# Behavior-based Malware Analysis using Profile Hidden Markov Models

Saradha Ravi, N. Balakrishnan and Bharath Venkatesh
*SERC, Indian Institute of Science, Bangalore, India*
*saradha.ravi@gmail.com, balki@serc.iisc.ernet.in, bharath.venkatesh85@gmail.com*

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Abstract: In the area of malware analysis, 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 being used in large malware analysis systems because of this reason. In these dynamic analysis systems, the malware samples are executed and monitored in a controlled environment using tools such as CWSandbox(Willems et al., 2007). In previous works, a number of clustering and classification techniques from machine learning and data mining have been used to classify the malwares into families and to identify even new malware families, from the behavior reports. In our work, we propose to use the Profile Hidden Markov Model to classify the malware files into families or groups based on their behavior on the host system. PHMM has been used extensively in the area of bioinformatics to search for similar protein and DNA sequences in a large database. We see that using this particular model will help us overcome the hurdle posed by polymorphism that is common in malware today. We show that the classification accuracy is high and comparable with the state-of-art-methods, even when using very few training samples for building models. The experiments were on a dataset with 24 families initially, and later using a larger dataset with close to 400 different families of malware. A fast clustering method to group malware with similar behaviour following the scoring on the PHMM profile database was used for the large dataset. We have presented the challenges in the evaluation methods and metrics of clustering on large number of malware files and show the effectiveness of using profile hidden model models for known malware families.

## 1 INTRODUCTION

With the pervasive use of the internet, a lot of malicious programs or malware that spread across it, pose a serious threat to the security of the systems. There are a variety of malware that are in the forms of viruses, trojans, worms and botnets. The malware uses the software vulnerabilities and other social engineering techniques to trick the users into running them, so that they can spread.The anti-malware companies receive thousands of sample files everyday, for analysis. These files are usually the ones that the user finds suspicious in his/her system, and whose functionality they are not sure of. It is important that we understand the operations that a particular malicious program does, in order to asses the seriousness of the threat and its malware family. We also notice the fact that, new files that are uploaded are usually the variants of some malicious program that is already existing. Though the action of the malware would be very similar, the signatures of the files may not match, even for very close variants. This makes the signature-based techniques fail for the metamorphic variants of the malware. Static malware analysis focuses on classifying malware based on features directly extracted from malware sample whereas dynamic analysis does it based on the behavioral patterns of the malware. Due to the increasing need, many automated malware analysis systems such as CWSandbox(Willems et al., 2007), Anubis (Bayer et al., ) are being used. In these systems, the uploaded malware programs are executed in a controlled environment. The operations performed by the program, characterized by the system calls and their arguments, or the registry changes are monitored carefully and logged. From these execution logs, the reports are generated and the analysts go through them to assess the threat. But when there are large number of programs, analysing them manually becomes a tough job. It would be easy if there is an automated way of classify a malware into already existing families or report a new behavior profile. A number of classification and clustering techniques from machine learning are used on the behavior reports(Rieck et al., 2011)(Lee and Mody,

2006)(Bayer et al., 2010)(Apel et al., 2009). Once the malware programs are grouped, we can then see what the common behavior of that particular family of malware is and use them later for proactively mitigating that threat beforehand in anti-malware software. In our work, we address the problem of malware classification and also clustering (based on similar behavior) using profile Hidden Markov Models.

# 2 RELATED WORK

In this section, we will look at some of the related work done in the behavior-based malware analysis and classification. The dynamic analysis techniques gained prominence because of the limitations in the static analysis techniques (Moser et al., 2007).Moser et al proposed a method where the normal model of programs were modelled 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(Bailey et al., 2007) tracked more abstract features like system state changes rather than system call sequences for malware classification.

Different distance measures are used to find the similarity within the files of the same malware family. Some of them are appropriate for the given problem whereas some are not, particularly when the order of the activities in the behavior isn't taken into consideration. Lee et al propose a malware clustering approach where a modified Levenshtein distance is used and a k-medoid partition clustering is performed(Lee and Mody, 2006). The complexity of computing distances between malware in their method is quadratic in the number of system calls and so expensive.

