Malware Analysis using Profile Hidden Markov Models and Intrusion Detection in a stream learning setting

A Thesis

Submitted For the Degree of

Master of Science (Engineering)

in the Faculty of Engineering

by

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May 2014

TO

Bhagawan Sri Ramana Maharishi and His grace

Acknowledgements

First of all I would like to thank my Research advisor Professor N.Balakrishnan for all his support and advice. He has encouraged and motivated me to learn about and work on some interesting problems in the area of computer security. He is been very instrumental in my growth as a researcher and gave the right perspective to view the problems, in very important junctures. He gave me and all his students the great opportunity to interact with and learn from some of the greatest minds in the country. I shall always hold the lessons I learnt from him about striving for excellence and results of hardwork, very close to my heart. He and Mrs. Jyothi Balakrishnan have been the pillar of support, during many tough times. I shall always remain indebted to him for all his kindness and guidance. I consider myself very privileged to be part of the Information Systems Lab in SERC, IISc.

Next I would like to thank the Chairman of Supercomputer Education and Research Centre, Prof. Govindarajan for his support and encouragement. The resources and facilities in SERC were always available for the students doing research. I also wholeheartedly thank my colleagues and friends in my lab., Bharath, Naimisha, Sudheep, Indira Ma'm, Prashant Kulkarni, Prashant Sharma, Nikhil Koul, Pritam padhy, Sachin Singh and Venkat Padhy for their unwavering support and help. Work gave me so much joy, when done in the company of such motivated and cheerful people. I wish to thank all my teachers who have been a great source of inspiration; especially Prof. P A Shastry, Prof. Vittal Rao, Prof. Joy Kuri, Prof. Veni Madhavan and Prof. Mathew

Jacob.

I also want to thank my friends Arun, Raman, Hariprasad, LakshmiNarasimhan, LP, Madhavan and the gang.Special thanks to my music Guru Deepak Paramashivam. They have motivated me so deeply to excel in whatever I do and have taught me the importance of staying humble and simple. I also wish to thank wholeheartedly, Ms.Nagarathna, Mrs Swarnalatha Ramesh and Mr.RaviKumar for their support and help, throughout. I thank my husband Dev for his unwavering support. And I thank all my friends, employees and colleagues at IISc for making it a memorable time of my life.

Publications based on this Thesis

1. Ravi S., Balakrishnan N. and Venkatesh B. (2013), Behavior-based Malware Analysis using Profile Hidden Markov Models. *In Proceedings of the 10th International Conference on Security and Cryptography, pages 195-206. DOI: 10.5220/0004528201950206*

2. Saradha R., Nikhil K., Balakrishnan N. (2011) Behavior-based malware classification using Profile Hidden Markov Models. Poster accepted at the *Women in Machine Learning Workshop* (NIPS 2011), Granada, Spain.

Abstract

In the last decade, a lot of machine learning and data mining based approaches have been used in the areas of intrusion detection, malware detection and classification and also traffic analysis. In the area of malware analysis, static binary analysis techniques have become increasingly difficult with the code obfuscation methods and code packing employed when writing the malware. The behavior-based analysis techniques are being used in large malware analysis systems because of this reason. In prior art, a number of clustering and classification techniques have been used to classify the malwares into families and to also identify new malware families, from the behavior reports. In this thesis, we have analysed in detail about the use of Profile Hidden Markov models for the problem of malware classification and clustering. The advantage of building accurate models with limited examples is very helpful in early detection and modeling of malware families.

The thesis also revisits the learning setting of an Intrusion Detection System that employs machine learning for identifying attacks and normal traffic. It substantiates the suitability of incremental learning setting(or stream based learning setting) for the problem of learning attack patterns in IDS, when large volume of data arrive in a stream. Related to the above problem, an elaborate survey of the IDS that use data mining and machine learning was done. Experimental evaluation and comparison show that in terms of speed and accuracy, the stream based algorithms perform very well as large

volumes of data are presented for classification as attack or non-attack patterns. The possibilities for using stream algorithms in different problems in security is elucidated in conclusion.

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Keywords

Malware analysis, Malware classification and clustering, Polymorphic viruses, Dynamic malware analysis, Profile Hidden Markov Models, Multiple Sequence Alignment, Huffman encoding, Phylogenetic trees, Intrusion Detection Systems, Misuse Detection, Anomaly Detection, Data mining, Batch learning, Online learning, Stream-based learning, Hoeffding trees, Weighted-Majority algorithm

Notation and Abbreviations

- IDS - Intrustion Detection System
- PHMM - Profile Hidden Markov Model
- IPS - Intrusion Prevention System
- MOA - Massive Online Analysis Framework
- HMM - Hidden Markov Model
- KDD - Knowledge Discovery in Databases
- DoS - Denial Of Service
- DoD - Department Of Defense (USA)
- F-Score - Figure of merit score
- TCP - Transmission Control Protocol
- IP - Internet Protocol
- Σ - The alphabet of symbols in a Hidden Markov Model
- Z - The set of hidden states in a Hidden Markov Model
- $E_{|Z|x|\Sigma|}$ - The emission probability matrix in a Hidden Markov Model
- $A_{|Z|x|Z|}$ - The state transmission matrix in a Hidden Markov Model
- π - The initial state distribution in a Hidden Markov Model

- $\mathcal{X}$ - The instance space in an online learning setting
- x^t - The data instance in round t of online learning algorithm
- N- Dimensionality of the Instance space
- y^t - True label of the data instance in round t of online learning algorithm
- $\hat{y}^t$ - Predicted label of the data instance in round t
- $\ell(y^t, \hat{y}^t)$ - Loss function defined over true and predicted labels

Chapter 1

Introduction

A cyber attack system is any kind of offensive system used by individuals or large organizations that targets infrastructures, computer networks and information systems, and other devices in various malicious ways. The threats or attacks usually originate from an anonymous source that either steals, changes, or completely destroys particular target by hacking into a vulnerable part of the system. Cyber-attacks have become increasingly sophisticated and dangerous and a preferred method of attacks against large entities, by attackers. Cyber-war or cyber-terrorism is synonymous with cyber attacks and exploits three main factors for terrorising people that further impairs tourism, development and smooth functioning of governments and other infrastructure in a country or a large business corporations. These factors are fear about security of lives, large scale economic loss that causes negative publicity about a corporation or government and vulnerability of government systems and infrastructure that raises questions about the integrity and authenticity of data that is published in them.

1.1 Types of cyber attacks

We can list down the different kinds of cyber attacks in an increasing order of sophistication and complexity of the attack itself. The order is also chronological in some ways since the attacks have become more sophisticated with time in order to stay ahead of the

security systems that are used in the networks and on individual systems. The initial attacks on computers were more social engineering attacks that were not very complicated and were aimed at individual hosts. The network sniffers, packet sniffing and session hijacking attacks came next, with the advent of internetworking. Automated probes and scans that came next, do reconnaissance following which widespread attacks such as the distributed denial of service type attacks were executed. Viruses that took advantage on the vulnerability in a software just by looking at compiled code came into picture. The more sophisticated viruses that spread through emails and widespread trojans came alongside. Anti-forensic malware and worms that escape the security systems by using encryption and code packing, are very rampant in recent times. So are the increasingly sophisticated network of compromised hosts, called botnets. Botnets have command and control capability within its own network and is capable of doing extremely large-spread attacks in the scale of internet.[58]

1.2 Role of malware in Cyber attacks

In all these different techniques from the early times to now, one component of the attack architecture necessarily needs to be detected and mitigated from spreading itself. These are the malicious executable files or the malware, that do the bulk of the intrusive activities on a system and that spreads itself across the hosts in a network.

Malicious software (malware) is defined as software performing actions intended by an attacker, mostly with malicious intentions of stealing information, identity or other resources in the computing systems. The different types of malware include worms, viruses, Trojan horses, bots, spyware and adware. They all exhibit different sort of malicious behaviour on the target systems and it is essential to prevent their activity and further proliferation in the network using different methods.

1.2.1 Viruses

A virus is a program that copies itself and infects a host, spreading from one file to another, and then from one host to another, when the files are copied or shared. The viruses usually attach themselves mostly to executable files and sometimes with master boot record, autorun scripts, MS Office Macros or even other types of files.The theoretical preliminary work on computer viruses goes back as far as 1949. John von Neumann (1903-1957) developed the theory of self-reproducing automatons. The function of a virus is to essentially destroy or corrupt files on the infected hosts. It was in 1984 that Fred Cohen introduced the implementation of computer virus and exhibited its capabilities on a unix machine.[59]. The "Brain" virus that infected the boot sector of the DOS operating system was released in 1986.

1.2.2 Worms

Computer worms send copies of themselves to other hosts in the network, usually through security vulnerabilities in the operating systems or the software. They spread automatically most often without any user intervention.The worms spread very rapidly over the network affecting many hosts in their path. They comprise the majority of the malware and are often mistakenly called viruses. Some of the most famous worms include the *ILOVEYOU* worm, transmitted as an email attachment, that cost businesses upwards of 5.5 billion dollars in damage. The Code Red worm defaced 359,000 web sites[60]. SQL Slammer had slowed down the entire internet for a brief period of time and the famous Blaster worm would force the host computer to reboot repeatedly.

1.2.3 Trojan horses

Trojan horses are applications that appear to be doing something innocuous, but secretly have malicious code that has intrusive behavior. In many cases, trojans usually

create a backdoor that allows the host to be controlled remotely either directly or as part of a botneta network of computers also infected with a trojan or other malicious software. The major difference between a virus and a trojan is that trojans do not replicate themselves. They are usually installed by an unsuspecting user. PC Writer was the first trojan horse pogram that came out in 1986. It pretended to be like a legitimate installable for the shareware PC Writer Word processing program. But on execution the trojan horse would start and delete all data on the hard disk and format the drive.

1.2.4 Spyware

Spyware is any software installed on a host which collects your information without the consent or knowledge of the user, and sends that information back to its author. This could include keylogging to learn about passwords,and other sensitive information. The spyware starts installing unwanted software and toolbars in the browsers without the knowledge or consent from the user. Many people have spyware running in their systems without even realizing it, but generally those that have one spyware application installed also have a dozen more. The sign for its presence is that the computer becomes very slow and many unknown software are usually automatically installed.

1.2.5 Botnets

Botnets are networks of compromised hosts which can be remotely controlled by an attacker who is usually referred to as the botmaster or the bot-herder. A bot is typically connected to the Internet, and mostly affected by a malware akin to a trojan horse. The botmaster can control each bot remotely over the network. It can instruct the bots to do malware update, send spam emails and steal information. The operation of the bots are controlled using a command and control (C2C) channel, which can be centralized or peer-to-peer[58]. The topology of the command and control channel determines the

efficiency and resilience of the botnet. The botnet detection is an active area of research due to the inherent complexity and scale of the problem.

1.3 Malware menace in recent times

The proliferation of malware in recent times is obvious from the statistics gathered, over the years.From the data gathered from an independent IT security company AV-Test, we see that the total number of malware on the internet has reached about 100 million in the year 2012. Over 30 million new malware instances have appeared in the year 2012 alone, which is twice the number of unseen malware that were introduced in the previous year. The plots in Fig. 1.1 and 1.2 show the total and the new types of malware that were seen over the years.

A range of malicious software/systems, ranging from classic computer viruses to Internet worms and bot networks, target computer systems linked to a private networks or the Internet. Proliferation of this threat is driven by a criminal industry which systematically comprises networked hosts for illegal purposes, such as gathering of confidential data, distribution of spam messages, and misuse of information for economic gains etc. According to McAfee, MyDoom is a massive spam-mailing malware that caused the most economic damage of all time, an estimated $38 billion. Conficker was a botnet employed for password stealing and it caused an estimated $9.1 billion damage. Unfortunately, the rising numbers and high diversity of malware render classic security techniques, such as anti-virus scanners, not very useful and have resulted in millions of hosts in the Internet infected with malicious software (Microsoft, 2009; Symantec, 2009)

From the above discussion, it is seen clearly that a huge task of improving the detection capability and methodology on the host lies on the antivirus products. They are

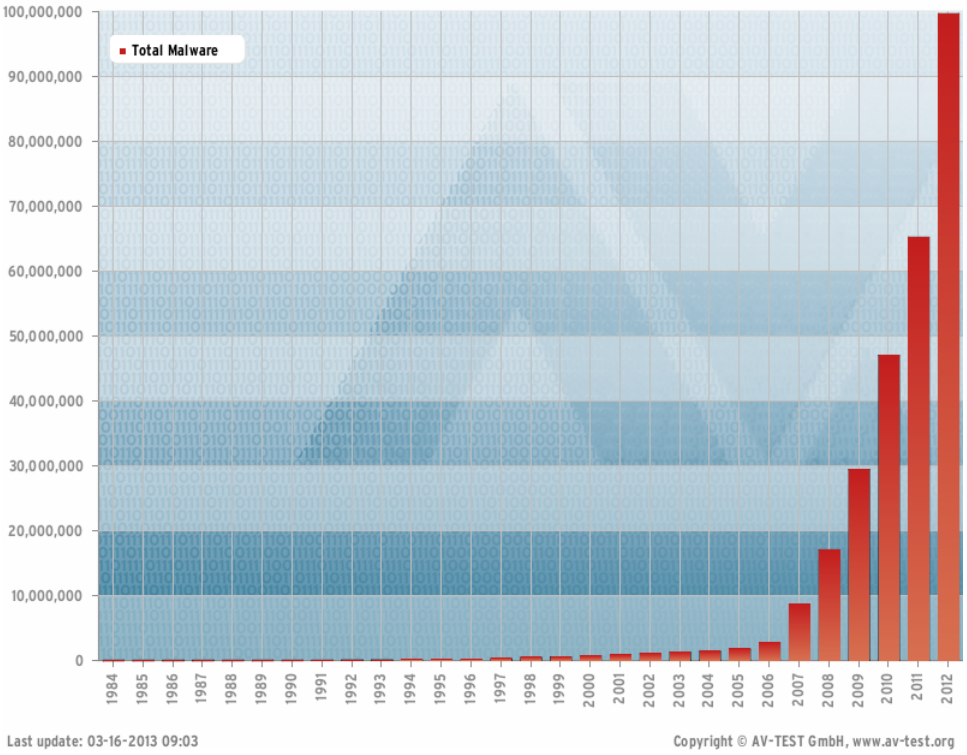


Figure 1.1: Total malware count over Years

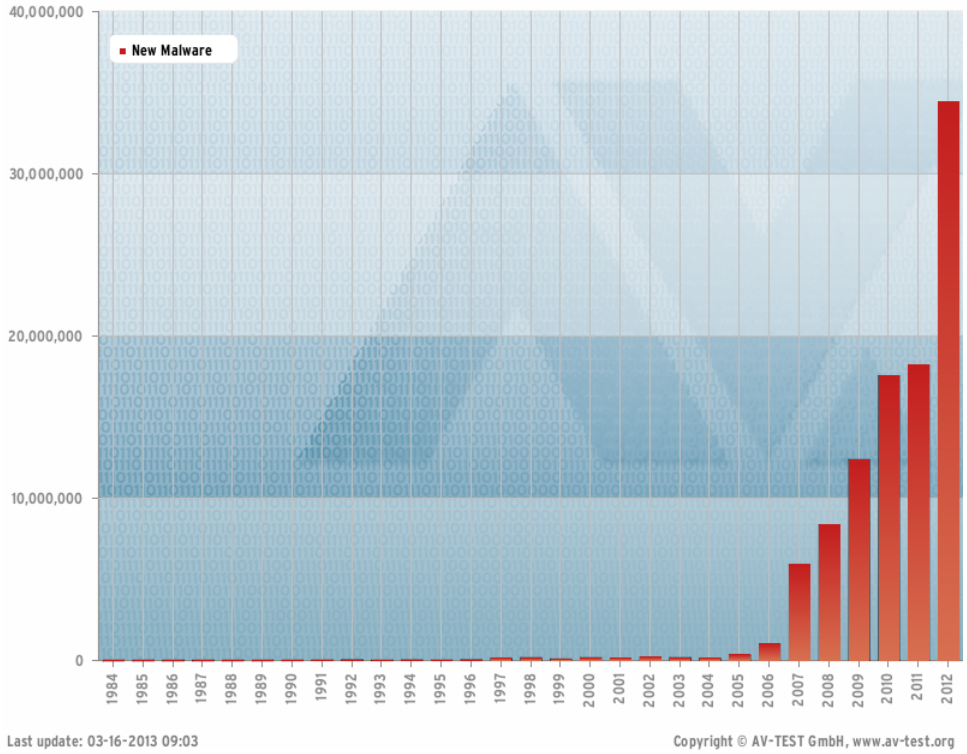


Figure 1.2: New malware count over Years

constantly challenged by the malware which make use of known or unknown vulnerabilities in the software or the network systems to come up with new kinds of attacking and hiding mechanisms. The antivirus companies employ many ways of creating the database of known *attack vectors* to detect known attacks. One of them is to collect any suspicious looking files or binaries (or those that were known to cause problems) that are identified by the end users or another system, and then analyse them. This process, called malware analysis, encompasses the steps of malware detection and malware classification. These need not be separate steps in the whole process, though in some practical implementations they may be.

