DATA MINING METHODS FOR MALWARE DETECTION

by

MUAZZAM AHMED SIDDIQUI
B.E. NED University of Engineering and Technology, 1999
M.S. University of Central Florida, 2004

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ABSTRACT

This research investigates the use of data mining methods for malware (malicious programs) detection and proposed a framework as an alternative to the traditional signature detection methods. The traditional approaches using signatures to detect malicious programs fails for the new and unknown malwares case, where signatures are not available. We present a data mining framework to detect malicious programs. We collected, analyzed and processed several thousand malicious and clean programs to find out the best features and build models that can classify a given program into a malware or a clean class. Our research is closely related to information retrieval and classification techniques and borrows a number of ideas from the field. We used a vector space model to represent the programs in our collection. Our data mining framework includes two separate and distinct classes of experiments. The first are the supervised learning experiments that used a dataset, consisting of several thousand malicious and clean program samples to train, validate and test, an array of classifiers. In the second class of experiments, we proposed using sequential association analysis for feature selection and automatic signature extraction. With our experiments, we were able to achieve as high as 98.4% detection rate and as low as 1.9% false positive rate on novel malwares.

To Asma, without you, this journey would not have been possible.

To Erum, for always keeping faith in me.

To Ammi & Abbu, for all your prayers.

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CHAPTER 1
INTRODUCTION

Computer virus detection has evolved into malicious program detection since Cohen first formalized the term *computer virus* in 1983 [Coh85]. Malicious programs can be classified into viruses, worms, trojans, spywares, adwares and a variety of other classes and subclasses that sometimes overlap and blur the boundaries among these classes [Szo05]. Both traditional signature based detection and generalized approaches can be used to identify these malicious programs. To avoid detection by the traditional signature-based algorithms, a number of stealth techniques have been developed by the malicious code writers. The inability of traditional signature based detection approaches to catch these new breed of malicious programs has shifted the focus of virus research to find more generalized and scalable features that can identify malicious behavior as a process instead of a single signature action.

We present a data mining approach to the problem of malware detection. Data mining has been a recent focus of malware detection research. Section 2.5 presents a literature review of the data mining techniques used for virus and worm detection. Our approach combines the ease of an automated syntactic analysis with the power of semantic level analysis requiring human expertise to reflect critical program behavior that can classify between malicious and benign programs. We performed initial experiments and developed a data mining framework that serves as a platform for further research.

1.1 Definitions

This section introduces various computer security terms to the reader. Since our work deals with computer virus and worms, a more detailed account of these categories is presented than any other area in security.

1.1.1 Computer Security

Computer security is the effort to create a secure computing platform, designed so that agents (users or programs) can only perform actions that have been allowed.

1.1.2 Malware

Any program that is purposefully created to harm the computer system operations or data is termed as malicious programs. Malicious programs include viruses, worms, trojans, backdoors, adwares, spywares, bots, rootkits etc. All malwares are sometimes loosely termed as virus (viruses, worms, trojans specifically) Commercial anti-malware products are still called antivirus.

1.1.3 Spam

Spam is abuse of electronic messaging systems to send unsolicited bulk messages Most widely recognized form is email spam. Also includes IM spam, blog spam, discussion forum spam, cell phone messaging spam etc.

1.1.4 Phishing

Phishing can be defined as a criminal activity using social engineering techniques. The most common example of phishing is an email asking to enter account/credit card information for e-commerce websites (ebay, amazon etc) and online banking.

1.1.5 Exploits

An exploit is a piece of software, a chunk of data, or sequence of commands that take advantage of a bug, glitch or vulnerability in order to cause unintended or unanticipated behavior to occur on computer software, hardware, or something electronic (usually computerized). This frequently includes such things as gaining control of a computer system or allowing privilege escalation or a denial of service attack.

1.2 Malware

Malware is a relatively new term that gets its name from malicious software. Many users are still unfamiliar with the term. Most of the time all malware are grouped under the umbrella term *virus*. For the detection of malware, the industry still use the term antivirus not antimalware, though the product caters all malware.

1.2.1 Virus

Computer virus is a self replicating code (including possibly evolved copies of itself) that infects other executable programs. Viruses usually need human intervention for replication and execution.

1.2.2 Worm

Computer worm is a self replicating stand alone program that spreads on computer networks. Worms usually do not need any extra help from a user to replicate and execute.

1.2.3 Trojan

Trojan horses or simply trojans are programs that perform some malicious activity under the guise of some normal program. The term is derived from the classical myth of the Trojan Horse.

1.2.4 Spyware

Spyware is computer software that is installed surreptitiously on a personal computer to intercept or take partial control over the user's interaction with the computer, without the user's informed consent.

1.2.5 Others

Other malware programs include *logic bombs*, that are an intended malfunction of a legitimate program, *rootkits*, that are a set of hacker tools intended to conceal running process from operating system, *backdoor*, that is a method to bypass normal computer authentication.

1.3 Virus

Computer virus is a self replicating code (including possibly evolved copies of itself) that infects other executable programs. Viruses usually need human intervention for replication and execution.

1.3.1 Classification by Target

This section define target as the means exploited by the virus for execution. Based upon the target viruses can be classified into three major classes.

1.3.1.1 Boot Sector Virus

Master Boot Record (Boot sector in DOS) is a piece of code that runs every time a computer system is booted. Boot sector virus infect the MBR on the disk, hence getting the privilege of getting executed every time the computer system starts up.

1.3.1.2 File Virus

File virus is the most common form of viruses. They infect the file system on a computer. File virus infect executable programs and are executed every time the infected program is run.

1.3.1.3 Macro Virus

Macro virus infect documents and templates instead of executable programs. It is written in a macro programming language that is built into applications like Microsoft Word or Excel. Macro virus can be automatically executed every time the document is opened with the application.

1.3.2 Classification by Self-Protection Strategy

Self-protection strategy can be defined as the technique used by a virus to avoid detection. In other words, the anti-antivirus techniques. Based upon self-protection strategies, viruses can be classified into the following categories.

1.3.2.1 No Concealment

Based upon the self-protection strategy the first category can be defined as the one without any concealment. The virus code is clean without any garbage instructions or encryption.

1.3.2.2 Code Obfuscation

Code obfuscation is a technique developed to avoid specific-signature detection. These include adding no-op instructions, unnecessary jumps etc, so the virus code look muddled and the signature fails.

1.3.2.3 Encryption

The next line of defense by the virus writers to defeat signature detection was code encryption. Encrypted viruses use an encrypted virus body and an unencrypted decryption engine. For each infection, the virus is encrypted with a different key to avoid giving a constant signature.

1.3.2.4 Polymorphism

Encrypted virus were caught by the presence of the unencrypted decryption engine that remain constant for every infection. This was cured by the mutating techniques. Polymorphic virus feature a mutation engine that generates the decryption engine on the fly. It consists of a decryption engine, a mutation engine and payload. The encrypted virus body and the mutating decryption engine refused to provide a constant signature.

1.3.2.5 Metamorphism

Metamorphic virus is a self mutating virus in its truest form of the word at it has no constant parts. The virus body itself changes during the infection process and hence the infected file represents a new generation that does not resemble the parent.

1.3.2.6 Stealth

Stealth techniques, also called code armoring, refers to the set of techniques developed by the virus writers to avoid the recent detection methods of activity monitoring, code emulation etc. The techniques include anti-disassembly, anti-debugging, anti-emulation, anti-heuristics etc.

1.4 Worm

A computer worm is a program that self-propagates across a network exploiting security or policy flaws in widely-used services.

Dan Ellis [Ell03], defined the life cycle of worms. Based upon the operations involved in each phase in the life cycle, worms can be classified into different categories. The following taxonomy was used by [WPS03] using similar factors.

1.4.1 Activation

Activation defines the means by which a worm is activated onto the target system. This is the first phase in a worms life cycle. Based upon activation techniques worms can be classified into the following classes.

1.4.1.1 Human Activation

This is the slowest form of activation that requires a human to execute the worm.

1.4.1.2 Human Activity-Based Activation

In this form of activation, the worm execution is based upon some action that the user perform not directly related to the worm such as launching an application program etc.

1.4.1.3 Scheduled Process Activation

This type of activation depends upon scheduled system processes such as automatic download of software updates etc.

1.4.1.4 Self Activation

This is the fastest form of activation where a worm initialize its execution by exploiting the vulnerabilities in the programs that are always running such as database or web servers.

1.4.2 Payload

The next phase in the worm's life cycle is payload delivery. Payload describes what a worm does after the infection.

1.4.2.1 None

Majority of worms do not carry any payload. The still cause havoc by increasing machine and network traffic load.

1.4.2.2 Internet Remote Control

Some worms open a backdoor on the victims machine thus allowing others to connect to that machine via internet.

1.4.2.3 Spam-Relays

Some worms convert the victim machine into a spam relay, thus allowing spammers to use it as a server.

1.4.3 Target Discovery

Once the payload is delivered, the worm start looking for new targets to attack.

1.4.3.1 Scanning Worms

Scanning worms scan for targets by scanning sequentially through a block of addresses or by scanning randomly.

1.4.3.2 Flash Worms

Flash worms use a pre-generated target list or a hit list to accelerate the target discovery process.

1.4.3.3 Metaserver Worms

This type of worms use a list of addresses to infect maintained by an external metaserver.

1.4.3.4 Topological Worms

Topological worms try to find the local communication topology by searching through a list of hosts maintained by application programs.

1.4.3.5 Passive Worms

Passive worms rely on user intervention or targets to contact worm for their execution.

1.4.4 Propagation

Propagation defines the means by which a worm spreads on a network. Based upon the propagation mechanism worms can be divided into the following categories.

1.4.4.1 Self-Carried

Self carried worms are usually self activated. They copy themselves to the target as part of the infection process.

1.4.4.2 Second Channel

Second channel worm copy their body after the infection by creating a connection from target to host to download the body.

1.4.4.3 Embedded

Embedded worms, embed themselves in the normal communication process as a stealth technique.

1.5 Trojans

While the words Trojan, worm and virus are often used interchangeably, they are not the same. Viruses, worms and Trojan Horses are all malicious programs that can cause damage to your computer, but there are differences among the three. A Trojan horse, also known as a Trojan, is a piece of malware, which appears to perform a certain action but in fact performs another such as transmitting a computer virus. At first glance it will appear to be useful software but will actually do damage once installed or run on your computer. Those on the receiving end of a Trojan horse are usually tricked into opening them because they appear to be receiving legitimate software or files from a legitimate source. When a Trojan is activated on your computer, the results can vary. Some Trojans are designed to be more annoying than malicious (like changing your desktop, adding silly active desktop icons) or they can cause serious damage by deleting files and destroying information on your system. Trojans are also known to create a backdoor on your computer that gives malicious users access to your system, possibly allowing confidential or personal information to be compromised. Unlike viruses and worms, Trojans do not reproduce by infecting other files nor do they self-replicate. Simply put, a Trojan horse is not a computer virus. Unlike such malware, it does not propagate by self-replication but relies heavily on the exploitation of an end-user. It is instead a categorical attribute, which can encompass many different forms of codes. Therefore, a computer worm or virus may be a Trojan horse. The term is derived from the classical story of the Trojan horse.

1.5.1 How Trojans Work

Trojans usually consist of two parts, a Client and a Server. The server is run on the victim's machine and listens for connections from a Client, which is used by the attacker. When the server is run on a machine it will listen on a specific port or multiple ports for connections from a Client. In order for an attacker to connect to the server they must have the IP Address of the computer where the server is being run. Some Trojans have the IP Address of the computer they are running on sent to the attacker via email or another form or communication. Once a connection is made to the server, the client can then send commands to the server; the server will then execute these commands on the victim's machine.

Today, with NAT infrastructure being very common, most computers cannot be reached by their external IP address. Therefore many Trojans now connect to the computer of the attacker, which has been set up to take the connections, instead of the attacker connecting to his or her victim. This is called a 'reverse-connect' Trojan. Many Trojans nowadays also bypass many personal firewall installed on the victims computer. (E.g. Poison Ivy)

Trojans are extremely simple to create in many programming languages. A simple Trojan in Visual Basic or C# using Visual Studio can be achieved in 10 lines of code or under. Probably the most famous Trojan horse is the AIDS TROJAN DISK that was sent to about 7000 research organizations on a diskette. When the Trojan was introduced on the system, it scrambled the name of all files (except a few) and filled the empty areas of the disk completely. The program offered a recovery solution in exchange of a bounty. Thus, malicious cryptography was born.

1.5.2 Trojan Types

Trojans are generally the programs that pose as legitimate programs on your computer and add a subversive functionality to it. That's when it's said a program is Trojaned. Common functions of Trojans include, but are not limited to, the following:

1.5.2.1 Remote Access Trojans

These are probably the most widely used trojans, just because they give the attackers the power to do more things on the victim's machine than the victim itself while being in front of the machine. Most of these trojans are often a combination of the other variations described below. The idea of these trojans is to give the attacker a total access to someone's machine and therefore access to files, private conversations, accounting data, etc.

1.5.2.2 Password Sending Trojans

The purpose of these trojans is to rip all the cached passwords and also look for other passwords you're entering and then send them to a specific mail address without the user noticing anything. Passwords for ICQ, IRC, FTP, HTTP or any other application that require a user to enter a login+password are being sent back to the attacker's email address, which in most cases is located at some free web based email provider.

1.5.2.3 Keyloggers

These trojans are very simple. The only thing they do is logging the keystrokes of the victim and then letting the attacker search for passwords or other sensitive data in the log file. Most of them come with two functions like online and offline recording. Of course, they could be configured to send the log file to a specific email address on a schedule basis.

1.5.2.4 Destructive

The only function of these trojans is to destroy and delete files. This makes them very simple and easy to use. They can automatically delete all the system files on your machine. The trojan is being activated by the attacker or sometimes works like a logic bomb and starts on a specific day and at specific hour. Denial Of Service (DoS) Attack Trojans These trojans are getting very popular these days, giving the attacker the power to start DDoS when having enough victims, of course. The main idea is that if you have 200 ADSL users infected and start attacking the victim simultaneously, this will generate a lot of traffic (more then the victim's bandwidth, in most cases) and its the access to the Internet will be shut down.

1.5.2.5 Mail-Bomb Trojan

This is another variation of a DoS trojan whose main aim is to infect as many machines as possible and simultaneously attack specific email address/addresses with random subjects and contents which cannot be filtered.

1.5.2.6 Proxy/Wingate Trojans

The interesting feature implemented in many trojans is turning the victim's computer into a proxy/wingate server available to the whole world or to the attacker only. It's used for anonymous Telnet, ICQ, IRC, etc., and also for registering domains with stolen credit cards and for many other illegal activities. This gives the attacker complete anonymity and the chance to do everything from your computer, and if he/she gets caught, the trace leads back to you.

1.5.2.7 FTP Trojans

These trojans are probably the most simple ones and are kind of outdated as the only thing they do is to open port 21 (the port for FTP transfers) and let everyone or just the attacker connect to your machine. Newer versions are password protected, so only the one who infected you may connect to your computer.

1.5.2.8 Software Detection Killers

There are such functionalities built into some trojans, but there are also separate programs that will kill ZoneAlarm, Norton Anti-Virus and many other (popular anti-virus/firewall) programs that protect your machine. When they are disabled, the attacker will have full access to your machine to perform some illegal activity, use your computer to attack others and often disappear. Even though you may notice that these programs are not working or functioning properly, it will take you some time to remove the trojan, install the new software, configure it and get back online with some sense of security.

1.6 Data Mining

Data mining has been defined as ”the nontrivial extraction of implicit, previously unknown, and potentially useful information from data” [FPM92] and ”the science of extracting useful information from large data sets or databases” [HH01].

Data mining can be divided into two broad categories.

- *Predictive data mining*, involves predicting unknown values based upon given data items.
- *Descriptive data mining*, involves finding patterns describing the data.

[Kan02] described the following tasks associated with data mining.

- *Classification*: the process of classifying data items into two or more pre defined classes.
- *Regression*: predicting the average value of one item on the basis of known value(s) of other item(s).
- *Clustering*: identifying a finite set of categories for the data.
- *Summarization*: finding a compact description of the data.
- *Dependency Modeling*: finding a local model that describes significant dependencies between variables.
- *Change and Deviation Detection*: discovering the most significant changes in the data set.

The final outcome of a data mining process is a model or a collection of models. A number of data mining techniques are available for the model building process. These techniques are not limited to the this final stage though. Any previous data mining stage e.g. data preprocessing may use these techniques.

CHAPTER 2
LITERATURE REVIEW

Chapter 1 provided a brief overview of the areas in computer security with special emphasis on viruses and worms. In this chapter, a literature survey is provided that structures the theoretical foundation for this research.

The term *computer virus* was first used in a science fiction novel by David Gerrold in 1972, When HARLIE Was One [Ger72], which includes a description of a fictional computer program called *virus* and was able to self-replicate. The first academic use of the term was claimed by Fred Cohen in 1983. The first published account of the term can be found a year later by Cohen in his paper *Experiments with Computer Viruses* [Coh84]. In his paper Cohen credits his advisor Professor Len Adleman for coining the term.

