University of Alberta

Static detection and identification of X86 malicious executables: A multidisciplinary approach

by

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A thesis submitted to the Faculty of Graduate Studies and Research
in partial fulfillment of the requirements for the degree of

Master of Science

Department of Computing Science

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Fall 2009
Edmonton, Alberta

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This thesis is dedicated to my parents and lovely wife.

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Abstract

In this thesis, we propose a novel approach to detect malicious executables in the network layer using a combination of techniques from bioinformatics, data mining and information retrieval. This approach requires translating malicious code into genome-like representations. Based on their "genetic" formats, we can easily extract features by constructing families for known malicious code using data mining algorithms. These features then can be stored in a router or an another device in the network to measure the similarity between payloads and extracted features. Once the similarity is over a threshold, the security device can block the entire session and report an alert before the threat reaches the intended host(s). Further more, attacks can be identified based on their features and the families where these features come from. Ultimately, our experiments showed that 95% accuracy of detection is possible with an identification rate of 83%.

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Acknowledgments

First of all, I would like to thank my supervisors, Dr. Mike MacGregor and Dr. Mario Nascimento. Without their extensive support and patience, this work would be impossible for me. I would also like to thank faculty members, Dr.Guohui Lin and Dr.Joerg Sander, for their generous assistance. Thanks to Sunil Ravinder for his comments during the meetings.

I really appreciate the financial support from the Computing Science Department at the University of Alberta, and from NSERC.

Finally, I would like to thank my parents and wife for their long-term understanding and love.

Chapter 1

Introduction

Malicious executables are programs that perform malevolent functions. They hide somewhere in the computer system, infect other benign files and execute harmful operations, such as destroying private data, consuming physical resources, providing unauthorized remote access to the system, stealing sensitive information and so on. Billions of dollars are lost every year due to damage from computer viruses alone. Therefore, detecting and identifying malicious executables play a crucial role in protecting computer systems.

The problem of malicious executables has become a serious security threat, especially with the growth of Internet usage. Networking provides not only an easy way to communicate between hosts, but it also provides a convenient tunnel to widely and quickly propagate dangerous attacks. Since the creation of the first computer virus in the mid-1980s, the number of malicious programs has been increasing very fast every year. Malicious code can now reach all aspects of the computer system.

The majority of the operating system market is taken by the series of Microsoft Windows® operating systems. These operating systems are highly popular, but they still have a large number of systemic holes that are vulnerable to attacks. Thus, the majority of malicious executables aim at Windows operating systems and applications. These programs, both malicious and benign, all run on the Intel processor that use the X86 instruction set architecture. Systemic defects demand some defense mechanisms to secure the system.

Currently, Windows-based security systems, anti-virus and internet security software, mainly use signatures from known malicious executables composed of binary sequences to prevent threats. These systems can only detect malicious executables, whose signatures were previously identified and are stored in a database. In this thesis, we aim at improving the effectiveness of detecting and identifying malicious X86 executables. For that, we apply techniques from multiple disciplines to packet classification in the network layer of computer networking.

1.1 Definitions of detection and identification

Detecting malicious executables is an interesting and important problem. Given dangerous executables, the detection problem is how to effectively discover threats to prevent system damage. Currently, dynamic analysis and static analysis are the main detection techniques. Dynamic detection monitors potential malicious attacks during their execution to observe abnormal behaviors. In contrast, static detection analyzes the properties of malicious attacks before their execution. Bergeron et al. [4] argue that static analysis has some advantages over dynamic analysis: it allows exhaustive analysis; it gives a verdict; and there is no run-time overhead. Probably because of these benefits, static analysis has been adopted widely and many static automated systems have been built using feature extraction techniques in recent years [17, 24, 38, 41], though all have their limitations. Feature extraction is the core component of these systems, and it is also a complicated task requiring a combination of different data processing algorithms. Although features provide important information to detect malicious executables, it is still difficult to completely understand various attacks. For this reason, dynamic analysis can be an accessorial supplement used to further improve the detection rate. Both static and dynamic analysis are helpful. But we concentrate on static detection in this thesis.

While many detection techniques have been proposed, the problem of identifying malicious executables has not been given the attention it deserves. Given harmful code, the identification problem is how to correctly recognize attacks and classify them into possible families. Currently, human experts are involved in the process of identifying and classifying new attacks. No automated system from our knowledge has been released to provide suggestions to label new attacks. We also aim at this problem beside the problem of detection. Algorithmic identification can offer us an opportunity for building a system with the ability to identify and classify previously unknown malicious executables automatically.

1.2 Previous Solutions

The ability to detect and identify malicious executables has evolved relatively slowly. Signature-based methods are still being commercially used; even though they cannot help detecting new attacks. New content-based solutions have been proposed, but they have not been implemented in real-time. Distributed security schemes provide a great potential to subvert the architecture of current anti-virus software. Since no work has addressed the problem of automated identification, in this section, we present only a brief introduction to different detection methods and their pros and cons.

1.2.1 Signature based methods

The first attempts to detect malicious executables (mainly viruses) were based on signatures. These approaches require the use of experts to manually extract signatures from destructive samples. These signatures are used to detect possible incoming attacks. However, signature extraction with human involvement is time consuming. Therefore, Kephart and Arnold [23] introduced an automatic method to extract signatures from samples of known viruses to remove the need for human experts. This has made the development of automated security systems possible. In fact, automated signature-based detection has been adopted to build commercial anti-virus software. The success of signature-based techniques has shown that they work very well for detecting known malicious executables, but they fail to prevent new attacks. After damage reports of new attacks are issued, the executables are sent to labs to analyze their functionalities. When the key binary sequences are found, client-side security programs have to update their malicious signature databases. According to Fitzgerald [15], "2007's total doubled the number of signatures F-Secure had built up over the previous 20 years." From this argument, it is obvious that lack of signatures for new attacks reduces the effectiveness of current anti-virus systems every year.

1.2.2 Heuristic methods

In academia, it has been recognized that the capabilities of signature-based security systems have faded away [2, 17, 24, 27, 33, 38, 41]. In order to overcome the shortcomings of signature-based solutions, some open problems about computer virus research were presented by White [39]. One of the problems is to develop heuristic techniques for detection. Actually, static analysis is a heuristic technique, where researchers analyze the features of malicious executables. These features are the core representations of the malicious executables. By using these features, we can inspect new attacks in a heuristic approach without exact signature matching. Unlike binary sequences, features have varied formats, and there are many different ways to extract features.

Byte patterns were one of the first features to be considered. Using an n-gram model [26], byte sequences in hex format are broken into multiple short subsequences, each with a length of n. Then the frequency of each unique n-gram subsequence is counted in order to determine whether it qualifies as a feature or not. The feature list may be pruned based on other constraints. A classifier is trained later using these features to label new malicious executables. Many researchers [2, 17, 24] use byte patterns as features to guide their classifiers, but there are problems with this type of the feature. All we can get from byte patterns are binary numbers. In this case, we have no knowledge of the malicious code at all. We need to use the features to understand the information hidden behind the binary digits.

Recently, the emphasis of feature extraction has shifted from binary analysis to content analysis, that is an analysis of assembly code. Reverse engineering techniques are involved in the process of content analysis. First of all, malicious executables are translated from binaries into low-level assembly code. This facilitates a better understanding of the functionality of the malicious executables. Depending on the contents of the assembly code, there are many types of features that may be extracted. Bergeron et al. [4] chose to use control-flow graphs of API function calls as features. Zhang et al. [41] applied the n-gram model to the sequences of API functions to refine their features. Here, the API is the application programming interface to the operating systems. A more novel approach is from Masud et al. [27]. They combined three types of features consisting of DLL (Dynamic Link Library) functions, assembly n-gram features and binary n-gram features, to build a hybrid model to discover new attacks. Besides these examples, there are many other types of features. In this thesis, we select opcode sequences to be our features.

1.2.3 Distributed system

All previous solutions to the problem of detecting malicious executables are isolated to run on a single host. Every client host, as a single entity, installs some security systems to protect itself. Recently, some commercial companies and researchers have been proposing a distributed approach. This distributes the task of detecting and identifying malicious executables across the whole network. An anti-virus company, Rising®, has already deployed its defense mechanism called "cloud security plan" using cloud computing. In their scheme, each client host becomes a sensor to detect abnormal behaviors and risky files. Identified malicious targets are sent to a central node for further processing. After analyzing them, solutions are returned to the source and are shared with all end users immediately. In this case, client hosts are not separated entities any more. They only carry small connected portions of the entire security system to protect all the users. Unfortunately, the current version of cloud-based security is aimed at trojan horses only.

1.3 Motivation and challenges

In the prior sections, we have briefly described the strategies to solve the problem of detecting malicious attacks. Signature-based systems perform poorly against new attacks, and recent research only focuses on the detection of destructive code. We then asked ourselves the question: can we find a technique to effectively detect new attacks and also identify them? To address the problems of both detection and identification, we propose a approach using a combination of techniques from multiple disciplines to statically analyze known malicious attacks, in order that extracted features can be used to detect and identify both previously known and unknown malicious executables.

1.3.1 Motivation

From our observation, some behaviors of malicious executables are similar to biological organisms, such as diseases and viruses. In some circumstances, attacks break out, self-replicate and propagate just like diseases and viruses. Usually, biologists analyze organisms using their DNA/RNA materials [5]. Inspired from biological genetic composition, we could analyze malicious executables using their simulated "genetic" representations. A new discipline of computing science, bioinformatics, has advanced biological analysis especially in the area of genome analysis. What we can do is to treat binary executables as "genomes". Important features obtained from binary "genomes" could be the "genes". In order to find them, we can analyze binary executables using their simulated "protein" sequences representations. Currently, researchers have already applied bioinformatics techniques to intrusion detection [8, 36]. Its algorithms combined with other techniques could be employed to address the problem of detecting and identifying new malicious attacks as well.

Detection using content analysis can potentially achieve higher accuracy than binary analysis. However, existing systems only focus on detecting malicious executables, they do not address the problem of identification. Commercially, new attacks must still be sent to human experts for identification and classification. Therefore, we believe a high detection rate is no longer enough. The next questions we have to ask ourselves are: what kinds of functionalities make programs virulent? Which families do they belong to? Security systems should be able to provide some advice about answering these questions.

1.3.2 Challenges and opportunities

Our challenge is to choose a proper format to represent characteristics of malicious executables. Byte sequences are one choice. However, in order to bypass detection through binary features, programmers of malicious programs try to disguise their work. For example, they may add extra instructions, or extend instruction sequences into longer equivalent sequences. Therefore, binary/hex representation by itself is not sufficient. At some level, similar malicious operations must have similar instruction sequences. If we reverse binary executables into assembly code, there must be some similar subsequences of instructions existing in all related malicious attacks, and these subsequences should also be unique compared to other types of attacks. Thus, the hypothesis in this thesis is that: there exists at least one unique common instruction subsequence in every member of the same malicious family. In other words, benign executables should not contain any of these characteristic instruction sequences. In order to test this hypothesis, we encounter the following challenges:

- To choose a proper representation to describe malicious executables. Binary/byte patterns, API functions, control-flow graphs and other types listed previously can all be used to represent malicious executables, but which type is more appropriate to our hypothesis?

- To algorithmically construct the families for malicious executables. To our knowledge, no solution has been proposed to automatically cluster malicious attacks, *i.e.,* they are classified manually by human experts. If our clustering approach works, then we have a solution or can at least provide some suggestions for algorithmically grouping malicious attacks.

- To extract features from each family, because each family contains many malicious members that include a large amount of information. It is difficult to find the feature that can represent the whole family.

- How to use features and how to take advantage of them to address the problem of detecting and identifying malicious executables.

1.4 Outline of the thesis

The remainder of this thesis is organized as follows. An overview of the existing systems for detecting malicious executables is discussed in Chapter 2. Also, Chapter 3 provides the discussion about the background of some fundamental algorithms from data mining, bioinformatics and information retrieval. In Chapter 4, we introduce the processes of our approach, including data preparation, clustering, feature extraction and application of features. Chapter 5 presents the details of experiments conducted to evaluate the accuracy of our system. Finally, conclusions and suggestions for future work are given in Chapter 6.

Chapter 2

Related work

The idea of using a signature was one of the methods used to detect malicious executables in the early days, and papers, *e.g.,* [11, 23] have been published about how to extract useful signatures from computer viruses. But it has been recognized afterwards that signatures cannot be used to protect against entirely new attacks. Researchers now apply heuristic analysis to potential malicious executables with the purpose of finding their essential features. In this case, data mining and information processing techniques become important tools to address the problem of detecting malicious executables. Features can then be employed to discover new attacks containing similar characteristics. Many different types of features have been proposed recently. Binary n-gram patterns [2, 6, 17, 24] are considered as features to examine the binary representations of malicious code. Instruction sequences and API function calls [4, 38, 41] have also been used to inspect the contents of malicious attacks. There are many other types of features as well, but it does not matter what kind of features one would like to use, the ultimate goal is to build an efficient classifier using these features to effectively and accurately detect new attacks.

In this section, we concentrate on the previous work regarding features. Binary feature extraction is presented in Section 2.1. Instruction-level feature extraction is discussed in Section 2.2. Finally, hybrid feature extraction by combining multiple formats of features is introduced in Section 2.3.

2.1 Binary-based detection

Malicious executables are in binary representations. The first attempt at extracting features was to find characteristics directly out of plain binary/byte sequences. Henchiri and Japkowicz used exhaustive search for unique binary n-gram sequences to discover helpful features [17]. By fixing a length n, they count the frequencies of different n-gram patterns, and the set of sequences with occurrence frequency over a certain threshold is selected for the subsequent processing. Additional thresholds such as intra-family and inter-family supports are introduced to further eliminate redundant sequences. Given the prior knowledge of computer virus families available from commercial anti-virus software, intra-family support is the constraint that limits the number of appearances of a feature in members of the same family. Inter-family support is the constraint that controls the number of occurrences of a feature in all malicious attacks. Only the n-gram patterns satisfying all constraints are chosen as features. These pruned features are used to evaluate their system.