1.4 Defense mechanisms

In this section, we review the detection and prevention solutions for cyber attacks in general and malware in particular. When we talk about security solutions it is obvious to start with defining an Intrusion Detection System. An Intrusion Detection System can be a device or a software that monitors a network or a system, for malicious activities and generates a reports for a management station[47]. They usually detect the intrusion that have already occurred or that which are in progress. The most early systems in 60s and 70s involved looking for suspicious or unusual events in system audit logs. The amount or granularity of audit logs that are analysed is a tradeoff between overhead and effectiveness. The host based IDS refers to a system that is deployed on individual hosts; This is usually an agent program that does event correlation, log analysis, integrity checking, policy enforcement etc. on a system level. The Anti-virus solutions are a type of HIDS that monitor the dynamic behavior of the host system. They monitor every user and system activity and raise alarm on any security policy violation at user and system level. The Anti-virus software products study and analyse the malware and come up with unique patterns or *signatures* to identify the

different types of malware. This is necessary since the cleanup, quarantine and removal procedures for each kind of malware is different from one another.

Everyday the anti-virus companies receive tens of thousands of instances of possible malicious files that have to be analysed, in a quick and efficient way. For this the *signature-based* malware detection techniques are widely used owing to their speed and effectiveness. But they may not give a complete coverage for all possible attacks, since the malware toolkits generate *polymorphic and metamorphic* variants of viruses and worms that easily outsmart the signature based systems. After analysis, the binaries are given labels and the signatures are extracted for newly seen variants and stored in the virus database.Throughout the thesis, we define malware analysis as classifying or clustering a malware to a particular family or group and do not address the problem of malware detection alone. The problem and the existing solutions for solving it are explained in detail in the coming sections.
We now will look at the role of IDS in detection of previously unseen zero-day attacks.

Apart from the Host-based IDS discussed before the other class of IDS that is used to monitor the activities and incidents going in a network form the class of Network Intrusion Detection Systems. Several rule-based and statistical methods have been employed in the existing NIDS. Some IDS use deep packet inspection in the network traffic data while some methods use header information in the packets or do sifting of the traffic data at various level of granularity, to look for abnormal patterns. The traffic data can be voluminous and sampling the data to look for patterns, especially for rare and previously unseen events such as a virus attack can be challenging task. Also the attacks can be crafted in such as way as to exhaust the resources that are used in the IDS platform.

The other main classification of IDS is done based on the choice of modeling the attack and the non-attack or benign data.There are misuse- detection systems or the signature-based detection systems that model the patterns of previously known attacks. These could be hand-crafted signatures or even rules learnt by a system, that characterised a known attack. These systems are fast in detecting known attacks but are very weak in detecting zero-day attacks. Also the speed of these systems tend to be slower as the database of signature grows and most often than not, the attacks are detected after they occur only. The other class of IDS is the anomaly detection systems, that models the normal non-malicious behavior of the system and ags any deviation from that as abnormal. They are very effective in identifying new unseen attacks, but suffer from the problem of high false-positive rates. Also the environment is so dynamic that the very definition of what is normal or abnormal data itself changes over time, posing more challenges in modeling the system. The Intrusion Detection Systems that make use of statistical features in the traffic patterns and/or payload data, have the inherent problem when it comes to relearning the model. An efficient strategy for relearning becomes very important and there are very few prior work that address this. Also the machine learning system itself can become vulnerable to manipulative training data injected by the hackers in order to mislead the system into modeling malicious code as non malicious. Thus the security of a batch-trained model itself becomes a serious concern [62].

1.5 Malware Analysis

The malware analysis that Anti-virus companies do, can be classified broadly into two categories; the static analysis techniques and the dynamic analysis techniques. The static techniques involve looking into the binaries directly or the reverse engineering

the code for patterns in the same. The dynamic analysis techniques involve capturing the behavior of the malware sample by executing it in a sandboxed environment or by program analysis methods and then use that for extracting patterns for each family of virus. Examples for these are systems like Anubis, [21] and CWSandbox. Of late static binary analysis techniques are becoming increasingly difficult with the code obfuscation methods and code packing employed when writing the malware. The behavior-based analysis techniques are preferred in more sophisticated malware analysis systems because of this reason. In previous works, a number of clustering and classification techniques from machine learning have been used to classify the malware into families and to also identify new malware families, from the behavior reports. In our experiments, we propose to use the Prole Hidden Markov Model[6] to classify the malware les into families or groups based on their behavior on the host system. We have looked at the challenges involving analysis of a large number of malware infected les, and show an extensive evaluation of our method in the following chapter.

1.5.1 Static malware analysis

Signature based detection is used to identify a virus or family of viruses. A signature based detector needs to update its list of signatures more often. Since the signature of a new virus would not be available in the database, it is not possible to detect it as a new virus. Detectors sometimes look into heuristics instead of relying on signatures. However, signatures form a formidable percentage in the detection process. Signature detection is fast and simple. Polymorphic and metamorphic viruses cannot be contained using signature detection. Metamorphic malware use a combination of various code obfuscation techniques. Storing signatures of each variant of a malware is practically not feasible since it increases the dictionary of the detector with unnecessary signatures.

1.5.2 Signature-based techniques

Signature-based detection provides undeniable advantages for operational use. It uses optimized pattern matching algorithms with controlled complexity and very low false positive rates. Unfortunately, form-based detection proves completely overwhelmed by the quick evolution of the viral attacks. The bottleneck in the detection process lies in the signature generation and the distribution process following the discovery of new malware. The signature generation is often a manual process requiring a tight code analysis that is extremely time consuming. Once generated, it must be distributed to the potential targets. In the best cases, this distribution is automatic but if this update is manually triggered by the user, it can still take days. In a context where worms such as Sapphire are able to infect more than 90% of the vulnerable machines in less than 10 min, attacks and protection do not act on the same time scale.

1.5.3 Problems in static analysis

In the past few years the number of observed malware samples has increased dramatically. This is due to the fact that attackers started to morph malware samples in order to avoid detection by syntactic signatures. McAfee, a manufacturer of malware detection products, reported that 1.7 million out of 2.8 million malware samples collected in 2007 are polymorphic variants of other samples. As a consequence a huge number of signatures need to be created and distributed by anti-malware companies. These have to be processed by detection products at the users system, leading to degradation of the systems performance. Malware behavior families can address this problem. So, all polymorphic variants of a particular sample are treated as members of the same malware behavior family. For this, we need an automatic method for appropriately grouping samples into respective behavior families.

1.5.4 Polymorphic malware

The variants produced by polymorphic malware constantly change. This is done by file-name changes, compression, encrypting with variable keys, etc. Polymorphic malware produce different variants of itself while keeping the inherent functionality as same. This is achieved through polymorphic code, which is core to a polymorphic malware.

1.5.5 Metamorphic malware

Metamorphic malware represent the next class of virus that can create an entirely new variant after reproduction. Unlike, polymorphic malware, metamorphic malware contain a morphing engine. The morphing engine is responsible for obfuscating malware completely. The body of a metamorphic malware can be broadly divided into two parts - namely Morphing engine and Malicious code Metamorphic malwares use code obfuscation techniques as opposed to encryption used by polymorphic viruses.

1.6 Code obfuscation techniques

Code obfuscation is a technique of deliberately making code hard to understand and read. The resulting code after obfuscation has the same functionality. There are a variety of code obfuscation techniques namely Garbage Code Insertion, Register Renaming, Subroutine Permutation, Code reordering and Equivalent code substitution that are heavily used in the metamorphic virus generation toolkits. The Table 1.1 is an example of equivalent code substitution and garbage code insertion. The following figure shows an example of code re-ordering that is done using unconditional jump instructions. Of all these methods the subroutine permutation is little easier to detect using signature-based technique since there is no actual modification of the instructions, as such.

Table 1.1: Samples of code obfuscation

Original	Obfuscated Version 1
call Delta Delta: pop ebp sub ebp, offset Delta	call Delta Delta: sub dword ptr[esp], offset Delta pop eax mov ebp, eax
Original	**Obfuscated Version 2**

call Delta
Delta: pop ebp
sub ebp, offset Delta
	add ecx,0031751B ; junk
	call Delta
	Delta: sub dword ptr[esp], offset Delta
	sub ebx,00000909 ; junk
	mov edx,[esp]
	xchg ecx,eax ; junk
	add esp,00000004
	and ecx,00005E44 ; junk
	xchg edx,ebp

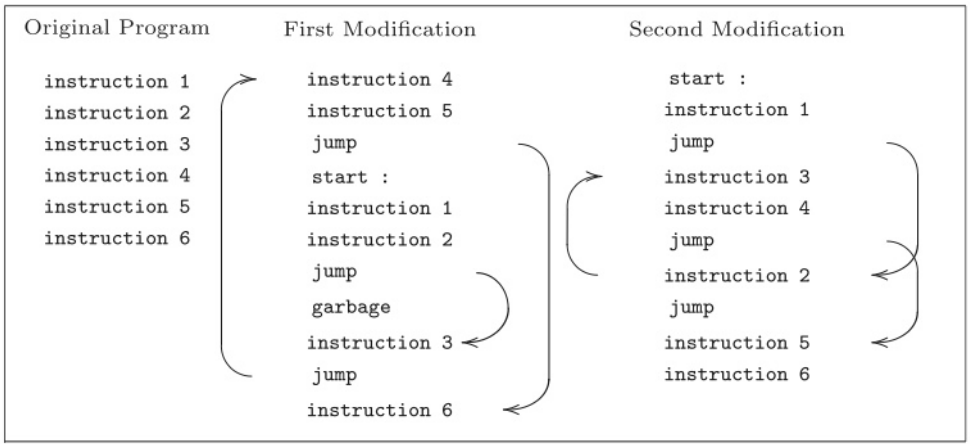


Figure 1.3: Example of code reordering

1.7 Dynamic malware analysis

Automated, dynamic malware analysis systems work by monitoring a programs execution and generating an analysis report summarizing the behavior of the program. These analysis reports typically cover file activities (e.g., what files were created), Windows registry activities (e.g., what registry values were set), network activities (e.g., what files were downloaded, what exploit were sent over the wire), process activities such as when a process was created or terminated and Windows service activities such as when the service was installed or started in the system etc. Several of them are publicly available on the Internet (Anubis, CWSandbox , Joebox , Norman Sandbox). The main thing to note about dynamic analysis systems is that they execute the binary for a limited amount of time. Since malicious programs do not reveal their behavior when only executed for several seconds, dynamic systems are required to monitor the binarys execution for a longer time. Thus dynamic analysis is resource-intensive in terms of necessary hardware and time. There is also the problem of multiple paths in the execution sequence and analysing all of them may not be possible in a sandbox environment.

1.8 Unsupervised and Supervised models on Dynamic analysis reports

Machine learning approaches like classification and clustering of malware have been proposed on reports generated from dynamic analysis. Models are built for malware families whose labels are available and used for predicting the malware labels for newly seen sample reports. These models can generalise well, depending on the learning algorithm and the sample training data from which they were built. The state-of-the-art malware analysis systems perform a step of classification followed by a step of clustering. In the next section, a detailed review of these systems and their performance

is presented.

1.9 Related work in Dynamic analysis

In this section, we will look at some of the related work done in the behavior-based malware analysis and classification. In malware analysis problem, there is not just one standard dataset in all previous research. Most malware datasets are collected over a certain periods of time using a honeynet setup and they comprise PE executables, aimed to attack Window based systems. The dynamic analysis techniques gained prominence because of the limitations in the static analysis techniques [14].Moser et al proposed a method where the normal model of programs were modeled using sequences of six system calls and any deviations from this was flagged as anomaly or a security threat.This was one of the first approaches of using behavior to differentiate malware from benign programs.

Bailey et al[15] tracked more abstract features like system state changes rather than system call sequences for malware classification. The clustering method they have used looks at overall system state and generates a behavioral fingerprint for each malware analysed. This is one of the earlier works that addressed the issue of anti-virus labeling inconsistencies.The Normalised Compression Distance is computed for every pair of malware samples and a simple hierarchical clustering method (using single linkage) was done on a dataset of malware collected in a sandbox system running Windows XP. There were 3360 malware that were analysed and resulting clustering had 403 clusters. In comparison with labellings by popular anti-virus systems like Symantec, McAfee, FProt and ClamAV, the behavior based method gave much better detection accuracy of 91% and consistent labeling for a given behavior profile. The authors however mention that behavior profiles can be looked at a finer level (rather than state changes alone) with modern system audit and trace systems such as CWSandbox, for better

performance. Also the length of malware behavior signatures differ a lot and this affects the clustering accuracy.

In the process of malware clustering, different distance measures have been used to find the similarity between every pair of files across different malware families. Some of these measures are appropriate for the analysis of metamorphic variants whereas some are not, particularly when the order of the activities in the behavior isn't taken into consideration. Lee et al proposed a malware clustering approach where a modified Levenshtein distance is used and a k-medoid partitional clustering[16]. The complexity of computing distances between malware in their method is quadratic in the number of system calls and may not scale for large number of files with a lot of variability.