Though Cohen first used the term, some early accounts of viruses can be found. According to [Fer92], the first reported incidents of true viruses were in 1981 and 1982 on the Apple II computer. *Elk Cloner* is considered to be the first documented example of a virus in mid-1981. The first PC virus was a boot sector virus called Brain in 1986 [JH90].

Worm also owe their existence to science fiction literature. John Brunner's Shockwave Rider [Bru75] introduced us to *worm*, a program that propagates itself on a computer network. [SH82] claim the first use of the term in academic circles.

Much has been written about viruses, worms, trojans and other malwares since then, but now we shift our focus, from fiction to the real world where both malware and anti-malware are big commercial industries now [Gut07]. As this work is related to malware detection, this chapter provides a literature survey of the area.

2.1 Hierarchy

We applied a hierarchical approach to organize the research into a four tier categorization. The actual detection method sits at the top level of the hierarchy, followed by feature type, analysis type and detection strategy. This work categorizes the malware detection methods into four broad categories; scanning, activity monitoring, integrity checking and data mining. File features are the features extracted from binary programs, analysis type is either static or dynamic, and the detection type is borrowed from intrusion detection as either misuse or anomaly detection. It provides the reader with the major advancement in the malware research and categorizes the surveyed work based upon the above stated hierarchy, which served as the one of the contributions of this research.

2.1.1 Detection Method

The first three categories have been mentioned in previous works, [Spa94], [Bon96]. We have added data mining as a fourth category. We define the detection mechanism as a two stage process: data collection and the core detection method. The above defined categories compete for the, second, core detection part. Otherwise, it is possible that activity monitoring is employed to collect data and extract features which are later used, either to train a classifier or as signatures in a scanner, after further processing. Based upon this criteria, we define the four categories as follows:

2.1.1.1 Scanning

Scanning is the most widely used industry standard. Scanning involve searching for strings in files. The strings being searched are pre-defined virus signatures and support exact matching as well as wildcards to look for variants of a virus.

2.1.1.2 Activity Monitoring

Activity Monitoring is the latest trend in virus research where a file execution is monitored for traces of malicious behavior.

2.1.1.3 Integrity Checking

Integrity Checking creates a cryptographic checksum for each file on a system and periodically monitors for any variation in that checksum to detect possible changes caused by viruses.

2.1.1.4 Data Mining

Data Mining involves the application of a full suite of statistical and machine learning algorithms on a set of features derived from malicious and clean programs.

2.1.2 Feature Type

Feature type describes the input data to the malware detection system. The source of this data serves as a classification criteria for many intrusion and malware detection systems. If the data source is a workstation, the detection is called *Host-Based Detection*. If the source is the network, the detection is termed as *Network-Based Detection*. Features extracted from programs are used in a host based detection system. Various reverse engineering techniques at different stages are applied to extract byte sequences, instruction sequences, API call sequences etc. Network-based detection systems use network connection records as their data source.

2.1.2.1 N-grams

An N-gram is a sequence of bytes of fixed or variable length, extracted form the hexadecimal dump of an executable program. Here, we are using n-grams as a general term for both overlapping and non-overlapping byte sequences. For the sake of this paper, we define n-grams to remain at a syntactic level of analysis.

2.1.2.2 API/System calls

An application programming interface (API) is a source code interface that an operating system or library provides to support requests for services to be made of it by computer programs [api]. For operating system requests, API is interchangeably termed as system calls. An API call sequences captures the activity of a program and, hence, is an excellent candidate for mining of any malicious behavior.

2.1.2.3 Assembly Instructions

In more recent developments, it was emphasized that since n-grams fail to capture the semantics of the program, instruction sequences should be used instead. Unlike extracting n-grams from hexdumps, instructions need disassembling the binaries. We define, assembly instruction features to be instructions of variable and/or fixed lengths extracted from disassembled files.

2.1.2.4 Hybrid Features

A number of techniques used a collection of features, either for different classifiers, or as a hybrid feature set for the same classifier. The work done by [SEZ01b] used three different features including n-grams, DLL usage information and strings extracted from the binaries. Since this work was made famous for its usage of n-grams, we finally decided to place it in the n-grams section.

2.1.2.5 Network Connection Records

A network connection record is a set of information, such as duration, protocol type, number of transmitted bytes etc, which represents a sequence of data flow to and from a well defined source and target.

2.1.3 Analysis Type

The analysis can be performed at the source code level or at the binary level where only the executable program is available. As mentioned by [BDD99], it is unrealistic to assume the availability of source code for every program. The only choice left are executables with certain legal bindings. The information from the executables can be gathered either by running them or performing static reverse engineering or by using both techniques. The reverse engineering method is called *Static Analysis* while the process in which the program is actually executed to gather the information is called *Dynamic Analysis*. A mixed approach is also utilized if needed.

Static analysis offers information about programs control and data flow and other statistical features without actually running the program. Several reverse engineering methods are applied to create an intermediate representation of the binary code. These include disassembling, decompiling etc. Once the data is in human readable format, other techniques can be applied for further analysis. The major advantage of static analysis over its dynamic counterpart is that its free from the overhead of execution time. The major drawback lies inherently in any static reverse engineering method being an approximation of the actual execution. At any decision point, it is only *guessed* which branch will be taken at the execution time, though the guess is often accurate.

Dynamic analysis require running the program and monitoring its execution in a real or a virtual machine environment. Though this gives the actual information about the control and data flow, this approach severely suffers from the execution overhead. A mixed analysis approach is often used that run portions of the code when static analysis fails to make a proper decision [Sym97].

2.1.4 Detection Strategy

All of these methods involve a matching/mismatching criteria to work. Based upon this criteria the method can be classified as an anomaly detection, a misuse detection or a hybrid detection method. *Anomaly Detection* involves creating a normal profile of the system or programs and checking for any deviation from that profile. *Misuse Detection* involves creating a malicious profile in the form of an exact or heuristic signature and checking for that signature in the programs. *Hybrid Detection* does not create any profile but uses data from both clean and malicious programs to build classifiers. An anomaly detection system looks for mismatches from normal profile, while a misuse detection system looks for matches for virus signatures.

[SL02] presented an excellent survey of virus and worm research where they cited important work in virus and worm theory, modeling, analysis and detection. [IM07] offers a taxonomy with their survey of malware detection research. Besides the hierarchical structure, the classification presented in this dissertation differs from [IM07] at two points.

- It includes literature describing theory, modeling and analysis besides detection.
- The definition used for dynamic and static analysis is different as [IM07] classified between

the two approaches based upon the data they are operating on. If it is execution data e.g. system calls, instructions etc. then the analysis is termed as dynamic whereas static analysis operates on non execution items e.g. frequencies.

The following sections review virus and worm research literature using the criteria defined above.

2.2 Scanners

Scanners are the necessary component of every commercial-off-the-shelf (COTS) antivirus program. As [Szo05] indicated, the scanners have matured from simple string scanning to heuristic scanning. Nevertheless the concept remains the same. Searching for signatures in the target file.

2.2.1 Static Misuse Detection

Scanning or file scanning as it sometimes referred to, is essentially a static misuse detection technique. [Szo05] reviewed a number of scanning techniques in his book including *string scanning*, that is simply exact string searching, *wildcard scanning*, that allows for wildcards to cover variants (signatures with slight modification), *smart scanning*, that discards garbage instructions to thwart simple mutations, *nearly exact identification*, that accompany the primary virus signature with a secondary one to detect variants, *exact identification*, that uses as many secondary signatures as required to detect all the variants in a virus family and *heuristic scanning*, that scans for malicious behavior in the form of a series of actions.

As [Bon96] pointed out with the advent of polymorphic viruses, the virus-specific scanners have exhausted themselves, [Gry99] argued that the new wave in virus detection research will be heuristic scanners.

2.2.2 Hybrid Misuse Detection

[Sym97] used the mixed approach in their Bloodhound technology where they supplement static analysis with code emulation in their heuristic scanner. The scanner isolate logical region of the target program and analyze the logic for each region for a virus like behavior.

Symantec's Striker technology [Sym96] also used code emulation and heuristic scanning to detect polymorphic viruses. Virus profiles were created for each polymorphic engine and mutation engine that were based upon behavioral signatures.

2.3 Activity Monitors

Activity monitors use both static and dynamic analysis. Though the term static activity monitoring carry some sense of being an oxymoron, nevertheless, static analysis make it possible to monitor the execution of a program without actually running it.

2.3.1 API/System Calls

The most common method to monitor the activity of a program is to monitor the API/system calls it is making.

2.3.1.1 Static Anomaly Detection

[WD01] proposed a technique that created a control flow graph for a program representing its system call trace. At execution time this CFG was compared with the system call sequences to check for any violation.

2.3.1.2 Hybrid Anomaly Detection

[RKL03] proposed an anomaly based technique where static analysis was assisted by dynamic analysis to detect injected, dynamically generated and obfuscated code. The static analysis was used to identify the location of system calls within the program. The programs can be dynamically monitored later to verify that each observed system call is made from the same location identified using the static analysis.

2.3.1.3 Static Misuse Detection

[BDE99] used a static misuse detection scheme where they used program slicing to extract program regions that are critical from a security point of view. Prior to this, the programs were disassembled and converted to an intermediate representation. Once the program slices are obtained, their behavior was checked against a pre-defined security policy to detect the presence of maliciousness.

In a related work [BDD01] extracted an API call graph instead of the program slices to test against the security policy. The programs were disassembled first and then an control graph is created from the disassembly. Next step was to extract the API call graph from the control graph.

[LLO95] proposed the idea of *tell-tale* signs which were heuristic signatures of malicious program behaviors. They created an intermediate representation of the program under investigation in the form of control flow graph. The CFG was verified against the tell-tale signs to detect any malicious activity. The approach was implemented in their system called Malicious Code Filter (MCF).

[SXC04] implemented signatures in the form of API calls in a technique called Static Analysis for Vicious Executables (SAVE). The API calls from any program under investigation were compared against the signature calls using Euclidean distance.

2.3.1.4 Dynamic Anomaly Detection

[HFS98] proposed anomaly detection based upon sequence of system calls. A normal profile was composed of short sequence of system calls. Hamming distance was used to compare the sequences of system calls. Large Hamming distances indicated longer sequences and were thus marked as anomalous.

In a similar approach [SBB01] used Finite State Automata (FSA) to represent system call sequences. The FSAs were created by executing the programs multiple times and recording the system calls. Anomalies were detected at runtime when a system call is made that did not have a transition from a given FSA state.

Similarly [KRL97] proposed an idea of trace policy which was essentially a sequence of system calls in time. Any deviation from this trace policy was flagged as anomaly. They implemented this approach in a system called Distributed Program Execution Monitor (DPEM).

[MP05] presented a tool called Dynamic Information Flow Analysis (DIFA) to monitor method calls at runtime for Java applications. Normal behavior was implemented in the form of an information flow policy. Deviations from this policy at runtime were marked as anomalies.

[SB99] created a system call detection engine that compares system calls modeled previously with the system calls made at runtime. An intermediate representation of a program was captured in the form of an Auditing Specification Language (ASL). The ASL was compiled into a C++ class that was then compiled and linked to create a model of a system call in the system call detection engine.

2.3.1.5 Hybrid Misuse Detection

[Mor04] presented an approach to detect encrypted and polymorphic viruses using static analysis and code emulation. The emulation part was implemented to extract system calls information from encrypted and polymorphic viruses once they are decrypted in the emulation engine. Next phase is the static analysis that compares the system calls to a manually defined security policy implemented in the form of Finite State Automata (FSA).

2.3.1.6 Dynamic Misuse Detection

[DGP01] proposed a dynamic monitoring system that enforces a security policy. The approach was implemented in a system called *DaMon*.

[Sch98] presented enforceable security policies in the form of Finite State Automata. The system was monitored at runtime for any violations against the security automata.

2.3.2 Hybrid Features

Some researchers have employed a hybrid set of features for activity monitoring.

2.3.2.1 Static Misuse Detection

[CJS05] created malware signatures using a 3-tuple template of instructions, variables and symbolic constants. An intermediate representation was obtained for any program under investigation.

Next step converted this intermediate representation to a control flow graph. This control flow graph was compared against the template control flow graph using a def-use pair. The program was deemed malicious if a def-use pair for the program under investigation matches a def-use pair from the template.

2.3.2.2 Dynamic Misuse Detection

[EAA04] proposed a dynamic signature based detection system that used behavioral signatures of worm operations. The system was monitored at runtime for these signatures. One such signature described by the authors was a server changing into client. As a worm needs to find other hosts after infecting a server, it sends request from a server thereby converting to a client. Another signature checks for same data flow links from in and out of a network node as a worm needs to send similar data across the network.

2.3.3 Network Data

Malware detection overlaps with intrusion detection if a network based detection mechanism is used. Activity monitoring can be carried out to monitor network data for traces of a spreading malware, especially worms.

2.3.3.1 Dynamic Anomaly Detection

[Naz04] discussed different traffic analysis techniques for worm detection. Three schemes were described for data collection; direct packet capture using tools such as tcpdump, using built-in SNMP statistics from switches, hubs routers etc. and using flow based exports from routers and switches. The techniques described for dynamic anomaly detection in the network traffic were:

- *Growth in traffic volume*: An exponential growth in network traffic volume is an indication of a worm.
- *Rise in the number of scans and sweeps*: Another anomaly in the normal traffic pattern is the rise in the number of scan and probe activities which are an indication of a worm scanning for new targets.
- *Change in traffic patterns for some hosts*: Worms change the behavior of traffic for some hosts. A server might start working as a client and start sending requests to other hosts in the system.

2.4 Integrity Checkers

The main force behind integrity checking programs is to protect programs against any modifications by viruses. To obtain this, a checksum based upon the program contents is computed and stored in encrypted form within or outside the program. This checksum is periodically compared against checksums obtained at later points in time. [Rad92] presented an excellent survey of checksumming techniques.

2.4.1 Static Anomaly Detection

Integrity checkers are inherently static anomaly detection systems where a checksum of the contents of the program under investigation is compared against a previously obtained checksum. Any difference would signal an anomaly.

Cohen argued and demonstrated in [Coh91], [Coh94] that integrity checking of computer files is the best generic methods.

2.5 Data Mining

Data mining has been the focus of many virus researchers in the recent years to detect unknown viruses. A number of classifiers have been built and shown to have very high accuracy rates. The most common method of applying data mining techniques for malware detection start from generating a feature set. These features include hexadecimal byte sequences (later termed as n-grams in the paper), instruction sequences, API/system call sequences etc. The number of features extracted from the files is usually very high. Several techniques from text classification [YP97] have been employed to select the best features. Some other features include printable strings extracted from the files and some operating system dependent features such as DLL information.

The following sections provide literature review of data mining techniques used in the virus detection research. Some of these methods might use activity monitoring as a data collection method but data mining remains the principal detection method.

2.5.1 N-grams

N-grams is the most common feature used by the data mining methods. Here, we are using n-grams as a general term for both overlapping and non-overlapping byte sequences. For the sake of this work, we define n-grams to remain at a syntactic level of analysis.

2.5.1.1 Dynamic Misuse Detection

The first major work that used data mining techniques for malware research was an automation of signature extraction for viruses by [KA94]. The viruses were executed in a secured environment to infect decoy programs. Candidate signatures of variable length were extracted by analyzing the infected regions in these programs that remained invariant from one program to another. Signatures with lowest estimated false positive probabilities were chosen as the best signatures. To handle large, rare sequences, a trigram approach was borrowed from speech recognition where the large sequence was broken down into trigrams. Then, a simple approximation formula can be used to estimate the probability of a long sequence by combining the measured frequencies of the shorter sequences from which it is composed. To measure algorithms effectiveness candidate signatures were generated and their estimated and actual probabilities were compared. Most of the signatures fell short of this criteria and were considered bad signatures. Another measure of effectiveness was false positive record of signatures, which was reported to be minimal. However no numerical values were provided for estimated and actual probability comparison and false positives.

2.5.1.2 Dynamic Hybrid Detection

This was followed by the pioneering work of [TKS96] where they extended the n-grams analysis to detect boot sector viruses using neural networks. The n-grams were selected based upon the frequencies of occurrence in viral and benign programs. Feature reduction was obtained by generating a 4-cover such that each virus in the dataset should have at least 4 of these frequent n-grams present in order for the n-grams to be included in the dataset. A validation set classification accuracy of 80-80% was obtained on viral boot sector while clean boot sectors received a 100%

classification.

In the continuation of their work in [TKS96], [AT00] used n-grams as features to build multiple neural network classifiers and adopted a voting strategy to predict the final outcome. Their dataset consisted of 53902 clean files and 72 variant sets of different viruses. For clean files, n-grams were extracted from the entire file while only those portions of a virus file are considered that remain constant through different variants of the same virus. A simple threshold pruning algorithm was used to reduce the number of n-grams to use as features. The results they reported are not very promising but it still presents a thorough work using neural networks.