After retrieving the most relevant binary n-gram sequences, Kolter and Maloof applied various types of classifiers to the feature set, including decision tree, naive Bayes and support vector machine [24]. First, they converted malicious executables into hexadecimal representations. Then, an n-gram term is generated by concatenating n continuous (hex) bytes; However, this n-gram selection produces millions of distinct byte sequences. In order to find the most pertinent n-gram patterns, Kolter and Maloof chose the top 500 n-grams independent of the length n based on their frequencies to be features. Finally, all classifiers listed above were used to evaluate the system using the extracted n-gram features. The work done by AbouAssaleh et al. [2] is very similar to the method from Kolter and Maloof. Using binary n-gram sequences, they selected the most frequent features to discover new attacks. Multiple experiments with 3-fold cross-validation are used in order to find the optimal length of an n-gram and the size of the feature list that can achieve the highest detection rate. In their experiment, AbouAssaleh et al. can achieve 98% accuracy; however, approximately two third of the data samples is required in training purposes. Now, the number of malicious attacks increases exponentially every year. We only have limited resources to preform the tasks of detection of identification. What we should do is to use the minimum resources to achieve the maximum results. Therefore, we believe using a large training set is not appropriate any more.

As we have shown in previous paragraphs, many researchers use n-gram patterns as features in their systems, but they have to struggle with choosing the proper length/size for both n-gram and the feature list to get the best result [2, 17, 24]. In addition to the problem of n-gram selection, Henchiri and Japkowicz in their work have to pre-group the virus samples into families according to the results from commercial anti-malware software [17].

In contrast to traditional classifiers trained with both sample malicious executables and benign programs, Cai et al. investigated only the profiles of benign programs using one-class classification [6]. In their paper, they extract distinct single bytes from benign programs as features. Principal component analysis [25] and a one-class support vector machine are applied to benign features to evaluate the accuracy of detecting malicious executables. This is an interesting approach to exclusively analyze the benign cases; however, single-byte features cause high false positive rates. In some circumstances, the classifier gives a roughly 70% false positive rate while the true positive rate is around 93% . At the same time, approximately three fourths of the data samples is required in training purposes.

2.2 Instruction-based detection

In recent years, content-based feature extraction has become a popular technique to detect malicious executables. Researchers now analyze attacks by disassembling them into low-level assembly code or languages such as C and C++. The disassembled code contains sequences of instructions, system calls and sub-functions; therefore, These assembly programs definitely provide more information about malicious executables than binary patterns.

Wang et al. proposed the features that are instructions in the byte representation [38]. However they only examine the first byte and the first two bytes of each four byte chunk. They believe the first byte is the opcode and the first two bytes are mainly composed of the opcode and the first operand. Information Gain [25] based on the frequencies of the features is applied to remove inappropriate patterns. Naive Bayes and decision tree classifiers are used to test the performance of the system. Their paper describes an interesting transition from binary sequences to the content of assembly code. However, it is unreasonable for the authors to assume every four-byte denotes an instruction because the Intel X86 instruction set contains variable-length instructions. The use of single-byte patterns provides insufficient support that causes a roughly 30% false positive rate while the best detection rate is around 93%.

Zhang et al. chose the features that are generated by a controlled sliding window through the sequences of API function calls while assuming that all viruses must interact with a 32-bit Windows operating system [41]. They first disassemble computer viruses to extract the sequences of system function calls. Then an n-gram sliding window is applied to break the sequences into several subsequences. The procedure of counting the frequencies of distinct n-gram subsequences is performed during the sliding process. Only the subsequences containing abnormal behaviors such as aggressive function calls are considered to be features. Finally, features are fed to a support vector machine to discover new attacks. That paper borrows the idea from Unix intrusion detection systems of using the abnormal sequences of Unix commands to prevent attacks.

Besides using the sequences of API function calls as the features, the use of an instruction-flow graph with the application of automatons is also interesting. Bergeron et al. converted instruction sequences into control-flow graphs [4]. An instruction-flow graph using assembly code is first constructed to imitate the processes of instruction execution. General-purpose instructions other than system function calls or sub-routine calls are removed from the graph later. Then the instruction flow graph is simplified into a finite state machine containing only the flows of API functions and sub-routines. At last, a verifier is used to compare the control-flow graphs of attacks and the predefined security automata. It is easy to construct the flows of function calls for malicious executables; however, the difficulty here is how to build the security automata to cover various types of malicious attacks.

2.3 Hybrid detection

Both binary-based and instruction-based detections only concentrate on one type of feature, either byte patterns or instruction sequences. Schultz et al. however used a set of experiments on varied features [33]. They extract three types of features, including strings that are printable sequences of characters in binary code, API function calls and byte sequences. Their classifiers are applied to features type by type to determine which one provides the best result. Interestingly, Schultz et al. take the point of view that various formats of features can be used to detect malicious executables.

As an extension, Masud et al. used a hybrid model of three types of features in the classifier training [27]. A combination of DLL functions, assembly n-gram features and binary n-gram features was extracted from the sample attacks. A combination vector containing these features was then applied to the classifier. The results show that the hybrid approach can achieve very high accuracy. The processing graph for this hybrid model is shown in Figure 2.1. Hybrid detection is very effective because it

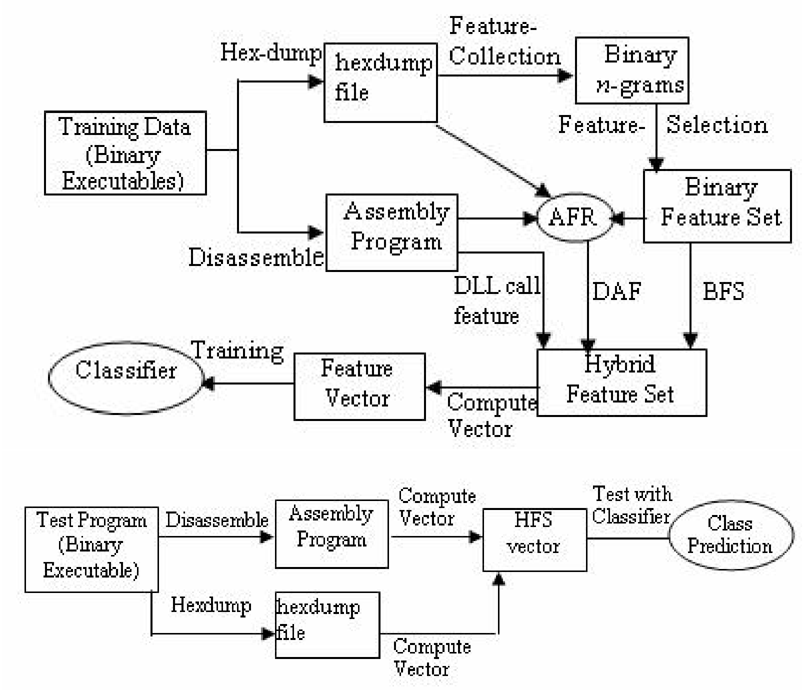


Figure 2.1: The hybrid model explanation for training phase and testing phase from Masud et al. [27].

takes advantage of many types of features. But this mechanism is relatively complex compared to the systems using traditional one-type feature extraction. The main shortcoming is that several parameters have to be carefully tuned to control various aspects of the system in order to achieve good results.

Like previous solutions, we use an n-gram sliding window as well. However, in order to reduce the complexity of selecting the proper length for the n-gram, we shrink its range by proposing a reasonable lower bound. Unlike Henchiri and Japkowicz [17] using commercial anti-virus software, we construct families using clustering algorithms instead. Also one-class classification using only malicious code instead of benign programs is implemented in this thesis. We will present more details about these approaches in Chapter 4.

Chapter 3

Background

We believe similar malicious executables contain one or more common characteristics. Since we cannot fully understand individual attacks at once, it is relatively easier to retrieve key features from a group of similar malicious executable because they share the same characteristics. Thus, analyzing malicious groups is strongly required. In this circumstance, grouping malicious executables requires the knowledge of clustering algorithms from data mining. It also demands some properties from attacks in order to distinguish them. Therefore, techniques from information retrieval are used to assign weights to malicious executables to differ similar or dissimilar ones. Once we have the groups, alignment algorithms from bioinformatics are applied to retrieve the common features that will be used to detect and identify new attacks. In this chapter, we provide the discussion about malicious attacks in Section 3.1, techniques from data mining, information retrieval and bioinformatics are represented from Section 3.2 to Section 3.4. At last, performance measurement is discussed in Section 3.5.

3.1 Malicious attacks

Generally, malicious attacks can be classified according to their functions and their approaches to propagation. Based on these characteristics, Skoudis and Ziltser [34] and McGraw and Morrisett [28] have categorized malicious attacks into the following major types:

- **Virus**: A virus is a self-replicating program that depends on human interaction such as opening malicious executables and reading e-mail. Once a virus is accessed, it infects benign programs by attaching itself to them, or simply by carrying out malicious acts. Computer viruses often have the ability to destroy data on the hard drive, or even destroy hard drives.

- **Worm**: A worm is also a self-replicating program that can spread itself through the network or through e-mail communication to other hosts. A worm does not need a benign program to act as a host. Massive replication activity can exhaust systems and network resources, leading to a crash. Well developed networks for data sharing provide convenient environments for them.

- **BackDoor**: A backdoor is a hidden program in the computer system that provides remote access that bypasses the normal authentication and security checks. It usually does not self-replicate, spread or infect other files; however, a backdoor program opens a tunnel for intruders to control the system, and collect private information and sensitive data.

- **Trojan horse**: A trojan horse is another type of attack that does not self-replicate. It arrives disguised as a legitimate program such as a screen-saver or mini-game. A trojan horse usually does not self-replicate and infect other clean files, but it actually executes unexpected and unauthorized operations. Trojan horses are often used to steal sensitive information and destroy data.

- **Spyware and Adware**: Spyware collects user' information such as online activities and file access history. It usually hides itself within other programs. Adware displays unwanted advertising. It can exhaust system resources and cause the poor system performance.

This list only contains the major categories. Other types of malicious code such as logic and time bomb and rootkit also exist. Since we are interested in Windows-based malicious attacks, any executable using Intel X86 instruction set architecture will be our target.

3.2 Clustering algorithms from data mining

Data mining or knowledge discovery is "a non-trivial extraction of implicit, previously unknown, and potentially useful information from data" [16]. It includes many techniques such as frequent pattern mining, sequential pattern mining, clustering, classification, outlier detection and so on. In this thesis, we are interested in grouping samples into classes without a priori knowledge of the resultant clusters. Hence clustering algorithms fit perfectly in the solution framework of our problem.

Clustering is a technique that groups a set of data objects into clusters or classes. Each cluster is a group of data objects that are similar to their cluster members and dissimilar to objects from other clusters. In other words, clustering maximizes the intra-cluster similarity and minimizes the inter-cluster similarity. In this case, a distance function between any pair of data objects and a threshold defining the meaning of closeness are required to construct the clusters containing similar data objects. Clustering is also called unsupervised learning because clustering algorithms do not require any dataset for the training purpose. Although many clustering algorithms have been proposed, each of them demands a different set of parameters to run. For example, the K-means [12], PAM [30] and CLARA [22] clustering algorithms require the user to specify the expected number of result clusters. Algorithms with this requirement are not adequate for our needs because we cannot specify the number of result classes in advance.

DBSCAN algorithm [13] on the other hand does not require the user to predefine the number of result clusters as an input. It is based on the connectivity and density functions to discover clusters with arbitrary shapes. There are two input parameters for DBSCAN, the minimum number of points (MinPts) and a radius (Eps). This algorithm relies on the following concepts (illustrated in Figure 3.1):

- **Eps-neighborhood**: number of neighbors within a radius Eps for a given point.
- **Core objects (CO)**: a set of points that each has at least MinPts points within its Eps-neighborhood.
- **Border objects (BO)**: a set of points that each has less than MinPts points within its Eps-neighborhood.
- **Directly density reachable (DDR)**:an point p is DDR from a CO q if p is within an Eps-neighborhood of q.
- **Density reachable (DR)**: a point p is DR from point q if there exists a chain of DDR point from p to q.
- **Density connected (DC)**: a point p is DC to point q if there exists a point r such that p and q are DR from r.

In order to find clusters, DBSCAN arbitrarily picks a data object out of the dataset. If the point is a border object, the algorithm just randomly picks other points until it is a core point. If this object is a core object, the algorithm creates a cluster with all its neighbors that are directly density reachable and further includes the rest of the points that are either density reachable or density connected to any point in this cluster. DBSCAN recursively repeats the same process until there is no

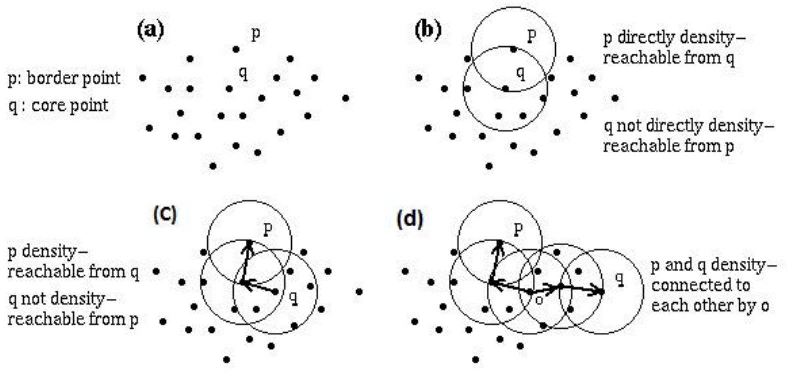

(a)
p: border point
q : core point
(b)
p directly density-reachable from q
q not directly density-reachable from p
(c)
p density-reachable from q
q not density-reachable from p
(d)
p and q density-connected to each other by o

Figure 3.1: Terminology explanation from Ester et al. [13].

point that is neither density connected nor density reachable. Once this cluster is built, the algorithm randomly selects the next un-clustered object, and repeats the same procedure until there is no point left un-clustered in the dataset.