In another work[11], Bayer et al have employed faster approximate nearest neighbor search using Locality Sensitive Hashing for comparison of the analysis reports with known behavior profiles that they have created (using data tainting methods to track system call dependencies). The behavior reports are then clustered using hierarchical clustering algorithm. Comparing the clusters to the true malware clusters gave them 0.98 and 0.93, precision and recall values. The issues in the performance evaluation of this method, given the nature of the dataset is explained in detail later in this chapter when we discuss the dataset we use for evaluation of the proposed PHMM based approach.

Another paper [64] discusses the concept of structural entropy for metamorphic detection problem. The technique proposed has two stages namely file segmentation and sequence comparison. In the segmentation stage, entropy measurements and wavelet analysis were used to segment files. The next stage measures the similarity of file by

computing an edit distance between the segments sequences that are got from the first step. The similarity measure within a particularly challenging group of metamorphic malware was shown.

The automatic classification system given by Rieck et al can be used to identify novel families of unseen malware using clustering and assign new instances of malware to these families by classification using SVMs[1]. In this method prototypes for each class of malware is generated and eventually used in the hierarchical clustering of the malware reports. The experiments for this work are conducted on a larger dataset with close to 33000 reports and a detailed study of resource utilization is also done.Their *malheur* implementation gave F-scores, around 0.95 for the clusters and 0.97 for the classification. In their previous work[2], the classification of malware using support vector machines is elaborated and the discriminative features in behavior reports are analysed to explain classification decisions. The authors also proposed a new representation for the monitored behavior of malware[3]. This representation is optimised to be efficient when applying machine learning and data mining techniques for building models for malware families. The CWSandbox reports are encrypted in the MIST format and all models are built from this representation. We also prefer this representation for our approach with PHMM.

Wagener et al [17] propose a dynamic analysis method where they couple a sequence alignment method to compute the similarities and leverage the Hellinger distances between malware reports. They also show how the use of phylogenetic tree improves their classification method. The zero-day attacks can be found by flagging the executables which have lowest average similarity with the existing classes of malware. Here relative frequencies of functions calls are taken into account in replacement of a global sequence alignment that can be expensive in case of highly varying sequence lengths.

The different distance measures used when clustering similar malware behavior are examined in a work by Apel eta al[23]. Their finding is that the *Manhattan* distance or some *similarity coefficient* used on *3-grams* of the report contents, stored in *tries* or *generalized suffix trees*, work the best. In case of polymorphic malware, 3-grams do not work as well as in others.

To detect similarity in workloads from NFS traces for storage systems, Neeraja et al [4] had proposed to build Profile Hidden Markov models on opcode sequences of the NFS traces. They also observe that very few training sequences for a particular type of workload, was enough for modeling. But the problem here was workload classification of known classes only. In another work by Attaluri et al [18], the profile HMM had been applied for x86 opcode sequences of the polymorphic malware binaries generated by the commonly available virus kits. VXHeavens is a popular website that provides a lot of metamorphic virus kits. Some popular virus kits like VCL32 and NGVCK have been used to generate variants for their study. NGVCK also implements anti-debugging and anti-emulation techniques apart from code obfuscation.The authors observe that the method works for some families better than the others because of the problems like subroutine permutation and the code reordering. Further, the study was done on a relatively small dataset with less than three hundred files only.

1.10 Motivation and Problem statement

The number of polymorphic and metamorphic variants of malware that cannot be easily detected by the signature detection techniques, is growing very rapidly. Standard static analysis techniques may not help much in detection of these kind of malware. Also it is important that a family or a group of malware is detected early in its life

cycle. Since most malware do a heavy code reuse with obfuscation on top of it, the behavioral signatures of malware can be used for detection and malware analysis. It should also be seen as an effective method for grouping a class of viruses and coming up with a taxonomy, since there are many inconsistencies in the labeling of a malware class just by searching or a binary signature. With very few number of malware samples, a powerful machine learning technique can be combined to help us with early detection of malware. Also we are in need of fast clustering or grouping mechanism that can scale well for a problem of this scale. We propose a method that uses Profile Hidden Markov models and a fast recursive bisection clustering method to solve the gaps in the chosen problem. We also address the efficiency of training and adding new models to an existing database of built models in an incremental fashion, in our proposed PHMM approach.

With regards to the network oriented malware attacks, many important issues remain with IDS that monitor them. IDS should detect more attacks with fewer false positives and must keep pace with modern networks of increased size, speed and dynamics. There is also the need for analysis techniques that help in identifying attacks in the network, at a higher level, for example like in case of botnet topology structures. The goal is to develop a system that detects close to 100 percent of attacks with minimal false positives. This goal is still not easily achievable. In practical scenarios, many businesses and corporate companies protect their networks by using an array of different IDS solutions that each address a certain kind of attack in an efficient way. This opens up a whole new area for research involving fusing the decisions of these individual systems to give a better detection accuracies and performance. Data mining or machine learning algorithms are algorithms that learn a model for any given pattern, from data. The model is then used for predictions in the live data. Many statistical,

probabilistic and rule based systems are designed to learn from sample data and used later for predicting the patterns in the new data. The algorithms are formulated in a way that they generalise well on data that may not be exactly the same as the sample. These make machine learning algorithms powerful when employed in a domain as dynamic as malware analysis or intrusion detection. Still there are challenges intrinsic to the domain of security where encryption is heavily used.

In case of network IDS many machine learning algorithms, such as SVM, Logistic regression, Regression splines, decision trees and boosting have all been tried before for classifying a data flow as benign and attack types. But the issue of retraining the models on the rapidly changing attack and normal data is still a challenge. It should be very important that this aspect is taken into consideration, since the models trained on some training data may not work well on a data that has certain differences from the trained data. Thus the learning algorithm is expected to model the data rapidly with fewer samples and also adapt quickly to any difference from a previous model. The class of stream learning algorithms are well suited for this kind of a problem where there continuous arrival of data in a stream. The online learning algorithms address the issue of differences in the distribution from which the training data and the actual data get generated. The superior performance of online and stream-based learning algorithms could pave the way for future statistical learning based IDS, that don't require frequent retraining.

1.11 Organisation of the thesis

The thesis is organised in the following manner. In Chapter 2, we explain in detail mathematical basis for the proposed methods, measures and metrics used in evaluation and comparison of results. The dataset used for experiments on the proposed approach

with PHMMs and clustering for malware analysis is referred as the *malheur* dataset [19]. The efficacy of stream based learning for IDS is shown on the famous KDD Cup 1999 Intrusion Detection dataset. Both the datasets are explained in detail in chapters 3 and chapter 4 respectively, before we explain our experiments. The proposed approach in using PHMM for building models for malware classification and clustering, based on their behaviour, is elaborated in Chapter 3. The initial set of experiments using PHMM for malware classification and the obtained results are elaborated. The initial experiments address the problem as a malware classification problem only. A closer look at malware analysis in a large scale systems is done later in Chapter 3 itself. The inherent issues in analysing large volumes of malware and evaluating the results of using various learning techniques is analysed in great detail here. The second set of experiments that were performed on a larger dataset, with steps of malware clustering and incremental building of models, have been explained too.

Chapter 4 addresses the problem of relearning in a data stream setting (as in a computer network). The data stream setting for a machine learning problem is described in great detail here. The theory of Hoeffding trees that are key to the stream learning paradigm are explained here. The online learning setting and comparison of these various types of learning algorithms on the KDD Cup 99 dataset is done subsequently. The thesis ends with a conclusion from this research work.

Chapter 2

Mathematical basis for chosen approach and Evaluation Metrics

2.1 Introduction

The Profile Hidden Markov Model is a probabilistic approach that was developed specially for modeling sequence similarity occurring in biological sequences such as proteins and DNA[6][8]. It is also a faster alternative to the traditional deterministic approaches used in sequence matching [8]. It is a modified implementation of HMM, which is basically a generative model and constructs a probabilistic finite state machines. For behavior-based analysis, we again assume that there is a sequence of operations common for a virus family and for a presented new sequence we would like to find the best known match from the database.

2.2 Profile Hidden Markov Models

The main reason for us to choose this approach for solving the problem of finding malware similarity is because the behavior of malware program has variablility, yet has a characteristic signature reflected in the sequence of system calls. For example if we look at the CWSandbox reports for two malware programs from same family, we notice that a sequence of malicious actions is preserved, interspersed with some other actions

introduced to confuse the malware detection system.

A *hidden markov model (HMM)* is very suitable for probabilistic modelling of such sequences, which is evident from past works. Thus it can be used for modelling different classes of malware. But as we have discussed above , there might be additions, deletions or changes to the system calls for different programs within same malware family. The *profile HMM* is exactly designed to model this kind of problem, because it also has non-emitting states or the *delete* states. We would now outline the concept of profile HMM before we proceed to show how it has been used in our work.

2.2.1 Hidden Markov Models

A hidden markov model(HMM) is a statistical tool which captures the features of one or more sequences of observable symbols by constructing a probabilistic finite state machine with some hidden states that are emitting the observed symbols [20]. When the state machine is trained, its graph and the transition probabilities are computed such that they best produce the training sequences. When we test with a new sequence, the HMM gives a *score* for how best the sequence matched with the known state machine. In our case, the observed symbols are the codes for each unique system call in the behavior report of the malware program(MIST codes).

An HMM is specified by the following parameters.

- the alphabet of symbols Σ
- the hidden state set Z
- the emission probability matrix $E_{|Z|x|\Sigma|}$
- the state transmission matrix $A_{|Z|x|Z|}$
- the initial state distribution π

Thus the HMM λ can be written as $\lambda = (\Sigma, Z, A, E, \pi)$. This model can thus be used to assign a probability to an observed sequence X as follows

$$P(X|\lambda) = \sum_{z} \prod_{k} A_{z_k, z_{k+1}} E_{z_k, X_k} \tag{2.1}$$

This probability as indicated by the formula, is that of emitting the observation sequence X after all possible state transitions (i.e state transmission sequences). of the model λ.

The model λ has to be learnt from training data consisting of independent and identically distributed sequences. This can be done by maximizing the probability $P(T|\lambda)$ where T is a training sequence. There is no analytical solution to this, however this can be done by using an iterative procedure that uses *E-M (Expectation-Maximization)* algorithm[20].

Given a sequence X, the *Viterbi* algorithm[20] can be used to compute the hidden state Z, so as to maximise $P(Z|X)$ i.e determine most probable sequence of hidden states that produced the observed sequence. Equation 1 can then be evaluated using the likelihood and *P(X)* got using the forward and backward procedures [20].

2.2.2 Profile Hidden Markov Model in detail

A PHMM is a specific formulation of a standard HMM that makes explicit use of positional information contained in the observation sequences[18]. PHMM is a strongly linear left-right model while HMM is not[6]. A PHMM model allows null transitions, so that it can match sequences that differ by point insertions and deletions happening by chance mutations. They were specifically formulated for use in bioinformatics, where such insertions and deletions to DNA sequences were natural during evolution. Thus PHMMs can be seen effective in modeling metamorphic malware, that also go through similar kind of evolution, both at binary level and at a behavioral level. Furthermore,

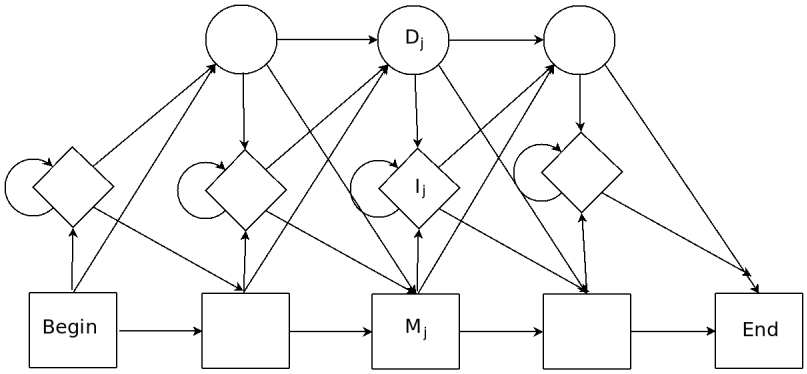


Figure 2.1: The transition structure of a profile HMM. For example, from an insert state (diamond), we can go to the next delete state (circle), continue in the insert state (self loop) or go to the next match state (rectangle). Note that while multiple sequential deletions are possible by following the circle states, each with a different probability, multiple sequential insertions are only possible with the same probability[4]

PHMM state transition matrices are essentially sparser than those of HMM, allowing quicker inference. Fig 2.1 shows a sample PHMM model with match, insert and delete states represented by M_i, I_i and D_i respectively.

A central concept to note here is that of sequence alignment. In DNA sequencing, multiple gene sequences which are significantly related are aligned. The alignment can be used to ascertain if the gene sequences where diverging out from some common ancestor. Now, for an unknown sequence, this *multiple sequence alignment* of a profile, can be used to determine if the sequence is related to it or not.

A *pairwise alignment* of two sequences yields a pair of sequences of equal length that captures the difference between the two original sequences by inserting '-' or gaps. The *global alignment* is an alignment such that the matches are maximised and the insertions/deletions are minimised[22]. The *local alignment* problem tries to locate two longest subsequences from each sequence, such that they are similar. This can be extended to align multiple sequences. This multiple sequence alignment represents a family of similar sequences, where some subsequences are conserved in all. While

```
>13506796c0eb3f5abe59fcc88f97eff1727b5c43.EJIK
TEEEEEEEEEEEEEEEAAAIDCRCRCIIAABIIKAAAEEAAEDECAABEEEEEABBCABE
XXABCECEECPABABCEPPTLPABBAADLD----E----CLTCELTEEEEEEEEEEEEEE
EEEEEEEEEEDECAABEEEEEABBCABEXXPABAAEEAAAEECCCCCCCCCCCCCCCCCC
CCCCCCCCCCCCCCCCCCCCCCCCCEEEKKKKPBKKKKPBABPBPBPBPLTTEEEEEEEEE
EEEEEEEEEE
>09d7bca7c6b0876872864403cb97174e26ce324f.EJIK
TEEEEEEEEEEEEEEEAAAIDCRCRCIIAABIIKAAAEEAAEDECAABEEEEEABBCABE
XXABCECEECPABABCEPPTLPABBAADLDECTCE----CLTCELTEEEEEEEEEEEEEE
EEEEEEEEEEDECAABEEEEEABBCABEXXPABAAEEAAAEECCCCCCCCCCCCCCCCCC
CCCCCCCCCCCCCCCCCCCCCCCCCEEEKKKKPBKKKKPBABPBPBPBPLTTEEEEEEEEE
EEEEEEEEEE
```

Figure 2.2: A sample MSA file for EJIK Malware Sequences

efficient dynamic programming based solutions exist to pair alignment, multiple alignment scales as $O(n^r)$ in both time and space. This makes it prohibitively expensive for implementation.