2.5.1.3 Static Anomaly Detection

[WS05] proposed a method of classifying various file types based upon their fileprints. An n-gram analysis method was used and the distribution of n-grams in a file was used as its fileprint. The distribution was given by byte value frequency distribution and standard deviation. These fileprints represented the normal profile of the files and were compared against fileprints taken at a later time using simplified Mahalanobis distance. A large distance indicated a different n-gram distribution and hence maliciousness.

2.5.1.4 Static Hybrid Detection

The most recent work that brought the data mining techniques for malware detection to the limelight was done by [SEZ01b]. They used three different types of features and a variety of classifiers to detect malicious programs. Their primary dataset contained 3265 malicious and 1001 clean programs. They applied RIPPER (a rule based system) to the DLL dataset. Strings data was used to fit a Naive Bayes classifier while n-grams were used to train a Multi-Naive Bayes classifier with a voting strategy. No n-gram reduction algorithm was reported to be used. Instead data set partitioning was used and 6 Naive-Bayes classifiers were trained on each partition of the data. They used different features to built different classifiers that do not pose a fair comparison among the classifiers. Naive-Bayes using strings gave the best accuracy in their model.

Extending the same ideas [SEZ01a], created MEF, Malicious Email Filter, that integrated the scheme described in [SEZ01b] into a Unix email server. A large dataset consisting of 3301 malicious and 1000 benign programs was used to train and test a Naive-Bayes classifier. N-grams were extracted by parsing the hexdump output. For feature reduction the dataset was partitioned into 16 subsets. Each subset is independently trained on a different classifier and a voting strategy was used to obtain the final outcome. The classifier achieved 97.7% detection rate on novel malwares and 99.8% on known ones. Together with [SEZ01b], this paved the way for a plethora of research in malware detection using data mining approaches.

A similar approach was used by [KM04], where they built different classifiers including Instance-based Learner, TFIDF, Naive-Bayes, Support vector machines, Decision tree, boosted Naive-Bayes, SVMs and boosted decision tree. Their primary dataset consisted of 1971 clean and 1651 malicious programs. Information gain was used to choose top 500 n-grams as features. Best efficiency was reported using the boosted decision tree J48 algorithm.

[ACK04b] created class profiles of various lengths using different n-gram sizes. The class profile length was defined by the number of most frequent n-grams within the class. These frequent n-grams from both classes were combined to form, what they termed as relevant n-grams, for each profile length. Experiments were conducted on a set of 250 benign and 250 malicious programs.

For classification, Dampster-Shafer theory of Evidence was used to combine SVM, decision tree and IBK classifiers. They compared their work with [KM04] and reported better results.

In a related work, [ACK04a] used a Common N-Gram classification method to create malware profile signatures. Similar class profiles of various lengths using different n-gram sizes were created. The class profile length was defined by the number of most frequent n-grams with their normalized frequencies. A k-nearest neighbor algorithm was used to match a new profile instance with a set of already created signature profiles. They experimented with combinations of different profile lengths and different n-gram sizes. A five-fold cross validation method gave 91% classification accuracy.

Building upon their previous work in [Yoo04], [YU06] experimented with a larger data collection with 790 infected and 80 benign files, thus landing in our static hybrid detection category. N-grams were extracted from octal dump of the program, instead of usual hexdump and then converted to short integer values for SOM input. Using the SOM algorithms, VirusDetector was created that was used as a detection tool, instead of a visualization tool. VirusDetector achieved an 84% detection with a 30% false positive rate. the technique is able to cater polymorphic and encrypted viruses.

In a recent n-grams based static hybrid detection approach [HJ06] used intra-family and inter-family support to select and reduce the number of features. First, the most frequent n-grams within each virus family were selected. Then the list was pruned to contain only those features that have a support threshold higher than a given value amongst these families. This was done for various n-gram sizes. Experiments were carried out on a set of 3000 programs, 1552 of which were viruses, belonging to 110 families, and 1448 were benign programs. With ID3, J4 decision tree, Naive

Bayes and SMO classifiers, they compared their results with [SEZ01b] and claimed better overall efficiency. In search of optimal feature selection criteria, they experimented with different n-gram sizes and various values of intra-family and inter-family selection thresholds. They reported better results with shorter sequences. For longer sequences, a low inter-family threshold gave better performance. Better performance was also noted, when features were in excess of 200.

2.5.1.5 Static Misuse Detection

[Yoo04] presented a static misuse method to detect viruses using self organizing maps (SOM). They claimed that each virus has its own DNA like character that changes the SOM projection of the program that it infects. N-grams were extracted from the infected programs and SOMs were trained on this data. Since the method only looks for change in the SOM projection as a result of virus infection, it is able to detect polymorphic and metamorphic malwares, even in the encrypted state. Experiments were performed on a small set of 14 viral samples. The algorithm was successfully able to detect virus patterns in the infected files.

2.5.2 API/System calls

Though API/system call monitoring is the most common method in activity monitoring systems, a number of data mining methods also employ these, to build classifiers.

2.5.2.1 Dynamic Anomaly Detection

[MS05] added a temporal element to the system call frequency and calculated the frequency of system call sequences within a specific time window. These windows were generated for independent peers and a correlation among them indicated a fast spreading worm. Similarity measures were calculated using edit distance on ordered sets of system calls windows and intersection on unordered sets. These similarity measures gave the probabilities of two peers running the same worm invoking the same system call sequence in a given time window. The technique works well for polymorphic worms.

2.5.2.2 Static Hybrid Detection

In the malware detection realm, the most important work using API sequences was done by [SXC04]. They created a signature based detection system called Static Analyzer of Vicious Executables (SAVE) that compares API sequences extracted from programs to sequences from a signature database. For matching cosine measure, extended Jaccard measure and Pearson correlation measures were used. Final outcome was the mean of all three measures. Using these statistical measures for similarity enables SAVE to capture polymorphic and metamorphic malwares, for which, traditional signature detection system are deemed incapable of.

In a recent approach using API execution sequences, [YWL07] developed Intelligent Malware Detection System (IMDS). IMDS used Objective-Oriented Association (OOA) mining based classification and is composed of a PE parser, an OOA rule generator and a rule based classifier. For rule generation, they developed a OOA Fast FP-Growth algorithm, an extension of FP-Growth algorithm, and claimed better performance than the Apriori algorithm for association rule generation. The experiments were conducted on a large data set consisted of 17366 malicious and 12214 benign executables. For detection, a Classification Based on Association rules (CBA) technique was used. They compared their results with popular anti-virus programs like Norton, McAfee, Dr

Webb and Kaspersky and claimed better efficiency on polymorphic and unknown virus detection. The IMDS was able to detect all the polymorphic viruses and 92% of the unknown viruses. For polymorphic virus detection a different dataset was created where for each virus a set of polymorphic versions were generated. IMDS was also compared with Naive-Bayes, J48 decision tree and SVM classifiers and proved to churn out better detection and false positive rates. A smaller dataset was sampled from the collection for this comparison.

2.5.3 Assembly Instructions

The first major work to include instructions in its features was Portable Executable Analysis Tool (PEAT) [WSS02]. PEAT used a number of other features also, so it will be explained in detail in the Hybrid Features section. Similarly [MKT07] used instruction sequences along with other features and will be discussed in the Hybrid Features section.

2.5.3.1 Static Misuse Detection

[KWL05] created a malware phylogeny using permutation of code. They extracted instruction sequences of fixed length (termed as n-grams in their paper) and created two datasets. First dataset contained all the n-grams while the second dataset featured n-perms, all possible permutations of the n-grams in the first dataset. Similarity scores were calculated using a combination of TFxIDF weighting and cosine similarity measures. Clustering on these similarity scores provided the phylogeny model. To measure the effectiveness of each feature set, an experiment was conducted on a small data collection of 170 samples. The results showed that n-perms produce higher similarity scores for permuted programs and produce comparable phylogeny models. A study was conducted to explore how the generated malware phylogeny can be used in naming and classification of malwares. Using a small dataset of 15 samples including an unknown malware, the created phylogeny model successfully identified the unknown malware family. The phylogeny model was also able to identify naming inconsistencies for names assigned by commercial antiviruses.

2.5.3.2 Static Hybrid Detection

Another recent work that solely used variable length instruction sequences, was [SWL08]. After disassembly, instruction sequences were selected based upon the frequency of occurrence in the entire dataset. A Chi-Square test was performed for feature reduction. They built logistic regression, neural network and decision tree models and reported 98.4% detection rate with decision tree model.

2.5.4 Hybrid Features

A number of techniques used a collection of features, either for different classifiers, or as a hybrid feature set for the same classifier. The work done by [SEZ01b] used three different features including n-grams, DLL usage information and strings extracted from the binaries. Since this work was made famous for its usage of n-grams, we finally decided to place it in the n-grams section.

2.5.4.1 Static Anomaly Detection

[WSS02] developed PEAT (The Portable Executable Analysis Tool) to detect structural anomalies inside a program. PEAT rested on the basic principle that the inserted code in a program disrupts its structural integrity and hence by using statistical attributes and visualization tools this can be detected. The visualization tools plot the probability of finding some specific subject of interest in a particular area of the program. These subjects include sequence of bytes, their ASCII representation, their disassembly representation and memory access via register offsets. Statistical analysis was done on instruction frequencies, instruction patterns, register offsets, jump and call offsets, entropy of opcode values and code and ASCII probabilities. The experimental results were provided for only one malicious program.

2.5.4.2 Static Hybrid Detection

[MKT07] created a hybrid feature set using n-grams, instruction sequences and API calls. For feature selection, Information Gain was used. They experimented with two non-disjoint datasets. The first dataset contains a collection of 1,435 executables, 597 of which are benign and 838 are malicious. The second dataset contains 2,452 executables, having 1,370 benign and 1,082 malicious executables. In addition to the hybrid feature set (HFS), two other datasets were also created using n-grams (BFS) and assembly features (AFS). The accuracy of each of the feature sets was tested by applying a three-fold cross validation using classifiers such as SVM, decision tree, Naive Bayes, Bayes Net and Boosted decision tree. Experiments were performed for different n-gram sizes. For the first dataset, best efficiency was reported for HFS using an n-gram size of 6, resulting in 97.4% classification accuracy. HFS performed better for the second dataset too. To compare classification accuracies of the HFS and BFS, a pairwise two-tailed t-test was performed. The test statistically proved that HFS performed slightly better than BFS.

2.5.4.3 Hybrid Hybrid Detection

[WHS06] presented a surveillance spyware detection system that used APIs and DLL usage information and changes in registry, system files/folders and network states to detect spywares. They collected 1147 samples over a period of time to experiment with. Information Gain and SVM runs were used for feature selection. An SVM was used to classify spywares from benign programs. They reported 97.9% detection with a 0.68% false positive rate.

CHAPTER 3
METHODOLOGY

This chapter provides a description of, the much required, theoretical foundation for our work and the general framework that we developed to carry out our experiments.

3.1 Research Contribution

[Kan02] describes the data mining process to be consisted of five steps.

- Problem statement and formulation of hypothesis
- Data collection
- Data preprocessing
- Model estimation
- Model interpretation

Once the problem was clearly stated as the malware detection problem, one of the main contributions of this work comes from the data collection step. We introduce the idea of using variable length instructions sequence, extracted from binary files as the primary classification feature. Unlike fixed length instructions or n-grams, the variable length instructions inherently capture the programs control flow information as each sequence reflects a control flow block.

The difference among our approach and other static analysis approaches mentioned in the related research section are as follows.

The framework we developed, used applied data mining as a complete process from problem statement to the model interpretation step. [Bon93] discussed the importance of maintaining a clean virus collection for research. We subjected the data to a malware analysis process where thousands of malwares as well as clean files were analyzed for corrupt and duplicate elements and packed, encrypted, polymorphic and metamorphic forms. Although data preparation is a very important step in a data mining process, most of the existing static analysis techniques mentioned in the 2 chapter did not discuss this step in detail except [WSS02]. Also, all features were sequences of instructions extracted by the disassembly instead of using fixed length of bytes such as n-gram. The advantages are:

1. The instruction sequences include program control flow information, not present in n-grams.
2. The instruction sequences capture information from the program at a semantic level rather than syntactic level.
3. These instruction sequences can be traced back to their original location in the program for further analysis of their associated operations.
4. The variable length instruction sequences inherently result in a smaller feature set as compared to n-grams.
5. A significant number of sequences that appeared in only clean program or malwares can be eliminated to speed up the modeling process.
6. The classifier obtained can achieve more than 98% detection rate for new and unseen malwares.

7. Instruction sequences are a domain-independent feature and the technique can be used without any modification to detect every type of malwares including virus, trojans, spywares etc.

The last four points have been experimentally proven in this work. It is worth noting that a dataset prepared for a neural network classifier might not be suitable for other data mining techniques such as decision tree or random forest. In this work, we compared different feature selection methods and different classifiers for optimum performance.

3.2 Learning Theory

The particular problem of labeling a program as malware or clean is an example of the general classification problem, which in turn belongs to a wider class of dependency estimation problems. Learning theory describes one approach to such problems. The process of learning from data manifests itself in two general steps.

- Learning or estimating dependencies, from given input data samples
- Using the estimated dependencies to predict output for new data samples

In the terms of statistical inference, the first step is referred to as *induction* (progressing from particular cases of input values to a general model), while the second step is *deduction* (progressing from a general model to particular cases of output values) [Kan02].

These two steps are implemented in a learning machine. The implementation details differ, but the main task is to learn from given data samples by searching through an n-dimensional space to form an acceptable generalization. The inductive learning, thus, takes the form of finding a function that estimates the dependencies in the data. More formally, given a collection of samples (x_i, $f(x)_i$), the inductive learning process returns a function h(x) that approximates f(x). The approximating function can be defined in terms of its internal parameters, and a more precise form can be expressed as h(X, w), where X is the input vector and w is the functions parameters. The quality of the approximation can be measured in terms of a function that can compare the output produced by the learning machine to the actual output. Such a function is called the *loss function L(y, h(X, w))*, where y is the actual output of the system, X is the set of inputs, w is the parameters of the approximation function, h(X, w) is the output produced by the learning machine using X as inputs and w as internal parameters.

The expected value of the loss function is called the *risk functional R(w)*

$$R(w) = \int \int L(y, h(X, w)) p(X, y) dX dy \tag{3.1}$$

where L(y, h(X, w)) is the loss function and p(X, y) is the unknown probability distribution of the input X. Inductive learning can be redefined as the process of estimating the function h(X, w_{opt}) that minimizes R(w), over the set of functions supported by the learning machine and using only the input data and not knowing the probability distribution p(X, y).

3.3 Vector Space Model

We used the *vector space model* to create our feature set. In information retrieval, a vector space model defines documents as vectors (or points) in a multidimensional Euclidean space where the axes (dimensions) are represented by terms. Depending upon the the type of vector components (coordinates), there are three basic versions of this representation: Boolean, term frequency (TF) and term frequency - inverse document frequency (TFIDF), [ML07]. In our case, the programs and instruction sequences mapped to documents and terms, respectively. Using these program vectors, we created a term-document matrix where programs were arranged in rows, while columns represent the potential features (instruction sequences). For feature selection we used boolean representation of the matrix, where a 1 represented presence, while 0 represented absence, of an instruction sequence in a given program. Assume there are n programs p_1, p_2, ... p_n, and m instruction sequences s_1, s_2, ..., s_m. Let n_{ij} be the number of times a sequence s_i was found in a program p_j. In the boolean representation a program p_j is represented as an m component vector, $p_j = p_j^1, p_j^2, \ldots p_j^m$,

$$p_j^i = \begin{cases} 0 & \text{if } n_{ij} = 0 \\ 1 & \text{if } n_{ij} > 0 \end{cases} \tag{3.2}$$

Using the boolean definition of p_j^i, let N_{ij} be the total number of times a sequence s_i was present in the program collection.

$$N_{ij} = \sum_{j=1}^{n} p_j^i \tag{3.3}$$

In order to be selected, a sequence s_i, must have its N_{ij} greater than a defined threshold. This threshold was set to 10% of the total number of the programs, as it is a common practice in data mining for defining unary variables.

$$N_{ij} > \frac{n}{10} \tag{3.4}$$

3.4 Models

We used an array of classification models in our experiments. The foundation of the inductive learning implemented in these models has been discussed in the learning theory section. Here, a short description of each of these models is provided.

3.4.1 Logistic Regression

Regression is a statistical technique that determines the best model that can relate an independent variable to various independent variables. Logistic regression is the type of regression that tries to estimate the probability that the dependent variable will have a given value, instead of estimating the value of the variable.

3.4.2 Neural Network

A neural network is a network of simple processing elements (neurons) that can exhibit complex global behavior, determined by the connections between the processing elements and element parameters. It can be used to model complex nonlinear relationship between inputs and outputs by learning from experiential knowledge expressed through the connections between the processing elements.