3.3 Techniques from information retrieval

Here, we use techniques from information retrieval which provide the ability to determine the distances between data objects. In this section, we introduce the tools from information retrieval: term frequency/inverse document frequency and cosine similarity.

3.3.1 Term Frequency/Inverse Document Frequency

Term Frequency/Inverse Document Frequency (TF/IDF) is a measure of the importance of terms within a document and across multiple documents [32]. In this thesis, these terms are fixed-length sequences. There are two steps in calculating this measurement. The first step is to calculate the occurrences of each individual term (TF). However, some terms are very common, appearing in almost every assembly code. Therefore, in the second step, IDF adds weights to balance the effects of common terms. Given terms t_i and documents d_j, TF/IDF values of terms can be calculated as follows:

$$tfidf_{i,j} = tf_{i,j} * idf_{i,j}$$

where

$$tf_{i,j} = \frac{n_{i,j}}{\sum_k n_{k,j}}$$

and

$$idf_{i,j} = \ln \frac{|D|}{|\{d_j : t_i \in d_j\}|}$$

where:

$n_{i,j}$: number of appearances of the term t_i in document d_j.

$\sum_k n_{k,j}$: number of terms in document d_j.

$|D|$: total number of documents.

$|\{d_j : t_i \in d_j\}|$: total number of documents in which term t_i appears.

According to this formula, the TF/IDF value for any term is greater or equal to 0.

3.3.2 Cosine similarity

Cosine similarity is a tool to measure similarity using the angle between two vectors. The elements of the vectors consist of a list of TF/IDF weights for each term. Given two vectors X and Y, cosine similarity is defined as follows:

$$similarity(X,Y) = \cos(\Theta) = \frac{X \cdot Y}{|X||Y|} = \frac{x_1 * y_1 + x_2 * y_2 + ... + x_n * y_n}{(x_1^2 + x_1^2 + ... + x_n^2)^{1/2} * (y_1^2 + y_2^2 + ... + y_n^2)^{1/2}}$$

where

$X \cdot Y$: inner product of two vectors

$|X|$ ($|Y|$) : the magnitude of vector X (Y)

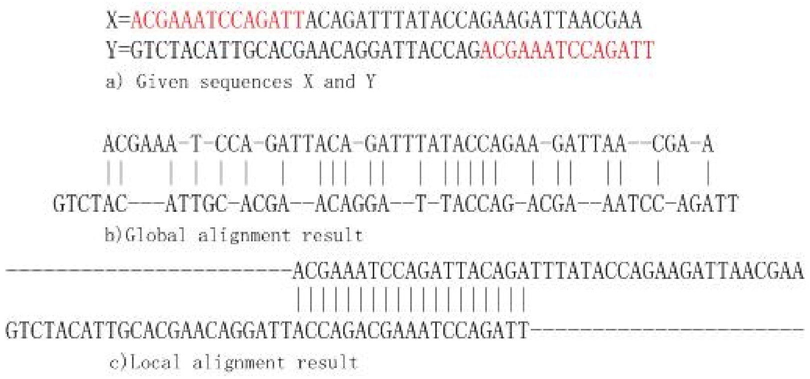
x_i (y_i) : the TF/IDF weight for term t_i in vector X (Y)

The value of cosine similarity originally is between 0 and -1. Since TF/IDF values are the input and they are greater or equal to 0, the value of cosine similarity is between 0 and 1. The closer the cosine similarity is to 1, the more similar the two vectors are.

3.4 Alignment algorithms from bioinformatics

Bioinformatics is the discipline used to process information about the molecular biology of organisms. Its objective is to analyze large amounts of data gathered from genome sequences and other molecular diagnostics [5]. One of the bioinformatics techniques is the sequence alignment. A sequence alignment is an approach of arranging the genetic sequences to identify similar regions that may be a consequence of functional relationships between the sequences. From the result of clustering algorithms, we have a set of clusters containing similar malicious executables. Therefore, the multiple alignment is used first to extract the common characteristic in members of each malicious family. Once we have this feature, the local alignment can help to find unknown sequences that are locally or globally similar to these common characteristics.

There are mainly two categories of sequence alignment, pairwise alignment and multiple sequence alignment. Both of them contain global and local alignment. Pairwise global alignment [29] aligns all residues in one sequence globally with the residues in another sequence; and pairwise local alignment [35] looks for identical contiguous subsequence between two inputs. Let us consider an example. Given two sequences X and Y in Figure 3.2 (a), the result of pairwise global alignment is in (b), and the result of pairwise local alignment is in Figure 3.2 (c). In our project, pairwise local alignment is used by applying features to detect new attacks. From our assumption in Section 1.3.2, each malicious family contains at least one unique subsequence of instructions that can represent the whole family. Once we retrieve these instruction subsequences, any new attack holding such characteristics can be detected and identified. Therefore, in order to measure the similarity regionally, pairwise local alignment is the appropriate alignment technique.



```
X=ACGAAATCCAGATTACAGATTTATACCAGAAGATTAACGAA
Y=GTCTACATTGCACGAACAGGATTACCAGACGAAATCCAGATT
a) Given sequences X and Y

    ACGAAA-T-CCA-GATTACA-GATTTATACCAGAA-GATTAA--CGA-A
    ||   | | | |  |  ||| ||  | |||||  | ||  ||  |   |
GTCTAC---ATTGC-ACGA--ACAGGA--T-TACCAG-ACGA--AATCC-AGATT
b)Global alignment result
----------------------------ACGAAATCCAGATTACAGATTTATACCAGAAGATTAACGAA
                            |||||||||||||||||||
GTCTACATTGCACGAACAGGATTACCAGACGAAATCCAGATT---------------------------
c)Local alignment result
```

Figure 3.2: Comparison between global and local alignments

Since pairwise local and global alignments only address the problem of aligning two sequences at a time, what if we want to align multiple sequences to analyze their similarities? This question leads us to the technique of multiple sequence alignment. Multiple sequence alignment is an extension of pairwise alignment to globally or local align more than two sequences at one time. There are many multiple alignment algorithms, including progressive methods, iterative methods, alignments based on locally conserved patterns, statistical and probabilistic methods and many others. Here, we choose to use the CLUSTALW algorithm [37]. CLUSTALW is a greedy method to globally align multiple sequences. First, it finds the two most similar sequences and aligns them together. It then progressively adds less similar sequences to adjust the result. CLUSTALW was originally designed to align a large number of sequences that are close to each other. Since we first need to group the malicious executables into classes before applying any multiple alignment algorithm, the CLUSTALW algorithm becomes an excellent choice for our implementation. More details about adopting multiple alignment to extract features can be found in Section 4.3.

3.5 Performance measurement

In order to evaluate the performance of our system, we use the following measurements:

- **For detection:**
  1. **True Positive (TP)**: number of malicious executables correctly classified.
  2. **True Negative (TN)**: number of benign executables correctly classified.
  3. **False Positive (FP)**: number of benign executables incorrectly classified as malicious.
  4. **False Negative (FN)**: number of malicious executables mistakenly classified as benign.
- **For identification:**
  1. **True Identification (TI)**: number of malicious executables correctly identified as members of their clustering family.
  2. **False Identification (FI)**: number of malicious executables not correctly identified as members of their clustering family.

For the problems of detecting and identifying malicious executables, the security system aims at accurately detecting both malicious and benign problems, and correctly identifying malicious executables as well. Thus, we are interested in the following quantities:

- **Detection Rate (DR)**: number of malicious executables correctly detected as malevolent regarding total number of malicious programs.

$$= \frac{TP}{TP + FN}$$

- **False Positive Rate (FPR)**: number of benign programs correctly detected regarding total number of benign programs.

$$= \frac{FP}{TN + FP}$$

- **Overall Accuracy For Detection (OAD)**: the summation of both correctly detected malicious and benign programs regarding the entire dataset.

$$= \frac{TP + TN}{TP + TN + FP + FN}$$

- **Identification Rate (IR)**: number of malicious executables correctly identified regarding total number of malicious programs.

$$= \frac{TI}{TI + FI}$$

Chapter 4

Malicious code detection and identification

In this chapter, we introduce the processes of our system: malicious data preparation in Section 4.1; clustering methodology in Section 4.2; feature extraction in Section 4.3 and the application of features in Section 4.4.

4.1 Data preparation

The epidemiology of malicious executables is similar to biological malicious diseases and viruses because of their ways to propagate, break out and self-replicate. In biology, diseases and viruses are simple organisms whose functionalities are mainly controlled by their genome sequences. Our first challenge is to find genome-like representations for malicious executables. As we stated previously, we assume programmers try to change opcodes or operands to bypass signature detection, but they cannot change the instruction sequences too much in order to keep similar functionalities. Each instruction is composed of an opcode and some operands, and the opcode primarily determines the intention of an instruction. In this case, the opcode is the core component of each instruction. Therefore, opcodes could be considered as the "nucleotides" within destructive attacks. In this section, we present our approach for transforming malicious executables from binary formats into their simulated "protein" sequences, which we call s-opcode sequences.

4.1.1 Disassembly

We know that malicious executables are programs represented in binary formats. Since we only examine the executables using 32-bit Intel® Instruction Set Architecture [21], binary executables can be translated into low-level assembly language to extract instruction sequences using a disassembler. In our project, we use a free tool, IDA disassembler [9], to decode malicious attacks. After disassembling them, each attack becomes a file containing thousands of lines of decoded instructions and their corresponding positions in binary files. The only data we need from each instruction is its opcode. By ignoring parameters and other disassembled information, the assembly code of each binary executable is simplified into a sequence of opcodes. Let us consider an example of the transformation from a binary sequence to its s-opcode sequence (see Figure 4.1). Given the binary sequence, "B430 CD21 86E0 3D1E 03BE B407 730A BEA5 103C 0A74 03BE C91E", this disassembly phase is shown in steps one and two of the figure.

4.1.2 Opcode grouping

A malicious executable can be seen as a sequence of opcodes. However, there are about two hundred opcodes within the Intel® instruction set [21]. It is easy for programmers of malicious executables to obfuscate attacks. For example, a for-loop with increment can be changed to a while-loop or for-loop with decrement or many other implementations. But no matter how they change, a loop has to include the arithmetic and control instructions. Under this circumstance, we try to categorize

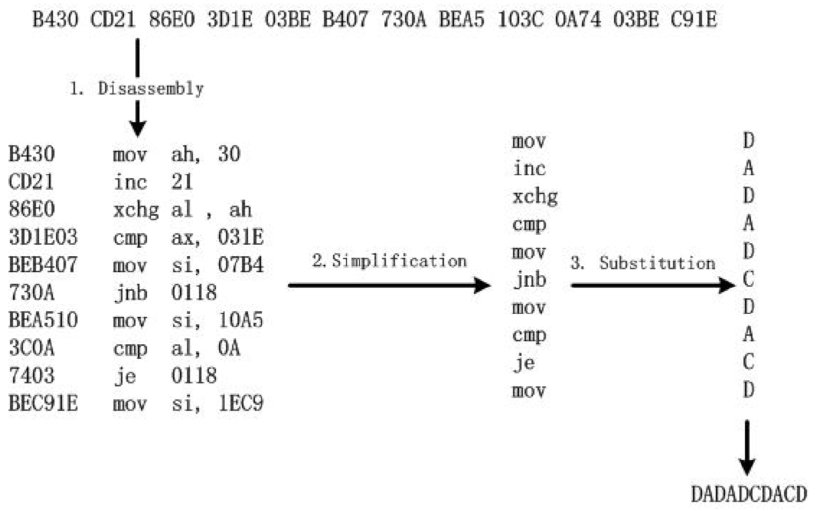


Figure 4.1: Binary to s-opcode sequence transformation

hundreds of opcodes into a relatively small number of groups whose opcodes have similar functionality. According to the guideline from Intel [21], the company has already classified its opcodes into thirteen categories. Because of the duplication of these categories, we further simplify the Intel grouping into eleven categories. More details about opcode grouping can be found in Appendix A. Just as genome sequences use a single character to denote each amino acid, our categories in Table 4.1 are also represented with unique single characters.

4.1.3 s-opcode sequence transformation

Each opcode in an opcode sequence is substituted by a single character according to the opcode grouping specified in Table 4.1. After opcode substitution, an opcode sequence is turned into the corresponding s-opcode sequence with single-character opcodes. In biology, both DNA and RNA sequences have four types of nucleotides and protein sequences are composed of twenty types of amino acids [5]. Since we group Intel opcodes into eleven groups, s-opcode sequences fit nicely into the domain

Intel instruction Category	**Character representation**
Data Transfer Instructions	**D**
Arithmetic Instructions	**A**
Logical Instructions	**L**
Shift and Rotate Instructions	**T**
Bit and Byte Instructions	**H**
Control Transfer Instructions	**C**
String Instructions	**S**
I/O Instructions	**I**
Flag Control Instructions	**F**
Segment Register Instructions	**R**
Miscellaneous Instructions	**M**

Table 4.1: Single character representation of opcode categories.

of bioinformatics algorithms. Now, we can treat s-opcode sequences as biological genome sequences, and apply bioinformatics techniques such as the alignment algorithms described in Section 3.4 to address the problem of detecting and identifying malicious executables. This transformation phase is shown in step three of Figure 4.1.

