroutine and thus does not hinder the functionality. For example, if a malware is composed of 8 subroutines, there are $8!$ ways, that is 40320 ways to mutate the malware [28].

In function call graph method, it may not be effective as we compute a graph from subroutines based on their calls and not by position.

4.4 Code transposition

Similar to the subroutine ordering, the code within the subroutine are re-ordered [15] if they do not demand computation in sequence. By shuffling the in-

structions, the signature detection can be defeated.

This technique may not be effective in our detection as the instruction sequence is not considered and only the list of opcodes are used to compute the score.

4.5 Code integration

The code integration is a more sophisticated means of obfuscating the code in which the virus on spreading the infection, attaches itself to the executable of the host. For example, **Zmist** virus [6] decompiles PE (Portable Executable) of the host file and smartly inserts the malware code by part, integrates itself and repackages the executable making it extremely hard to detect.

4.6 Dead code insertion

Dead code insertion is the most commonly used detection technique. Dead code is the piece of code that just performs meaningless actions which does not produce any results. When dead code is appended to any program it will not affect the code. For example, the No Operation (NOP) on being inserted will not perform any action but may tamper the signature of the malware [14, 13]. The dead code can be inserted in two ways:

1. Block morphing: In this type of morphing, a block of the dead code is inserted in the malware [15]. This may hinder the signature based detection and prove effective based on the malware. If the block added is not part of the unique part of malware extracted to make signature then it may not prove effective.
2. Random morphing: In random morphing, single or few of lines of the dead code are inserted at random all through the malware code. Sometimes, when

the percentage of benign code added to malware code increases there may be a chance all the mutated codes are quite similar. The dead code used to be inserted has to be varied in each generation to fetch better results.

Dead code insertion technique used to defeat the function call graph score may result in any of the three scenarios:

1. On using block morphing, if the benign dead code is added as a block in between two subroutines or at start or end of program, the score will not be affected as the detection method only takes the subroutines and the instructions in it into consideration.
2. On using block morphing, if block of dead code is added within a subroutine, it will only affect one sub-routine and hence will not make a big difference
3. On using random morphing, if significant number of lines of dead code are inserted in all subroutines, it may be deter or boost the scores depending on whether the code is inserted to a an already obfuscated dead coded subroutine (as we are dealing with metamorphic malware) or a matching sub-routine respectively.

The same random morphing technique when applied using external function calls as dead code is very effective in defeating the function call graph based detection.

CHAPTER 5

Experiments

In this chapter, we will be discussing on the results obtained on scoring metamorphic malware files using function call graph analysis and few experiments on defeating the score by using code morphing.

5.1 Chosen Dataset

We have used NGVCK, Zbot, ZeroAccess and Harebot files to be scored. The New Generation Virus Generation Kit (NGVCK) is a metamorphic worm that has been created to defeat the Hidden Markov Model (HMM) detection technique [6] using obfuscation techniques as dead code insertion and instruction substitution. Zbot [23] and ZeroAccess [24] are trojans that infects the host system and uses stealth techniques to collect sensitive data. Harebot [8] is a backdoor which usually attacks the Operating system and consumes the system resources bringing down the system's productivity. For this research, we have used 30 cygwin files for the benign dataset. Table 10 lists the number of files used in each malware family.

Table 10: Malware files

Malware family	Number of files
Zbot	22
NGVCK	38
Zeroaccess	38
Harebot	52

5.2 Receiving Operating Characteristics

Receiving Operating Characteristics(ROC) is a graphical plot that is used to measure the accuracy of detection. The ROC curve is drawn using the true positive rate(TPR) and false positive rate(FPR) by assessing several other criteria. The area under the curve (AUC) is the measured value from the plot that is used for comparing the performance from experiments. The best case of obtaining an AUC of 1.0 implies that it was a perfect classification with no false positives or false negatives. The value of the ROC may range between 0.5 and 1. Figure 4 shows the an ROC curve with an AUC value of 1.0.

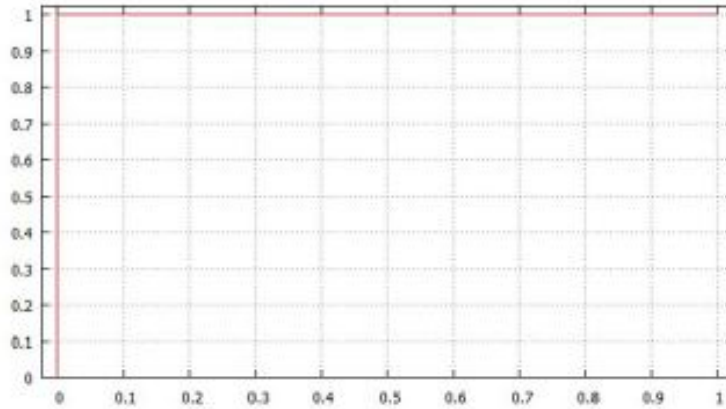


Figure 4: An ROC curve with $AUC = 1.0$ [25]

5.3 Scoring of the files

We have implemented the function call graph detection method using Java as discussed in Chapter 3. Initially, the executable in assembly language format is pre-processed to obtain the sub-routines of the specific file. After the first set of trial experiments in NGVCK family as shown in Fig 5, we had to adjust the threshold values of α , β and γ as 0.80, 0.5 and 0.5 respectively as it produced more accurate results for the chosen dataset.