MUSCLE is a freely available program used commonly for MSA. It uses fast distance estimation using k-mer counting, a progressive alignment using a new profile function, and refinement using tree dependent restricted partitioning method[10]. We have used MUSCLE for generating the MSA files in the *.afa format. The MSA step essentially serves as a training phase where we align sequences of selected few malware reports in each class, in our approach to using PHMM. A sample of sequences that were aligned using MSA is shown in the Figure 2.2. The samples belonged to a malware family commonly named EJIK

The Viterbi algorithm, forward-backward procedure and Expectation-Maximization are naturally extended to PHMMs. In PHMM, the emission probabilities are position dependent unlike in standard HMM. Learning a profile HMM from data involves computing the emission probability matrix E and the state transition probability matrix A using the multiple sequence alignment data. These are given by

$$A_{uv} = \frac{N_{uv}^A}{\sum_v N_{uv}^A} \tag{2.2}$$

$$A_{uv} = \frac{N_{ut}^{E}}{\sum_t N_{ut}^{E}} \tag{2.3}$$

Where N_{uv}^{A} represents the number of transitions from the state u to v and N_{uv}^{E}, the number of emissions of t given a state u.[8] After the model λ has been learnt from the training multiple alignment data, the problem of identifying the family that a new sequence X belongs to, is decided by the rule

$$y(X) = argmax_k P(X|\lambda_k) \tag{2.4}$$

HMMER[7] is an open source implementation of PHMM and its architecture gives flexibility in deciding between local and global alignments. It is a very powerful tool and can used to perform operations like building HMM profiles from MSA, compressing a HMM profile database for efficiency and for searching the most matched profile for a new sequence. We have used hmmer for building HMM profiles for all malware families and for searching the 'best suited' profile for new sequences, that are essentially the malware reports in the test dataset.

Assuming we build a model using PHMM for known malware families, we need to now measure the generalisability or the fit of the model to actual data. The most common metrics used in the classification problem are the Precision, Recall and the F-Score.

2.3 Classification Evaluation Metrics

In machine learning, the binary classification problem can be stated as follows. Given a sample of n training instances (x, y), the learning algorithm typically gives back a model *h(x)*, that minimises the expected error in output with respect to the actual joint distribution D over the input and output variables. In multi class setup, we use what

are called the Type I and Type II errors to measure the performance of a classifier. The terms true positives, true negatives, false positives, and false negatives compare the results of the classifier under test with trusted external labeling. The terms positive and negative refer to the classifier's prediction, and the terms true and false refer to whether that prediction matches the external judgment.

2.3.1 Precision

Precision is also called the positive predictive value (PPV) . It is the ratio of true positives or the number of samples classified correctly by the classifier to the total number of positive samples in observation (true positives + false positives). Therefore

$$Precision = \frac{tp}{tp+fp}$$

2.3.2 Recall

Recall is defined as the true positive rate . It is the proportion of true positives or the number of samples classified positive by the classifier to the total number of positive samples in the predicted result (true postives + false negatives). Therefore

$$Recall = \frac{tp}{tp+fn}$$

2.3.3 F- Score

The F-score or the F-measure is the harmonic mean of the precision and recall. The traditional F-measure or the balanced F-measure is given by the following formula.

$$FScore = 2 * \frac{(Precision*Recall)}{(Precision+Recall)}$$

2.3.4 Confusion Matrix

This is a matrix used for easy visualisation of performance of a classifier over multiple class data. Each column of the matrix represents the instances in a predicted class, while each row represents the instances in an actual class. The darkness of the cell

signifies what proportion of the actual class samples were classified into the observed class. A dark diagonal in the matrix signals a good classifier and the gray cells account for the misclassification. In our study we have used this confusion matrix to prove the effectiveness of PHMM in malware family classification.

2.3.5 Accuracy

Accuracy is the most commonly used metric in many classification problems, though it may just not be sufficient by itself. It is the ratio of the total number of correctly classified datapoints to the total number of datapoints in the dataset.

$$Accuracy = \frac{tp+tn}{tp+fn+tn+fp}$$

2.3.6 Kappa statistic

The Kappa statistic refers to several measures that denotes the measure of agreement on categorical data, generally used in a rating problem with different raters. The kappa value of agreement is given by the following equation where $\mathcal{P}(\mathcal{A})$ refers to the probability of agreement among the raters and $\mathcal{P}(\mathcal{E})$ is the probability that the raters agree by chance alone.

$$\kappa = \frac{\mathcal{P}(\mathcal{A}) - \mathcal{P}(\mathcal{E})}{1 - \mathcal{P}(\mathcal{E})} \tag{2.5}$$

2.4 Clustering Comparison Metrics

Clustering of data is an unsupervised learning approach where the data samples are given without any label. The purpose of clustering is to identify hidden structures and patterns that explain the data. Though it is hard to identify the number of clusters in a given dataset, certain tests on the properties of the obtained clustering indicate the quality of clusters. However, in our research we have concentrated on comparing a clustering, with another reference clustering. This was because we assumed that the labels for malware samples supplied by an antivirus software was akin to a cluster ID. Few

clustering methods were applied to the data and then compared to the ground labels(for clusters). The commonly used metric in cluster comparison were again Precision and Recall. Let us carefully look at these measures.

2.4.1 Precision and Recall

Let M denote a collection of m malware instances to be clustered. Let $\mathcal{C} = \{C_i\}_{1 \leq i \leq c}$ and $\mathcal{D} = \{D_i\}_{1 \leq i \leq d}$ be two partitions of M, and let $f : \{1 \dots c\} \rightarrow \{1 \dots d\}$ and $g : \{1 \dots d\} \rightarrow \{1 \dots c\}$ be functions. Many prior techniques evaluated their results using two measures:

$$Precision(\mathcal{C}, \mathcal{D}) = \frac{1}{m} \sum_{i=1}^{c} |C_i \cap D_{f(i)}|$$

$$Recall(\mathcal{C}, \mathcal{D}) = \frac{1}{m} \sum_{i=1}^{d} |C_{g(i)} \cap D_i|$$

where C is the set of clusters resulting from the technique being evaluated and D is the clustering that represents the right answer. More specifically, in the case of classification, C_i is all test instances classified as class i, and D_i is all test instances that are really of class i. In clustering, there is no specific label to a cluster in $\mathcal{D}$ that corresponds to a cluster in $\mathcal{C}$, as in classification. So usually we resort to have the functions that map the clusters between $\mathcal{C}$ and $\mathcal{D}$ as the cluster that has maximal overlap with the one in its domain. Or

$$f_i = \text{argmax}_{\ i'} |C_i \cap D_{i'}|$$

$$g_i = \text{argmax}_{\ i'} |C_{i'} \cap D_i|$$

The pros and cons of using different metrics are explained in detail, with respect to the problem in malware clustering. This is done so because the reference clustering that we use for evaluation, matters in determining the effectiveness of one malware clustering method over another. F-Score can be calculated using the same formula mentioned in the classification metrics section.

Chapter 3

Malware Classification and Clustering using PHMM based approach

3.1 Initial Experiments

The initial experiments are conducted on the publicly available dataset that comprises of behavior reports generated by CWSandbox, for nearly 3130 malware binaries collected over three years from many sources[3]. The malware files in this dataset were annotated by choosing the majority of the labels given independently by six different anti-virus products. Each malware family has a number of files ranging from 30 to 300. The details of the reference dataset that we have used for our experiments is shown in Figure 3.1. It says the name of the malware and the corresponding number of files belonging to each family. The distribution of files over these 24 classes is similar to real world situation in the sense that it is skewed. The initial experiments were conducted for the problem of malware classification, in which case we assume the label given by antivirus as ground truth label.

Our approach to the classification problem employing PHMM employs the following steps:

1. The behavior reports (which are XML files) obtained from the dynamic analysis

Malware class	#	Malware class	#
ADULTBROWSER	262	PRONDIALER	98
ALLAPLE	300	RBOT	101
BANCOS	48	ROTATOR	300
CASINO	140	SALITY	85
DORFDO	65	SPYGAMES	139
EJIK	168	SWIZZOR	78
FLYSTUDIO	33	VAPSUP	45
LDPINCH	43	VIKING_DLL	158
LOOPER	209	VIKING_DZ	68
MAGICCASINO	174	VIRUT	202
PODNUHA	300	WOIKOINER	50
POSION	26	ZHELATIN	41

Figure 3.1: The different malware families and the number of files in each, as in Malheur reference dataset[19]

tool such as CWSandbox(currently called the GFISandbox), can be encoded using a more simpler representation such as the MIST[3]. The MIST format that we chose for experiments can be processed at different levels considering how much of system call argument information we look at. Refer to Fig. 3.2 for a sample MIST encoding. We can also directly encode every unique type of a system call to a particular alphabet in the range (A-T) and eventually the behavior report looks like a protein sequence.

2. A small number of such *sequences* belonging to a known malware family (ranging from 3 to 15 files) is given to a *multiple sequence alignment* module to get an alignment file.

3. The multiple alignment file for a malware family is used for constructing a profile hidden markov model for that family. Many such HMM profiles can be combined to create a *malware profile database*.

4. When a new malware file is given, it is again encoded as a sequence and searched for in the malware profile database. The profile HMM gives a score for the most similar malware families for that new sequence.The one with the highest score is taken as the

malware class prediction.

Given that we see how PHMM is a very effective method for doing sequence based modeling, we will look at how the method is practically applied for our problem in dynamic malware analysis involving classification and clustering in the next chapter, in detail.

3.2 Methodology

The main reason for us to choose this approach for solving the problem of finding malware similarity is because the behavior of malware program has variablility, yet has a characteristic signature reflected in the sequence of system calls. For example if we look at the CWSandbox reports for two malware programs from same family, we notice that a sequence of malicious actions is preserved, interspersed with some other actions introduced to confuse the malware detection system.

In this thesis , it is shown that polymorphic malware are better detected when we look at their behavior, where we expect a certain common sequence of actions to be preserved, in spite of obfuscation in the code. We choose PHMM mainly because it intuitively fitted the kind of sequence search problem, which we have in classifying malware behavior. The initial experiments are done on a fairly diverse dataset that has close to 24 families of malware and we see that the results are quite promising. The F-scores for most of the classes considered,(including polymorphic families) are above 0.96. This way, we show that the method is comparable to some of the best of the techniques used for this problem. Later we extend the experiments on a larger and more varied dataset of malware infected files, which poses more challenges to the analysis and grouping of similar files. The challenges are explained and the results of

using PHMM models on the dataset is also presented.

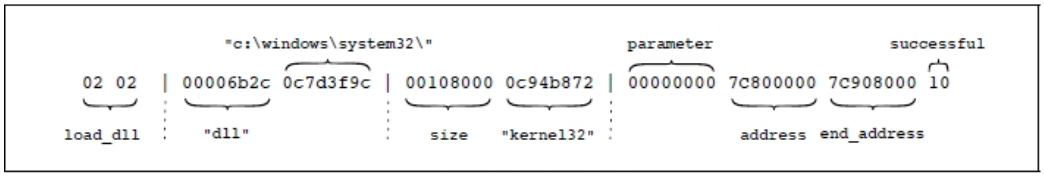
The Profile Hidden Markov Model is a probabilistic approach that developed specially for modeling sequence similarity occurring in biological sequences such as proteins and DNA[6][8]. It is also a faster alternative to the traditional deterministic approaches used in sequence matching [8]. It is a modified implementation of HMM, which is basically a generative model and constructs a probabilistic finite state machines. For behavior-based analysis, we again assume that there is a sequence of operations common for a virus family and for a presented new sequence we would like to find the best known match from the database.

A *hidden markov model (HMM)* is very suitable for probabilistic modeling of such sequences, which is evident from past works. Thus it can be used for modeling different classes of malware. But as we have discussed above , there might be additions, deletions or changes to the system calls for different programs within same malware family. The *profile HMM* is exactly designed to model this kind of problem, because it also has non-emitting states or the *delete* states. The reports are available in the MIST format too. For our experiments, we consider only the *MIST Level 0* in the reports.That is, we look at only the system call type and not the argument values. This level is actually sufficient for discrimination of various classes of malware.

The MIST Level 0 reports have close to eighty five different mist codes or system call operations, out of which, 20 operations are very frequent. The Fig 3.2(a) shows the XML representation of a dynamic analysis report on CWSandbox. The corresponding MIST representation is seen in 3.2(b). As the figure explains the corresponding information are coded in way such that the most important and relatively static information about the system call is on the left and less important parameters (those that change in value for different executions) such as memory addresses or file locations are towards

```
<load_dll filename="C:\WINDOWS\system32\kernel32.dll" successful="1"
 address="#7C800000" end_address="#7C908000" size="1081344"
 filename_hash="c88d57cc99f75cd928b47b6e444231f26670138f"/>
```

(a) CWSandbox representation



(b) MIST representation

Figure 3.2: Sample of MIST representation of a portion of CWSandbox report[3] (a) and (b)

the right. Now we map every *category operation* code with a unique alphabet in the range [A-T]. The remaining category operation codes are also mapped to alphabets in the accepted range.This facilitates the sequence representation to be compatible with the protein sequence format such as the *FASTA* or the *STOCKHOLM* formats.

Now for every family of malware, say *Allaple*, we choose few *(typically between 5-20)* files and add their sequence representation to FASTA (*.fa) file. The number of samples was chosen proportional to the number of samples in the dataset and often chosen at random. And when more than 10 samples were used for a family, we resorted to choosing samples that had varying sequence length. This variability would help in building better models that give higher accuracy in prediction. The FASTA file with the sequences is given to the multiple sequence alignment module and the output is an *aligned FASTA (*.afa)*, which has the multiple alignment. The alignment file for that malware family is now given to the *hmmbuild* step in hmmer, which now creates a profile HMM for the class.This is done for all the families of malware. The *malware profile database* is the concatenation of all the HMM profiles created for the known malware families in hand.

Presented with an unknown malware instance, we convert the MIST encoded file to a FASTA sequence file. The *hmmsearch* operation of the hmmer triggers a search on the profile database. The result of the hmmsearch operation gives the scores for the different malware families profiles, that were closely related to the presented sequence. The score values for the overall sequence match and best domain matches are obtained. Choosing the family which gets the maximum score, gives the classification result. The score differences between the families can also help us get some insight into how close the match was, to each of it.

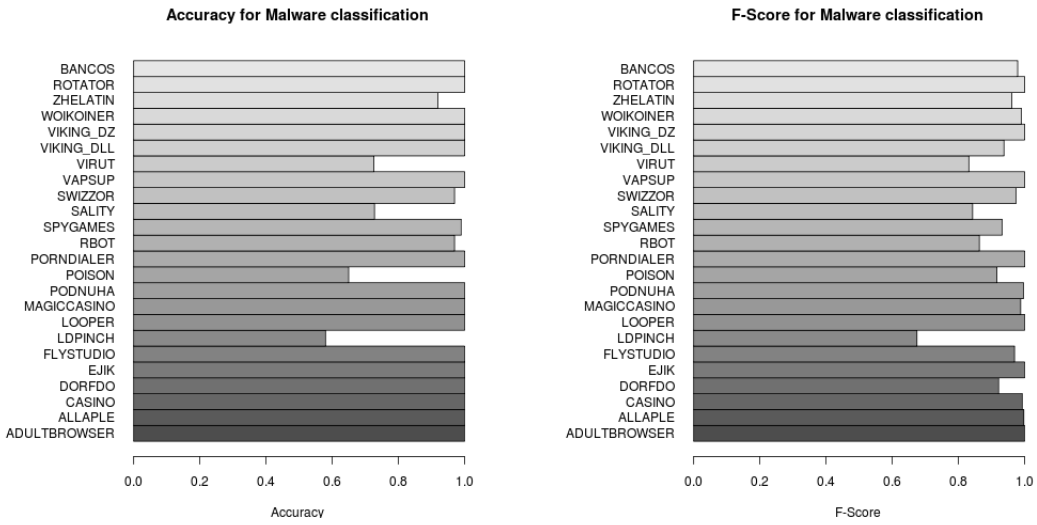
The hmmsearch operation takes longer time for identifying very long sequences with more than 50000 operations in a single report. Multiple sequence alignment and hmmsearch operations were run on a system with quad-core Intel(R) Xeon(R)E5440 @ 2.83GHz processor with 32GB of RAM. Some sequences in the family *SALITY* were too long and we haven't used them for testing in our experiment. But we plan to look at how to handle such sequences in our future work.