4.2 Clustering

There are at least two ways to detect new attacks. The first approach is to find the key features from the existing malicious executables, then use these characteristics to recognize new malicious executables. The second approach is to construct malicious families based on the properties of attacks. Using these families, we can extract features from each family to discover new attacks. Between these two approaches, the first one is more like an idealistic method. It is very complex to find the crucial information directly from attacks. The second approach on the other hand is more practical. Malicious families can be formed based on their properties, for example s-opcode sequences, and it is easier to retrieve key data from members in the same family since they share similar characteristics. In contrast with malicious families, a single executable alone provides insufficient information to find its characteristics. In our project, we apply the second method to extract features from clustered malicious families.

After the transformation from binary code to s-opcode sequences, our task now is to find a way to cluster malicious attacks algorithmically. In commercial industry, security software programs have their own approaches to classify malicious executables. A new malicious attack is analyzed for its functionalities, propagation and many other characteristics by experienced analysts. Then, these newly reported attacks are manually classified into families. In this case, human beings play an important role in forming the groups of malicious executables. For the same reason, different companies have different understandings of attacks, and therefore, have slightly different identification results for existing malicious executables. In order to construct malicious families algorithmically, clustering algorithms from data mining can be used to address the problem of grouping.

In clustering algorithms, there are two important components, a distance function and a distance threshold. The distance function is also called the distance measurement or similarity measurement and quantifies the difference between any pair of data objects. The distance threshold is a constraint that determines whether two data objects are close enough or not. In this thesis, we use a combination of cosine similarity and TF/IDF to measure the difference. Heuristic approaches introduced with the DBSCAN algorithm help choosing the distance threshold.

4.2.1 Distance measurement

Given a s-opcode sequence with a length of n, we choose a fixed window length k where $k \leq n$. By sliding the length k window through the s-opcode sequence, we obtain a vector containing $(n-k+1)$ subsequences where each subsequence is a term with k-opcodes. An example is shown in Figure 4.2 with sliding window of length 8. The s-opcode sequence with length 13 can be decomposed into 6 subsequences with length 8. Using this vector representation, each vector has a list of subsequences which have length k. The TF/IDF value for each subsequence is calculated over all the available subsequences. After calculating the value for TF/IDF, each vector has a list of terms associated with their TF/IDF values. Every malicious executable is now represented in vector space as pairs of k-length subsequences and their TF/IDF values.

Many distance functions such as Euclidean distance, Manhattan distance and Jaro distance [14] have been developed to measure the differences between two data objets of their coordinates in metric space. In our project, instead of measuring geometrical distances between two vectors, we are interested in estimating the direction and angle of them. The direction and angle between two vectors provides precise information about how they differ in functionalities that are instruction sequences in our case. This is the reason that cosine similarity is chosen to measure the angle between two vectors. Our next step is to apply the vector representations to the cosine measurement.

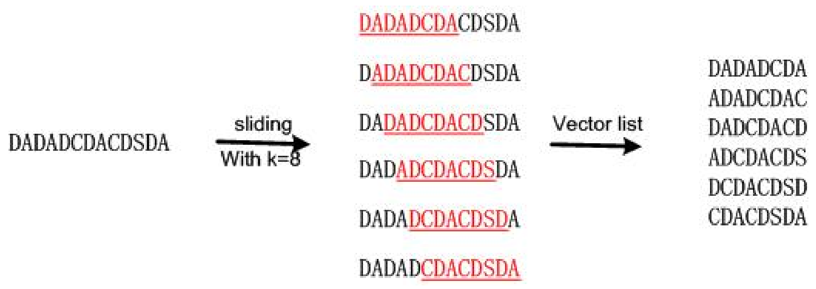


Figure 4.2: Sliding window used to retrieve length k term list.

Applying the formula of cosine similarity described in Section 3.3.2, the distance between vectors A and B can be found in a numeric range of 0 to 1. By collecting all results of cosine similarity, a score matrix can be generated to represent the distance between any pair of vectors in the dataset. In cosine similarity, the closer to value 1 the distance is, the more similar the two vectors are. In order to follow the meaning of distance in a natural way, we subtract all the elements in the score matrix from 1. After this adjustment, the adjusted score matrix in Table 4.2 as an example gives an opposite meaning to the cosine value. The value 0 means that two vectors are identical. The closer to the value 0 the score is, the more similar the two vectors are. For example, object "NB-P.COM" is more similar to object "NB-O.COM" than object "A_204.COM" because the score between object "NB-O.COM" and object "NB-P.COM" is smaller.

	A_204.COM	NB-O.COM	NB-P.COM	NB-T.COM	NB-U.COM
A_204.COM	0				
NB-O.COM	0.9904101	0			
NB-P.COM	0.9919908	0.1834956	0		
NB-T.COM	0.990327	0.1748854	0.0487555	0	
NB-U.COM	0.9903327	0.1708549	0.0556605	0.046651	0

Table 4.2: Adjusted score matrix.

4.2.2 Clustering algorithm

Once we have the distance matrix for all data objects, the next challenge is to choose a proper clustering algorithm. We use the implementation of hierarchical clustering from R [40] with the input of a TF/IDF-Cosine distance matrix to find the potential number of result groups of our dataset and the possible threshold to determine the neighborhood. The result from hierarchical clustering is shown in Figure 4.3. The height at value 0 according to cosine similarity is for objects that have exactly the same angle (identical). At this distance, every malicious executable forms a cluster for itself. When we increase the distance from a value of 0 to around 0.1, several clusters are built by merging similar attacks. As the distance further increases, some lines merge together into bigger classes. Fewer and fewer classes can be formed as the distance approaches 1. A relatively small number of clusters is constructed overall because we randomly select training samples from the dataset. The graph shows that similarities between malicious executables within the same cluster are lower than the similarities between malicious executables from different families. If we can choose a proper threshold, the clustering algorithm is capable of constructing some clusters from malicious samples based on their TF/IDF-Cosine similarity. However, from the result of the hierarchical clustering algorithm, there is no way in advance to predict the possible number of result classes given the fixed threshold. All similar malicious executables should be able to be grouped into the same class without predefined clusters. Because of this constraint, there are only a few clustering algorithms such as nearest neighbor and DBSCAN algorithms that we can choose. By testing these clustering algorithms, we find that DBSCAN generates the categorization that is the closest to the result from commercial anti-malware products.

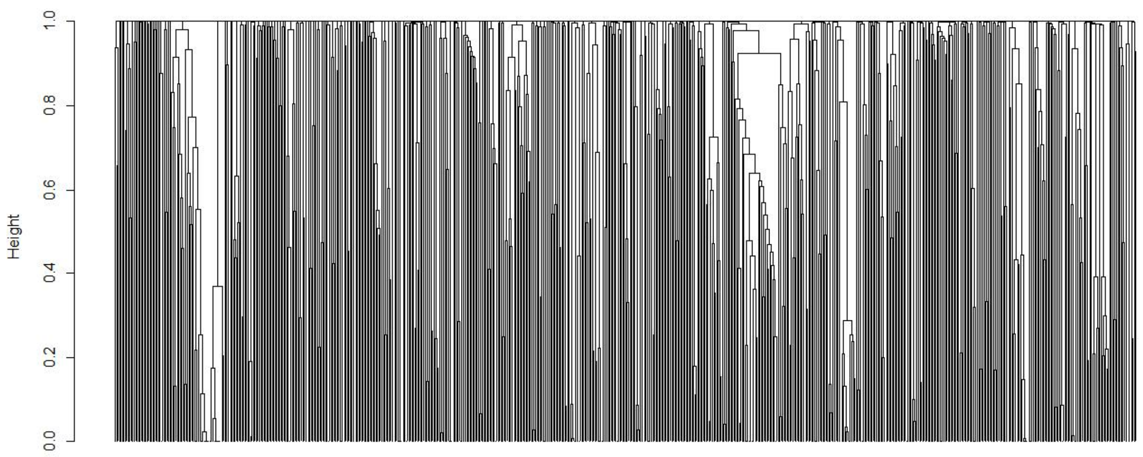


Figure 4.3: Result from a complete hierarchical clustering algorithm.

DBSCAN is a density-based algorithm. We introduced DBSCAN in Section 3.2

along with its two main parameters. The first parameter is the minimum number of points within the neighborhood. In our domain, no attack is considered noise. Therefore, minPts can be set to 1. This allows the smallest family to have at least two members (a core object and a neighbor). The attack without neighbors builds a cluster only with itself. The second parameter is the radius used to form the neighborhood. From the result of the hierarchical clustering algorithm in Figure 4.3, there are clusters existing in the range of approximately 0.4 to 0.8. Thus, the radius can be chosen within this range. A detailed heuristic method to choose the DBSCAN radius is presented in Section 5.3.1.

4.3 Feature extraction

After applying the clustering algorithm, malicious executables are grouped into different families containing similar attacks. The next obstacle is how to retrieve the feature from each family. But first of all, what is a "feature" in our domain? As we stated in Section 1.3, there exists at least one common subsequence of instructions that is similar or identical among all malicious members from the same family. This common subsequence is relatively different from other attacks because different families contain comparatively different s-opcode sequences. In this case, these unique instruction sequences from malicious families become our features. Now we understand the domain of our features, but how can we find specific features? When we prepared the data objects, we translated the instruction sequences into genome-like s-opcode sequences. Then all the s-opcode sequences in each class can be aligned according to their best local sequences using the multiple alignment algorithm described in Section 3.4. By searching through the output of multiple alignment, we can extract the most common s-opcode subsequences as features. In other words, features are the local subsequences from each class that appear in every member of that cluster. The example in Table 4.3 shows a malicious family with two common subsequences. In the table, the subsequences $DSDDCDCDDARDDSDDDDDDD$ and $ADADDADD$ are the common s-opcode sequences that could be features.

NB-P.COM	DSDDCDCDDARDDSDDDDDDDSAHADADDADD
NB-T.COM	DSDDCDCDDARDDSDDDDDDDDDDADADDADD
NB-U.COM	DSDDCDCDDARDDSDDDDDDDSDHADADDADD
NB-O.COM	DSDDCDCDDARDDSDDDDDDDDDMADADDADD

Table 4.3: Multiple alignment that has common subsequences.

Common subsequences generated from multiple alignment can have various lengths from family to family. We have found that their lengths vary from 1 to 20 or even more. The question is how to gather the important features. There are many options here. The first choice is that we can define a threshold according to the length of the sliding window. Any common subsequence with length greater than this threshold can be selected as the feature. The rest are considered to be insignificant. A second choice is that we ignore the threshold, but choose the longest or the top two longest common subsequences as features. We have decided to use the subsequences that are the longest or the two longest common subsequences whose length is greater than the length of the sliding window as features.

Using common subsequences as the feature suggests a matching threshold with value 100%. It means that all members in the family have to carry a or some specific subsequence(s). Unfortunately, some clusters do not have any common subsequence at all or the length of the common subsequences is not long enough. For these special clusters, we can reduce the value of the threshold to retrieve proper features other than common subsequences. But how do we choose the proper value? Should it be 70%, 80% or 90%? In this circumstance, we introduce a simple approach to determine the value of the threshold. If we choose the length of the sliding window to be a fixed value n in the process of data preparation, then the length of the features should also be greater than n. While the threshold is changing, we can examine the changes of the size and the content of the resulting subsequences to choose a proper value for the threshold.

For illustration, Figure 4.4 shows how the size of the feature list changes by varying the threshold for a cluster without any common subsequence. Tables 4.4 lists changes of the content of the feature list.

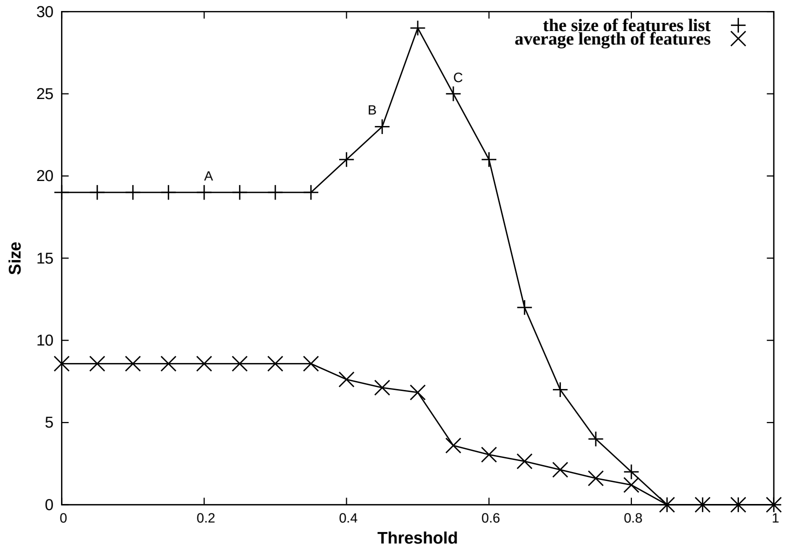


Figure 4.4: Feature list size.