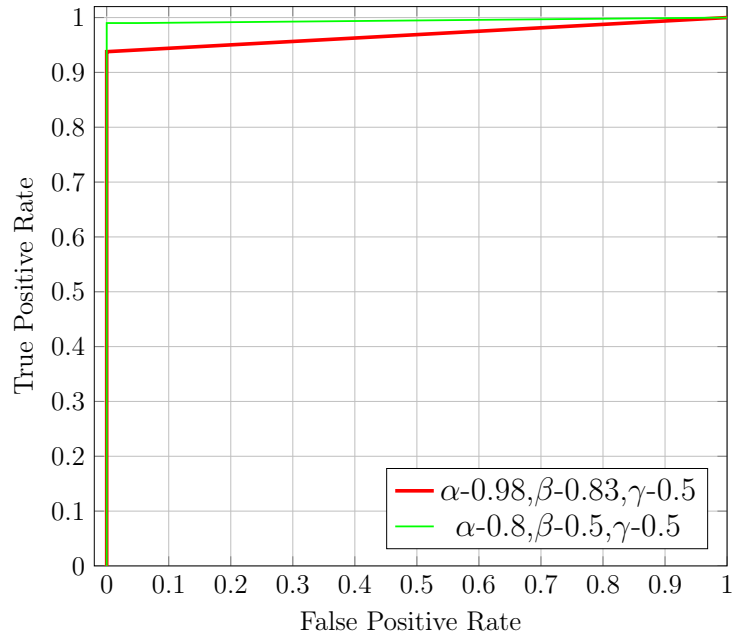


Figure 5: NGVCK ROC curve with change in threshold values

5.3.1 NGVCK files

We scored the NGVCK files using our detection method and was able to classify the benign files and malware variants. On scoring the malware files with benign files, most of the scores were 0.0 denoting no similarity between the files and the maximum score was 0.044 whereas scoring the malware variants within themselves most of the scores were above 0.2.

Figure 6 shows the scatter plot that clearly classifies the files and Figure 7 shows an ROC curve based on the scores obtained which gives an AUC of 0.99 which is good as it is very close to 1.0.

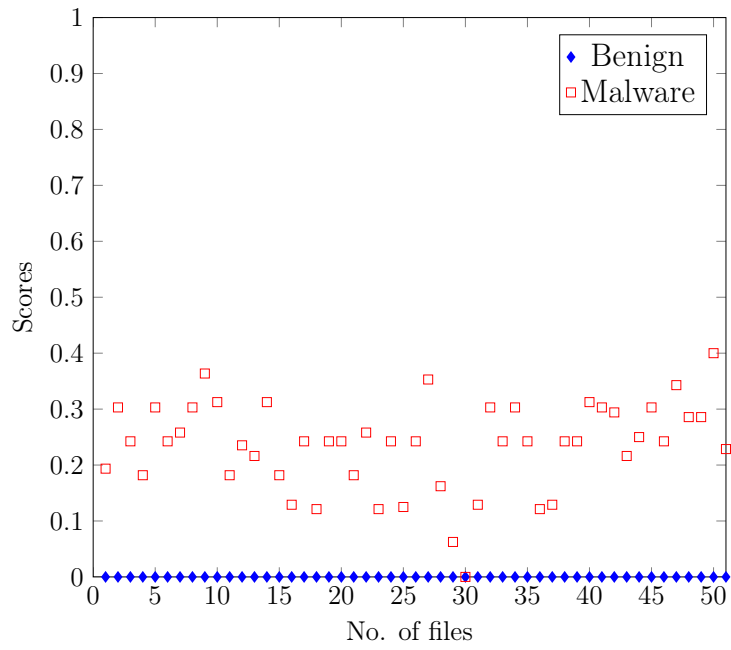


Figure 6: NGVCK Scatterplot

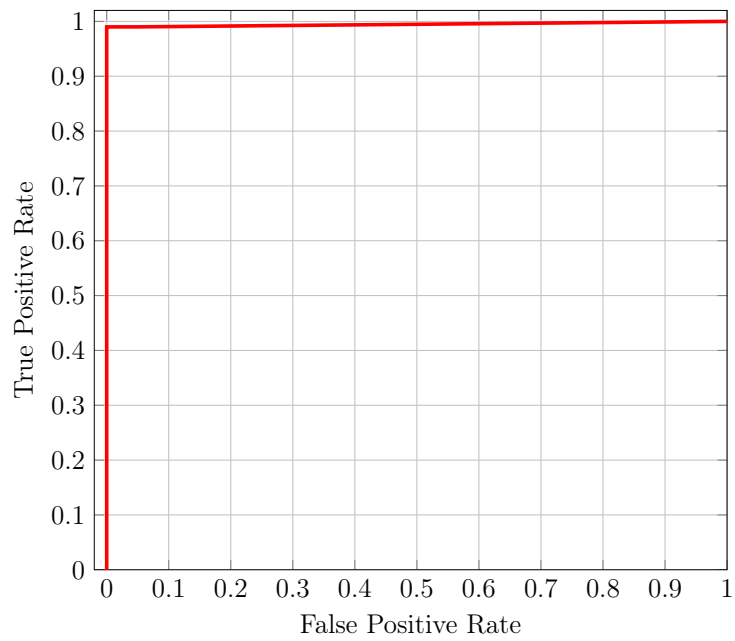


Figure 7: NGVCK ROC Curve

5.3.2 Zbot files

The Zbot files were also scored using the function call graph implementation and successfully classified the benign and malware files. The malware variants when scoring within themselves gave high values and on scoring with benign files they showed no similarity by scoring 0.0 for most files.

Figure 8 displays the differentiation between benign and malware files and Figure 9 shows the ROC curve which are plotted using the scores and it provides an AUC of 0.96.