3.3 Results

We already saw that, around 5 to 20 files are used to construct the profile HMM for every malware family considered. The testing set consisted of the remaining files in the dataset[19]. The predictions of the HMM for all the malware programs spanning the 24 families is given in the form of a confusion matrix in Figure 3.4. We see that the overall accuracy for the dataset is around 95% and the classification accuracy for most of the classes is close to 100%. This shows that our approach is comparable with the state-of-the-art approaches as the *Malheur*[1], in terms of prediction accuracy.

The overall accuracy rate over the entire dataset is about 0.964. The accuracy of

classification for every class of malware is shown as a histogram in the Figure 3.3(a). We see that for most of the classes the accuracy is close to 1.0. For classes such as *Allaple*, which is polymorphic, all 300 instances were classified correctly. It was noticed that the scores given for the dominating profile or malware class was very high when compared to all other closely matched profiles. Also, whenever there was misclassification, the difference in the scores for the closely matched profiles is small.



(a) Histogram of classification accuracy

(b) Histogram of F-scores

Figure 3.3: (a) Histogram of accuracy and 3.3(b)Histogram of F-Scores

The Figure 3.3 b) shows a plot of the F-scores and Figure 3.3 a) shows that of the accuracies obtained for the classification results. The average F-score taken over most of the classes are more than 0.96 and there are families like *Looper, Adultbrowser etc.* with values 1.0. We would like to compare this with results from [1] and [12] which give average F-scores of about 0.88 and 0.97 respectively, which are considered state-of-the-art.

The confusion matrix for the multi-class prediction of malware families is presented in the Figure 3.4. By observing this matrix we see how the diagonal blocks are dark,owing to high prediction accuracy. There are lighter grey blocks outside the diagonal reflecting the proportion of files that were misclassified for every target malware family. The confusion plot gives us some insight on how closely related different families are.

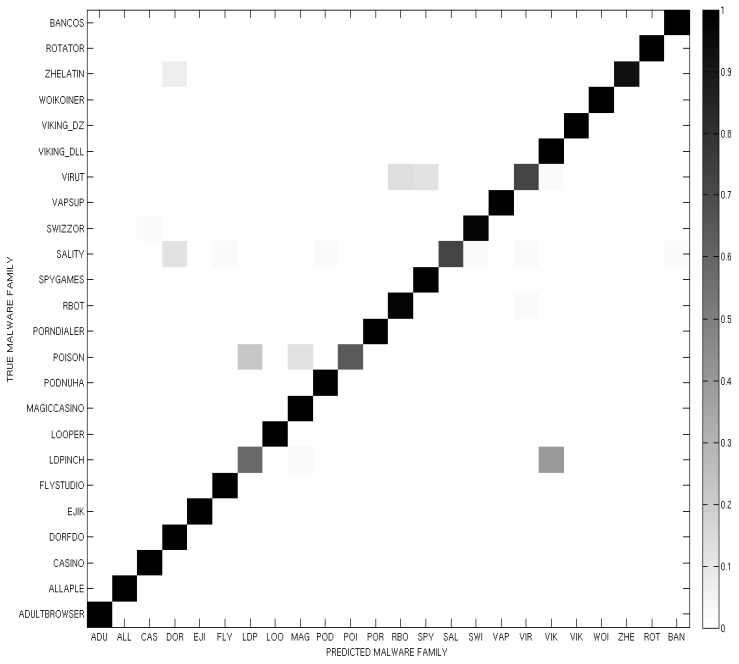


Figure 3.4: Confusion matrix for malware classification

For some classes like *Ldpinch*, owing to the small size of the reports and high variability, the accuracy is low. Programs of the family *virut* and *rbot* are very close in the behavior pattern which is reflected in the accuracy.

3.4 Closer look at malware analysis

In this section, we extend our approach on larger collection of malware to show its usefulness in real-time malware analysis, motivated by the initial results. The publicly available malheur application dataset[19] has close to about 400 different families of malware reports available, on which we wanted to test our approach and do a comprehensive study.

3.5 Challenges in practice

It is known that there are many challenges in the analysis on such large and varied dataset when using the PHMM approach. To encode a broader range of MIST instructions, a better and efficient encoding scheme was required. The encoding also had to take into account the larger range of malware classes that had to be analysed. Since there are many classes of malware with just very few (1 to 3) instances available for analysis, a pure classification approach may not be very suited. So we resort to a clustering approach that would work on the PHMM scores that we obtain for every malware report against stable malware profiles.

If we assume the malware family name given by an antivirus as the ground truth, then the cluster size distribution for the labeling is still skewed. So in addition to precision and recall for clustering, measures like dispersion index are also calculated to assess the purity of the clusters. The reference dataset that was used in our initial experiments has a few shortcoming when evaluating the performance of any methodology. The behaviour of different classes of malware in the dataset were distinct from one another. As pointed in a work by Li et al [26] , most of the discriminative classification models built on such datasets give good results and the effectiveness of one method over another does not account for the intrinsic characteristics of a malware. In the same work it is been analysed that biased cluster size distribution in the dataset reduces the significance of a high precision and recall of the clustering results of the malware as observed in the dataset used for a fast scalable clustering approach[12]. Also the issue of inconsistency in the labels used for this evaluation across different anti-virus vendors renders the evaluation metric not so effective. It is pointed that even a plagiarism detection software gave comparable results for the dataset and metrics while still the *Locality Sensitive Hashing* based clustering technique considered in [12] is far more scalable. In essence, our analysis emphasizes on the clustering of malware mainly based on its behaviour

that we obtain and study of malware evolution on this large dataset using the PHMM approach.

3.6 Detailed Experiments

We present the details of experiments in testing the usefulness of PHMM to create malware family profiles and how one can use the PHMM scores to cluster a large set of malware instances. The malware analysis using this approach involves the following steps.

1. We choose to use the MIST[3] approach for representing the instructions of the CWSandbox report.

2. The *MIST 0* level is what we have used for the current experiments. In future, we will consider using the arguments of the MIST instructions too (higher mist levels).

3. Since the number of unique instructions in the MIST set is more than the number of legitimate alphabets in the protein encoding(20), we choose to use an efficient encoding algorithm which will be described in the following subsection.

4. The choice of the malware instances to create the family's PHMM profile was an important question that arose. We have addresed the issue, by choosing the most variable sequences in terms of the sequence length and malware behaviour.

5. As in the previous experiment, the subsequent steps are the MSA of the chosen sequences and building of the HMM profiles for those families that we have enough samples of.

6. The new unseen sequences of all the malware instances are scored against the profile database. The resulting scores for the top scoring families(above an inclusion threshold) are then normalised across all known families in the database.

7. This normalised vector is then used for clustering the malware into families. We have used a fast repeated bisection method for clustering the set of malware reports.

3.6.1 Encoding the behaviour reports

The behaviour reports of the malware dataset[19] are encoded using the MIST codes as in the paper[3]. When converting this encoding to that of the protein sequences we have fewer codes to represent a larger set of MIST instructions. We resorted to use the *huffman encoding* algorithm for the same. The idea behind Huffman coding is to give less frequent characters and groups of characters longer codes. Also, the coding is constructed in such a way that no two constructed codes are prefixes of each other. This property about the code is crucial with respect to easily deciphering the code. We observed that even in the MIST opcode vocabulary for all of the reports, the frequency distribution of the opcodes is very skewed and obeys the Zipf's law. Hence Huffman coding works as an optimal prefix coding for the behavioral sequences and the data loss is minimum. The lengths of the sequence also don't grow beyond a factor of 3. The smallest amino sequence had about 300 symbols and longest was about 4000 and the average length was around 1600 characters in the sequence after the multiple alignment step. Also the rare behaviour opcodes, that occur commonly in an aligned sequence or that are absent in majority of the aligned sequences for a malware family, PHMM gives higher probabilities to the Hidden state paths and emission for match or insertion, for the amino coding symbols representing the opcode. This makes rare events in malware behaviour, to be captured well by the model.

3.6.2 Incremental setting for the detailed experiments

The dataset that we used for the detailed experiments mainly focuses on the analysis of the malware families that exhibit varied behaviour across samples. The malheur application set has malware files spanning over 403 families, among which, around 146 families have more than three samples each. To see how an incremental analysis can be done, we did a profile creation for about 130 families and the malware belonging

to these families were scored over the profile database. This covered about 7700 files whose precision and recall was about 0.67 and 0.46 respectively.

In the incremental step, we add the PHMM profiles for 15 more prominent families to the database. The total number of files in the dataset is around 18990 and the reports of all the 400 families of malware are presented for scoring and later clustering using a fast recursive bisection method. The vectors of PHMM scores for each report is normalised and the cosine similarity measure was used for clustering. The recursive bisection algorithm is very fast and the clustering results for nearly 19000 malware reports was available in less than one minute. This is of a great advantage in malware analysis where thousands of files are typically getting uploaded everyday for analysis. The classification results for some of the initially seen samples from newly added families (in the incremental) can be explained with the help of phylogenetic analysis that will be introduced in the coming section. It is assumed that, at some point of time the phylogenetic analysis on the aligned MIST sequences helps us discover a new class of malware branching steadily from an existing family. Once that discovery is done, the exemplary samples of the new family is used for building its own profile and the database is updated. However, completely new families of malware generally do not surface on the web so frequently as the polymorphic variants or extensions of already existing families of malware. The results of the final clustering is shown in Table 3.1. The clusterings obtained on this dataset with n-gram features (with $n = 4$) (malheur approach) and the proposed method with PHMM scoring features, are compared. We obtained a higher precision in our method slightly. The recall going down is not a bad sign since we have more even-sized clusters than the malheur approach. The number of clusters was varied and was seen to give steady precision and recall for values around $n = 400$, which is close to the true number of labels in the dataset. The comparison of

Table 3.1: Malware Clustering Comparision of PHMM based method and N-grams method

Features	*Precision*	*Recall*	*Number of clusters*
PHMM Scores	*0.7058*	*0.3106*	400
4-gram frequencies	0.7000	0.3700	400

the two clusterings was done using the function that mapped the clusters with maximum intersection of data points, as explained in the subsection 2.4.1 in Chapter 2.

3.7 What is Phylogeny?

The phylogenetic analysis is usually done in the field of evolutionary biology to find the hierarchical relationships between the organisms belonging to different taxonomic groups that form the leaves in the tree. The physical or the genetic characeteristics are used for the same. The cladograms or the phylogenetic trees are constructed with the branch lengths representing the evolutionary distance between the organisms in consideration.

The trees can be built from two forms of the genomic data. They are the distance matrices for the genetic sequences and the molecular data comprising the aligned sequences themselves. The distance methods build the phylogenetic tree by clustering the sequences based on their distances obtained from the matrix, in an iterative manner. Character-based tree building methods can use both types of data, and search for the best hierarchical tree from a set of possible tree topologies. They are slower than the distance methods as they come with optimality guarantees, but there are heuristics that speed up the process.

3.7.1 Malware Phylogeny

The term malware is in common use as the generic name for malicious code of all sorts, including viruses, trojans, worms, and spyware. Malware authors use generators, incorporate libraries, and borrow code from others. Malware also frequently evolves due to rapid modify-and release cycles, creating numerous strains of a common form. The

result of this reuse is a tangled network of derivation relationships between malicious programs. In biology such a network is called a phylogeny; an important problem in bioinformatics is automatically generating meaningful phylogeny models based on information in nucleotide, protein, or gene sequences. Generating malware phylogeny models using techniques similar to those used in bioinformatics may assist forensic malware analysts. The models could provide clues for the analyst, particularly in terms of understanding how new specimens relate to those previously seen. Phylogeny models could also serve as a principled basis for naming malware. Despite a 1991 agreement on an overall naming scheme and several papers proposing new schemes, malware naming continues to be a problem in practice [52][53]. We hope that using phylogenetic trees built from malware behaviour, naming conventions and the virus removal methods can be more standardised, than how it is done now.

Phylogeny from Our Observations

The tool *ClustalW* was used for phylogenetic analysis of the encoded MIST sequences of the malware. It takes in the prealigned homologous sequences, initially computes rough distance matrices based on pairwise alignment scores. It then uses a simple Neighbor-Joining clustering method to cluster the leaves of the tree under branches. In biology, the *homologous sequences* refer to the nucleic acid or protein sequences that are similar because they have a common evolutionary origin. The phylogenetic tree for the families Virut and Kies are shown in Figure 3.5. The initially seen few samples of Virut were misclassified as Kies and it is seen that the tree reflects the common behaviour that they share. A similar tree for the families Palevo and Buzus are shown in Figure 3.6. In the trees the length of the branch is proportional to the distance of the leaf or leaves from that node to the parent. Palevo was a worm that surfaced in 2009 and it opens a back door on the compromised computer and attempts to connect to the following IRC server to receive commands and the Buzus shared similar behaviour too. In the

tree diagrams (Figure 3.5 and Figure 3.6), the length of each branch is proportional to the actual evolutionary distance between the variant in leaf node to its ancestor. The diagram is scaled accordingly.

3.8 Analysis of the results

In the malheur dataset, the distribution of files over different families of viruses is very skewed, with popular polymorphic viruses like *Allaple*, *Texel*, *Swizzor* with over 1000 samples and nearly 200 classes of viruses with just one sample each. From a little bit of analysis into the behaviour profiles, it was observed that some of the majority classes like *Basun* had a stable behaviour pattern with minimal variations and constituted a third of the malware collection itself. With such a distribution in the data, a high precision and recall may not help us distinguish the effectiveness of one method over another. So for our study and comparison, we have used the malware families with the most variable behaviour across instances, forming the majority of the samples used in the study for comparison. The typical example is the class of viruses called *Texel*. It has many aliases used in the antivirus companies and has a varying behaviour. It behaves like a virus because of its self replicating nature. Some instances of Texel may frequently pop up advertising messages to interrupt computer users, while more severely they may destroy the data in computers. The lower recall and higher precision in the clustering obtained from PHMM features is because the Texel files have a varied behavior forming different clusters of big and small sizes. The cluster distribution for the top fifteen clusters are shown in the Figure 3.7. It is seen that the clusters are pure and that the cluster size distribution obtained is not too skewed, so it appropriate for comparing methods. The results show that the performance of our methodology is comparable with the state-of-the-art malheur, and uses very few sequences to actually model a behaviour profile.