3.4.3 Decision Tree

A decision tree recursively partitions the predictor space to model the relationship between predictor variables and categorical response variable. Using a set of input-output samples a tree is constructed. The learning system adopts a top-down approach that searches for a solution in a part of the search space. Traversing the resultant tree gives a set of rules that finally classified each observation into the given classes.

3.4.4 Support Vector Machines

SVMs are set of tools for finding the optimal hyperplane that separates the linear or non-linear data into two categories [Web05]. The separating hyperplane is the hyperplane that maximizes the distance (margin) between the two parallel hyperplanes. The non-linear classification is obtained by applying a kernel function to these maximum-margin hyperplanes.

3.4.5 Bagging

Bagging or Bootstrap Aggregating is a meta-algorithm to improve classification and regression models in terms of accuracy and stability. Bagging generates multiple versions of a classifier and uses plurality vote to decide for the final class outcome among the versions. The multiple versions are created using bootstrap replications of the original dataset. Bagging can give substantial gains in accuracy by improving on the instability of individual classifiers. [Bre96]

3.4.6 Random Forest

Random forest provides a degree of improvement over Bagging by minimizing correlation between classifiers in the ensemble. This is achieved by using bootstrapping to generate multiple versions of a classifier as in Bagging but employing only a random subset of the variables to split at each node, instead of all the variables as in Bagging. Using a random selection of features to split each node yields error rates that compare favorably to Adaboost, but are more robust with respect to noise.[Bre01]

Besides classification, random forest also gives the important variables used in the model. The importance is calculated as the mean decrease in accuracy or mean decrease in Gini index if the variable is removed from the model.

3.4.7 Principal Component Analysis

Another technique that was used for feature reduction in our experiments was Principal Component Analysis (PCA). PCA is a technique used to reduce multidimensional data sets to lower dimensions for analysis. PCA involves the calculation of the eigenvalues that represent the linear combination of original variables such that the lower order eigenvalues explain most of the variance in the data.

3.5 Performance Criteria

We tested the models using the test data. Confusion matrices were created for each classifier using the actual and predicted responses. The following four estimates define the members of the matrix.

True Positive (TP): Number of correctly identified malicious programs.

False Positive (FP): Number of wrongly identified benign programs.

True Negative (TN): Number of correctly identified benign programs.

False Negative (FN): Number of wrongly identified malicious programs.

The performance of each classifier was evaluated using the detection rate, false alarm rate and overall accuracy that can be defined as follows:

Detection Rate: Percentage of correctly identified malicious programs.

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

False Alarm Rate: Percentage of wrongly identified benign programs.

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

Overall Accuracy: Percentage of correctly identified programs.

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

CHAPTER 4
SUPERVISED LEARNING EXPERIMENTS

This chapter describes the experiments that are distinguished by the use of supervised learning algorithms on a collection of datasets that used the frequency of occurrence of a feature as a primary selection criterion. In principle, our approach is similar to other data mining approaches described in the previous chapter. Our major contribution comes from the unique set of features that we identified by analyzing the malware samples and the application of data mining as a complete process from problem statement and data collection to model interpretation and drawing conclusions. In these experiments we worked with different malware types and compared different classification and feature selection methods. We also compared our feature type with other the most common feature type, used in data mining for malware detection research.

The basic unit of our analysis is a computer file. A file can be defined as a block of arbitrary information, or resource for storing information that is available to a computer program. Based upon the contents, files can be divided into two major categories; *data files*, that store information and *executable files*, that are composed of a collection of instructions describing some task, to be carried out by a computer. In terms of files, a computer program consists of at least an executable file supplemented by a collection of data files. As malware are mostly identified as programs, they necessarily consist of an executable file. Worms, trojans, spywares etc. are stand alone programs while viruses are injected into other executable programs making them malicious.

Our research deals with Windows malwares only. The executable file for Windows is called PE (Portable Executable) [Cor99], that defines the format of the file. Figure 4.1 displays the layout of a PE file.

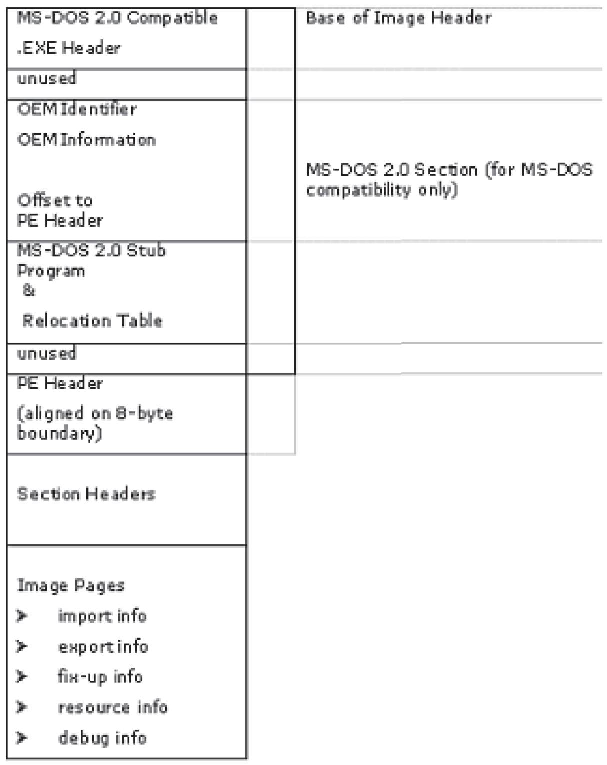


Figure 4.1: Typical 32-Bit Portable .EXE File Layout

In a more simplified form the PE file can be considered as consisting of two main portions; header and body. Header contains information about the file including statistics e.g. number of sections, starting address etc. while body contains the actual contents of the file.

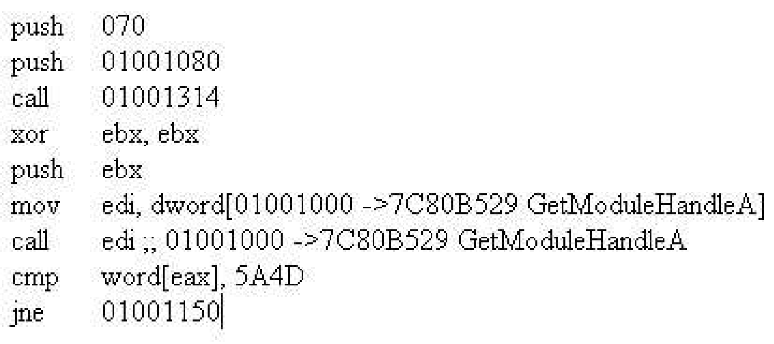
We performed experiments with three types of malwares; virus, trojan and worm. The following sections describe experiments with each of these malwares types. First section describes experiment with a subset containing all three types. Next sections are dedicated to trojans and worms only.

4.1 Subset Data

The initial experiment was carried out to build a data mining framework. Once the framework was built, experiments with large collection of malwares were carried out.

4.1.1 Data Processing

The dataset consisted of 820 Windows PE files. Half of them were malicious and the other half consisted of clean programs. The clean programs were obtained from a PC running Windows XP. Each malicious program in our dataset belongs to one of the three main categories of virus, worm and trojan. The virus files were mostly small windows application programs such as notepad, calc, wordpad, and paint etc, infected with different types of viruses and their variants. We only considered Win32 malwares. The dataset did not contain any encrypted, polymorphic or metamorphic viruses, as the static disassembly analysis of a virus in its encrypted form would be meaningless as any other infection would contain a mutated copy of the virus with different instructions performing the same malicious task. Figure 4.6 displays the data preprocessing steps.



```
push    070
push    01001080
call    01001314
xor     ebx, ebx
push    ebx
mov     edi, dword[01001000 ->7C80B529 GetModuleHandleA]
call    edi ;; 01001000 ->7C80B529 GetModuleHandleA
cmp     word[eax], 5A4D
jne     01001150
```

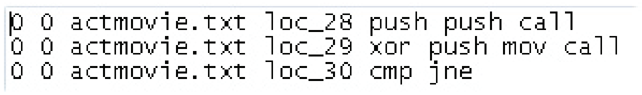
Figure 4.2: Portion of the output of disassembled actmovie.exe.

4.1.1.1 Malware Analysis

[Bon93] discussed the importance of maintaining a clean virus collection for research. We purged our collection of corrupt and duplicate files. Next the samples were categorized based upon the malware type (virus, worm, trojan etc), concealment strategy (no concealment, encryption, polymorphism etc.) and in memory strategy (memory resident, non memory resident).

4.1.1.2 Disassembly

For further analysis the binaries were transformed to an intermediate representation. This transformation was obtained by applying reverse engineering to the binaries. The intermediate representation thus obtained was in the form of assembly language code using a disassembly program. The disassembly was obtained using Datarescues' IDA Pro [IDA]. From these disassembled files we extracted the variable length instruction sequences that served as the primary source for the features in our dataset. We only considered the opcode and the operands were discarded from the analysis. Figure 4.2 shows a portion of the disassembly of the program actmovie.exe.



```
0 0 actmovie.txt loc_28 push push call
0 0 actmovie.txt loc_29 xor push mov call
0 0 actmovie.txt loc_30 cmp jne
```

Figure 4.3: Instruction sequences extracted from actmovie.exe

4.1.1.3 Parsing

The disassembly in figure 4.2 was parsed to create the instruction sequences. Figure 4.3 displays the sequences obtained from the disassembled portion shown in figure 4.2. Each row in figure 4.3 represents a single instruction sequence. The first column indicates if it is a clean file or malware, second column carries the file name. Third column carries the sequence name that the parser assigned to it. From fourth column and on, the instruction sequence starts.

4.1.1.4 Feature Extraction

The raw disassembly of the virus and clean files resulted in 1510421 sequences. Among them 62608 unique sequences were identified with different frequencies of occurrence. Each sequence was considered as a potential feature. Figure 4.4 displays the scatter plot of sequence frequencies and the number of times those frequencies were spotted in the files. Points close to Y-axis are rare sequences while the points close to X-axis and on the farther right corner of the plot represents the most occurring sequences. Figure 4.5 displays the same plot with outliers removed. This shows the actual operating region from where the dataset can be built. Rare sequences will reduce the classifier to a signature detection engine while the ones that are too frequent cannot be used as identifiers.

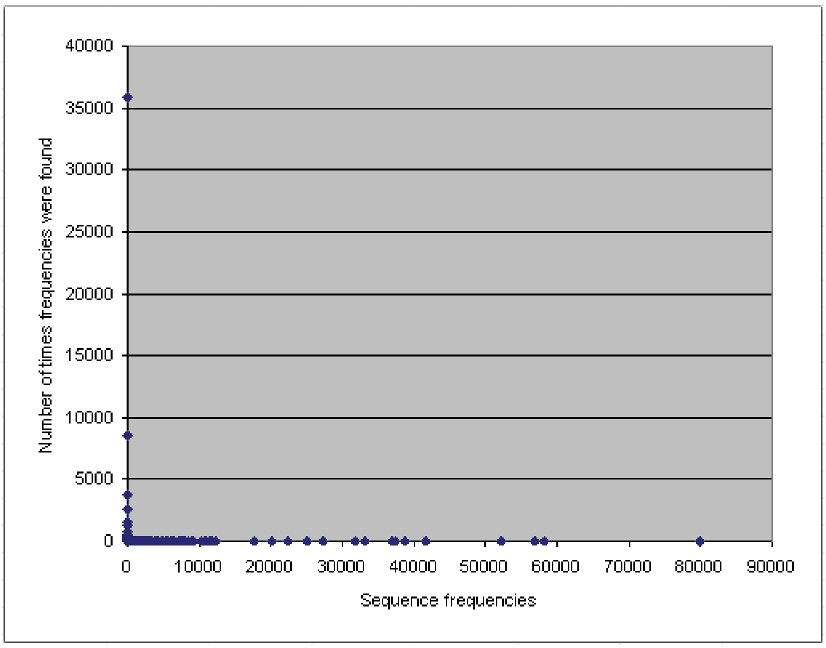


Figure 4.4: Scatter plot of sequence frequencies and their frequency of occurrence.

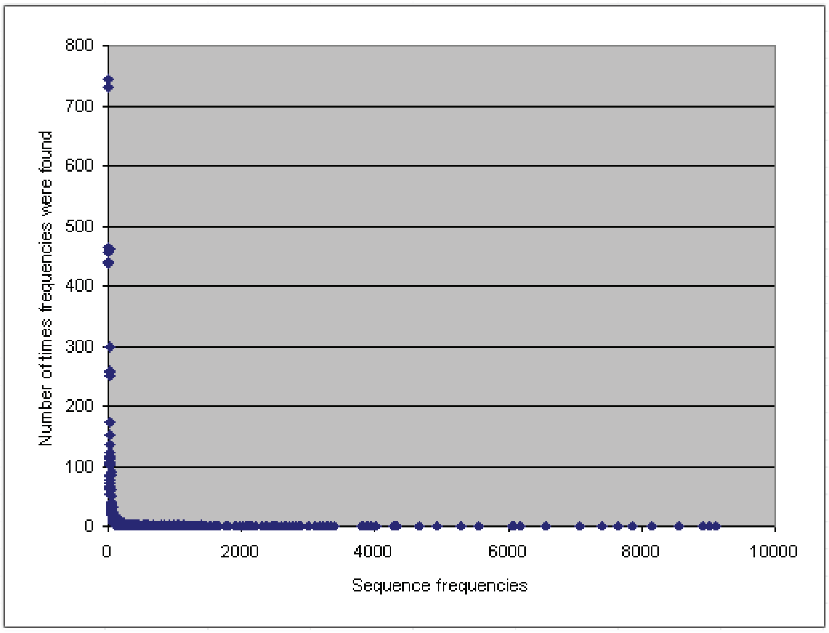


Figure 4.5: Scatter plot of sequence frequencies and their frequency of occurrence with outliers removed.

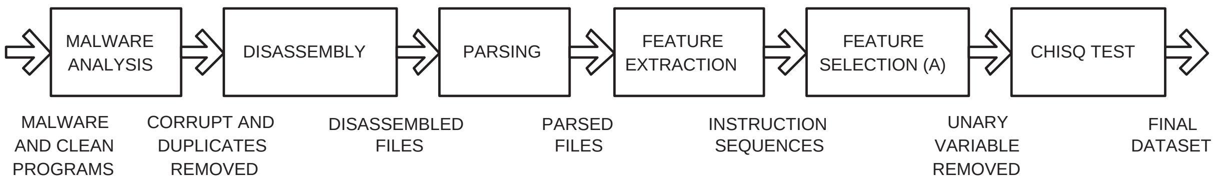


Figure 4.6: Data preprocessing steps for experiments with the malware subset.

4.1.1.5 Feature Selection

We used the vector space model to transform the unstructured data into a structured form. Each program was considered a vector in a n dimensional space where n was the number of distinct instruction sequences. A term document matrix was created where each program represented a document, while instruction sequences were considered as terms. Using the unary variable removal method described in the section 3.3, we selected the most important instruction sequences. This removed 98.2% of the sequences and only 1134 sequences were selected. After the removal, the term document matrix contained the term frequency representation of the model. A binary target variable identified each program as malware or clean.

4.1.1.6 Independence Test

A Chi-Square test of independence was performed for each feature to determine if a relationship exists between the feature and the target variable. The term document matrix was transformed to a binary representation to get a 2-way contingency table. Using a p-value of 0.01 for the test resulted in the removal of about half of the features that did not showed any statistically significant relationship with the target. Features that have their entire occurrence in one class only are also removed from the analysis, as they tend to bias the classifier. Out of initial 1134 features, 633 remained after this step. Some features have too many levels to implement data mining methods such as logistic regression and neural networks efficiently. An m-to-n mapping was used by applying the ChiMerge technique to collapse the number of levels within a feature.

4.1.2 Experiments

The data was partitioned into 70% training and 30% test data. We fitted three models to the training data using SAS Enterprise Miner. These include logistic regression, neural networks and decision trees.

4.1.2.1 Logistic Regression

Logistic regression model was used to calculate the posterior probabilities that a given observation belonged to malicious class or benign. In the Enterprise Miner implementation of logistic regression, we only considered main effects due large number of input features. Two-factor interactions and polynomial terms were not considered.

4.1.2.2 Neural Network

Neural network model was used to learn to classify between malicious and benign class by repetitively presenting observations from both classes. The model used MLP architecture with 10 hidden units and misclassification as the model selection criteria.

4.1.2.3 Decision Tree

Decision tree model was used to obtain a set of rules that can classify each sample into either malicious or benign class. The decision tree model we used in Enterprise Miner used entropy as split criterion with a maximum depth of 30.