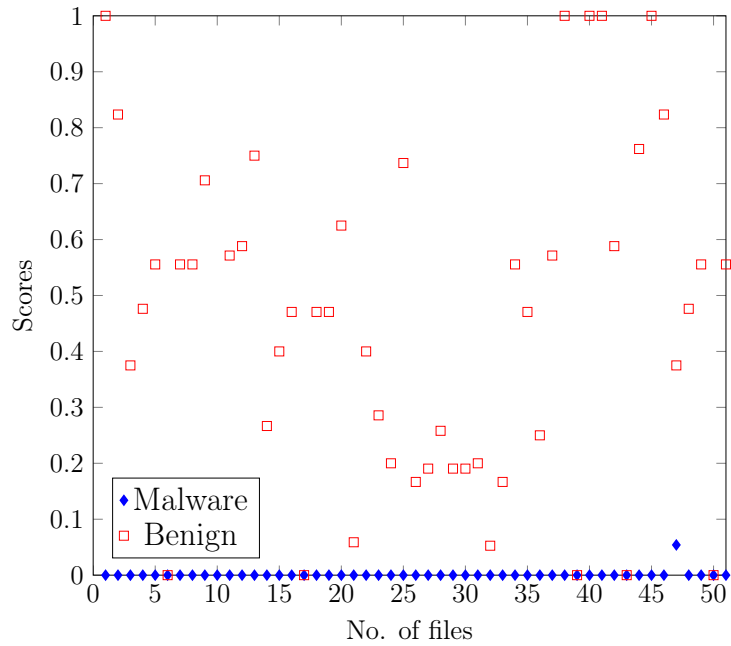


Figure 8: Zbot Scatterplot

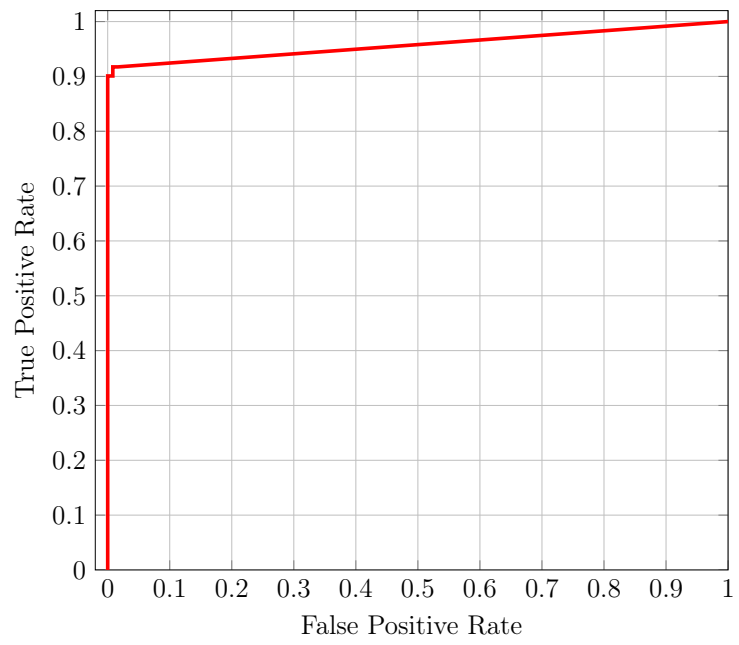


Figure 9: Zbot ROC Curve

5.3.3 ZeroAccess files

On scoring the ZeroAccess files using our detection method, we found that it failed to get classified as clear as the previous families. The benign files when scored with malware files had the maximum score of 0.03 and on scoring with its malware variants scores an average of 0.07.

Figure 10 shows the scatter plot of the ZeroAccess files in which the benign and malware files seem to score similar except for a few outliers and Figure 11 shows an ROC curve of the ZeroAccess files with an AUC of 0.77.

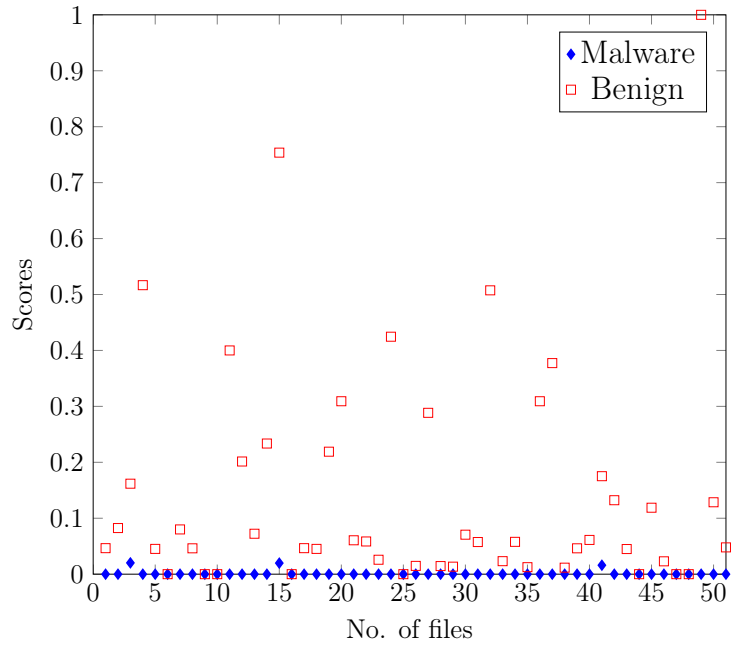


Figure 10: ZeroAccess Scatterplot

5.3.4 Harebot files

On scoring the Harebot files, the results were relatively worse than the ZeroAccess family. Most of the benign files and malware files score the same and there is no distinct classification between the two files.