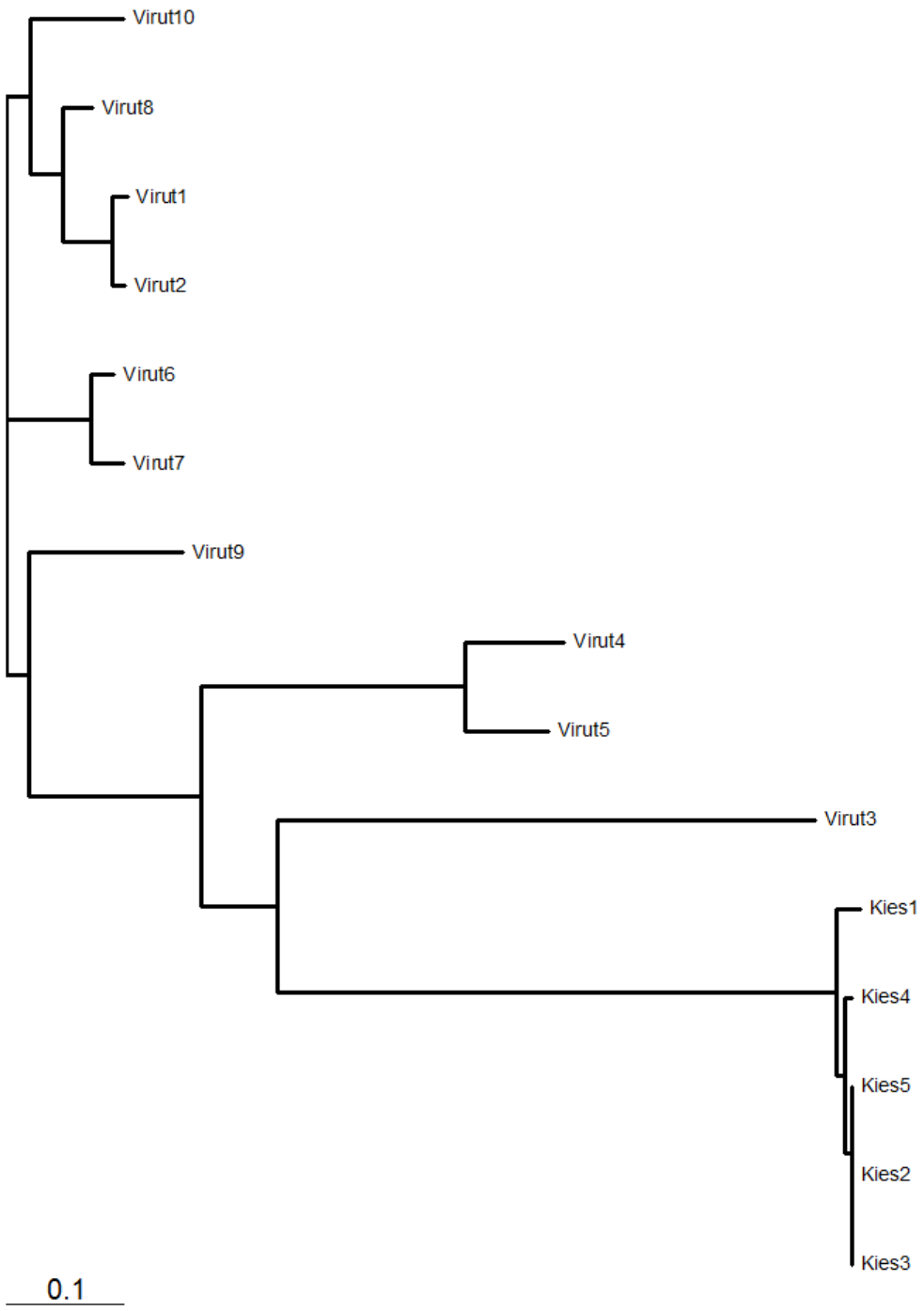


Figure 3.5: Phylogenetic tree for Virut and Kies

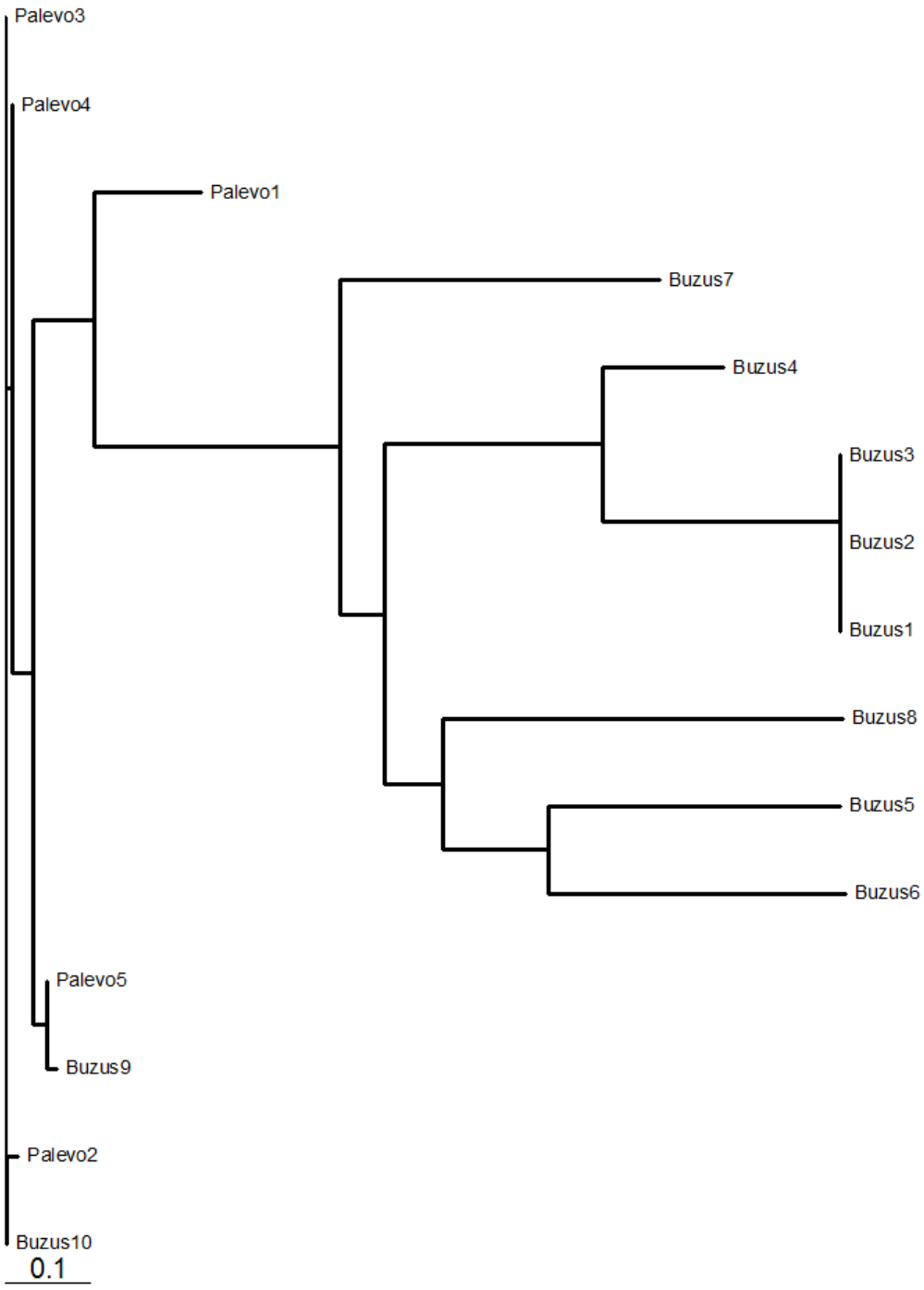


Figure 3.6: Phylogenetic tree for Palevo and Buzus

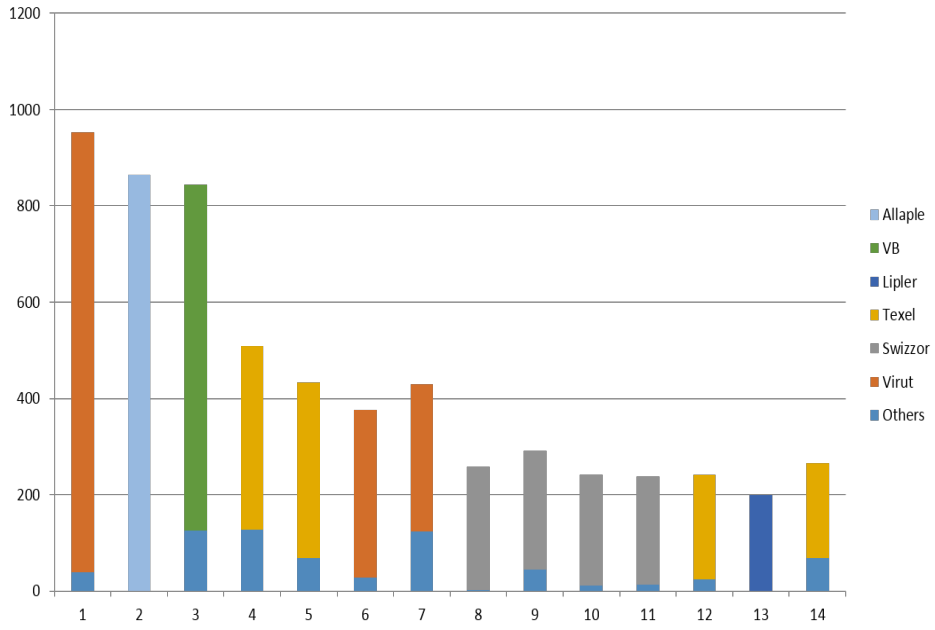


Figure 3.7: Clustering Results - Top 15 clusters

Chapter 4

Intrustion Detection in a Data Stream

Though IDSs can be classified based on a number of attributes, there are two major classes of IDSs. First of them are misuse-detection systems or the signature-based detection systems that model the patterns of previously known attacks. These could be hand-crafted signatures or even rules learnt by a system, that characterised a known attack. These systems are fast in detecting known attacks but are weak in detecting zero-day attacks. The other class of IDS is the anomaly detection systems, that models the normal non-malicious behavior of the system and flags any deviation from that as abnormal. They are very effective in identifying new unseen attacks, but suffer from the problem of high false-positive rates in detecting attacks. Some of the modern IDS/IPS solutions use a combination of rules, statistical, and deep packet inspection techniques for identifying attacks. The signature based detection is effective in identifying and existing class of attack, but the signature database requires constant update from someone with expert knowledge.

4.1 Brief Introduction to machine learning

Machine learning deals with the construction and study of systems that can learn from data. In figure 4.1 , we have shown the broad classes of learning algorithms with examples. The table also talks briefly the differences in the different learning approaches. Though there are technically 4 classes of algorithms, the Supervised and Unsupervised learning algorithms are very prominently used in the problem of intrusion detection. Machine learning has historically concentrated on learning from small numbers of examples, because only limited amounts of data were available when the field emerged. Though not currently in practical use, sophisticated algorithms that can learn highly accurate models from limited training examples have been explored in the field of machine learning. It is commonly assumed that the entire set of training data can be stored in working memory. More recently the need to process larger amounts of data has motivated the field of data mining.It explores methods to reduce computation time and memory when working with large, static datasets. If the data cannot fit into memory, it may be necessary to sample a smaller training set. Otherwise, an algorithm may process only subsets of data at a time. Commonly the goal is to create a learning process that is linear in the number of examples. The essential learning procedure is treated like a scaled up version of classic machine learning, where a set of training examples are processed to output a final static model. The data mining approach does not address the problem of a continuous supply of data even if it allows larger data sets to be handled. Typically, a model that has already been learned cannot be updated with new information arrives. Instead, the entire training process must be repeated with the new examples included. This limitation can be inefficient and undesirable for certain situations.

4.2 Stream-based learning paradigm

The data stream paradigm is used to address the problem of continuous data. Algorithms written for data streams can naturally cope with data sizes many times greater than memory, and can extend to challenging real-time applications not previously tackled by machine learning or data mining. The core assumption of data stream processing is that training examples can be briefly inspected a single time only. The algorithm processing the stream has no control over the order of the examples seen, and must update its model incrementally as each example is inspected. Another useful property, the "anytime" property, requires that the model be applied at any point between training examples. Studying purely theoretical advantages of algorithms is certainly useful , but the demands of data streams require this to be followed up with empirical evidence of performance. Claiming that an algorithm is suitable for data stream scenarios raises the doubt as to whether these claims cannot be backed by reasonable empirical evidence. Data stream classification algorithms require proper evaluation practices. The evaluation should allow users to be sure that particular problems can be handled, to quantify improvements to algorithms, and to determine which algorithms are most suitable for their problem.

4.3 Intrusion detection systems employing machine learning - *A survey*

Intrusion detection systems have evolved a lot since the Denning's seminal work on intrusion detection[27]. Besides network-based detection, these systems have also been used for host protection in the operating system level, by modeling system call sequences[29]. PAYL[35], which is a payload-based network anomaly detection system, models the byte frequencies in the packet payloads of various lengths and various services. It is proved to be fast and the problem of retraining the model is also addressed well.

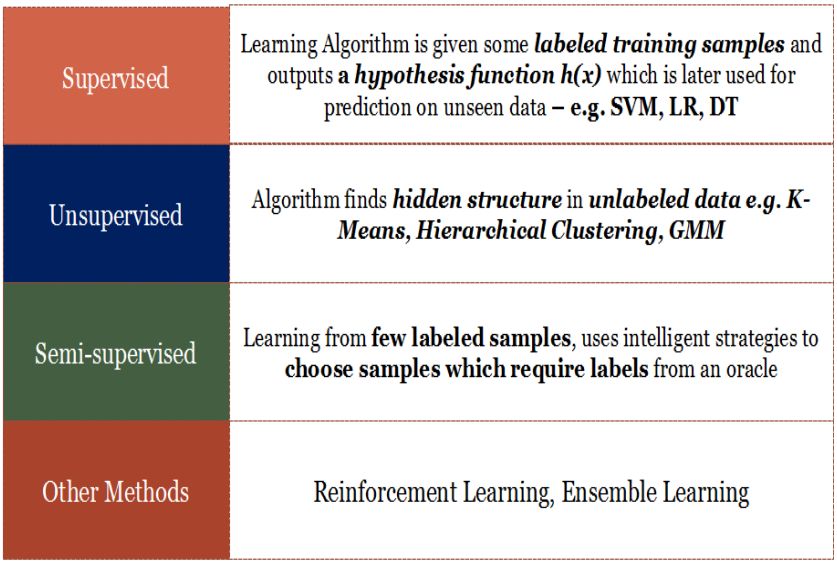


Figure 4.1: Broad Classification of machine learning

In general, the anomaly detection problem has been solved using different formulations for the one-class SVM or density-based outlier detection methods.[55][57] The work on Support vector Data Description(SVDD)[56] introduces the concept of finding a spherical boundary around the training data considered to be from one single class, say normal traffic. The problem is formulated as a *constrained minimisation* problem with the objective function being the square of radius of a *minimal enclosing hypersphere*, for all given training data. A regularisation term with a cost variable is included to avoid over-fitting problem. The training data is transformed to a higher dimensional hyper-space using the transformation $\phi(\mathbf{x}_i)$. The centre of the hypersphere is represented by w. The constraint is that all datapoints x_i must lie within the radius of this sphere , when transformed to the hyperspace. The basic formulation that is used for the shown in Equations 4.1 and 4.2 represent the problem, just explained. Once the solution is found by solving the dual of this problem, for any incoming packet or datapoint it is enough to find its distance from the center of hypersphere and verify if it is within the radius. Else the data is flagged as an anomaly.

$$\min_{w,R,\xi_i} \quad R^2 + C\sum_i \xi_i$$

$$\text{s.t.} \quad \|\phi(\mathbf{x}_i) - w\|_2^2 \leq R^2 + \xi_i \quad \forall\ i \tag{4.1}$$

$$\xi_i \geq 0 \quad \forall\ i \tag{4.2}$$

The area of intrusion detection is well studied and the use of data-mining and pattern recognition algorithms for the same have been researched. A variety of learning algorithms such as the SVMs, decision trees, neural nets etc. have been widely used for attack detection and classification. In the context of misuse detection, where we try to model different type of attacks and non-attack data together, a classification approach is very often used. The main issue in doing research in intrusion detection is the lack of publicly available dataset that are representative of the current activity patterns. Most of the previous studies have been done on mainly two publicly available datasets. They are the DARPA Dataset 1999 and the KDD Cup 99 Intrusion detection dataset. Though the relevance of these synthetic datasets is much argued about in literature, they do serve as a benchmark for analysis of various new techniques used in IDS.[37].