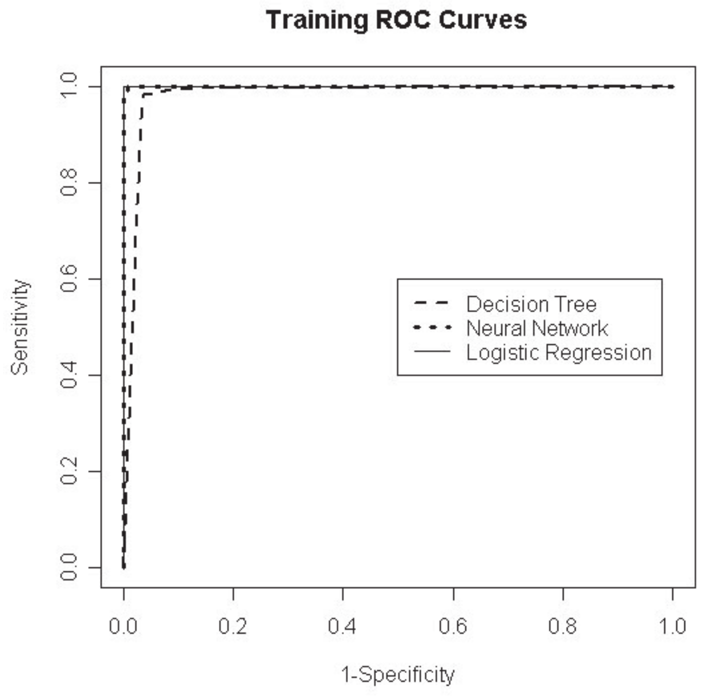


Figure 4.7: ROC curve comparing regression, neural network and decision tree training results.

Figure 4.7 displays the training ROC curves for each model.

4.1.3 Results

The models were tested on the 30% test data that we set aside before the experiments. The test data contain the malwares and clean programs that were not part of the model fitting process. In data mining terms it was scoring data, while in the malware research terminology, this set contained new and unknown malwares.

Table 4.1 displays the experimental results for each classifier.

Figure 4.8 displays the ROC curves for test data for each model. The slight bent in the curve for decision tree exhibits that the classifier was more prone to false positive rate although it displayed a slightly better detection rate. Neural network gave a slightly better false positive rate with a

Table 4.1: Experimental results for new and unknown viruses.

Classifier	Detection Rate	False Alarm Rate	Overall Accuracy
Logistic Regression	95%	17.5%	88.6%
Neural Network	97.6%	4.1%	97.6%
Decision Tree	98.4%	4.9%	96.7%

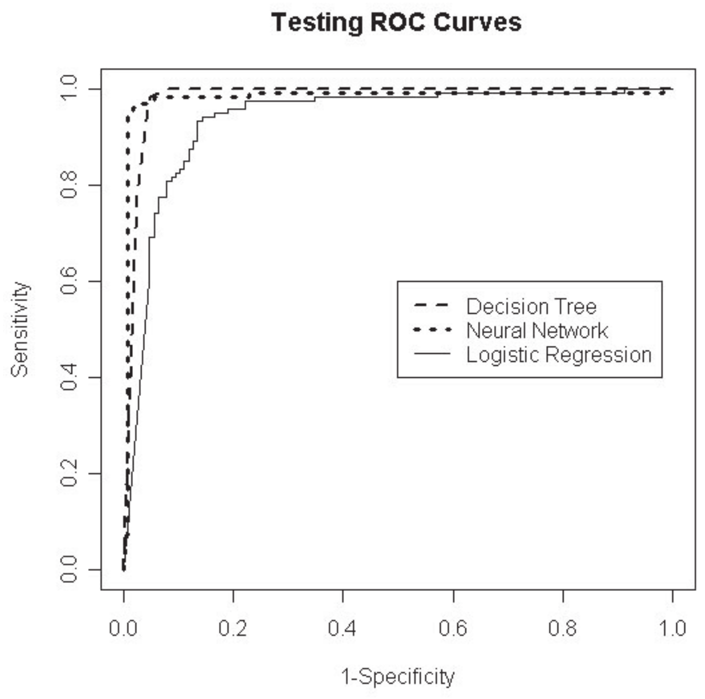


Figure 4.8: ROC curve comparing regression, neural network and decision tree test results.

less detection rate. Logistic regression didn't perform well on the test data as the ROC curve for training displayed overfitting for the model. Table 4.2 displays the area under the ROC curve for each model.

4.2 Trojans

Our decision to exclusively use trojans in an experiment was based upon last year's malware distribution statistics. Figure 4.9 displays the 2007 malware distribution statistics from Trend Micro.

Table 4.2: Area under the ROC curve for each classifier.

Classifier	AUC
Logistic Regression	0.9357
Neural Network	0.9815
Decision Tree	0.9817

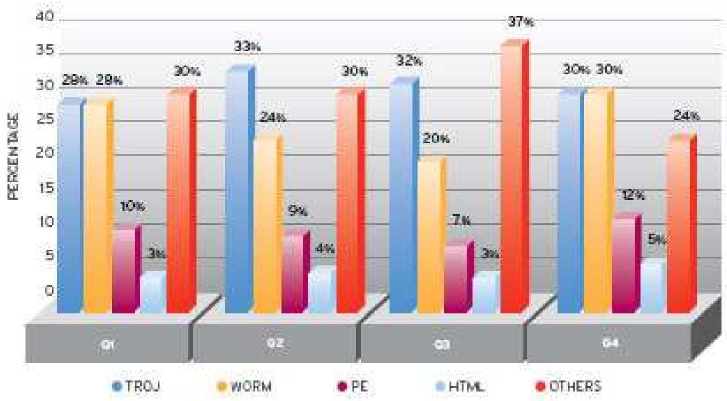


Figure 4.9: 2007 Malware distribution statistics from Trend Micro.

The number of trojans in each quarter is equal to or more than the number of any other malware type including worms.

4.2.1 Data Processing

Our collection of trojans and clean programs consisted of 4722 Windows PE files, of which 3000 were trojans and the 1722 were clean programs. The clean programs were obtained from a PC running Windows XP. These include small Windows applications such as calc, notepad, etc and other application programs running on the machine. A number of clean programs were also downloaded from [Dow] to get a representation of programs downloaded from the Internet. The trojans were all downloaded from [vx]. The dataset was thus consisted of a wide range of programs, created using different compilers and resulting in a sample set of uniform representation. Figure 4.12 displays the data processing steps.

Table 4.3: Packers/Compilers Analysis of Trojans

Packer/Compiler	Number of Trojans	Number of Clean Programs
ASPack	349	2
Borland	431	39
FSG	38	1
Microsoft	1031	937
Other Not Packed	229	597
Other Packed	118	24
PECompact	48	2
Unidentified	174	72
UPX	582	48

Table 4.4: Packers/Compilers Analysis of Trojans and Clean Programs

Type of Program	Not Packed	Packed	Unidentified
Clean	1573	77	72
Trojan	1691	1135	174
Total	3264	1212	246

4.2.1.1 Malware Analysis

We ran PEiD [PEi] on our data collection to detect compilers, common packers and cryptors, used to compile and/or modify the programs. Table 4.3 displays the distribution of different packers and compilers in the collection. Table 4.4 displays the summary of packed, not packed and unidentified trojans and clean programs.

Before further processing, packed programs were unpacked using specific unpackers such as UPX (with -d switch) [UPX], and generic unpackers such as Generic Unpacker Win32 [GUW] and VMUnpacker [VMU].

4.2.1.2 File Size Analysis

Before disassembling the programs to extract instruction sequences, a file size analysis was performed to ensure that the number of instructions extracted from clean programs and trojans is

Table 4.5: File Size Analysis of the Program Collection

Statistic	Trojans Size (KB)	Cleans Size (KB)
Average	176	149
Median	66	51
Minimum	1	3
Maximum	1951	1968

approximately equal. Table 4.5 displays the file size statistics for trojans and clean programs.

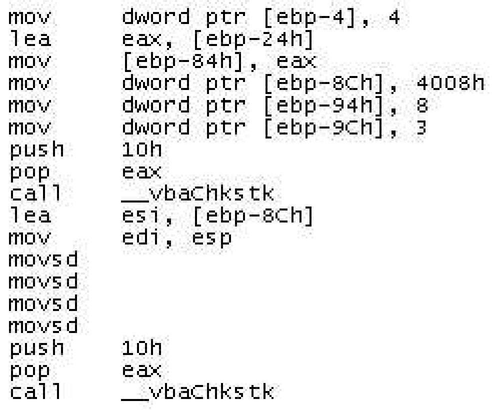
To get an even distribution of the number of programs in the collection, we finally chose 1617 trojans and 1544 clean programs after discarding unidentified programs and large trojans that were pulling the average program size a little higher than the clean programs.

4.2.1.3 Disassembly

Binaries were transformed to a disassembly representation that is parsed to extract features. The disassembly was obtained using Datarescues' IDA Pro [IDA]. From these disassembled files we extracted sequences of instructions that served as the primary source for the features in our dataset. A sequence is defined as instructions in succession until a conditional or unconditional branch instruction and/or a function boundary is reached. Instruction sequences thus obtained are of various lengths. We only considered the opcode and the operands were discarded from the analysis. Figure 4.10 shows a portion of the disassembly of the Win32.Flood.A trojan.

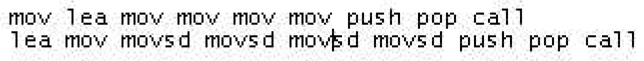
4.2.1.4 Parsing

A parser written in PHP translates the disassembly in figure 4.10 to instruction sequences. Figure 4.11 displays the output of the parser. Each row in the parsed output represented a single instruction sequence. The raw disassembly of the trojan and clean programs resulted in 10067320 instruction



```
mov     dword ptr [ebp-4], 4
lea     eax, [ebp-24h]
mov     [ebp-84h], eax
mov     dword ptr [ebp-8Ch], 4008h
mov     dword ptr [ebp-94h], 8
mov     dword ptr [ebp-9Ch], 3
push    10h
pop     eax
call    __vbaChkstk
lea     esi, [ebp-8Ch]
mov     edi, esp
movsd
movsd
movsd
movsd
push    10h
pop     eax
call    __vbaChkstk
```

Figure 4.10: Portion of the output of disassembled Win32.Flood.A trojan.



```
mov lea mov mov mov mov push pop call
lea mov movsd movsd movsd movsd push pop call
```

Figure 4.11: Instruction sequences extracted from the disassembled Win32.Flood.A trojan.

sequences.

4.2.1.5 *Feature Extraction*

The parsed output was processed through our Feature Extraction Mechanism. Among the 10067320 instruction sequences, 2962589 unique sequences were identified with different frequencies of occurrence. We removed the sequences that were found in one class only as they will reduce the classifier to a signature detection technique.

4.2.1.6 *Primary Feature Selection*

We used the vector space model to transform the unstructured data into a structured form. Each program was considered a vector in a n dimensional space where n was the number of distinct instruction sequences. A term document matrix was created where each program represented a document, while instruction sequences were considered as terms. Using the unary variable removal

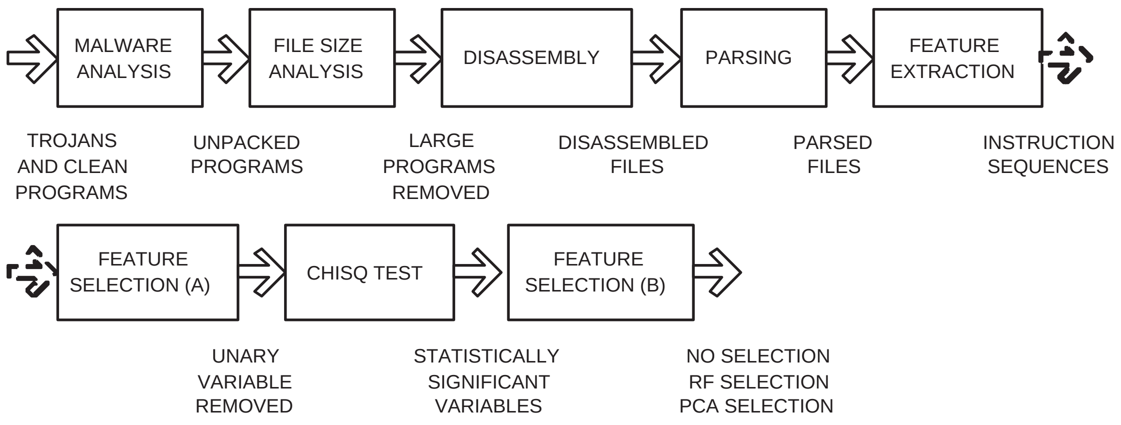


Figure 4.12: Data preprocessing steps for experiments with trojans.

method described in the section 3.3, we selected the most important instruction sequences. This removed 97% of the sequences and only 955 sequences were selected. After the removal, the term document matrix contained the term frequency representation of the model. A binary target variable identified each program as trojan or clean.

4.2.1.7 Independence Test

A Chi-Square test of independence was performed for each feature to determine if a relationship exists between the feature and the target variable. The term document matrix was transformed to a binary representation to get a 2-way contingency table. Using a p-value of 0.01 for the test resulted in the removal of about half of the features that did not showed any statistically significant relationship with the target. The resulting number of variables after this step was 877.

4.2.1.8 Secondary Feature Selection/Reduction

After performing the primary feature selection and independence test, we applied two more feature selection/reduction algorithms to create three different datasets. These algorithms include random forest and principal component analysis. The first dataset retained all the original 877 variables. In the results section 4.2.3, this set is referred to as *All variables*.

Random Forest: While using the random forest model for feature selection, we rejected the variables for which the mean decrease in accuracy was less than 10%. Only 84 variables were selected. In the results section 4.2.3, this set is referred to as *RF variables*.

Principal Component Analysis: During the PCA feature reduction process, we obtained the 146 variables that explained 95% variance in the dataset and rejected others. In the results section 4.2.3, this set is referred to as *PCA variables*.

4.2.2 Experiments

The data was partitioned into 70% training and 30% test data. Similar experiments showed best results with tree based models for the count data [SWL08]. We built bagging and random forest models using R [R]. We also experimented with SVMs using R.

4.2.2.1 Bagging

Classification trees were used with 100 bootstrap replications in the Bagging model.

4.2.2.2 Random Forest

We grew 100 classification trees in the random forest model. The number of variables sampled at each split was ranged from 6 to 43 depending upon the number of variables in the dataset.

4.2.2.3 Support Vector Machines

We used C-Classification with a radial basis kernel function.

Table 4.6: Experimental results for new and unknown trojans.

Classifier	Variables	Detection Rate	False Alarm Rate	Overall Accuracy
Random Forest	All	93.1%	6.3%	92.6%
Random Forest	RF	92.4%	9.2%	94.0%
Random Forest	PCA	89.7%	10.1%	89.6%
Bagging	All	91.1%	7.4%	89.8%
Bagging	RF	91.1%	9.6%	91.9%
Bagging	PCA	89.4%	10.5%	89.4%
SVM	All	83.6%	15.0%	82.6%
SVM	RF	83.3%	12.3%	79.7%
SVM	PCA	82.5%	19.8%	84.7%

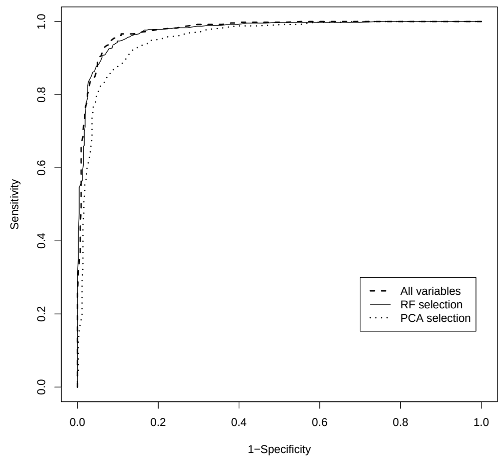


Figure 4.13: ROC curve comparing random forest test results on datasets with all variables, RF variables and PCA variables.

4.2.3 Results

Like, in the experiments described in the previous section, we tested the models using the 30%test data. Table 4.6 displays the experimental results for each classifier over the three training sets.

4.2.4 Discussion

Random forest stood out to be the winner among all the classifiers and dimension reduction methods in our experiments. The best results for overall accuracy, false positive rate and area under

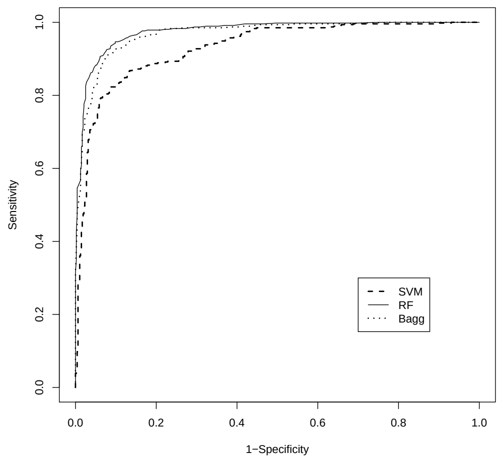


Figure 4.14: ROC curve comparing random forest, bagging and SVM test results on dataset with RF selection.

Table 4.7: Area under the ROC curve for each classifier for each dataset.