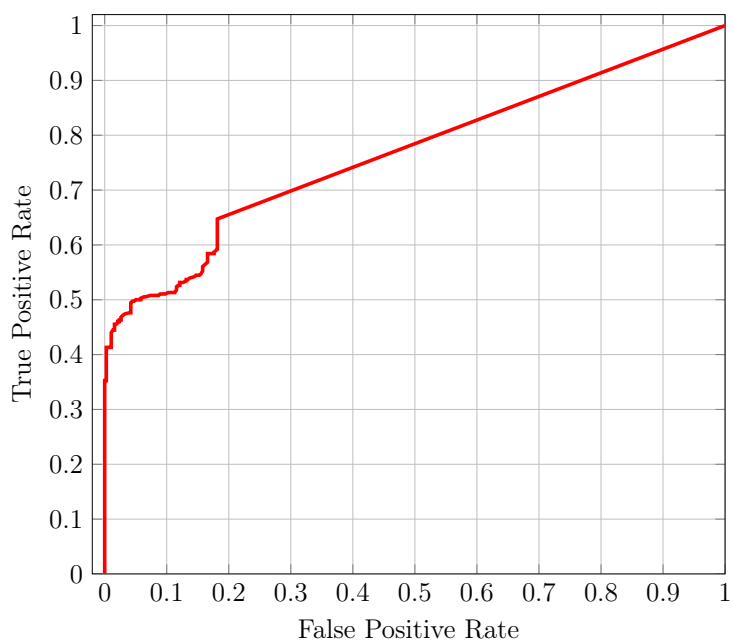


Figure 11: ZeroAccess ROC Curve

Figure 12 shows the scatter plot in which it is evident that the benign and malware files are not distinctly clear and Figure 13 shows an the ROC plotted with the results fetching an AUC of 0.60.

5.3.5 Analysis of scores

In the four families, NGVCK and Zbot have scored well by using function call graph analysis. But, function call graph detection failed to classify the malwares in ZeroAccess and Harebot families. On having a closer look at the files, it was evident that in cases when two files which had big difference in their file sizes did not score well. In Chapter 3, when computing similarity between the graphs using Formula (4) as the common edges are not normalized with respect to the total number of edges in each graph they fail to score well. To clarify the assumption we scored the ZeroAccess and Harebot files in sets classified based on file size.

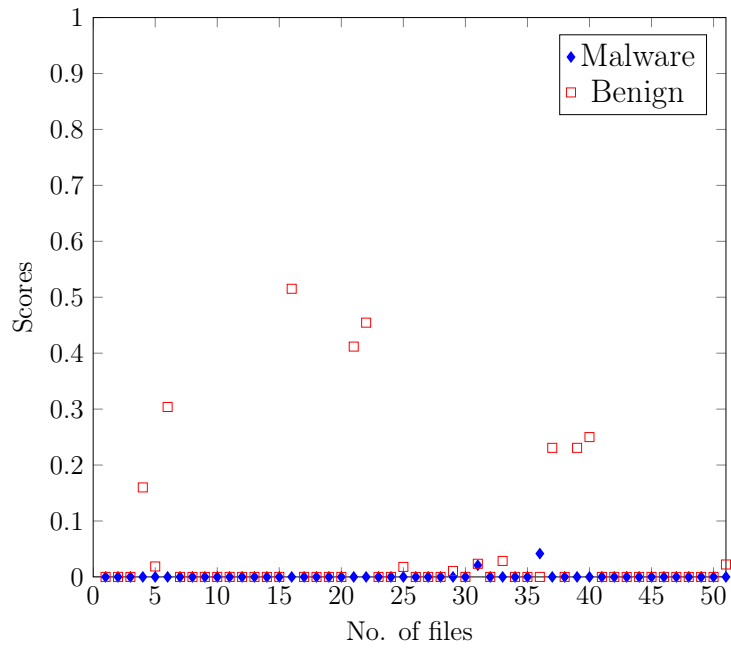


Figure 12: Harebot Scatterplot

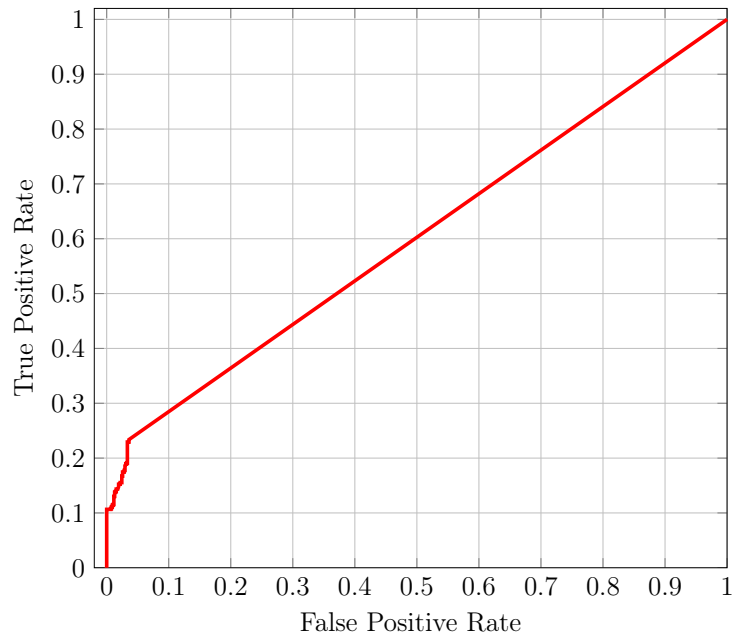


Figure 13: Harebot ROC Curve

5.4 Scoring the files in sets

The files are partitioned in sets based on file sizes and scored using the function call graph analysis.