Lee and Stolfo [32] proposed the association rules algorithm and the frequent episodes algorithm for Intrusion Detection. These algorithms were used to compute audit record patterns, and propose an agent-based architecture for updating the models from the statistics collected over time. Several learning algorithms like the neural networks, functional networks, adaptive regression splines have all been used on the features obtained from Lee's method. The winner of the 1999 KDD cup contest had employed an ensemble of decision trees with bagged boosting, but different groups published better methods and algorithms. The work of Mukkamala etal [40] that used the Support Vector Machines for 2-class classification of attack and non attack records on KDD dataset

reported a high accuracy of about 99.5%. In order to reduce the size of the dataset, several researches proposed to apply feature selection methods to the training dataset ([Chebrolu et al., 2005], [Kayacik et al., 2005] and [Mukkamala and Sung, 2002]).

4.4 Commonly used datasets for validation of an IDS

4.4.1 DARPA 1999 Dataset for Intrusion Detection

At Lincoln Labs, MIT Lippman etal.,[31]developed an intrusion detection evaluation test bed which generated normal traffic similar to that on a government site containing 100s of users on 1000s of hosts. More than 300 instances of 38 different automated attacks were launched against victim UNIX hosts in seven weeks of training data and two weeks of test data. The attacks were broadly of 4 types namely, probe, denial of-service (DoS), remote-to-local (R2L), and user to root (U2R) attacks. They analysed the performance of 6 different IDSs that had handcrafted rules or signatures, or expert systems to detect the attacks.Their results suggested that further research had to focus on developing techniques to find new attacks instead of extending existing rule-based approaches. This dataset that was created for the test-bed is most commonly known as the DARPA 1999 dataset[30] for Intrusion Detection.

Lee and Stolfo [32] proposed two general data mining algorithms that were the association rules algorithm and the frequent episodes algorithm for Intrusion Detection. These algorithms were used to compute the intra- and inter-audit record patterns, on the system call traces and network audit logs and they propose an agent-based architecture for updating the models from the statistics collected over time. In their subsequent work[33], a detailed data mining framework was proposed. The features that are collected from network dump files and system audit logs were clearly classified

as connection-based and time-based features. The framework made it easy for crafting rules for detection of different types of attacks based on the 'features' that they built.

PAYL[35], which is a payload-based network anomaly detection system, models the byte frequencies in the packet payloads of various lengths and various services. It is proved to be fast and the problem of retraining the model is also addressed well.

The KDD Cup 99 contest winner employed an ensemble of decision trees with bagged boosting. Several authors in the literature have used this dataset in order to test their classifiers and trying to improve the results achieved by the winner. Earlier studies have utilized neural networks and support vector machines (SVMs) [40]. These approaches were used again later by Fugate and Gattiker (2003) together with an ANOVA model, and they outperformed some of the results of the KDD winner, but the drawback of these methods is that they are very time and computational consuming and it is necessary to deal with reduced training datasets. Lately, functional networks were also applied to this dataset, obtaining similar results and the same inconvenient. In order to reduce the size of the dataset, several researches proposed to apply feature selection methods to the training dataset [40] [41]. However, these works were more focused in determining the more relevant features than in achieving better performance with fewer attributes.

4.4.2 The KDD Cup 1999 Dataset

The KDD Cup 99 dataset, taken from the DARPA IDS evaluation dataset [31], was used for the KDD Cup 99 Competition[34]. The complete dataset has almost 5 million input patterns and each record represents a TCP/IP connection that is composed of 41 features that are both qualitative and quantitative in nature[37] [33]. The dataset used in our study is a smaller subset (10% of the original training set), that contains 494,021 instances and it was already employed as the training set in the competition. For the

test set, we used the original KDD Cup 99 dataset containing 331,029 patterns. Around 20% of the two datasets are normal patterns (no attacks). As for attack patterns, the 39 types of attacks are grouped into four categories[43].

1. Denial of Service (DoS) attacks, where an attacker makes some computing or memory resource too busy or too full to handle legitimate requests.

2. Probe attacks, where an attacker scans a network to gather information or find known vulnerabilities.

3. Remote-to-Local (R2L) attacks, where an attacker sends packets to a machine over a network, then exploits machines vulnerability to illegally gain local access as a user.

4. User-to-Root (U2R) attacks, where an attacker starts out with access to a normal user account on the system and is able to exploit vulnerability to gain root access to the system.

The 1998 DARPA Intrusion Detection Evaluation Program was prepared and managed by MIT Lincoln Labs. The objective was to survey and evaluate research in intrusion detection. A standard set of data to be audited, which includes a wide variety of intrusions simulated in a military network environment, was provided. Lincoln Labs acquired nine weeks of raw TCP dump data for a typical U.S. Air Force Local Area Network (LAN). They operated the LAN as if it were a true Air Force environment, but peppered it with multiple attacks. The raw training data was about four gigabytes of compressed binary TCP dump data from seven weeks of network traffic, which was processed into about five million connection records. The two weeks of test data yielded two million connection records.

Attacks fall into four main categories as explained above in KDD 99 Dataset section.

It is important to note that the test data and training data do not have the same probability distribution (including specific attack types not in the training data). This

makes the task more realistic. Some intrusion experts believe that most novel attacks are variants of known attacks and the "signature" of the latter can be used to catch the former. The datasets contain a total of 24 training attack types, with an additional 14 types in the test data only.

4.5 Stream based learning algorithm

The incremental learning algorithms are used in KDD systems that operate indefinitely and continuously arriving examples. There exist a number of online or sequential learning algorithms that are efficient but offer no performance guarantees.
The Hoeffding Tree algorithm[46] is an anytime algorithm that is used for classification tasks, and can be used for learning from large datasets. Every example is seen exactly once. Its performance increases smoothly with time. The Hoeffding Tree algorithm uses the *Hoeffding bound* result from statistics to determine the number of examples necessary to do the testing of an attribute value.

The MOA framework [45] implements several algorithms that learn from data streams in an online fashion. The framework has implementations of the classical Naive Bayes, Hoeffding trees, Random Hoeffding trees, OZBoost, Weighted Majoriy Algorithm etc. The OZBoost is a boosting algorithm that uses a forest of hoeffding trees in learning.The framework also supports the generation of data points as in a stream, with preset time intervals for a concept drift. Parameters of the learning algorithm such as the prior distributions and their parameters, number of trees to use for bootstrapping etc., can also be tuned up.

4.6 Hoeffding Trees

We shall now look at the Hoeffding tree algorithm in detail. The classification problem is generally defined as follows. A set of N training examples of the form (x; y) is given, where x is a vector of d attributes, and y is a discrete class label each of which may be symbolic or numeric.From this sample data we wish to learn a model $y = f(x)$ that will predict the classes y of future examples x. One of the most widely-used classification methods is decision tree learning. Learners of this type induce models in the form of decision trees, where each node contains a test on an attribute, each branch from a node corresponds to a possible outcome of the test, and each leaf contains a class prediction. The label y = DT(x) for an example x is obtained by passing the example down from the root to a leaf, and following the branch corresponding to the attribute's value in the example. A decision tree is learned by recursively replacing leaves by test nodes, starting at the root. The attribute to test at a node is chosen by choosing the best one according to some heuristic measure. Classic decision tree learners like ID3, C4.5 and CART assume that all training examples can be stored simultaneously, and are therefore severely limited in the number of examples they can learn from. Disk-based decision tree learners like SLIQ and SPRINT assume the examples are stored on disk, and learn by repeatedly reading them in sequentially. While this greatly increases the size of usable training sets, it can become too expensive. Our goal is to design a decision tree learner for extremely large datasets. This learner should require each example to be read at most once, with small processing time. This will make it possible - without ever storing the examples - to directly mine online data sources, and to build potentially very complex trees with acceptable computational cost. We achieve this by noting with Catlett [2] and others that, in order to find the best attribute to test at a given node, it may be sufficient to consider only a small subset of the training examples that pass through that node. Thus, given a stream of examples, the first ones will be

used to choose the root test. We solve the problem of deciding how many examples are necessary at each node by using the Hoeffding bound (or additive Chernoff bound) [7, 9]. Consider a real-valued random variable r whose range is R. Suppose we have made n independent observations of this variable, and computed their mean r.

The Hoeffding bound states that, with probability $1-\delta$, the true mean of the variable is at least $\bar{r} - \epsilon$ where

$$\epsilon = \sqrt{\frac{R^2 ln(1/\delta)}{2n}} \tag{4.3}$$

4.6.1 Special properties of the Hoeffding trees

The Hoeffding bound has the very attractive property that it is independent of the probability distribution generating the observations. The price of this generality is that the bound is more conservative than distribution-dependent ones (i.e., it will take more observations to reach the same δ and ϵ). Let $G(X_i)$ be the heuristic measure used to choose test attributes (e.g., the measure could be information gain as in C4.5, or the Gini index as in CART). We wish to ensure that, with high probability, the attribute chosen using n examples (where n is as small as possible) is the same that would be chosen using infinite examples. Assume G is to be maximized, and let X_a be the attribute with highest observed G after seeing n examples, and X_b be the second-best attribute. Let $\Delta\bar{G} = G(X_a) - G(X_b) \geq 0$ be the difference between their observed heuristic values. Then, given a desired δ, the Hoeffding bound guarantees that X_a is the correct choice with probability $1-\delta$ if n examples have been seen at this node and $\Delta\bar{G} > 0$.

If d is the number of attributes, v is the maximum number of values per attribute, and c is the number of classes, the Hoeffding tree algorithm requires O(dvc) memory to store the necessary counts at each leaf. If l is the number of leaves in the tree, the

total memory required is O($ldvc$). This is independent of the number of examples seen, if the size of the tree depends only on the true concept and is independent of the size of the training set.

A key property of the Hoeffding tree algorithm is that it is possible to guarantee under realistic assumptions that the trees it produces are asymptotically arbitrarily close to the ones produced by a batch learner (i.e., a learner that uses all the examples to choose a test at each node). In other words, the incremental nature of the Hoeffding tree algorithm does not significantly affect the quality of the trees it produces.

4.7 Online learning

Online machine learning is a model of induction that learns one instance at a time. The goal in on-line learning is to predict labels for instances. For example, the instances could describe the current conditions of the stock market, and an online algorithm predicts tomorrow's value of a particular stock. The key defining characteristic of on-line learning is that soon after the prediction is made, the true label of the instance is discovered. This information can then be used to refine the prediction hypothesis used by the algorithm. The goal of the algorithm is to make predictions that are close to the true labels.

More formally, an online algorithm proceeds in a sequence of trials. Each trial can be decomposed into three steps. First the algorithm receives an instance. Second the algorithm predicts the label of the instance. Third the algorithm receives the true label of the instance. The third stage is the most crucial as the algorithm can use this label feedback to update its hypothesis for future trials. The goal of the algorithm is to minimize some performance criteria. For example, with stock market

prediction the algorithm may attempt to minimize sum of the square distances between the predicted and true value of a stock. Another popular performance criterion is to minimize the number of mistakes when dealing with classification problems. In a two-class classification scenario, the N training set instances (x, y) are given. The incurred loss for a wrong prediction $\hat{y}^t$ is given by the loss function $\ell(y^t, \hat{y}^t)$, at the third stage.

4.7.1 Online Prediction from Experts

A general online prediction problem proceeds as follows.

Online (binary) prediction using multiple experts

For $t = 1, \ldots, T$:

- Receive instance $x^t \in \mathcal{X}$
- Receive expert predictors $\xi_1(x^t), \ldots, \xi_N(x^t) \in \{\pm 1\}$
- Predict $\hat{y}^t \in \{\pm 1\}$
- Receive true label $y^t \in \{\pm 1\}$
- Incur loss $\ell(y^t, \hat{y}^t)$ If $\hat{y}^t \neq y^t$
  - Modify predictor function for $\hat{y}^t$

4.7.2 Weighted Majority algorithm

Weighted Majority Algorithm (WMA) is a meta-learning algorithm used to construct a compound algorithm from a pool of prediction algorithms, which could be any type of learning algorithms, classifiers, or even real human experts. The algorithm assumes that we have no prior knowledge about the accuracy of the algorithms in the pool, but there are sufficient reasons to believe that one or more will perform well. The algorithm uses a multiplicative update on the weights, for the predictors whose predictions go wrong in every round by a factor $\eta > 0$ Consider a two-class classification scenario where the N training set instances (x, y) are given. The weights $\mathbf{w}$ are initialised equal for all the predictors (or hypothesis or classifiers) in consideration. When the first instance

is presented the algorithm goes by the decision of the majority of the classifiers. Now the weights are reduced by a multiplicative factor $\eta > 0$, for those classifiers that erred. And the process iteratively continues for all the training instances in the sequence.

Weighted Majority Algorithm

Initiate weights $w_i^1 = 1 \forall i \in [N]$

Choose parameter $\eta > 0$ that would be used in the weight update rule.

For $t = 1, \ldots, T$:

- Receive instance $x^t \in \mathcal{X}$
- Receive expert predictors $\xi_1(x^t), \ldots, \xi_N(x^t) \in \{\pm 1\}$
- Predict $\hat{y}^t = sign(\sum_{j=1}^{n} w_j^t . \xi_j^t)$ (majority vote)
- Receive true label $y^t \in \{\pm 1\}$
- Incur loss $\ell(y^t, \hat{y}^t)$
- Update:- If $\hat{y}^t \neq y^t$

  $\forall i \in 1 \ldots N$

  $\mathbf{w}_i^{t+1} \leftarrow \mathbf{w}_i^t \exp^{(\eta . \mathbf{I}(y^t \neq \xi_i^t))}$

There are good performance guarantees for the weighted majority algorithm.