While we are altering the threshold from 5% to 100% with 5% granularity, both the content and the size of the result list change. The size of the list is first flat on a fixed value, then increases to a peak value and at last goes down to the value zero as the threshold approaches 100%. Let us examine the contents as well. As the size of the subsequence list approaches the peak value (point B in both Figure 4.4 and Table 4.4), the average length of subsequences decreases. But, some of the subsequences are still long enough to be features. Once the size starts dropping (point C in both Figure 4.4 and Table 4.4), subsequences become shorter and irrelevant to the problem of detecting and identifying malicious attacks. Therefore, we select a value on the up-slope curve as the threshold. Then, the longest sequences are picked

Point A	Point B	Point C
D	D	C
CD	C	D
DS	CD	S
CDD	DS	DC
DDMD	DD	DD
AAACCD	CDD	DS
CDCCDD	CDC	AD
SSDDMC	CDMD	AA
CACDMCC	DACD	CD
DDDDDDM	DDMD	DCD
MDMDDDD	LDCA	DDD
LDCACDACD	MDDDM	CDD
CDMDSMDDDM	AAACCD	CCD
CDDDMDLDCDMD	SSDDMC	DACD
DDAMMSMDDAADD	CACDMCC	MDDD
ACDAACCACDDDCD	MDMDDDD	DDCC
DDCCLCDCDDMDCD	DDDDDDM	DDMD
AADDTTFADLDDDDDC	ACDAACCACD	DDMC
RDDRDDDDTDRDDDAADADDDDDDD	CDDDMDLDCDMD	DDDA
	DDAMMSMDDAADD	CDMCC
	DDCCLCDCDDMDCD	DAACC
	AADDTTFADLDDDDDC	DADDDD
	RDDRDDDDTDRDDDAADADDDDDDD	CDDDMD
		MDMDDDD
		DDAMMSMDDA

Table 4.4: The content of the feature list changes by varying the threshold referring to Figure 4.4.

as features according to the selected threshold. Since the threshold is arbitrarily chosen in a range, the result of the feature list is slightly different at each time of extracting features. By applying this approach, the priority of the feature extraction is to find common subsequences as features. Then, for those clusters without any common subsequence, the secondary goal is to find the feature that satisfies the chosen matching threshold.

4.4 Applying features to the problems of detection and identification

After clustering and feature extraction, we have a set of families of known malicious executables and a list of s-opcode sequences as features that can represent the characteristics of these malicious families. The next step is to apply features to detect and identify attacks. For any incoming attack, we use the same transformation processes: disassembling it into a sequence of instructions; retrieving its opcode sequence and translating it into an s-opcode sequence. Then, a bioinformatics-based classifier using s-opcode sequences is applied to perform the tasks of detection and identification.

Given a set of features and their families, our challenge is to apply the advantages of bioinformatics analysis. According to our hypothesis, each malicious family has at least one key subsequence that is unique compared to other families. If any subsequence from a program is similar or identical to the features appearing in our database, then this executable can be flagged as a malicious program. The question is how we are going to compare them. This question requires the knowledge of the local alignment algorithm. We have described the local alignment in Section 3.4. Pair-wise local alignment is used to find the similar subsequences in both inputs. Therefore, for any possible incoming executable, we locally align its decoded s-opcode sequence with all the features in our database. In order to tell whether two sequences are close enough or not, we introduce a similarity threshold to distinguish them. This threshold can vary from 0% to 100%. If the value of the threshold is 100%, then the local alignment is a scheme with exact matching. On the other hand, decreasing this threshold gives a better tolerance of detecting new attacks with mutated s-opcode sequences. However, the threshold cannot be too low. Too low a threshold will generate a large number of false alerts. We will investigate this in Chapter 5.

In addition to the detection, if there is a match between an incoming attack and the feature in the database, we can retrieve its most similar feature(s). By using these features and the families where they appear, we can signal the families to which the attack belongs.

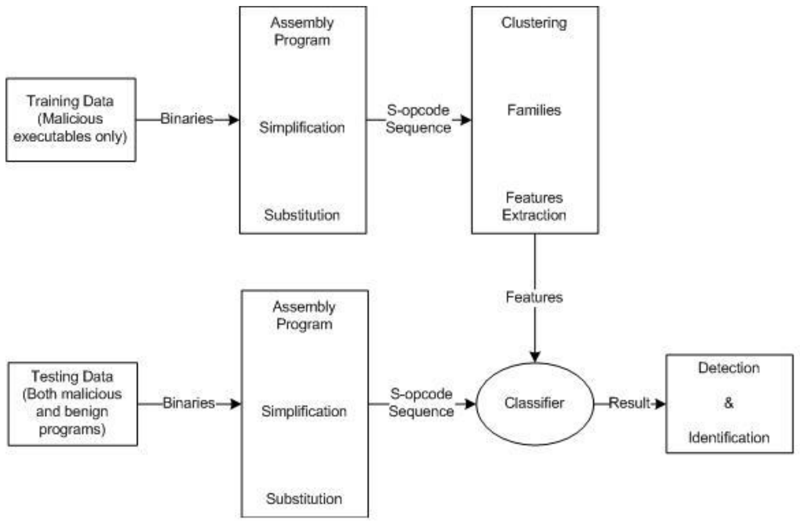


Figure 4.5: Processes of our approach

4.5 Summary

In summary, the procedures of our approach are outlined in Figure 4.5. First of all, malicious samples are randomly selected from the dataset, and we apply the processes of decoding, simplifying and substituting to obtain their s-opcode sequences. Features extracted from clustered malicious families are then used by the classifier. The classifier uses these features to achieve the goal of detecting and identifying new incoming attacks.

Chapter 5

Experiments and Performance Evaluation

The features we extract from binary executables can be applied at either the application level or the networking level. This chapter presents results for our approach in detecting and identifying attacks at the network layer in simulated network traffic. As we will see in Section 5.3, we try to optimize system parameters in order to achieve the highest accuracy. Shortcomings that affect the results are analyzed afterwards, and possible alternative solutions are also presented.

5.1 Datasets

We have a dataset containing 3548 malicious executables and 200 benign files. The malicious executables were gathered from VX Heavens [1], and the benign programs come from the Windows XP operating system. The malicious executables consist of a large number of DOS viruses, Windows malicious EXE or application programs and a small number of trojan horses. The malicious attacks and benign files were disassembled and then stored for the purposes of either training or testing.

We input one fifth of the set of malicious executables into the training phase. After their features are extracted, both malicious and benign files are used to test the performance of this system.

If we could deploy our system in the field, then we would use all attacks from our dataset for training purposes to predict unknown threats online. However, in order to evaluate our technique, the dataset is divided into two sets, a training set and a testing set. The idea is to mimic the current knowledge with the training set and have the testing set serve as the new and unknown threats. Thus we can estimate how effective our technique would be in realistic settings. Having a relatively small training set would put an unfair stress on the system since it is unreasonable to expect that one could learn anything effectively from a small sample. Having the training set too large , on the other hand, would also be unfair because it would be strongly biased towards our proposal. We have thus decided to use only 20% of our dataset as the training set. As we shall see this is enough for us to deliver very good performance, but also offers a scenario to illustrate how well the technique might perform when one knows much less about the real set of threats that exist.

5.2 Experiment setup and simulation

All implementations were developed in Java with JDK 1.6. We used an external Java package, Similarity Measurement Library [7], which implements the local alignment algorithm [35] to measure the similarity between two s-opcode sequences. In addition, a Java version of CLUSTALW [19] was used for aligning malicious s-opcode sequences in the same cluster.

For our simulations, we simulated a device in the network layer of the Internet. In this layer, communication data is organized in the form of a series of TCP/IP segments. The payload of a TCP segment is assumed to be 1400 bytes, and the average length of an instruction is assumed to be four bytes. Therefore, each segment contains approximately 1400/4=350 instructions with 350 opcodes. In order to simulate the network traffic, we break each malicious s-opcode sequence into several subsequences, each with a length of 350 or less if the length of the s-opcode sequence is not divisible by 350. A classifier is deployed in the simulated device to examine each incoming segment to determine whether its contents are malicious. If one or more segments from a session are identified as malicious, then the whole session is blocked.

5.3 Results

First, we randomly selected 710 malicious executables (20% of the dataset) as the training set. After their transformation, DBSCAN was applied to this training set by using the measurements of TF/TDF and cosine similarity. As a result, roughly 300 clusters were built. These clusters contain an unbalanced number of members that are relatively similar to each other; we call each cluster a malicious family. By assumption, similar malicious executables contain one or a few opcode subsequences that are unique compared to other attacks. These key opcode subsequences can be gathered by using multiple alignment among the members in each family. We used the CLUSTALW algorithm to extract features (the most common subsequences) from each family. After extracting the subsequences, there are approximately 300 features. The classifier then applies the local alignment technique to detect and identify unknown malicious attacks using these features.

The procedures described above depend on various parameters. Next, we introduce these parameters and possible ways for selecting their values.

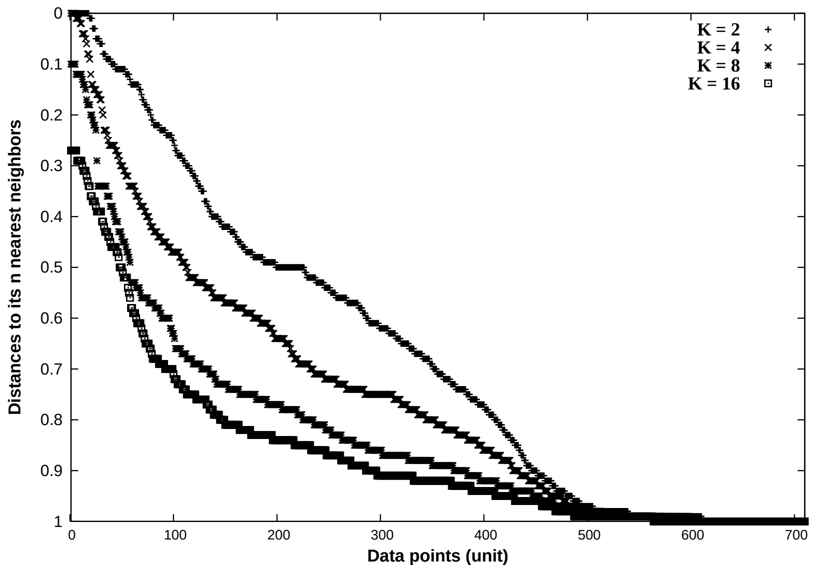
5.3.1 Parameter selection

There are four parameters in our approach:

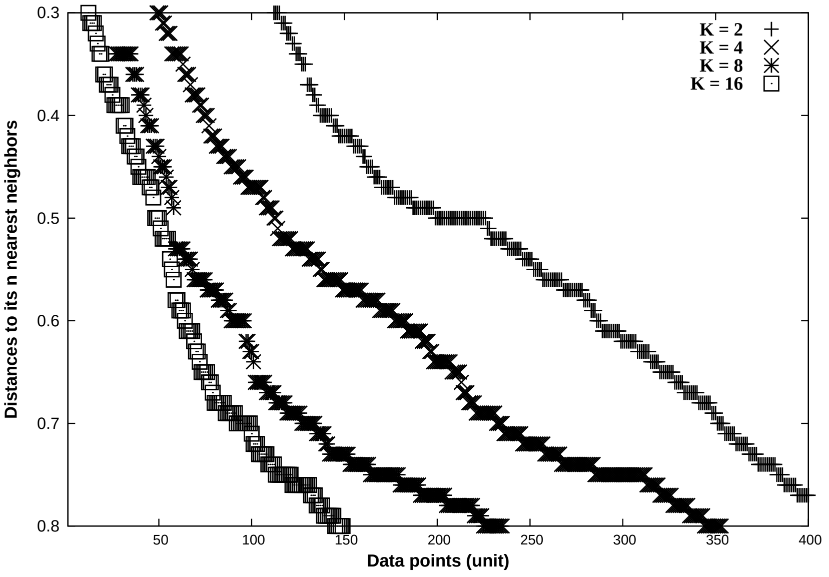
1. The length of the n-gram for sliding through the s-opcode sequence.
2. The minimum number of points within the neighborhood, needed by DBSCAN.
3. The radius used to build the neighborhood, needed by DBSCAN.
4. The threshold for local alignment similarity used to measure the distance between two s-opcode sequences.

The length of the n-gram can take values from 1 to the length of the maximum s-opcode sequence, but we are interested in the size of basic blocks in assembly codes. A basic block is defined as "a sequence of consecutive statements (instructions) in which the flow of control enters at the beginning and leaves at the end" [3]. Previous analysis shows the size of basic blocks from SPEC benchmark programs varies roughly from 5 to 15 instructions [20]. For example, blocks such as if-else and for-loop statements require at least 4 to 5 instructions. In order to perform some extra functions besides basic control statements, we assume a meaningful malicious block has to be over 8 instructions long. Our experiments test the basic blocks starting at length 8. Also, the minimum s-opcode length of an important feature corresponds to the length of the n-gram.

The minimum number of points in the neighborhood and the neighborhood radius are required parameters for DBSCAN. According to Ester et al., the radius to build the neighborhood can be found approximately using a graphical representation [13]. We calculate the average distance for each data object to its k nearest neighbors. After sorting the distances among all points, we can plot the sorted values in a graph, which will have a "valley" shape. We select the value of the radius somewhere around the valley. In this thesis, we follow this process by varying k values from 2 to 16. Figure 5.1(a) shows the "valley" shapes with a broken or shifted line around value from 0.5 to 0.7. If we zoom in the graph using distances from 0.3 to 0.8, we obtain more details about this area (see Figure 5.1(b)). The "valley" representing the sorted



(a) Sorted average distance to k nearest neighbors.



(b) Enlarged area for distance from 0.3 to 0.8.

Figure 5.1: Sorted average distance to k nearest neighbors.

average distance to two nearest neighbors shifts approximately at value 0.5, and the sorted average distance to eight nearest neighbors breaks roughly at value 0.65.

Values around where the "valley" is shifted or broken can be selected as the radius to create the neighborhood with the specified number of neighbors. From Figure 5.1, the radii match the result from our hierarchical clustering analysis in Section 4.2.2 that malicious families exist in a range of approximately 0.4 to 0.8. Using this approach, we can determine the value of the radius to create the proper neighborhood. For determining the minimum number of points, we have to consider the problem of detecting malicious executables. In clustering malicious attacks, there is no noise. Malicious executables with neighbors create families to include them, and the rest of the attacks without any neighbors build singleton families.