5.4.1 ZeroAccess family

On scoring the 120 ZeroAccess files as sets, the ZeroAccess family scored well. In fact, it achieved a perfect AUC of 1.0 in one of the sets. Table 11 shows the details of the files in the sets and the corresponding AUC values. Figure 14 shows the ROC curves of the sets in the ZeroAccess family.

Table 11: Zero Access files set

	No. of files	Filesize Range	AUC Values
Set 1	20	25 - 30 KB	0.91
Set 2	40	31 - 40 KB	0.74
Set 3	40	110 - 112 KB	0.96
Set 4	20	114 - 128 KB	1.0

5.4.2 Harebot family

On scoring 40 Harebot files in two sets, though there is a substantial increase in the AUC values the classification is not discrete. On further analysis on the files, we found that the reason for low scores in Harebot was because it had only a couple of external functions in each program. Since atleast two external functions from same sub-routine has to match to be considered common vertex, Harebot may not have any similarity in the external functions attribute. Table 12 shows the details of the files in the sets and the corresponding AUC values. Figure 15 shows the ROC curves of the sets in the ZeroAccess family.

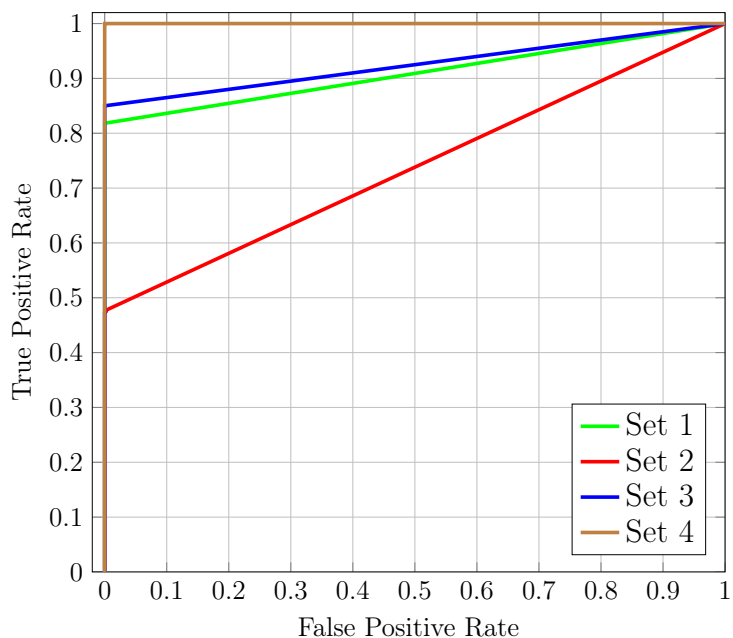


Figure 14: ZeroAccess ROC curve of the sets

Table 12: Harebot file sets

	No. of files	Filesize Range	AUC Values
Set 1	20	7 - 11 KB	0.74
Set 2	20	13 - 31 KB	0.62

5.5 Defeating the score

In this section, we have defeated the function call graph scoring method. The code obfuscation used to morph the malware is dead code insertion. As discussed in Chapter 4, block morphing will fail to defeat the method as it only affects one sub-routine. We have used external functions as dead code and randomly inserted it as chunks of code in all subroutines.

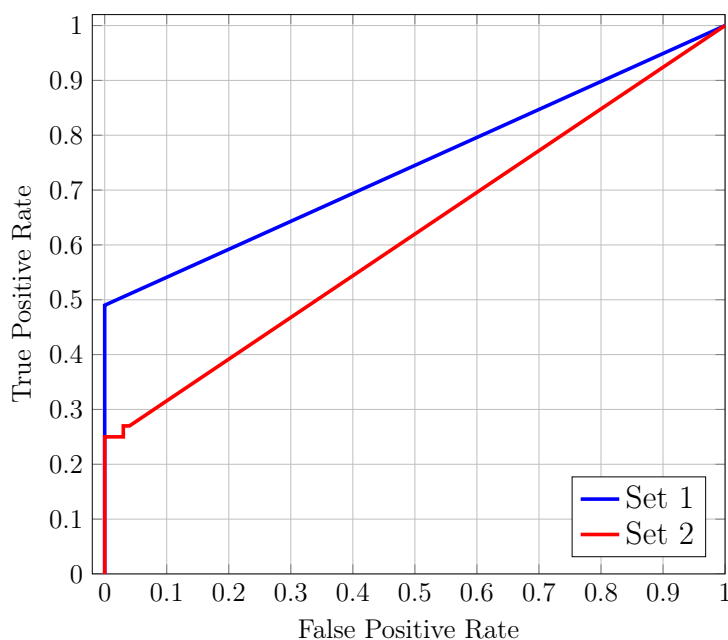


Figure 15: Harebot ROC curve of the sets

5.5.1 NGVCK family

Starting from 15% random morphing, we can see the effect in the AUC values. Figure 16 shows the ROC curves starting from 5% to 40% in which there is a significant change from 10% to 15%. Since there is a hill climb behavior in 35% we plotted the morphed values from 10% to 200% in which the score gradually increases. This indicates that a threshold of 15% to 35% should be set for morphing to defeat the NGVCK score. Figure 17 clearly visualizes the necessity to set a threshold value for morphing.