4.8 Experiments and Results

We have for the first time used and compared the stream learning algorithms to perform the multilabel classification of attack and normal data on the KDD Cup1999 dataset. Several algorithms like the Naive Bayes, Hoeffding Trees, Weighted Majority algorithm, RandomHoeffding trees etc. were used and the classification performance on the whole of dataset were studied. The classification accuracies of various algorithms were compared. We notice that the Hoeffding trees and Random Hoeffding trees perform better in terms of evaluation time and accuracy as the data size grows, whereas Naive Bayes performs poorly as the data size grows.

Table 4.1: Accuracies and Kappa-statistic for various Stream learning algorithms on the KDD Cup 99 dataset

Algorithm	*Accuracy*	*Kappa*	*Model Parameters*
Hoeffding Trees	99.4069	98.9841	Gaussian10
Random Hoeffding tree	98.7202	97.8121	
Weighted Majority	99.9266	99.8743	HT,HT-NB,HT-NBAdaptive,NB
NaiveBayes	95.6028	92.5854	

The weighted majority algorithm[48] is an online method that gives a weighted decision from the predictions of four different classifiers, which explains the increase in its evaluation time, inspite of the high accuracy. It is noted that, with the first 1 million examples, Hoeffding Tree predictor gets the maximun weight of about 0.98, when other classifiers get rest of the weight, over 1. The weights vary very little from there and ends at 0.994 for HT,0.03 each for Random HT and Naive Bayes. The online algorithms also generally don't have the i.i.d assumptions on the training and testing data. It allows us to see, how every component algorithm predicted over a length of time, which is reflected in its weight. Thus, Hoeffding trees are proven to perform the best of all in terms of performance and speed. This shows the need for looking closely into incremental learning for IDS, as there will be space and time constraints when learning from huge data.

The incremental learners perform well with time, even when there is a concept drift in the data. Most previous results on KDD Cup 99 dataset[40][43][44], were done on the 10% Train and Test sample dataset whereas we use the complete dataset with over 4.8 milion samples and the dataset we used has 22 classes of attacks and 1 class of normal patterns.

The results for different algorithms are tabulated in Table 4.1. The Naive bayes method was used as a baseline for batch processing method. And the results for Hoeffding trees with Gaussian priors (with SD = 10.0) were shown to have an accuracy of 99.409. Random Hoeffding trees (where a subset of features are only used at each step) give a better accuracy. The online weighted majority algorithm that combined the decisions

from other classifiers like Hoeffding Trees, Hoeffding Trees with Naive bayes assumption and Plain Naive Bayes algorithm was seen to work the best. The Figures 4.2 and 4.3 show the graphical comparison of the accuracies and kappa values with every sample, for the algorithms in study. It is clearly seen that performance of Naive Bayes drops with time when the number of samples keep increasing. Whereas the other stream algorithms perform steadily better with more samples. In terms of CPU execution times, Hoeffding and Random Hoeffding trees learn the model under 100 ms for the same data. The comparison of CPU execution times of these algorithms with growing sample sizes is shown in Figure 4.4. The above results encourages us to look more deeply at the learning setting in the Intrusion Detection problem. If we can obtain a tagged dataset at any point, the stream learning algorithm can incrementally update the model for the newly accounted attacks and benign traffic and not lose prior knowledge too. The online learning algorithms are analysed and compared against each other based on the factor of Regret as opposed to the Empirical risk as in a batch learning setting. Fast optimisation algorithms such as the stochastic gradient methods can be used in case of high dimensional data as in the case of IDS problem. When the power of hardware is utilised with these powerful algorithms, we can surely see some improvements in the performances of statistics based IDSs.

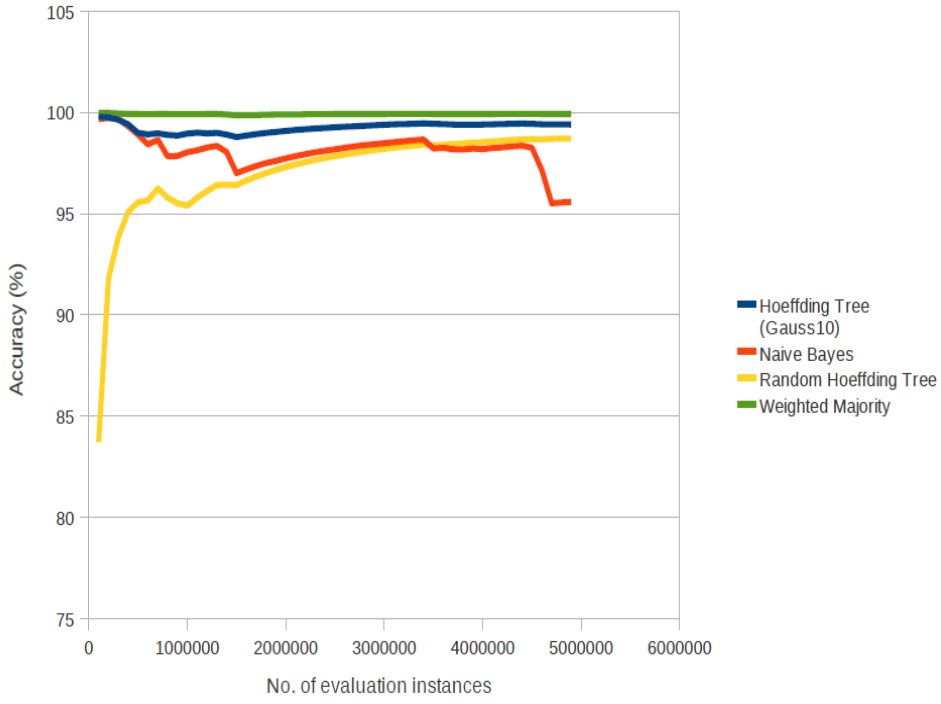


Figure 4.2: Accuracy Comparison Graph

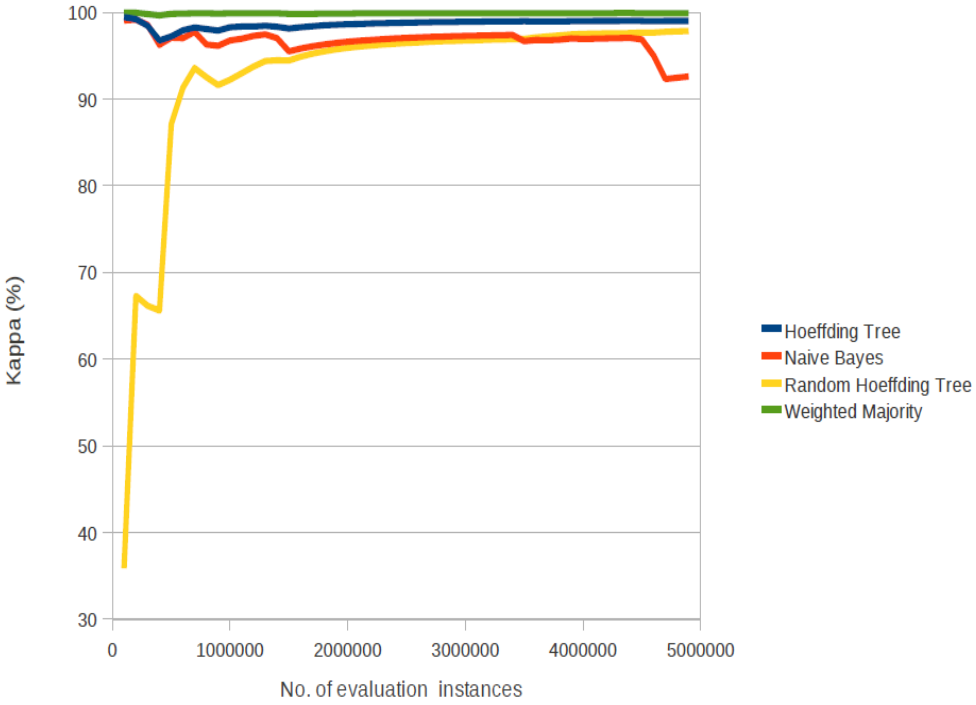


Figure 4.3: Kappa Comparison Graph)

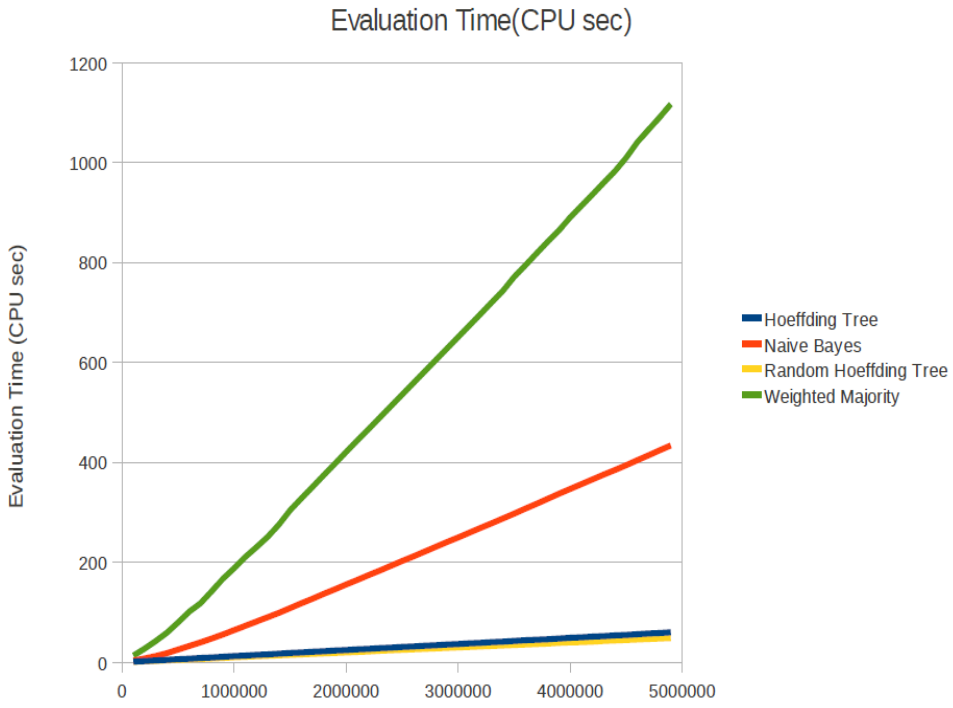


Figure 4.4: Evaluation Time (in CPU secs)

Chapter 5

Conclusion

In this chapter we will review the main contributions of this thesis and directions for future work.

5.1 Contribution of the thesis

From earlier research work, we see that polymorphic malware are better detected when we look at their behavior, where we expect a certain common sequence of actions to be preserved, in spite of obfuscation in the code. In this thesis, we have shown that Profile Hidden Markov Models are very effective mainly because it intuitively fitted in solving the kind of sequence search problem, which is also very commonly encountered in bio-informatics. It has been experimentally verified that, even with limited examples, accurate models can be built and the results using these models were comparable to some of the best of the techniques used for this problem. The initial set of experiments were done on a diverse set of 24 malware families and the PHMM models were used for classification.

Later we extended the experiments on a larger and more varied dataset of malware infected files, which poses more challenges to the analysis and grouping of similar files. The challenges are explained and the results of using PHMM models on the dataset is also presented. Malware clustering was performed on the large dataset to cluster or

group the files purely based on their behaviour. We also present a phylogenetic analysis done on the malware samples, purely based on behavioural features. All the results are comparable to that of state of the art, but this has been acheived with very few training samples (in between 3-20).

We also proceeded to address the issue of relearning in IDS. A set of stream based learning algorithms based on the Hoeffding trees have been tried on the KDD Cup 99 Intrusion Detection dataset for the classification of non- attack data and 22 different kinds of attack. Online learning algorithm such as weighted majority algorithm is observed to be effective as an ensemble technique in trying to combine many classifiers. The thesis does a comparison of these algorithms in terms of accuracy, speed and resource consumption, for the problem of attack classification.

5.2 Directions for future work

The experiments and general trend in security engineering show that, the identification and mitigation of malware attack on our networks and systems are going to get more challenging in the times to come. The polymorphic variants of malware generated using different virus toolkits pose a major threat and many of the security product companies are moving towards using more elaborate dynamic analysis based or program verification based techniques for identification and removal of malware. Software vulnerabilities in the system and application software also need to be addressed and fixed with due diligence, when we address the issue of malware. When there are scalable systems to analyse malware and a standard taxonomy for naming malware families, it would be easier to compare and evaluate the performance of different anti-malware products. Though there have been multiple ways suggested through researches, none of them have been employed across all major anti-virus vendors.

We see from research that dynamic malware analysis is gaining prominence. In a more recent work,[63], Ying etal., describe a method for extracting a set of minimal abstract behavioral features from the API call sequences, that would serve well for many graph based data mining approaches. The features they have extracted has advantages such as resistance to redundant data and ease to embed in very high dimensional space. With such features made available, more sophisticated machine learning can be done for classification, detection or clustering of malware.

The advances in the areas of machine learning and statistical analysis can be used for addressing some of the problems of pattern recognition in computer security. The recent surge in the consumption and use of mobile devices opens a whole new area in security research. With the data speeds increasing rapidly in networks, having intelligent IDS that constantly relearns in a dynamic environment, has become all the more necessary. To support the improvements in software and network speeds, hardware also have improved a lot, over the years.

The GPUs are the graphics processing units that are separate computational units specially designed to do hardware optimisation for graphics. These units are much faster than CPUs since they have the capacity of running several parallel threads. Having GPUs takes away significant computing load from the CPU for graphic-rich applications and systems. Slowly GPUs have been utilised for other non-graphic computational purposes and the advent of architectures such as CUDA (compute unified device architecture) and standards such as OpenCL have made a breakthrough in fast and parallel computing. It is evident from previous research the GPU tends to improve the performance of CPU-intensive operations, so it is possible to load some of the computations in the anti-virus program to the GPU. Typically this could be done for fast signature

matching techniques used in popular anti-virus. In fact, the anti-virus makers Kaspersky released a GPU version which they have said runs 360 times faster than a CPU version[68].

We also see some recent work on utilising GPUs for multiple pattern matching algorithms[66]. This paper describes how the GPUs were used for comparing the contents of single packet in parallel, during the phase of deep packet inspection. In experiments, it is seen that the proposed algorithm gives twice the performance of the existing multi-pattern matching algorithm (WM algorithm) that was already used in the Snort IDS.

As always, in the area of security, there is also the flip side to the story involving GPUs. A recent work describes a prototype that was developed to show how polymorphic malware can evade detection using GPU architecture.

The paper explains that unpacking of the malicious code can be done by GPU and be placed in memory that is accessible to the CPU. This process calls for the majority of the code to be written for the GPU, and little that is executed on the Intel x86 architecture. Thus there are very little remnants of the executed code in the memory. This could subsequently make it harder for the current malware detection solutions that may use methods such as call graph traces or tainting[65]. GPU assisted malware are even hard when using reverse engineering techniques because the encoding and decoding of the virus code is done very quickly on the GPU leaving very little time for analysis. Even with existing debugging techniques, reverse engineering such code is a challenge for malware analysts.

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