Classifier	Variables	AUC
Random Forest	All	0.9772
Random Forest	RF	0.9754
Random Forest	PCA	0.9537
Bagging	All	0.9714
Bagging	RF	0.9686
Bagging	PCA	0.9549
SVM	All	0.9295
SVM	RF	0.9305
SVM	PCA	0.8971

the ROC curve were obtained using random forest classifier on all the variables. The best detection rate was obtained using random forest model with feature selection using a previous run of random forest. This comes with a slight sacrifice in overall accuracy but a much simpler model. Tree based method performed better on the count data. More specifically random forest performed slightly better than Bagging which is an endorsement of its superiority over Bagging as claimed in [Bre01]. ROC curves are provided to compare results for each classifier and each dataset. For space considerations, we are only providing ROC curves for RF Dimensions dataset for each classifier in figure 4.13. To compare the results over each dataset figure 4.14 displays ROC curve for random forest test results for the three datasets.

4.3 Worms

Worms claim more damage to the economy than any other type of malware. In the recent years the most notable malwares were mostly worms including Melissa, ILoveYou, Code Red I & II, Nimda, SQL Slammer, Blaster, SoBig, Sober, MyDoom, Witty and Sasser worms. The same framework that we developed for trojans and viruses was extended to include worms.

4.3.1 Data Processing

Our collection of 3195 Windows PE files consisted of 1473 worms and 1722 clean programs. The clean programs were obtained from a PC running Windows XP. These include small Windows applications such as calc, notepad, etc and other application programs running on the machine. A number of clean programs were also downloaded from [Dow] to get a representation of downloaded programs. The worms were downloaded from [vx]. The dataset was thus consisted of a

Table 4.8: Packers/Compilers Analysis Details of Worms and Clean Programs

	Before Unpacking		After Unpacking	
Packer/Compiler	Worms	Cleans	Worms	Cleans
ASPack	79	2	1	0
Borland	118	39	258	45
FSG	31	1	3	0
Microsoft	350	937	649	976
Other Not Packed	205	597	234	601
Other Packed	104	24	135	28
PECompact	26	2	7	0
Unidentified	161	72	161	72
UPX	399	48	24	0
Total	1473	1722	1473	1722

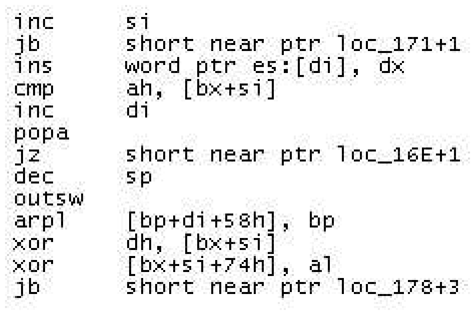
Table 4.9: Packers/Compilers Analysis Summary of Worms and Clean Programs

	Before Unpacking		After Unpacking	
Packer/Compiler	Worms	Cleans	Worms	Cleans
Not Packed	672	1573	1140	1622
Packed	640	77	171	28
Unidentified	161	72	162	72
Total	1473	1722	1473	1722

wide range of programs, created using different compilers and resulting in a sample set of uniform representation. Figure 4.17 displays the data processing steps.

4.3.1.1 Malware Analysis

We ran PEiD [PEi] on our data collection to detect compilers, common packers and cryptors, used to compile and/or modify the programs. Table 4.8 displays the distribution of different packers and compilers in the collection. Before further processing, packed programs were unpacked using specific unpackers such as UPX (with -d switch) [UPX], and generic unpackers such as Generic Unpacker Win32 [GUW] and VMUnpacker [VMU]. Table 4.9 displays the summary of packed, not packed and unidentified trojans and clean programs.



```
inc      si
jb       short near ptr loc_171+1
ins      word ptr es:[di], dx
cmp      ah, [bx+si]
inc      di
popa
jz       short near ptr loc_16E+1
dec      sp
outsw
arpl     [bp+di+58h], bp
xor      dh, [bx+si]
xor      [bx+si+74h], al
jb       short near ptr loc_178+3
```

Figure 4.15: Portion of the output of disassembled Netsky.A worm.

A number of clean programs were removed to keep an equal class distribution. The unidentified programs were also removed.

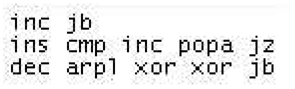
4.3.1.2 Disassembly

Binaries were disassembled to obtain a source code representation using Datarescues' IDA Pro [IDA]. Programs with disassembly errors were removed from the dataset.

4.3.1.3 Feature Extraction

The core of the Feature Extraction Mechanism consisted of a parser that parsed the disassembled files to generate instruction sequences. A sequence is defined as instructions in succession until a conditional or unconditional branch instruction and/or a function boundary is reached. Instruction sequences thus obtained are of various lengths. We only considered the opcode and the operands were discarded from the analysis. Figure 4.15 shows a portion of the disassembly of the Netsky.A worm.

The parser was written in PHP and it translated the disassembly in figure 4.15 to instruction sequences. Figure 4.16 displays the output of the parser. Each row in the parsed output represented a single instruction sequence. For comparison purposes we also extracted non-overlapping fixed



```
inc jb
ins cmp inc popa jz
dec arpl xor xor jb
```

Figure 4.16: Instruction sequences extracted from the disassembled Netsky.A worm.

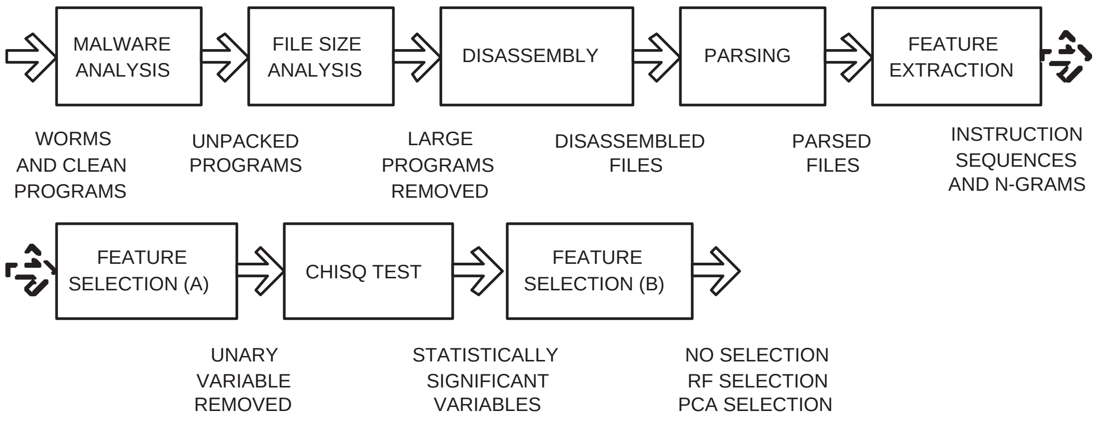


Figure 4.17: Data preprocessing steps for experiments with worms.

length instruction sequences from the disassembly. These fixed length sequences will be termed n-grams in this paper, where n is the length of the sequence. The value of n was varied from 2 to 10 in our experiments.

4.3.1.4 Feature Selection/Reduction

We used the vector space model to transform the unstructured data into a structured form. Each program was considered a vector in a n dimensional space where n was the number of distinct instruction sequences. A term document matrix was created where each program represented a document, while instruction sequences were considered as terms. Using the unary variable removal method described in the section 3.3, we selected the most important instruction sequences. After the removal, the term document matrix contained the term frequency representation of the model. A binary target variable identified each program as worm or clean. We also added a heuristic flag variable indicating if the worm or clean program was originally found in a packed or an unpacked

Table 4.10: Features Statistics

	No of Features			
Feature Size	Total	Distinct	10% Presence	Ind. Test
2	16365620	6728	630	537
3	10910413	45867	1583	1334
4	8182810	156572	1823	1483
5	6546248	361715	1771	1466
Variable	5487145	509778	574	492
6	5455206	640863	1114	906
7	4675891	949233	458	363
8	4091405	1236822	112	71
9	3636804	1474690	37	27
10	3273124	1618698	20	15

state.

4.3.1.5 Independence Test

A Chi-Square test of independence was performed for each feature to determine if a relationship exists between the feature and the target variable. The term document matrix was transformed to a binary representation to get a 2-way contingency table. Using a p-value of 0.01 for the test resulted in the removal of about half of the features that did not showed any statistically significant relationship with the target.

Table 4.10 displays the features statistics for datasets generated for each n-gram size and the variable length instruction sequences. Each n-gram or instruction sequence is considered a feature.

4.3.1.6 Feature Reduction

After performing the feature selection and independence test, we applied two different feature reduction techniques to create two datasets. These techniques include random forest and principal component analysis. In addition to these two datasets we also kept the original dataset with all the

Table 4.11: Reduced Feature Sets

Feature Size	All Variables	RF Variables	PCA Variables
2	537	79	124
3	1334	124	148
4	1483	138	133
5	1466	138	120
Variable	492	89	164
6	906	148	164
7	363	99	200
8	71	35	68
9	27	15	27
10	15	10	15
20	0	0	0

features retained from the chi-square test output. In the results section 4.4, this dataset is referred to as *All variables*.

4.3.1.7 Random Forest

We followed the same procedure for feature selection using random forest, that we developed for the trojan dataset. The variables for which the mean decrease in accuracy was less than 10% were rejected. In the results section 4.4, this dataset is referred to as *RF variables*

4.3.1.8 Principal Component Analysis

PCA was also employed under the similar conditions. We kept the variables that explained 95% variance in the dataset and rejected others. In the results section 4.4, this dataset is referred to as *PCA variables*

Table 4.11 displays the number of features in each dataset after applying the random forest and principal component analysis, for each feature size.

4.3.2 Experiments

Experiments were conducted on 30 different datasets. As explained in the previous section these were generated by using a combination of feature size and selection mechanism. Each dataset was partitioned into 70% training and 30% test data. Similar experiments showed best results with tree based models for the count data [SWL08]. We built bagging and random forest models using R [R].

4.3.2.1 Bagging

We used classification trees with 100 bootstrap replications in the Bagging model.

4.3.2.2 Random Forest

We grew 100 classification trees in the Random forest model. Each random forest model was first tuned to obtain the optimal number of variables to be sampled at each node.

4.4 Results

As explained in the previous experiments, the 30% test data was used to test the efficiency of the models. Table 4.12 displays the experimental results for each classifier, selection strategy and n-gram size combination.

Table 4.12: Experimental results for new and unknown worms.

Classifier	Variables	Size	Detection Rate	False Alarm Rate	Overall Accuracy
Random Forest	All	variable	94.3%	5.64%	94.24%
Random Forest	RF	variable	93.85%	7.6%	95.38%
Random Forest	RF	5	93.04%	7.46%	93.56%
Random Forest	RF	2	92.85%	5.74%	91.47%
Random Forest	All	2	92.7%	6.85%	92.29%
Bagging	RF	2	92.55%	6.65%	91.76%
Bagging	All	variable	92.5%	7.12%	92.12%
Bagging	RF	variable	92.35%	8.48%	93.23%
Random Forest	RF	4	91.63%	7.45%	90.78%
Random Forest	RF	8	91.63%	7.45%	90.78%
Random Forest	RF	9	91.63%	7.45%	90.78%
Bagging	RF	5	91.57%	8.28%	91.41%
Random Forest	RF	3	91.51%	5.49%	88.63%
Random Forest	PCA	4	91.38%	8.06%	90.8%
Random Forest	PCA	5	91.38%	8.06%	90.8%

Continued on next page

Table 4.12 – Experimental results for new and unknown worms.

Classifier	Variables	Size	Detection Rate	False Alarm Rate	Overall Accuracy
Random Forest	PCA	6	91.38%	8.06%	90.8%
Random Forest	PCA	7	91.38%	8.06%	90.8%
Random Forest	PCA	8	91.38%	8.06%	90.8%
Random Forest	PCA	9	91.38%	8.06%	90.8%
Random Forest	All	3	91.21%	7.01%	89.5%
Random Forest	All	6	91.15%	7.42%	89.86%
Random Forest	All	5	90.92%	8.96%	90.8%
Bagging	All	3	90.76%	7.01%	88.63%
Bagging	PCA	5	90.62%	10.75%	92.02%
Bagging	RF	3	90.61%	7.32%	88.63%
Bagging	PCA	variable	90.55%	9.5%	90.61%
Random Forest	PCA	variable	90.4%	8.31%	89.09%
Bagging	All	2	90.31%	6.85%	87.71%
Random Forest	All	4	90.28%	8.39%	89.05%
Bagging	All	5	90.17%	10.15%	90.49%
Random Forest	PCA	2	90.01%	10.91%	90.96%
Random Forest	PCA	3	89.57%	8.23%	87.46%

Continued on next page

Table 4.12 – Experimental results for new and unknown worms.

Classifier	Variables	Size	Detection Rate	False Alarm Rate	Overall Accuracy
Random Forest	RF	7	89.29%	11.21%	89.81%
Random Forest	All	7	89.29%	10.91%	89.49%
Bagging	PCA	3	89.27%	8.23%	86.88%
Random Forest	RF	6	88.7%	10%	87.54%
Bagging	RF	4	88.64%	8.7%	86.17%
Bagging	RF	8	88.64%	8.7%	86.17%
Bagging	RF	9	88.64%	8.7%	86.17%
Bagging	RF	6	88.55%	7.42%	84.93%
Bagging	PCA	2	88.23%	13.27%	89.76%
Bagging	All	6	87.94%	9.03%	85.22%
Bagging	PCA	4	87.29%	13.76%	88.3%
Bagging	PCA	6	87.29%	13.76%	88.3%
Bagging	PCA	7	87.29%	13.76%	88.3%
Bagging	PCA	8	87.29%	13.76%	88.3%
Bagging	PCA	9	87.29%	13.76%	88.3%
Bagging	RF	7	87.27%	12.12%	86.62%
Bagging	All	7	87.11%	13.03%	87.26%

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Table 4.12 – Experimental results for new and unknown worms.

Classifier	Variables	Size	Detection Rate	False Alarm Rate	Overall Accuracy
Random Forest	All	8	81.13%	12.5%	75%
Bagging	All	8	80.81%	11.84%	73.73%
Random Forest	All	10	79.66%	12.35%	72.36%
Random Forest	RF	10	79.66%	12.35%	72.36%
Bagging	All	10	78.14%	15.14%	72%
Random Forest	All	9	77.93%	22.64%	78.43%
Bagging	RF	10	77.76%	15.94%	72%
Random Forest	PCA	10	77.76%	14.34%	70.55%
Bagging	PCA	10	77.57%	12.75%	68.73%
Bagging	All	9	74.61%	27.92%	76.8%

Table 4.12 indicates that the variable length instruction sequences resulted in a higher detection and a lower false positive rate than the fixed length instructions of various sizes. Combining the statistics of table 4.10 with the results of table 4.12, it is also evident that variable length instruction sequences resulted in a better overall accuracy with a dataset of lesser dimensions, than the fixed length instruction sequences. Among the classifiers, random forest performed better than bagging which is endorsement of its superiority over bagging as claimed in [Bre01].

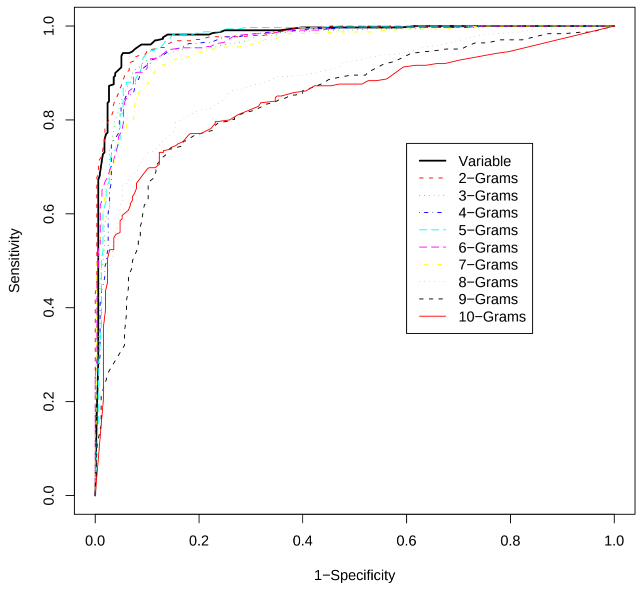

Figure 4.18: ROC curves comparing random forest results for each n-gram size using all variables.

Figures 4.18 - 4.25 display ROC curves comparing various combinations of classifiers, selection strategies and n-gram sizes. Figure 4.18 compares ROC curves for each n-gram size using random forest classifier on all the variables. Figure 4.19, compares similar curves on the random forest selection datasets, while figure 4.20, compares ROC curves on the PCA selection datasets. Figures 4.21, 4.22 and 4.23, compare similar ROC curves using bagging as the classification method. Figure 4.24 compares the results from each classifier on the random forest selected, variable length instruction sequences dataset. Another area of interest is to compare the different feature selection and reduction mechanisms used in these experiments. Figure 4.25 compares the ROC curves using random forest classifier on the variable length instruction sequences dataset using all variables, RF variables and PCA variables.