5.5.2 Zbot family

Similar to the NGVCK family, Zbot also has low AUC values starting from 15% and the pattern continues until 35% after which a gradual increase is to be noted. The difference in the scores from 10% to 15% is graphically depicted using ROC curves in

Figure 16: NGVCK Morphed ROC Curve

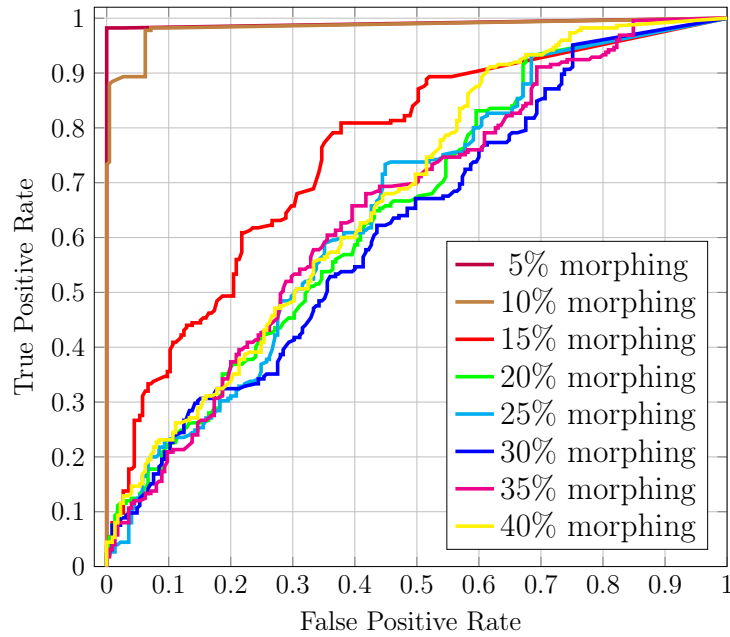


Figure 18.

5.5.3 Consolidated results

The consolidated results from the external function dead code random morphing is displayed in Table 13. Both NGVCK and Zbot files starting 15% show promising results. Notably, as the morphing % increases the malware variants are found similar within themselves. Hence, a threshold must be set on the level of morphing to defeat the method consistently.

5.6 Scoring files on a larger number of files

To find whether the results are consistent, the function call graph scoring is experimented on more no. of files. Table 14 shows the malware families and the

Figure 17: NGVCK Morphed 10% - 200%

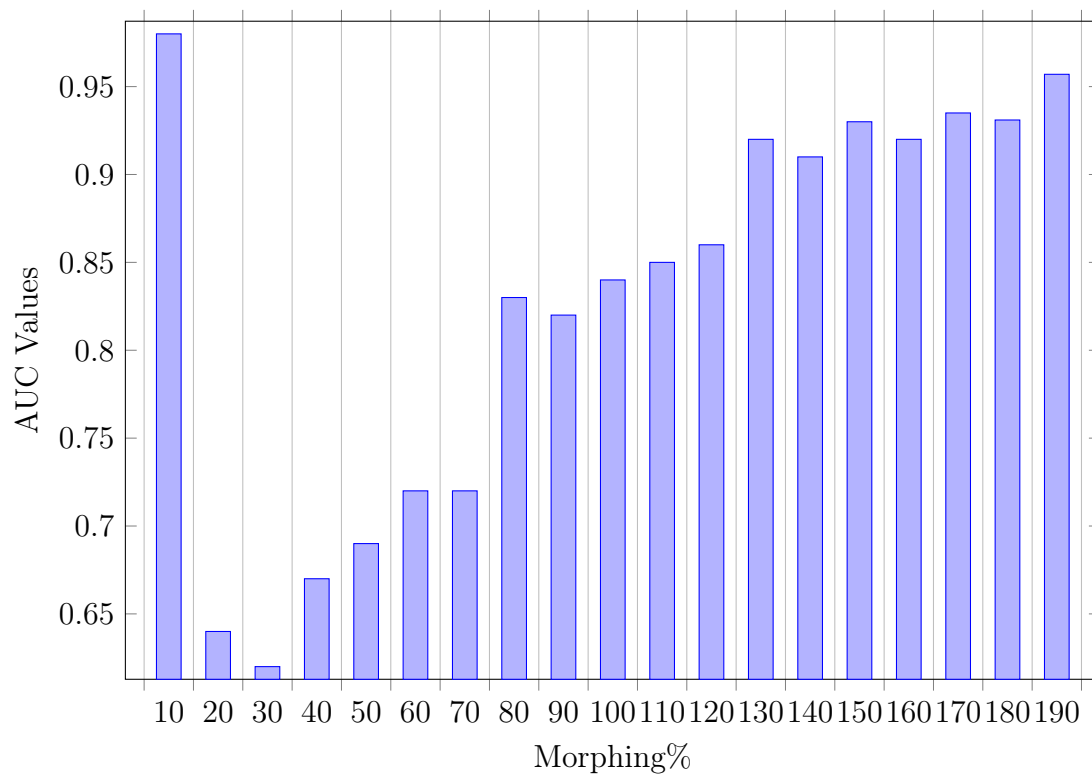


Table 13: AUC curve results for morphed NGVCK and Zbot files

Morphing	AUC	
	NGVCK	Zbot
0%	0.99	0.96
5%	0.99	0.96
10%	0.98	0.93
15%	0.75	0.84
20%	0.64	0.87
25%	0.65	0.84
30%	0.62	0.83
35%	0.65	0.84
40%	0.67	0.83