The last parameter is the threshold measuring the local alignment similarity. Its value varies from 0 to 1. If the value is 1, then the local alignment is an exact match. Otherwise, we are loosening the constraints of the local alignment.

In summary, the two parameters we have to address are the length of the n-gram and the threshold measuring the local alignment similarity. Hence, we focus on the performance of the system using various combinations of these two parameters.

5.3.2 Analysis

Since we have narrowed the system parameters down to two, we first run experiments against the training set. These are divided into two parts. First, we fix the threshold of local alignment similarity and test the system by varying the n-gram length. Next, we use the n-gram length from the first part which achieves the highest accuracy, and change the value of the local alignment threshold.

5.3.2.1 Experiments against the training set

***n*-gram length**

Threshold	n-gram Length			
	10	14	18	22
0.6	0.57	0.578	0.577	0.621
0.8	0.578	0.627	0.922	0.929
1	0.749	0.916	0.921	0.9175

Table 5.1: Overall accuracy of detection.

Single segment examination In this test, we first need to select a value for the local alignment threshold. But, how do we choose a proper value? As we know, this threshold should not be too low because a low threshold will cause false alarms. A local alignment threshold of 0.6 is a reasonable lower bound. However, in order to select a proper value within this range, we have to further understand macro behaviors of our system using both the local alignment threshold and the n-gram length as parameters. Applying individual segment examination, Table 5.1 provides a high-level view of changes of overall accuracy of detection (OAD) using various combination of both parameters. In the table, the highest OAD values appear when the threshold is at 0.8. Therefore, we select the threshold to be 80%.

As we discussed in previous sections, a basic instruction block is assumed to be at least 8 instructions long. Therefore, our experiments start with an 8-gram length. After running the clustering algorithm using the information provided from the n-gram length, we extract from each family the most common longest subsequences, as features, whose length is greater than n. In this case, each family only contributes one feature to represent its characteristics. We assume the classifier resides in a network device and examines each individual segment. Before we examine any segment, we choose the threshold to be 0.8 to define the meaning of similarity. If there is a match between a disassembled payload and a feature from our database with a similarity over this threshold, the classifier will report the segment and block the session. In this scenario, the classifier only examines one segment at a time, and reports the alert as soon as it identifies the examined segment as malicious. The classifier does not require any memory to store the information about blocked sessions. We call this approach the individual segment examination. Results for the individual segment examination using different n-gram length are shown in Figure 5.2. The corresponding numeric data of this graph and the following graphs can be found in Appendix B. In this and the next graphs, Detection Rate (DR) is the fraction of malicious executables correctly detected. False Positive Rate (FPR) is the fraction of benign files mistakenly detected as malicious. Identification Rate (IR) is the fraction of malicious executables correctly predicted from their own families, and Overall Accuracy of Detection (OAD) is the overall accuracy of both detection and false positive rates. These definitions can be found in Section 3.5.

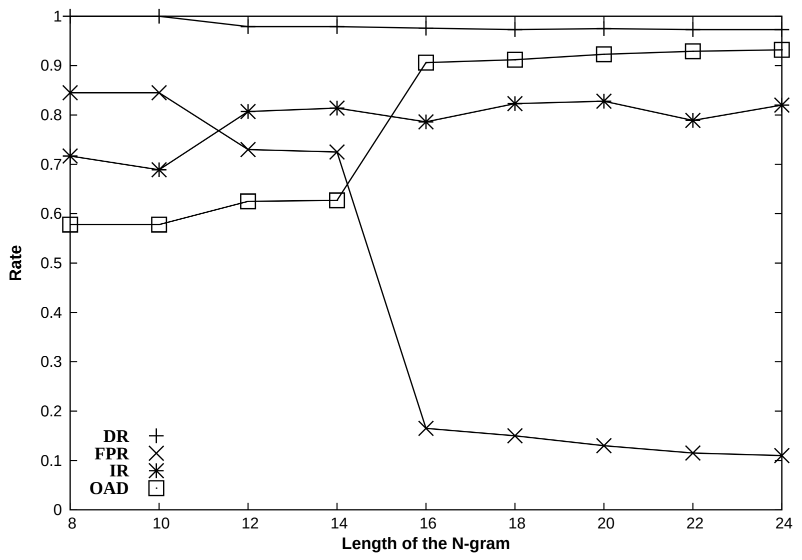


Figure 5.2: Individual segment examination

The graph shows detection rates of over 97%. Individual segment examination gives a good detection rate because once there is a match in any one of the segments, the session will be reported and blocked. However, the false positive rate is relatively high. This is because of the noise feature. When the length of the n-gram is small, there are many s-opcode sequences in the feature list that commonly appear in the assembly code. Benign programs containing these common s-opcode sequences are also reported. Therefore, both detection and false positive rates are affected by false alarms. Actually, as we increase the length of n-gram, the false positive rate drops quickly. However, its value is still above 10%. For example, with the 18-grams sliding window, even though we have a detection rate above 95%, the false positive rate is roughly 17%. In contrast to the detection rate, the identification rate increases as the length of the n-gram increases because the longer n-gram becomes more characteristic and provides more information about targets. We want to select the n-gram length which can achieve both the highest OAD and IR. In this case, our experiments suggest that an n-gram length above 18 provides the highest accuracy for individual segment examination.

The main drawback of checking a individual segment is the relatively high false positive rate. Our next job is to reduce false positives while maintaining the same detection rate. There are two options to ameliorate the current situation: improving the quality of features or introducing more features.

Single segment examination using merged features In the previous experiments using features to examine individual segment, we get high detection and false positive rates because of the noise feature. To remove noise from features, we can merge similar features. When a feature is extracted from a family, a scanner will search the feature list for either its super-sequences or subsequences or features that are similar enough in other similarity measurements, for example local alignment [35], Euclidean distance [14] and so on. If the scanner finds a super-sequence feature, the newly generated feature will be dropped. If the scanner observes sub-sequence features, the current feature will be included in the feature list by eliminating its children. Otherwise, if similar features are found, only the longest one among them is kept. By merging the features, approximately 20% to 30% of the original features are pruned out.

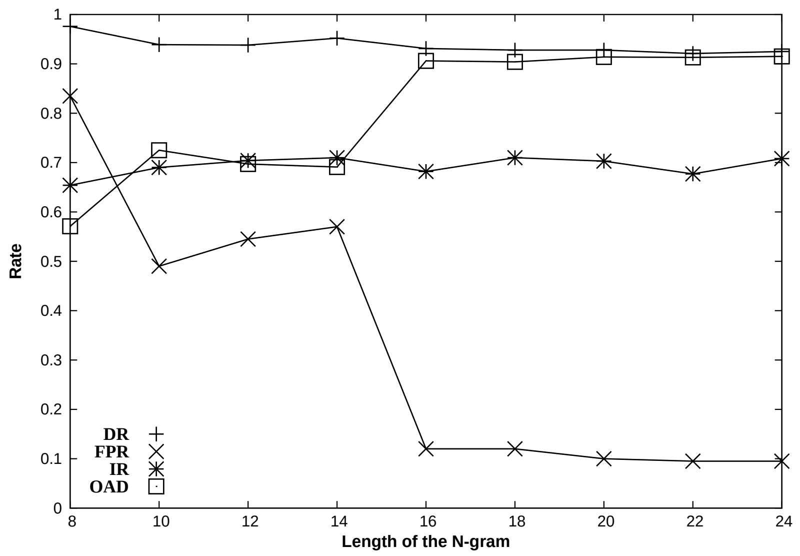


Figure 5.3: Individual segment examination with merged features

Figure 5.3 shows the experimental results for the merged features generated from different n-gram length. The detection rate is sacrificed a little as a compromise for the drop of the false positive rate for merged features compared to original features. For example, using the 18-grams, the false positive rate drops by roughly 1% to 12% while the detection rate is maintained at 93%. However the false positive rate is still above 10%. After merging the feature list, the effect of noise features has been reduced. The high false positive rate now could be due to the organization of executables. The assembly code consists of both execution and data segments. Lots of data segments or “NOP” operations mix with executable instructions. In our simulation, we have to remove all unrelated segments to retrieve s-opcode sequences. This removal causes s-opcode sequences from some segments to be shorter and non-characteristic. These non-characteristic s-opcode sequences trigger false alarms. Therefore, merging similar features does not improve accuracy very much. In our experiments, the identification rate drops quickly because merging features causes the loss of information about the families they belong to. Eventually, this leads to a lower identification rate. Interestingly, false positive rates from 10-grams and 12-grams drop significantly compared to the rate from 14-grams. This is because short noise features from both 10-grams and 12-grams are comparatively easier to merge. The more noise features are merged, the better the quality of the feature list. The graph shows that the n-gram with a length above 18 provides the highest accuracy.

Threshold	n-gram Length			
	10	14	18	22
0.6	0.613	0.618	0.621	0.646
0.8	0.63	0.745	0.945	0.951
1	0.8105	0.927	0.93	0.909

Table 5.2: OAD using double segments examination

Double segments examination The last two sets of experiments show that the false positive rate generated from examining individual segment is affected by either feature noise or the quality of segment payloads. Since examining one segment is not enough, we can check two or more successive segments from one session. If double segments from a session match two features from one family, the classifier issues an alarm. In this case, the classifier has to include a memory to record at least the first detected malicious segment for each session.

As far individual segment examination, we need to understand system's behavior. Macro results in Table 5.2 shows that a threshold of 0.8 provides the highest OAD to examine double segments. Therefore, we set the local alignment threshold to be 0.8. Also, we now have to retrieve the two longest features instead of one from each family. Features stored in the feature list are associated with their families' name. Comparing two successive segments with two features from one family can relieve the

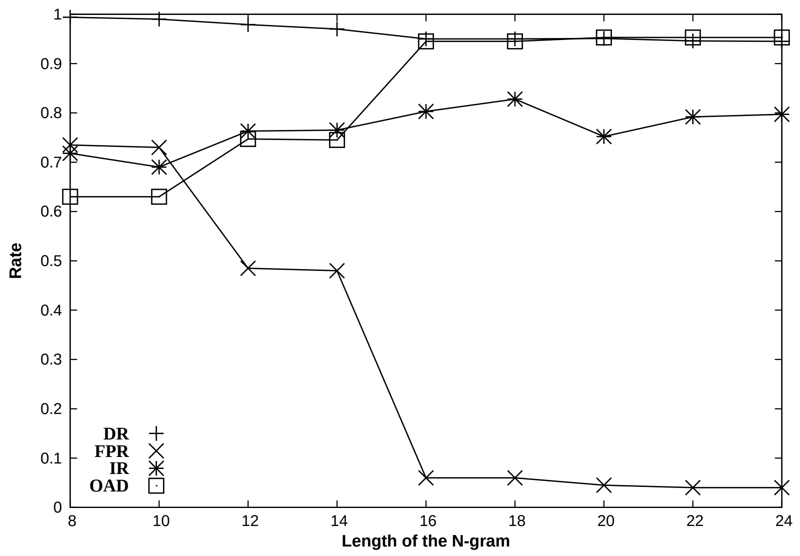


Figure 5.4: Double segments examination

impact of both feature and payload noise. The same scenario applies when checking multiple segments as well. Figure 5.4 gives more details about the experimental results.

In this graph, the detection rate with an n-gram length of 18 is 95%, for example, compared to 97% from examining individual segment. The reason the detection rate drops is because the classifier adds more constraints in detection by examining one additional segment. As a result, the false positive rate drops significantly from 13% to 6%. Sacrificing 2% in detection rate can actually reduce the false positive rate by 55%. From experiments, we learn that using an n-gram length of 18 to 22 provides the highest accuracy.

Double segments examination using merged features Besides using the approach for examining two successive segments, we can improve the quality of the feature list containing two features from each family by merging similar ones as well. The experimental results shown in Figure 5.5 are similar to those in Figure 5.3. The reason that both 10-grams and 12-grams provide better false positive rates is still the same. The merged feature list can reduce the number of features about 15% and improve the false positive rate from 6% to roughly 2% while the detection rate drops from 95% to 90%. Similar to Figure 5.4, experiments show that using an n-gram length from 18 to 22 provides the highest accuracy.

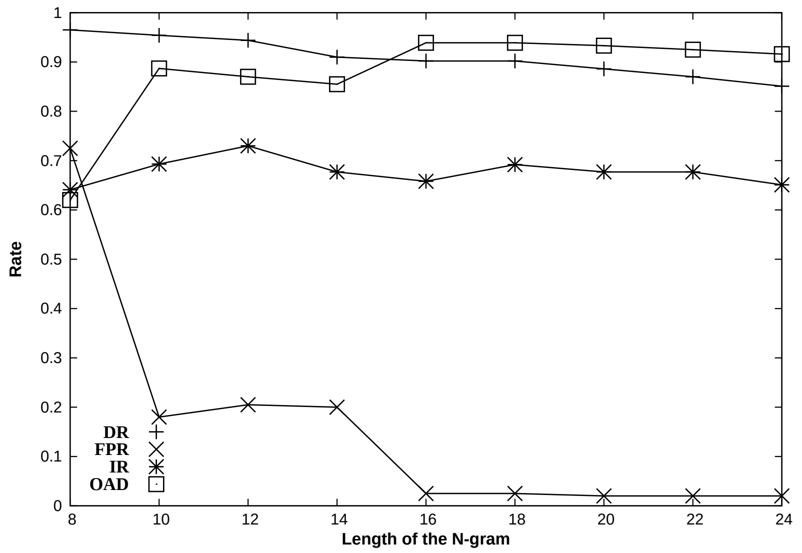


Figure 5.5: Double segments examination with merged features

Multiple segments examination The result is comparatively better by checking two successive segments, but what would the result be if checking more than double segments for a session? If we examine more segments, we have to extract the corresponding number of features from each family. One would hope that examining more segments for a session would improve the result meaning a higher detection rate and a lower false positive rate. However, our results (see Figure 5.6) are the opposite of these expectations.