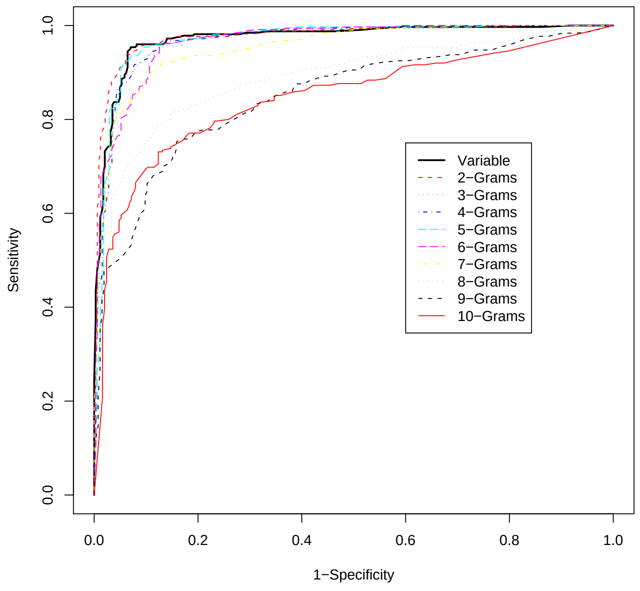

Figure 4.19: ROC curves comparing random forest results for each n-gram size using random forest feature selection.

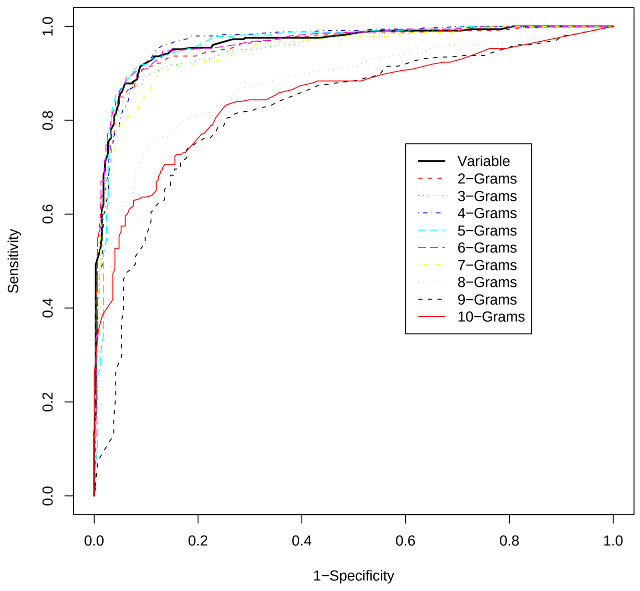

Figure 4.20: ROC curves comparing random forest results for each n-gram size using PCA feature reduction.

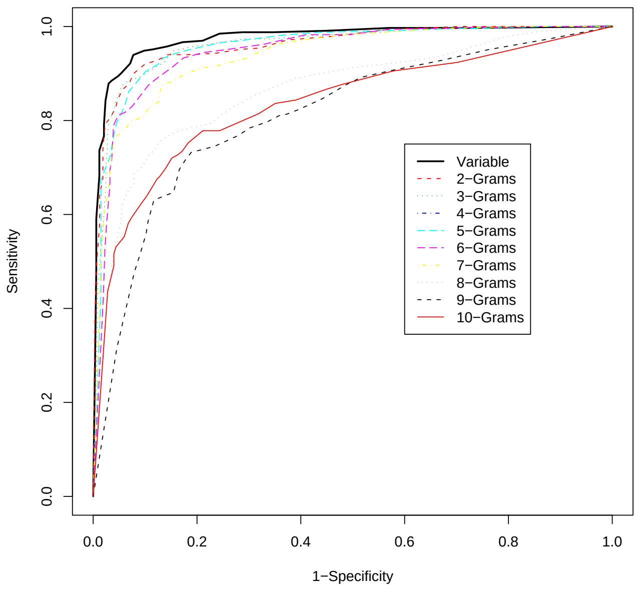

Figure 4.21: ROC curves comparing bagging results for each n-gram size using all variables.

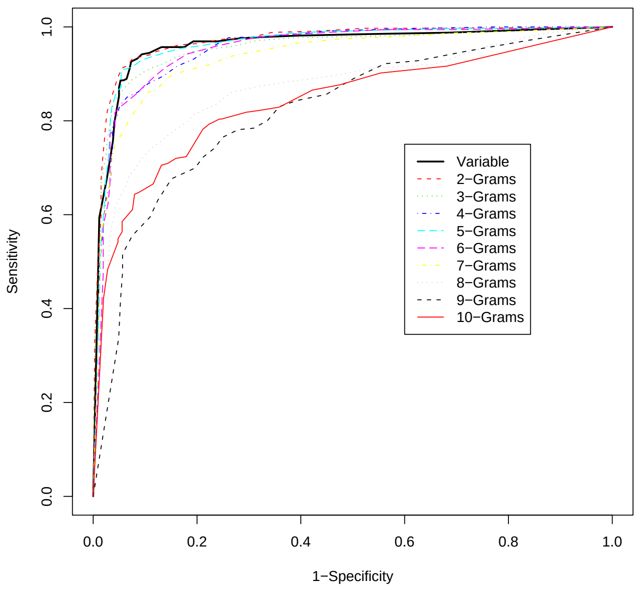

Figure 4.22: ROC curves comparing bagging results for each n-gram size using random forest feature selection.

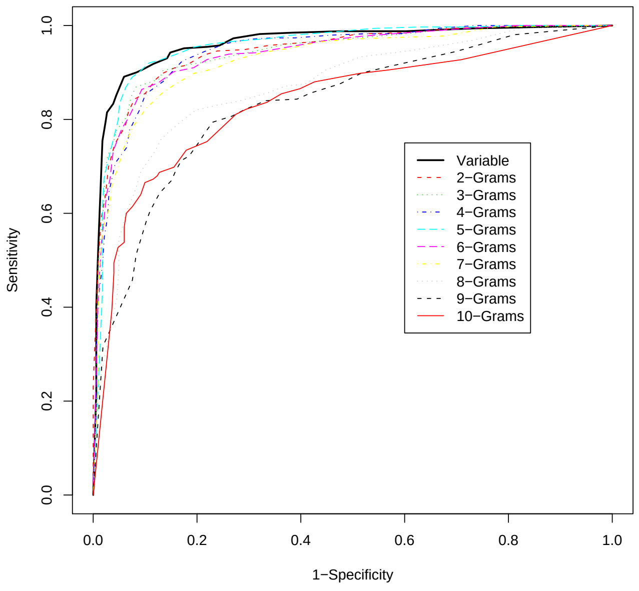

Figure 4.23: ROC curves comparing bagging results for each n-gram size using PCA feature reduction.

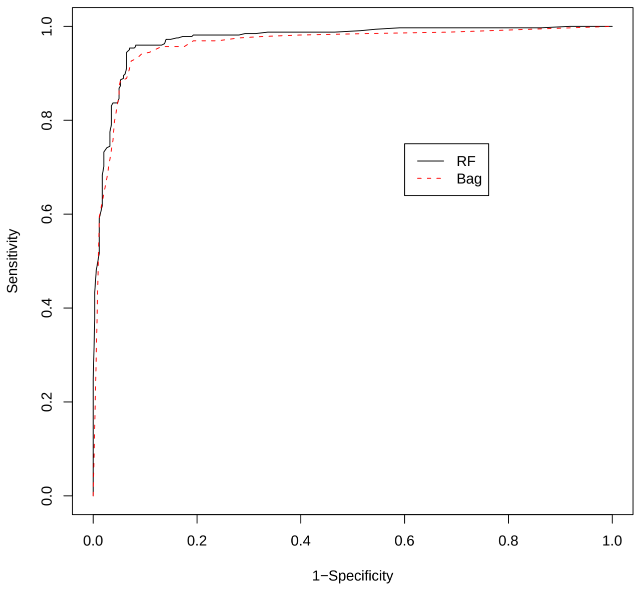

Figure 4.24: ROC curves comparing random forest and bagging results using random forest feature selection.

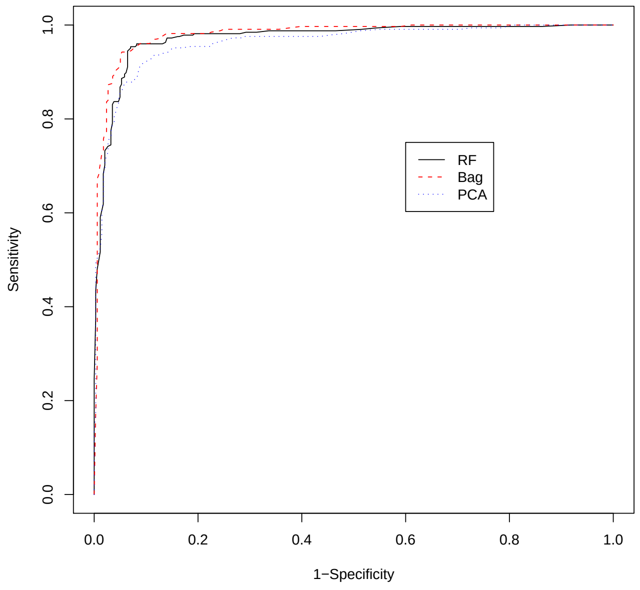

Figure 4.25: ROC curves comparing the variable selection methods (all variables, RF variables, PCA variables)

Table 4.13: Area under the ROC curve for each classifier.

Classifier	Variables	Size	AUC
Random Forest	All	var	0.9797275
Random Forest	All	2	0.9769337
Random Forest	RF	2	0.9765461
Bagging	All	var	0.974773
Random Forest	RF	var	0.9722357
Bagging	RF	2	0.9708548
Random Forest	RF	5	0.9691695

Continued on next page

Table 4.13 – Area under the ROC curve for each classifier.

Classifier	Variables	Size	AUC
Random Forest	All	5	0.9689085
Random Forest	RF	4	0.9677985
Random Forest	RF	3	0.9668456
Random Forest	RF	6	0.9656194
Random Forest	All	6	0.9647966
Random Forest	PCA	4	0.9640092
Bagging	RF	5	0.9629567
Random Forest	PCA	6	0.9628565
Bagging	PCA	var	0.9625978
Random Forest	All	3	0.9624724
Random Forest	PCA	var	0.961695
Bagging	RF	var	0.9611786
Random Forest	All	4	0.9611399
Bagging	All	2	0.9604272
Random Forest	PCA	5	0.9602692
Bagging	All	3	0.9595703
Random Forest	PCA	2	0.9570894
Bagging	All	5	0.9569957

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Table 4.13 – Area under the ROC curve for each classifier.

Classifier	Variables	Size	AUC
Bagging	RF	3	0.9562282
Bagging	PCA	5	0.9562128
Bagging	RF	4	0.9546736
Random Forest	All	7	0.9543331
Random Forest	RF	7	0.9534163
Bagging	RF	6	0.9519028
Random Forest	PCA	3	0.951264
Bagging	All	6	0.9464049
Bagging	PCA	2	0.9459697
Random Forest	PCA	7	0.9448514
Bagging	PCA	3	0.9435753
Bagging	PCA	4	0.9434564
Bagging	PCA	6	0.9399018
Bagging	All	7	0.9380911
Bagging	RF	7	0.93674
Bagging	PCA	7	0.9280979
Random Forest	RF	8	0.8872366
Random Forest	All	8	0.8855346

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Table 4.13 – Area under the ROC curve for each classifier.

Classifier	Variables	Size	AUC
Random Forest	PCA	8	0.8729024
Bagging	RF	8	0.8710807
Bagging	PCA	8	0.8692018
Bagging	All	8	0.8684002
Random Forest	RF	9	0.8493587
Random Forest	PCA	10	0.8482651
Random Forest	All	10	0.8458964
Random Forest	RF	10	0.8458964
Bagging	RF	10	0.8404781
Random Forest	All	9	0.8399124
Bagging	PCA	10	0.836762
Bagging	All	10	0.8354075
Bagging	PCA	9	0.8332223
Bagging	RF	9	0.8211247
Random Forest	PCA	9	0.8211
Bagging	All	9	0.8115304

CHAPTER 5
UNSUPERVISED LEARNING EXPERIMENTS

The unsupervised learning experiments involved using sequential association analysis on the malware collection. Association analysis is a form of descriptive data mining, where the focus is to mine the data for patterns that describe association among data elements and are easily understandable by humans. It is the most common form of local pattern discovery in an unsupervised learning environment. Association analysis discovers patterns in the form of association rules that describes the elements that are frequently found together in the data and assign confidence scores to these rules.

Association analysis can be best explained by *Market Basket Analysis*, which searches for items that are frequently found together in a random market basket. In the malware detection realm, association analysis can be used to discover features that are found together in each class of programs, i.e. malware or clean, and use this information for the detection of new and unknown malwares. Market basket analysis works at transaction level and finds items that are found together in many transactions. An extension of association analysis is sequential association analysis, that works at the user level, instead of transaction level. The user level analysis considers all the transactions done by a specific user in a sequence.

As explained previously, the basic feature for our experiments is a variable length instruction sequence. Intuitively, sequence mining was the method that we adopted for our experiments, where each candidate item was an instruction sequence. We devised two types of experiments using the association analysis for malware detection. One was to use association analysis for feature extraction/selection and in the second class of experiments we used association analysis for automatic malware signature extraction.

5.1 Feature Extraction

Chapter 4 described the use of occurrence frequency as the main feature selection method. This section explains the use of sequence mining as the primary feature extraction/selection mechanism. We used the same collection of malware and clean programs that was used previously in 4.3. The malware analysis, disassembly and feature extraction steps remained the same. The feature extraction mechanism was different as we used sequential association mining as the primary feature extraction/selection method, instead of unary variable removal. Features were originally extracted from the parsed files. The sequential association mining extracted rules from these features that can be used as features for a subsequent supervised learning process.

5.1.1 Data Processing

The vector representation of programs was no longer valid in sequence mining as the frequent instruction sequences were searched globally in the entire data collection, instead of locally, within a program.

5.1.1.1 Data Partitioning

Malware and clean sequences were separated prior to transforming the data into the form required by the sequence node in the SAS/Enterprise Miner. This was done because sequence mining is an unsupervised operation, so a target variable is not included during the process.

5.1.1.2 Data Transformation

For each partition, the sequences from each program were stacked in a dataset and each sequence was assigned an ID. For sequence mining, the sequence node in SAS/Enterprise Miner requires the data to be in a $N \times 3$ table, where $N = \sum_i^n l_i$, n is the total number of sequences and l is the length of each sequence. The first column holds the global ID for the sequence. Second column contains the transposed sequence and the third column carries the within sequence ID, that displays the position of each item in the sequence.

5.1.2 Sequence Mining

Sequential association mining was carried out with a 2% support on both the partitions separately, resulting in a malware rules dataset and a clean rules dataset. These rules represent the instruction sequences that were frequently found together in their respective partitions. The malware dataset contained 758 rules while the clean dataset had 535 rules. The malware and clean rules datasets were combined into one dataset with 831 rules.

5.1.2.1 Feature Extraction Process

We propose the idea of using these rules as potential features for a vector space model and build a classifier that uses this data to classify between malware and clean programs. So, the next step after combing the malware and clean rules into one dataset, was to choose the best rules among them. We defined a signature rule to be a rule that is only found in one class. These signature rules were removed, so were the rules that were too common in both the classes. The signature rules were identified with a greater than 0% support in its signature class a 0% support in the other class. To identify the common rules the absolute difference in the support level in each class was calculated and a 1% threshold was set, below which every rule was considered as too common, and hence, rejected. After this step we were left with only 227 rules and that was considered the final rule set. As explained previously, these rules represent the instruction sequences that were frequently found together in the malware and clean data.

5.1.2.2 Dataset

We used the vector space model for final dataset representation. Each program was considered a vector in a n dimensional space where n was the number of features selected using the sequential association mining procedure described in the last section. A term document matrix was created where each program represented a document, while rules representing instruction sequences were considered as terms. A term frequency was computed for each rule within each program. A binary target variable identified each program as malware or clean. We also added a heuristic flag variable indicating if the malware or clean program was originally found in a packed or an unpacked state.

5.1.2.3 Independence Test

A Chi-Square test of independence was performed for each feature to determine if a relationship exists between the feature and the target variable. The term document matrix was transformed to a binary representation to get a 2-way contingency table. Using a p-value of 0.01 for the test resulted in the removal of about half of the features that did not showed any statistically significant relationship with the target.

Table 5.1: Experimental results for new and unknown malwares using sequential association analysis as well as a combined selection method.