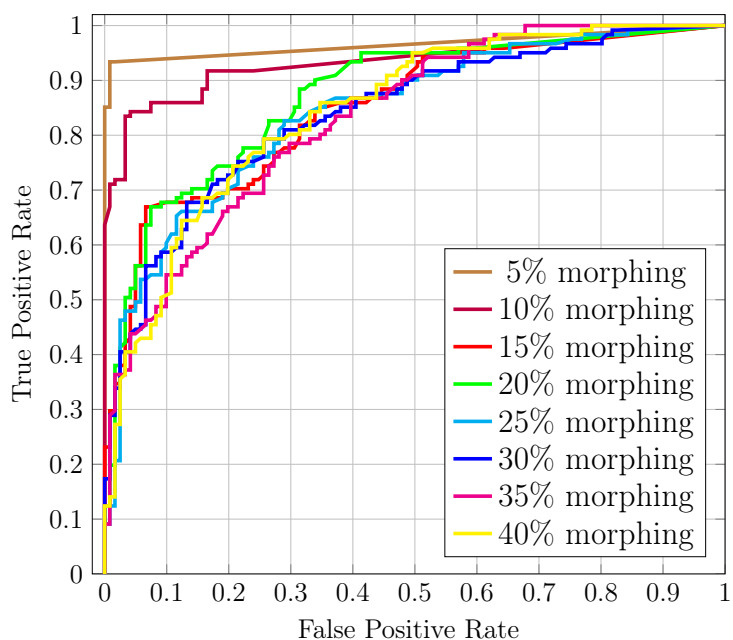


Figure 18: Zbot Morphed ROC Curve

number of files used for this experiment.

Table 14: Number of files used in each family

Malware family	Number of files
Zbot	100
NGVCK	100
Zeroaccess	100

5.6.1 NGVCK family

On scoring the larger dataset, the AUC values are lower which maybe because of a few outliers in the total files used. Figure 19 shows an AUC of 0.94 which is still a good score and classifies most malwares from the files.

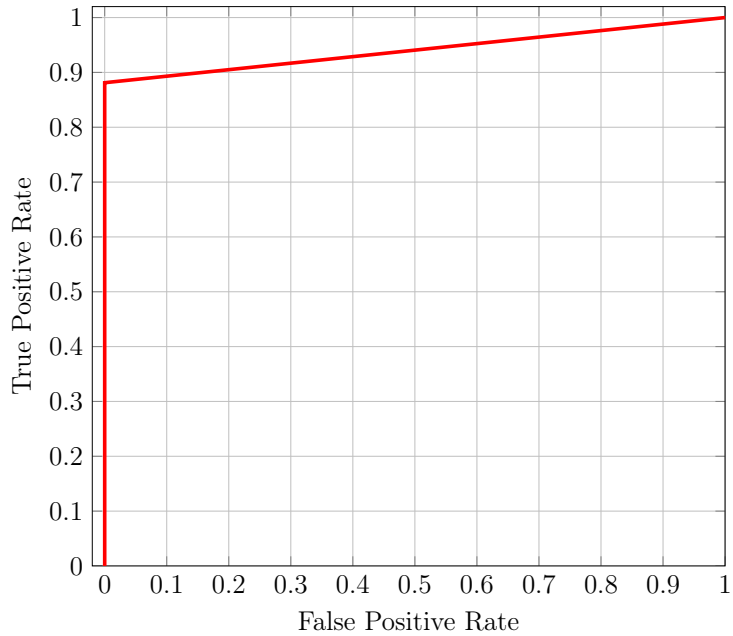


Figure 19: NGVCK ROC Curve (100 files)

5.6.2 Zbot family

The Zbot family seem to have a setback in the AUC value. As shown in Figure 20 has an AUC of 0.8 which fails to classify the malware effectively. At a closer look on the files used, similar to ZeroAccess it has a larger difference in the file sizes used. By dividing it into sets based on filesize, we can have a clearer picture of the overall score for Zbot family. Table 15 shows the details about each set and Figure 21 shows the AUC values of the sets.

Table 15: Zbot sets

	No. of files	Filesize Range	AUC Values
Set 1	30	4 KB	0.84
Set 2	60	5 KB	0.72
Set 3	20	6 - 8 KB	0.96
Set 4	40	9 - 13 KB	0.8

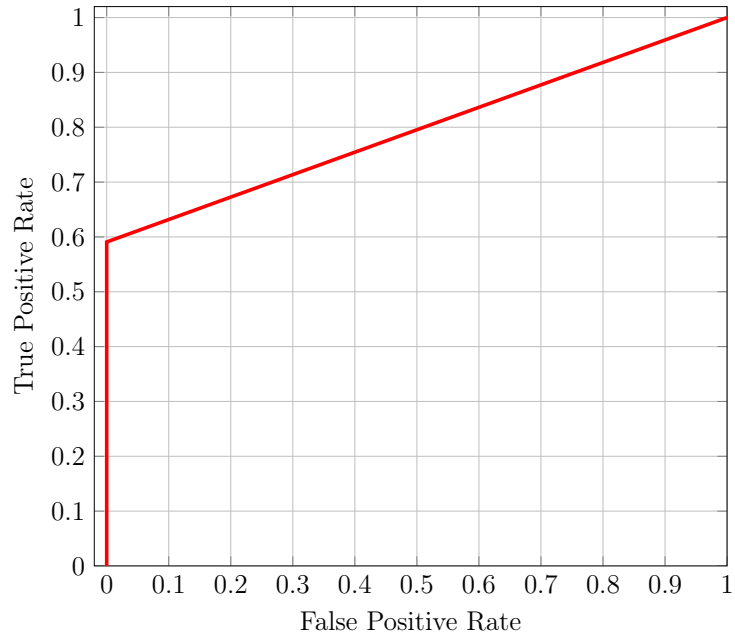


Figure 20: Zbot ROC Curve (100 files)