Both detection and identification rate drop after examining more than double segments because of adding extra constraints when checking additional segments.

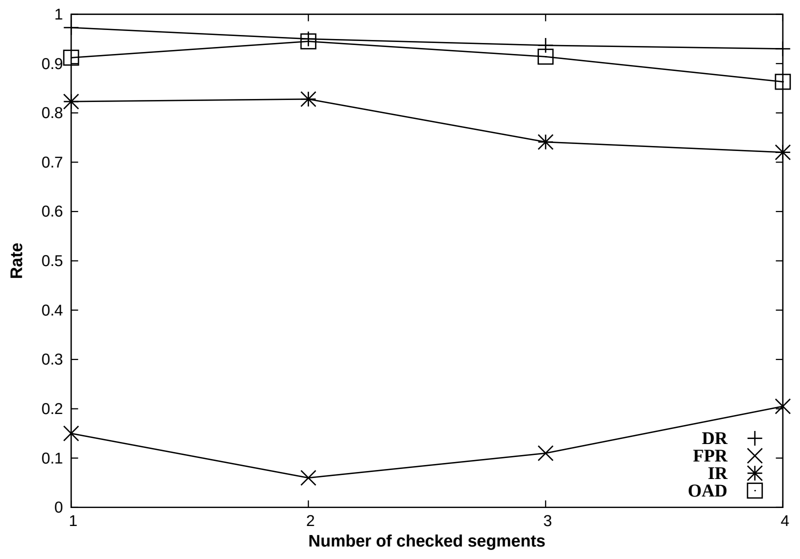


Figure 5.6: Varying number of segments examined

The false positive rate increases because the quality of features is declining. In order to examine more segments in the session, we have to extract more features from each family. The most significant feature from each family is the longest common s-opcode sequence. As we increases the number of features extracted from each family, the quality (length) of features drops. Once the length of the feature falls too much, they will become non-typical and start generating false alarms. Our results suggest that checking double segments for each session gives the best result. It is not necessary to go beyond this point.

Threshold selection

Overall, the results in the previous section show that the n-gram length from 18 to 22 provides the best accuracy regardless of the value of local alignment threshold. Therefore, in this section, we arbitrarily select the n-gram length to be 18, and vary the alignment threshold to appraise the system.

First, we test the system using the individual segment examination by changing

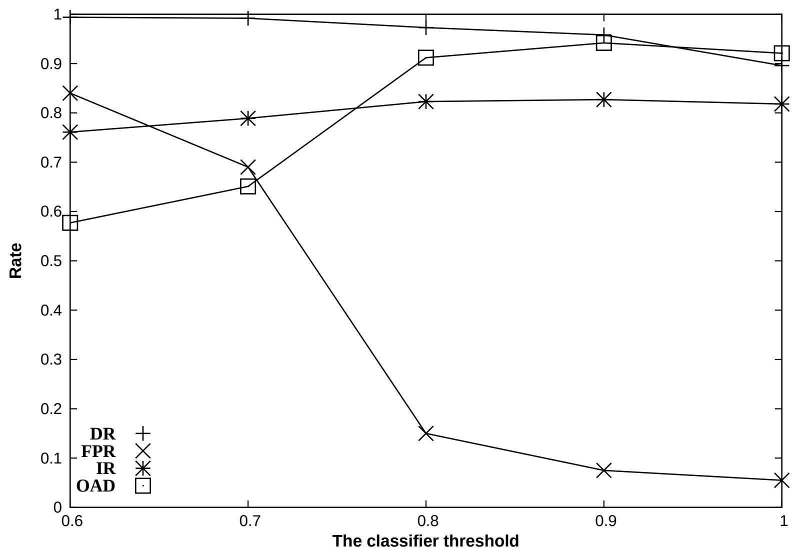


Figure 5.7: Individual segment examination with varied alignment thresholds

the threshold. The experiment results are shown in Figure 5.7. The value of the threshold varies from 0.6 to 1.0. Since we are using local alignment to measure the similarity, reducing the threshold below 0.7 creates meaningless results. For example, a 0.6 threshold gives a 99% detection rate, but it also reports 84% false positives. If we further lower the threshold, both detection and false positive rates will reach 100%. It is apparent that the smaller the value of the threshold is, the higher the detection rate. However, the high detection rate results from false alerts and therefore does not help improve the overall accuracy. We find that a threshold of 0.9 gives the highest identification rate and best overall accuracy of detection.

Second, we vary the threshold for examining double segments. The result shown in Figure 5.8 is very similar to the result of individual segment examination except it illustrates a lower false positive rate. In general, experiments show that increasing the threshold reduces the false positive rate, and the detection rate is decreased because of severely increasing the threshold value. From results of both individual and double segments examination, the experiments suggest that setting the threshold within the range of 0.8 to 0.9 using double segments examination provides the highest accuracy.

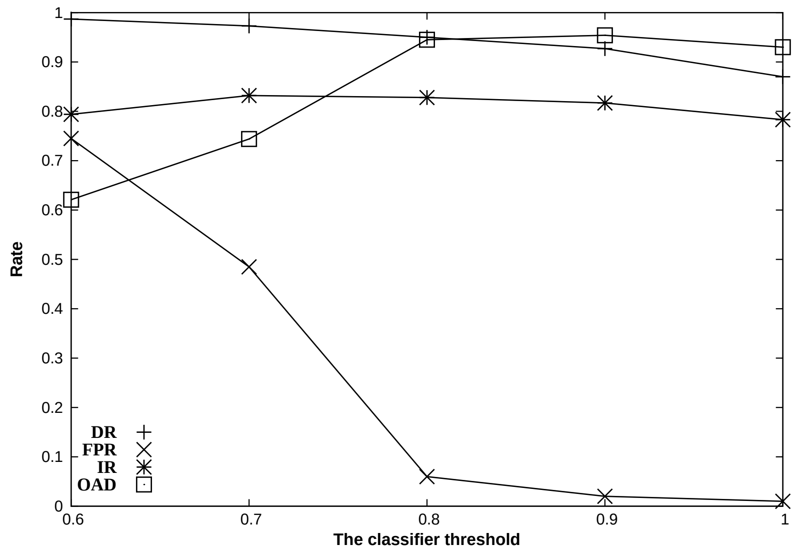


Figure 5.8: Double segments examination with varied alignment thresholds

5.3.2.2 Experiments against the entire dataset

The experiments so far only test malicious executables from the training set. The next step is to apply the features to all malicious executables. We randomly select 710 malicious executables as the training set which is 20% of the original dataset. From previous experiments, the n-gram length of 18 and the threshold value of 0.8 generate the best overall accuracy. We apply these parameter values to double segments examination to detect executables from the entire dataset. The results show that features generated this way can be used to achieve a detection rate of roughly 69.2% (2456/3548) while maintaining a 4.5% false positive rate. We definitely can use a large training set to increase the final detection rate, but this is misleading.

In summary, our experiments suggest that double segments examination using a threshold within the range of 0.8 to 0.9 provides the highest accuracy, a 95% overall accuracy of detection is possible and an identification rate of 83% can be achieved.

Chapter 6

Conclusions

In this thesis, we start with a hypothesis regarding the unique characteristics among members in the same family of malicious X86 executables. Our whole project is encircled with this assumption and we have applied techniques from data mining, information retrieval and bioinformatics. Feature-based characteristics are employed to solve the problems of detecting and identifying malicious executables. By introducing the automated identification system and the idea of extracting the "genetic" information from malicious executables, our research differs from previous related work that purely focuses on detection. The main contributions of our work can be summarized as follows:

1. We treat malicious attacks as biological organisms by transforming binary executables into genome-like s-opcode sequences. Alignment algorithms from bioinformatics and tools from other disciplines are combined in the training and testing processes of our system.

2. In contrast to traditional two-class classification, we use one-class classification. Exclusively examining the properties of malicious executables makes it possible to classify both malicious and benign programs.

3. Malicious samples are grouped into classes by the clustering algorithm. This approach provides an opportunity to automatically group malicious attacks instead of human experts.

4. Besides the problem of detecting malicious executables, our system also provides ways to identify unknown attacks by identifying their closest families.

Our approach provides an alternative view to the problem by using a combination of many techniques to discover "genetic" features from malicious executables. Our experimental results show that our system can accomplish an identification rate at approximately 83% while achieving an overall detection rate of roughly 96%.

6.1 Limitations

Even though our system has relatively high accuracy, there are still limitations:

1. There are four parameters in the system, which we believe is too many. Some of them are related to each other, but it is really complicated to control them all. Although we propose boundaries for some of the parameters, lots of experiments are still required in order to find the best values to achieve the best results.

2. The feature list has to be rebuilt after a certain period of time after detecting and identifying new attacks. If we want to distribute the features, when and how to update them become the problem.

6.2 Future work

All limitations listed above are our future work, and there are still many places for improvement.

First, the clustering algorithm is not good enough. In our experiments, the identification rate is affected by the conjunction of distinct clusters. Since DBSCAN cannot construct completely disjoint clusters, some families still contain very similar features after clustering. A possible solution could either improve the clustering algorithm or post-process the result clusters. We suggest proposing a threshold to measure inter-family similarity. After clustering the samples, we can merge some of the close families according to their similarities. Merging clusters could significantly improve the quality of features in contrast to what we did in Section 5.3.2 by merging the result features. However, the measurement of inter-family similarities is going to introduce more parameters to the system.

Second, the present alignment scoring scheme is not very accurate. We are currently using the simplest pair-wise scoring scheme. The value -1 denotes that a residue aligns with a different type of residue; the value -2 denotes that a residue aligns to an empty spot; the value 1 means that a residue matches with the same type of residue. In bioinformatics, researchers use better scoring matrixes such as PAM [10] and BLOSUM [18] that are calculated statistically to measure the score of the alignment. However, we do not have any supporting scoring matrix for the alignment of s-opcode sequences. If we can build a scoring matrix based on the sequence of malicious executables, it might improve the accuracy of our similarity measurement.

Last, host-based security is not effective any more. Oberheide et al. propose a distributed approach to subvert the architecture of current antivirus software [31]. By using the same concept, we could distribute the features of our system among network devices such as routers and firewalls across the Internet. First, we could deploy a special cache storing features in some network devices to examine network traffic to prevent attacks before their arrival to hosts. If this scheme works, we could further distribute this mechanism among all devices in the network. Instead of containing all features, network devices could include a hierarchical distribution of the feature set. Distinct levels of the network could contain different levels of features for blocking attacks with different severity. Features within each network device do not have to be static. A feature-routing protocol could be designed for devices to exchange features automatically according to their roles in the distributed security system.

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Appendix A

Intel opcode grouping

This section is the detailed table to illustrate how we group about two hundreds of Intel opcode. According to Intel® IA-32 Architectures Software Developer's Manual from [21], general purpose opcodes are grouped into 13 groups. With a slight modification, we group all the opcodes into 11 groups.

Intel group	**Opcode**	**Our group**
Data Transfer	**MOV**	Data Transfer(D)
Data Transfer	**CMOVE**	Data Transfer(D)
Data Transfer	**CMOVZ**	Data Transfer(D)
Data Transfer	**CMOVNE**	Data Transfer(D)
Data Transfer	**CMOVNZ**	Data Transfer(D)
Data Transfer	**CMOVA**	Data Transfer(D)
Data Transfer	**CMOVNBE**	Data Transfer(D)
Data Transfer	**CMOVAE**	Data Transfer(D)
Data Transfer	**CMOVNB**	Data Transfer(D)
Data Transfer	**CMOVB**	Data Transfer(D)
Data Transfer	**CMOVNAE**	Data Transfer(D)
Data Transfer	**CMOVBE**	Data Transfer(D)
Data Transfer	**CMOVNA**	Data Transfer(D)
Data Transfer	**CMOVG**	Data Transfer(D)
Data Transfer	**CMOVNLE**	Data Transfer(D)
Data Transfer	**CMOVGE**	Data Transfer(D)
Data Transfer	**CMOVNL**	Data Transfer(D)
Data Transfer	**CMOVL**	Data Transfer(D)

Continued on next page

Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
Data Transfer	**CMOVNGE**	Data Transfer(D)
Data Transfer	**CMOVLE**	Data Transfer(D)
Data Transfer	**CMOVNG**	Data Transfer(D)
Data Transfer	**CMOVC**	Data Transfer(D)
Data Transfer	**CMOVNC**	Data Transfer(D)
Data Transfer	**CMOVO**	Data Transfer(D)
Data Transfer	**CMOVNO**	Data Transfer(D)
Data Transfer	**CMOVS**	Data Transfer(D)
Data Transfer	**CMOVNS**	Data Transfer(D)
Data Transfer	**CMOVP**	Data Transfer(D)
Data Transfer	**CMOVPE**	Data Transfer(D)
Data Transfer	**CMOVNP**	Data Transfer(D)
Data Transfer	**CMOVPO**	Data Transfer(D)
Data Transfer	**XCHG**	Data Transfer(D)
Data Transfer	**BSWAP**	Data Transfer(D)
Data Transfer	**XADD**	Data Transfer(D)
Data Transfer	**CMPXCHG**	Data Transfer(D)
Data Transfer	**CMPXCHG8B**	Data Transfer(D)
Data Transfer	**PUSH**	Data Transfer(D)
Data Transfer	**POP**	Data Transfer(D)
Data Transfer	**PUSHA**	Data Transfer(D)
Data Transfer	**PUSHAD**	Data Transfer(D)
Data Transfer	**POPA**	Data Transfer(D)
Data Transfer	**POPAD**	Data Transfer(D)
Data Transfer	**CWD**	Data Transfer(D)
Data Transfer	**CDQ**	Data Transfer(D)
Data Transfer	**CBW**	Data Transfer(D)
Data Transfer	**CWDE**	Data Transfer(D)
Data Transfer	**MOVSX**	Data Transfer(D)
Data Transfer	**MOVZX**	Data Transfer(D)
Binary Arithmetic	**ADD**	Arithmetic(A)
Binary Arithmetic	**ADC**	Arithmetic(A)
Binary Arithmetic	**SUB**	Arithmetic(A)
Binary Arithmetic	**SBB**	Arithmetic(A)