Classifier	Selection	Detection Rate	False Alarm Rate	Overall Accuracy
Random Forest	Assoc	66.6%	21.4%	72.1%
Random Forest	Merged	94.6%	10.2%	92.2%

5.1.3 Experiments

To perform the experiments, we constructed two datasets. The first contained the features selected from the sequence mining process and another dataset that combined the features selected from the sequence mining process and the occurrence frequency process. The datasets were partitioned into 70% training and 30% test data. Similar experiments showed best results with tree based models for the count data [SWL08]. We built random forest models using R [R].

5.1.3.1 Random Forest

We grew 100 classification trees in the Random forest model. Each random forest model was first tuned to obtain the optimal number of variables to be sampled at each node.

5.1.4 Results

We tested the model using the 30% test data from both the datasets. Table 5.1 displays the experimental results.

Figure 5.1 compares the ROC curves for the results from the feature set, selected using sequence association mining only and the combined feature set with features from sequence association mining and occurrence frequency.

It is obvious from table 5.1 and figure 5.1, that the features selected using sequence association

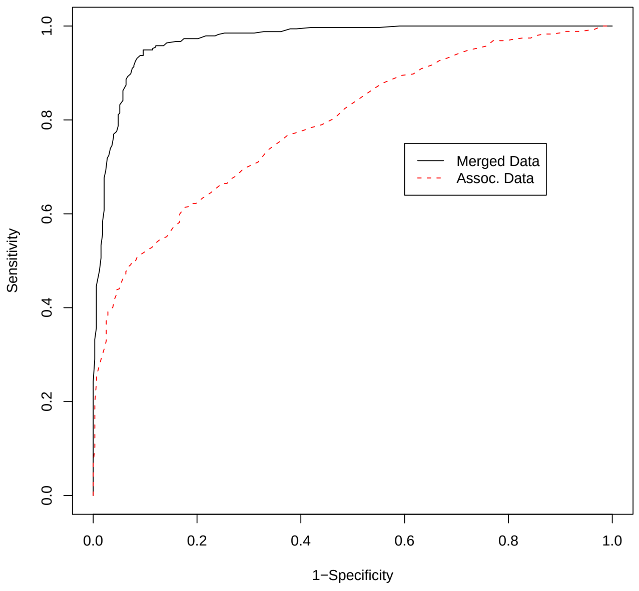

Figure 5.1: ROC curves comparing the results for the features selected using sequence association mining only and the combined feature set.

mining cannot be used towards a classification application, alone. The feature set can be merged with another feature set to create a hybrid set of two distinct feature selection mechanism. The 94.6% detection rate on new and unknown malwares validates this point.

5.2 Automatic Malware Signature Extraction

Signature detection is the industry standard for fighting against malwares [ACK04a]. These signatures are usually hand crafted by security experts. The first known data mining application for malware detection was for automatic signature extraction by [KA94]. Results were not very impressive but it opened the gate for data mining research in malware detection.

We propose a new idea of based upon association analysis to extract malware signatures. The underlying idea is to extract instruction sequences that are found frequently in a collection of malicious programs and then filter the ones that have any occurrence in a collection of clean programs. The result will be a generalized set of malware signatures that are not specific to any particular malware. Such a general set of malware signatures can thwart zero day attacks and do not need any human expertise.

5.2.1 Data Processing

We used the same collection of malware and clean programs that was used previously in 4.3. The malware analysis and disassembly steps remained the same. Features were extracted using the similar process but instead of saving the features from all the programs in one file, this time the features from each program were saved individually in separate files. No feature selection mechanism was used as the vector representation of programs was not used in the signature extraction scheme. Feature selection was implicit in the signature extraction algorithm. No partitioning is required for these experiments as individual malware and clean data is used.

5.2.1.1 Data Transformation

Each program was converted from its instruction sequence representation to the conform the requirements of the association node in SAS/Enterprise Miner. For sequence mining, the sequence node in SAS/Enterprise Miner requires the data to be in a $N \times 3$ table, where $N=\sum_i^n l_i$, n is the total number of sequences and l is the length of each sequence. The first column holds the global ID for the sequence. Second column contains the transposed sequence and the third column carries the within sequence ID, that displays the position of each item in the sequence.

5.2.2 Signature Extraction

The signature extraction mechanism used an incremental process to create the signature database. This databases was built by constantly adding new and unique class signatures from the program collection and removing the ones that were found in both classes. We performed a series of experiments by modifying the basic signature extraction algorithm for improved efficiency.

5.2.2.1 Basic Algorithm

The basic algorithm creates and updates a malware signature database. The database is updated every time a new malware signature is found or an existing signature is found in a clean program. The basic algorithm can be described as,

```
Input: A Collection of Files
Output: Malware Signature Database
Read a malware file;
Run assoc analysis on the file with 0% support;
Output the generated rules to create the signature database;
for each file do
    Read the file;
    Run assoc analysis on the file with 0% support;
    Output the generated rules;
    Search the signature database for the generated rules;
    if True Positive or True Negative then
        Goto next file;
    end
    else if False Positive then
        Remove the signature from the signature database;
    end
    else if False Negative then
        Add the signature to the signature database;
    end
end
```

Algorithm 1: Basic algorithm for signature extraction

The main update is the step where the algorithm searches the signature database for the gen-

Table 5.2: Truth table for the basic algorithm.

Malware	Found	Verdict
0	0	TN
0	1	FP
1	0	FN
1	1	TP

erated rules. Four scenarios arise from this situation that are described as a truth table in table 5.2.

Scenario 1: The file being processed is a *clean file* and no match is found. A *true negative (TN)* is generated in this case.

Scenario 2: The file being processed is a *clean file* and a match is found. A *false positive (FP)* is generated in this case.

Scenario 3: The file being processed is a *malware file* and no match is found. A *false negative (FN)* is generated in this case.

Scenario 4: The file being processed is a *malware file* and a match is found. A *true positive (TP)* is generated in this case.

Scenarios 1 and 4 do not trigger any update to the malware database. The update is required for scenarios 2 and 3. In the case of a false positive, the subject file is a clean file, therefore the matching signature has to be removed from the malware signature database. Similarly in the false negative case, the signature has to be added to the signature database, as the subject file is a malware and the signature database do not carry a matching signature.

The algorithm is nothing more than an online version of the batch processing described in the feature selection section of 5.1. The main difference is the nature and number of features that were finally selected. In the feature selection scheme, signatures were removed and only the features that were common to both classes were kept. The signature extraction scheme kept the signatures belonging to the malware class only. As the signatures are usually rare items, the signature extraction ran the association analysis with 0% support while the feature selection mechanism was interested in the most frequent features only, therefore the support level was 2%. The experiments were carried out using SAS/Enterprise Miner on a Pentium 4, 3.0 GHz machine with 1 GB of memory. Initially the batch version was tried with 0% support but upon receiving memory problems, the online version of the algorithm had to be developed.

The basic algorithm did not proved to be very efficient in terms of detection rate and false positive rate. A very high false positive rate of 30% for the test dataset suggested that too many signatures remained in the malware signature database that should have been filtered. Poor performance of the basic algorithm led to the development of the modified algorithm.

5.2.2.2 Modified Algorithm

The basic algorithm was modified to include clean signatures also and a plurality vote on clean and malware signatures decided if the subject file should be labeled as clean or malware. The modified algorithm can be described as,

The modified algorithm treated clean programs also as target for clean signatures. This resulted in two truth tables, one for each class. Table 5.3 gives the truth table for clean programs. In this table a clean program whose signature is not found in the clean program is considered to be a false negative. Similarly, table 5.4 gives the truth table for malwares.

These two truth tables can be combined to cover the eight possible scenarios at each iteration of the algorithm.

```
Input: A Collection of Files
Output: Malware and Clean Signature Databases
Read a malware file;
Run assoc analysis on the file with 0% support;
Output the generated rules to create the malware signature database;
Read a clean file;
Run assoc analysis on the file with 0% support;
Output the generated rules to create the clean signature database;
for each file do
    Read the file;
    Run assoc analysis on the file with 0% support;
    Output the generated rules;
    Search the malware signature database for the generated rules;
    Search the clean signature database for the generated rules;
    if True Positive or True Negative then
        Goto next file;
    end
    else if False Positive then
        if Subject File is a Malware then
            Remove the matching signatures from the malware signature database;
        end
        else if Subject File is a Clean File then
            Remove the matching signatures from the clean signature database;
        end
    end
    else if False Negative then
        if Subject File is a Malware then
            Add the new signatures to the malware signature database;
        end
        else if Subject File is a Clean File then
            Add the new signatures to the clean signature database;
        end
    end
end
```

Algorithm 2: Modified algorithm for signature extraction

Table 5.3: Truth table for the modified algorithm for clean files.

Malware	Found	Verdict
0	0	FN
0	1	TP
1	0	TN
1	1	FP

Table 5.4: Truth table for the modified algorithm for malwares.

Malware	Found	Verdict
0	0	TN
0	1	FP
1	0	FN
1	1	TP

Table 5.5: Truth table for the modified algorithm for malwares and clean programs

Malware	Found in Clean	Found in Malware	Clean	Malware
0	0	0	FNC	TNM
0	0	1	FNC	TNM
0	1	0	FNC	TNM
0	1	1	FNC	TNM
1	0	0	FNC	TNM
1	0	1	FNC	TNM
1	1	0	FNC	TNM
1	1	1	FNC	TNM

The scenarios described in the table 5.5, are explained below,

Scenario 1: The file being processed is a *clean file* and no matching signature is found in the clean signature database and no matching signature is found in the malware signature database. We defined this as a *false negative clean (FNC)* and a *true negative malware (TNM)* situation.

Scenario 2: The file being processed is a *clean file* and no matching signature is found in the clean signature database and matching signatures are found in the malware signature database. We defined this as a *false negative clean (FNC)* and a *false positive malware (FPM)* situation.

Scenario 3: The file being processed is a *clean file* and matching signatures are found in the clean signature database and no matching signature is found in the malware signature database. We defined this as a *true positive clean (TPC)* and a *true negative malware (TNM)* situation.

Scenario 4: The file being processed is a *clean file* and matching signatures are found in the clean signature database and matching signatures are found in the malware signature database. We defined this as a *true positive clean (TPC)* and a *false positive malware (FPM)* situation.

Scenario 5: The file being processed is a *malware file* and no matching signature is found in the clean signature database and no matching signature is found in the malware signature database. We defined this as a *true negative clean (TNC)* and a *false negative malware (FNM)* situation.

Scenario 6: The file being processed is a *malware file* and no matching signature is found in the clean signature database and matching signatures are found in the malware signature database. We defined this as a *true negative clean (TNC)* and a *true positive malware (TPM)* situation.

Scenario 7: The file being processed is a *malware file* and matching signatures are found in the clean signature database and no matching signature is found in the malware signature database. We defined this as a *false positive clean (FPC)* and a *false negative malware (FNM)* situation.

Scenario 8: The file being processed is a *malware file* and matching signatures are found in the clean signature database and matching signatures are found in the malware signature database. We defined this as a *false positive clean (FPC)* and a *true positive malware (TPM)* situation.

5.2.3 Results

The basic algorithm was not able to stand the test for new and unknown malwares and gave a high false positive rate of around 30%. This indicated the flaw in the filtering method as only those signatures were filtered out that were found in the training data. A high number of signatures were found in the clean programs in the test dataset. The modified algorithm remedied this problem. Assigning the final class outcome based upon the majority vote for malware and clean signatures in a file decreased the false positive rate significantly. Besides counts of the signatures, the signature databases also carried the scores for each signature that described the probability of finding that

Table 5.6: Experimental results for new and unknown malwares using automatically extracted signatures by applying sequential association mining.

Method	Detection Rate	False Alarm Rate	Overall Accuracy
Count	73.1%	2.2%	85.9%
Score	85.9%	7.0%	89.6%
Combined	86.5%	1.9%	92.5%

signature in the entire program collection. Besides count of the signatures, we used these scores also to reach a final class verdict. The last measure that we used was a combination of scores and counts.

CHAPTER 6
CONCLUSIONS

This dissertation provided an introduction to the malware research using data mining techniques. We applied a four tier hierarchy to organize the research and included data mining in the top tier of detection methods. Our work closely resembles information retrieval and classification techniques, where we replaced text documents with computer programs and applied similar techniques. Unlike previous attempts at applying data mining techniques at a syntactic level, using n-grams, we introduced a variable length instruction sequence, that inherently captures program control flow information and hence provides a semantic level interpretation to the program analysis. In our quest to choose the best classification model, we compared different feature selection methods and classifiers and provided empirical results. We proposed using association analysis for feature selection and automatic signature extraction and were able to receive as low as 1.9% false positive rate and as high as 93% overall accuracy on novel malwares with the algorithms that we devised. In the end future work is proposed to extend the association analysis method for improved classification and time and space complexity for the algorithms.

CHAPTER 7
FUTURE WORK

The malware detection using association analysis research is still in its initial stages. There are many ideas and methods that are yet to be implemented. We present a number of ideas as future research directions for using association analysis for malware detection.

7.1 Feature Extraction

Association analysis did not prove to be very effective for feature selection from malware and clean files. The selected features performed poorly when used alone to classify between new unknown malware and clean programs. Although we removed signature features and features that were too common to both the classes, the performance was still poor.

For experimentation purposes, several other representations of the term document matrix that resulted after the feature selection process, can be used. These include a normalized term count by total number of terms or by the maximum number of terms. A log scale can also be used, but the most notable representation is the TF-IDF representation. In the vector space model with a term frequency or boolean representation, each coordinate of the document vector is computed locally, taking into account only the particular term and document. This gives equal importance to all the coordinates, that may not be the case. Some terms occur frequently in a number of documents, but they may not be related to the defining contents of the document. On the other hand, there may be terms that are not found in many documents, but may provide a better definition of the document. This can be cured by the *Inverse Document Frequency (IDF)* method, that scales down the contribution of frequent terms across the documents and scales up the rare terms. IDF is multiplied by TF, to get the feature representation. A series of experiments can be conducted for these representation types.

7.2 Signature Extraction

The signature extraction method needs improvement on two grounds. First is to increase the detection rate and second is to reduce the time and space complexity of the algorithm. The combined measure of signature scores and count proved efficient with false positives but false negatives remained high and that amounts for a bigger problem.

Signatures are essentially rare items and this should be the direction, the extraction mechanism should proceed. Traditionally association analysis, gives the items that frequently occur together. To extract the signatures as rare items, the *negative border* can be considered, where negative border is the set of all *infrequent* items, that were rejected at each step. This would automatically improve the space complexity.

We used SAS for the sequential association analysis that uses Apriori algorithm to perform the task. It has been proven that the Apriori, is not the most efficient method for sequential pattern analysis [Kan02]. For improved efficiency, Frequent Pattern-Growth (FP-Growth) method should be used instead.

7.3 PE Header

Another area of experimentation is to use the information from the PE header. We initially developed a rule based system to detect malwares [SWL05]. Instead of using hand crafted heuristic rules, association analysis can be employed to extract these rules from the malicious PE headers.

7.4 Stratified Sampling

We did a random sampling to create training and test datasets with a holdout method with 70/30 split. For a better representation of the various malware families and variants a stratified sampling approach can be applied. A temporal element can be added to the sampling procedure to reflect the timeline of the appearance of different malwares. Malwares appearing later in a chronological sequence of events should be part of test sample to represent newer malwares.

7.5 Real Time Implementation

This work was focused on academic research and the real time implementation of the proposed data mining framework for malware detection was not discussed. The following issues needs to be considered for a real time implementation of such a system.

7.5.1 Time and Space Complexity:

The major hindrance for such the real time implementation of such a data mining framework is the time and space complexity of the machine learning and other algorithms involved. The disassembly, parsing and feature extraction are time consuming processes and require a lot of space also. In an automated framework these processes need to be streamlined for better efficiency.

7.5.2 Cost Sensitive Learning:

One thing that was not discussed in this work, is cost sensitiveness of the learning process. False negatives carry a different cost than false positives. Leaving out a computer virus is not the same as wrongly identifying a clean program as a virus. To address the issue, cost sensitive learning can be used, where a cost matrix can be defined carrying costs for different true and false identifications.

7.5.3 Class Distribution:

In the malware or fraud detection realm, the class distributions are highly skewed [PAL04], [BJL08]. Cost sensitive learning mentioned in the last paragraph, addresses this issue also. Other methods include under sampling and over sampling. [MB02].

7.6 Combining Classifiers

In this work, we compared different classifiers and gave experimental results for the best one based upon classification accuracy and ROC curves. [Web05] gave an excellent account of combining classifiers. Using this approach we can combine the output of different classifiers instead of choosing the best one among them. The classifiers can be trained on the same dataset or different datasets. For different datasets, one suggestion is, to combine the classifiers learned on PE header information and instruction sequences to assign one final class to the output. For the same dataset, several classifiers including random forest and neural networks, can be built and the final class output can be assigned using a voting strategy.

7.7 More Classifiers

We covered an array of classifiers in out work. These include random forest, bagging, decision tree, neural networks, support vector machines and logistic regression. Several other classifiers can be added to this list including logic regression (using the Boolean representation of the term-document matrix), Bayesian methods and nearest neighbor methods.

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