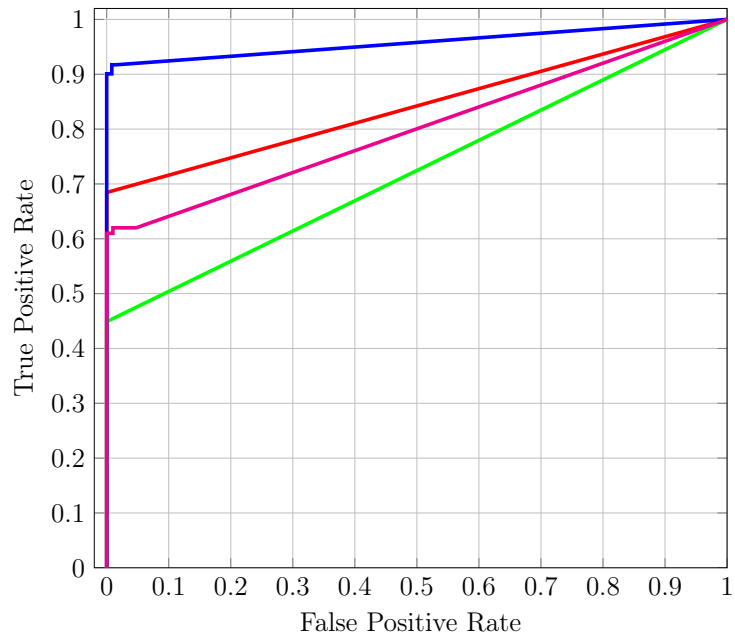


Figure 21: Zbot ROC curve in sets

5.6.3 ZeroAccess family

The score of the ZeroAccess family is consistent with the previous experiment.

Figure 22 shows the AUC value of 0.75 in the Zero Access ROC curve.

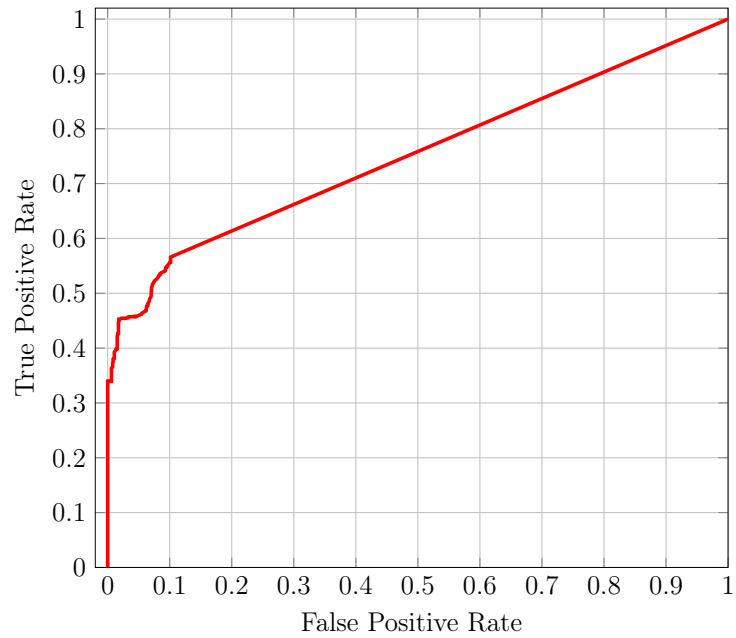


Figure 22: ZeroAccess ROC Curve (100 files)

CHAPTER 6

Conclusion and Future Work

The main goal of our project was to study the function call graph analysis [6, 17, 21], implement and score it on metamorphic malware families and defeat the score to understand how the detection method can be made more effective and efficient. The function call graph analysis scores the metamorphic malware based on similar external functions, local functions that have similar external functions, cosine similarity based on frequency of opcodes which are classified and color coded based on the purpose of the instructions and matching neighbors of similar local functions. Additionally, the length of the functions and degree similarity are also added as thresholds to make the detection effective. From all the above comparisons, the common vertices between the function call graphs of the two malware variant is found. Using these common vertices, the total number of common edges between the vertices of the graphs are found and used to score the malwares.

We scored four malware families: NGVCK, Zbot, ZeroAccess and Harebot to analyze how the detection technique is effective in these families. The NGVCK and Zbot detected the malware and classified them by scoring higher than the benign files. But the ZeroAccess and Harebot families were not very successful in detecting the malwares. We also tried to defeat the NGVCK and Zbot scores using random block morphing and achieved considerable success in it.

For future work, these experiments can be implemented in comparison of different threshold parameters α , β and γ , as some malware families perform well at higher thresholds and some at lower thresholds. The annotated call graph similarity [1],

external functions similarity [29], opcode graph similarity [20] and the function call graph similarity [17] can be incorporated to build a hybrid robust detection technique that can overcome all the limitations of the detection methods. The common vertices by external functions happen to be the most contributing factor in the score which can be exploited by random morphing of benign external function calls. The external function based match has to be normalized based on total number of external function calls. The function call graph detection technique is more effective in files with same number of sub-routines. On considering two malware variants, in which one is obfuscated extensively by adding dead code the function call graph method fails to identify one file as the subset of other which implies it is similar. To rectify this flaw, the common edges need to be normalized not just by the total number of edges in both graphs but by total number of edges in each graph.

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