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Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
Binary Arithmetic	**IMUL**	Arithmetic(A)
Binary Arithmetic	**MUL**	Arithmetic(A)
Binary Arithmetic	**IDIV**	Arithmetic(A)
Binary Arithmetic	**DIV**	Arithmetic(A)
Binary Arithmetic	**INC**	Arithmetic(A)
Binary Arithmetic	**DEC**	Arithmetic(A)
Binary Arithmetic	**NEG**	Arithmetic(A)
Binary Arithmetic	**CMP**	Arithmetic(A)
Decimal Arithmetic	**DAA**	Arithmetic(A)
Decimal Arithmetic	**DAS**	Arithmetic(A)
Decimal Arithmetic	**AAA**	Arithmetic(A)
Decimal Arithmetic	**AAS**	Arithmetic(A)
Decimal Arithmetic	**AAM**	Arithmetic(A)
Decimal Arithmetic	**AAD**	Arithmetic(A)
Logical	**AND**	Logical(L)
Logical	**OR**	Logical(L)
Logical	**XOR**	Logical(L)
Logical	**NOT**	Logical(L)
Shift and Rotate	**SAR**	Shift and Rotate(T)
Shift and Rotate	**SHR**	Shift and Rotate(T)
Shift and Rotate	**SAL**	Shift and Rotate(T)
Shift and Rotate	**SHL**	Shift and Rotate(T)
Shift and Rotate	**SHRD**	Shift and Rotate(T)
Shift and Rotate	**SHLD**	Shift and Rotate(T)
Shift and Rotate	**ROR**	Shift and Rotate(T)
Shift and Rotate	**ROL**	Shift and Rotate(T)
Shift and Rotate	**RCR**	Shift and Rotate(T)
Shift and Rotate	**RCL**	Shift and Rotate(T)
Bit and Byte	**BT**	Bit and Byte(H)
Bit and Byte	**BTS**	Bit and Byte(H)
Bit and Byte	**BTR**	Bit and Byte(H)
Bit and Byte	**BTC**	Bit and Byte(H)

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Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
Bit and Byte	**BSF**	Bit and Byte(H)
Bit and Byte	**BSR**	Bit and Byte(H)
Bit and Byte	**SETE**	Bit and Byte(H)
Bit and Byte	**SETZ**	Bit and Byte(H)
Bit and Byte	**SETNE**	Bit and Byte(H)
Bit and Byte	**SETNZ**	Bit and Byte(H)
Bit and Byte	**SETA**	Bit and Byte(H)
Bit and Byte	**SETNBE**	Bit and Byte(H)
Bit and Byte	**SETAE**	Bit and Byte(H)
Bit and Byte	**SETNB**	Bit and Byte(H)
Bit and Byte	**SETNC**	Bit and Byte(H)
Bit and Byte	**SETB**	Bit and Byte(H)
Bit and Byte	**SETNAE**	Bit and Byte(H)
Bit and Byte	**SETC**	Bit and Byte(H)
Bit and Byte	**SETBE**	Bit and Byte(H)
Bit and Byte	**SETNA**	Bit and Byte(H)
Bit and Byte	**SETG**	Bit and Byte(H)
Bit and Byte	**SETNLE**	Bit and Byte(H)
Bit and Byte	**SETGE**	Bit and Byte(H)
Bit and Byte	**SETNL**	Bit and Byte(H)
Bit and Byte	**SETL**	Bit and Byte(H)
Bit and Byte	**SETNGE**	Bit and Byte(H)
Bit and Byte	**SETLE**	Bit and Byte(H)
Bit and Byte	**SETNG**	Bit and Byte(H)
Bit and Byte	**SETS**	Bit and Byte(H)
Bit and Byte	**SETNS**	Bit and Byte(H)
Bit and Byte	**SETO**	Bit and Byte(H)
Bit and Byte	**SETNO**	Bit and Byte(H)
Bit and Byte	**SETPE**	Bit and Byte(H)
Bit and Byte	**SETP**	Bit and Byte(H)
Bit and Byte	**SETPO**	Bit and Byte(H)
Bit and Byte	**SETNP**	Bit and Byte(H)
Bit and Byte	**TEST**	Bit and Byte(H)
Control	**JMP**	Control(C)

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Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
Control	**JE**	Control(C)
Control	**JZ**	Control(C)
Control	**JNE**	Control(C)
Control	**JNZ**	Control(C)
Control	**JA**	Control(C)
Control	**JNBE**	Control(C)
Control	**JAE**	Control(C)
Control	**JNB**	Control(C)
Control	**JB**	Control(C)
Control	**JNAE**	Control(C)
Control	**JBE**	Control(C)
Control	**JNA**	Control(C)
Control	**JG**	Control(C)
Control	**JNLE**	Control(C)
Control	**JGE**	Control(C)
Control	**JNL**	Control(C)
Control	**JL**	Control(C)
Control	**JNGE**	Control(C)
Control	**JLE**	Control(C)
Control	**JNG**	Control(C)
Control	**JC**	Control(C)
Control	**JNC**	Control(C)
Control	**JO**	Control(C)
Control	**JNO**	Control(C)
Control	**JS**	Control(C)
Control	**JNS**	Control(C)
Control	**JPO**	Control(C)
Control	**JNP**	Control(C)
Control	**JPE**	Control(C)
Control	**JP**	Control(C)
Control	**JCXZ**	Control(C)
Control	**JECXZ**	Control(C)
Control	**LOOP**	Control(C)
Control	**LOOPZ**	Control(C)
Control	**LOOPE**	Control(C)

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Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
Control	**LOOPNZ**	Control(C)
Control	**LOOPNE**	Control(C)
Control	**CALL**	Control(C)
Control	**RET**	Control(C)
Control	**IRET**	Control(C)
Control	**INT**	Control(C)
Control	**INTO**	Control(C)
Control	**BOUND**	Control(C)
Control	**ENTER**	Control(C)
Control	**LEAVE**	Control(C)
Control	**RETF**	Control(C)
String	**MOVS**	String(S)
String	**MOVSB**	String(S)
String	**MOVS**	String(S)
String	**MOVSW**	String(S)
String	**MOVS**	String(S)
String	**MOVSD**	String(S)
String	**CMPS**	String(S)
String	**CMPSB**	String(S)
String	**CMPS**	String(S)
String	**CMPSW**	String(S)
String	**CMPS**	String(S)
String	**CMPSD**	String(S)
String	**SCAS**	String(S)
String	**SCASB**	String(S)
String	**SCAS**	String(S)
String	**SCASW**	String(S)
String	**SCAS**	String(S)
String	**SCASD**	String(S)
String	**LODS**	String(S)
String	**LODSB**	String(S)
String	**LODS**	String(S)
String	**LODSW**	String(S)
String	**LODS**	String(S)

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Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
String	**LODSD**	String(S)
String	**STOS**	String(S)
String	**STOSB**	String(S)
String	**STOS**	String(S)
String	**STOSW**	String(S)
String	**STOS**	String(S)
String	**STOSD**	String(S)
String	**REP**	String(S)
String	**REPE**	String(S)
String	**REPZ**	String(S)
String	**REPNE**	String(S)
String	**REPNZ**	String(S)
I/O	**IN**	I/O(I)
I/O	**OUT**	I/O(I)
I/O	**INS**	I/O(I)
I/O	**INSB**	I/O(I)
I/O	**INS**	I/O(I)
I/O	**INSW**	I/O(I)
I/O	**INS**	I/O(I)
I/O	**INSD**	I/O(I)
I/O	**OUTS**	I/O(I)
I/O	**OUTSB**	I/O(I)
I/O	**OUTS**	I/O(I)
I/O	**OUTSW**	I/O(I)
I/O	**OUTS**	I/O(I)
I/O	**OUTSD**	I/O(I)
Flag Control	**STC**	Flag Control(F)
Flag Control	**CLC**	Flag Control(F)
Flag Control	**CMC**	Flag Control(F)
Flag Control	**CLD**	Flag Control(F)
Flag Control	**STD**	Flag Control(F)
Flag Control	**LAHF**	Flag Control(F)
Flag Control	**SAHF**	Flag Control(F)

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Table A.1 continued from previous page

Intel group	**Opcode**	**Our group**
Flag Control	**PUSHF**	Flag Control(F)
Flag Control	**PUSHFD**	Flag Control(F)
Flag Control	**POPF**	Flag Control(F)
Flag Control	**POPFD**	Flag Control(F)
Flag Control	**STI**	Flag Control(F)
Flag Control	**CLI**	Flag Control(F)
Segment Register	**LDS**	Segment Register(R)
Segment Register	**LES**	Segment Register(R)
Segment Register	**LFS**	Segment Register(R)
Segment Register	**LGS**	Segment Register(R)
Segment Register	**LSS**	Segment Register(R)
Miscellaneous	**LEA**	Miscellaneous(M)
Miscellaneous	**NOP**	Miscellaneous(M)
Miscellaneous	**XLAT**	Miscellaneous(M)
Miscellaneous	**XLATB**	Miscellaneous(M)
Miscellaneous	**CPUID**	Miscellaneous(M)
Miscellaneous	**MOVBE**	Miscellaneous(M)

Table A.1: Opcode grouping

There is one group, Enter and Leave Instructions, from Intel manual that only contains two instructions, ENTER and LEAVE. Both of the ENTER and LEAVE instructions appear in the group of Control Transfer Instructions as well. According to their functionality, we ignore this group and categorize both instructions into the group of Control Transfer. Therefore, we obtain eleven groups by ignoring one group and combining Binary and Decimal Arithmetic groups into one.

Appendix B

numerical experimental results

This appendix contains a list of tables with experimental results referring to graphs in Chapter 5.

	***N*-gram**								
	8	10	12	14	16	18	20	22	24
DR	1	1	0.979	0.979	0.976	0.973	0.975	0.973	0.973
FPR	0.845	0.845	0.73	0.725	0.165	0.13	0.13	0.115	0.11
IR	0.717	0.689	0.807	0.814	0.786	0.823	0.828	0.789	0.82
OAD	0.578	0.578	0.625	0.627	0.906	0.922	0.923	0.929	0.932

Table B.1: Numerical results for individual segment examination referring to Figure 5.2.

	***N*-gram**								
	8	10	12	14	16	18	20	22	24
DR	0.976	0.939	0.938	0.952	0.931	0.928	0.928	0.921	0.925
FPR	0.835	0.490	0.545	0.57	0.12	0.12	0.1	0.095	0.095
IR	0.654	0.69	0.704	0.71	0.682	0.71	0.703	0.677	0.708
OAD	0.571	0.725	0.697	0.691	0.906	0.904	0.914	0.913	0.915

Table B.2: Numerical results for individual segment examination using the merged feature list referring Figure 5.3.

	***N*-gram**								
	8	10	12	14	16	18	20	22	24
DR	0.994	0.99	0.979	0.97	0.95	0.95	0.951	0.946	0.945
FPR	0.735	0.73	0.485	0.48	0.06	0.06	0.045	0.045	0.04
IR	0.718	0.69	0.763	0.765	0.803	0.828	0.752	0.792	0.797
OAD	0.63	0.63	0.747	0.745	0.945	0.945	0.953	0.951	0.953

Table B.3: Numerical results for double segments examination referring to Figure 5.4.

	***N*-gram**								
	8	10	12	14	16	18	20	22	24
DR	0.965	0.954	0.944	0.91	0.902	0.902	0.886	0.87	0.851
FPR	0.725	0.18	0.205	0.2	0.025	0.025	0.02	0.02	0.02
IR	0.641	0.693	0.73	0.677	0.658	0.692	0.677	0.677	0.651
OAD	0.62	0.887	0.87	0.855	0.939	0.939	0.933	0.925	0.916

Table B.4: Numerical results for double segments examination using the merged feature list referring to Figure 5.5.

	Number of segments			
	1	2	3	4
DR	0.973	0.95	0.937	0.93
FPR	0.15	0.06	0.11	0.205
IR	0.823	0.828	0.741	0.72
OAD	0.912	0.945	0.914	0.863

Table B.5: Numerical results for varying the number of examining segments referring to Figure 5.6.

	Threshold				
	60%	70%	80%	90%	100%
DR	0.994	0.992	0.973	0.958	0.896
FPR	0.84	0.69	0.13	0.075	0.055
IR	0.761	0.789	0.823	0.827	0.818
OAD	0.577	0.651	0.922	0.942	0.921

Table B.6: Numerical results for varying classifier threshold for one segment examination referring to Figure 5.7.

	Threshold				
	60%	70%	80%	90%	100%
DR	0.987	0.973	0.95	0.927	0.87
FPR	0.745	0.485	0.06	0.02	0.01
IR	0.794	0.832	0.828	0.817	0.783
OAD	0.621	0.744	0.945	0.954	0.93

Table B.7: Numerical results for varying classifier threshold for double segments examination referrring to Figure 5.8.