In more recent work(Bayer et al., 2010), 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 automatic classification system given by Rieck et al was used to identify novel families of unseen malware using clustering and assign new instances of malware to these families by classification using SVMs(Rieck et al., 2008). 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(Rieck et al., 2008), 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 propose a new representation for the monitored behavior of malware(Trinius et al., 2010). This representation is optimised to be efficient when applying machine learning and data mining techniques.

Wagener et al (Wagener et al., 2008) propose a dynamic analysis method where they couple a sequence alignment method to compute the similarities and leverage the Hellinger distances. They also show how the use of phylogenetic tree improves their classification method. The different distance measures used when clustering similar malware behavior are examined in a work by Apel eta al(Apel et al., 2009). 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.

To detect similarity in workloads from NFS traces for storage systems, Neeraja et al (Yadwadkar et al., 2010) have applied the PHMM on the opcode sequences of the NFS traces. They also observe that very few training sequences for a particular type of workload, was enough for modeling. In another work (Attaluri et al., 2009), the profile HMM had been applied for x86 opcode sequences of the polymorphic malware binaries generated by the commonly available virus kits. But they observe that the method works for some families better than the others because of the problems like subroutine permutation and the code reordering.

# 3 PROPOSED APPROACH

## 3.1 Our Contribution

In this paper , 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 re-

sults 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(Eddy, 1998)(Durbin et al., 1998). It is also a faster alternative to the traditional deterministic approaches used in sequence matching (Durbin et al., 1998). 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. 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 tool such as CWSandbox(currently called the GFISandbox), can be encoded using a more simpler representation such as the MIST(Trinius et al., 2010). 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. 4 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 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.

## 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.

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. We would now outline the concept of profile HMM before we proceed to show how it has been used in our work.

## 3.3 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 (Rabiner, 1989). 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 $\Sigma$
- 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 $\pi$

Thus the HMM $\lambda$ 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

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

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(Rabiner, 1989).

Given a sequence *X*, the *Viterbi* algorithm(Rabiner, 1989) 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 (Rabiner, 1989).

## 3.4 Profile Hidden Markov Model

A PHMM is a specific formulation of a standard HMM that makes explicit use of positional information contained in the observation sequences(Attaluri et al., 2009). PHMM is a strongly linear left-right model while HMM is not(Eddy, 1998). 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, PHMM state transition matrices are essentialy sparser than those of HMM, allowing quicker inference.

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(Needleman et al., 1970). The *local alignment* problem tries to locate two longest subsequences from each sequence, such that they are similar. This can be extended to align

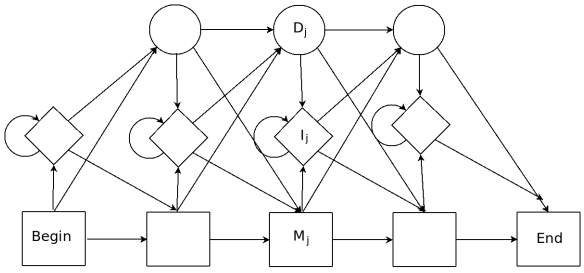



Figure 1: The transition structure of a profile HMM. For example, from an insert state (diamond), we can go to the next delete state (circle), continue in the insert state (self loop) or go to the next match state (rectangle). Note that while multiple sequential deletions are possible by following the circle states, each with a different probability, multiple sequential insertions are only possible with the same probability(Yadwadkar et al., 2010).

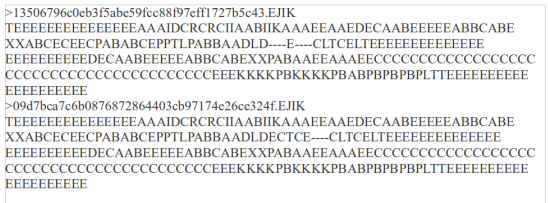

>13506796c0eb3f5abe59fcc88f97eff1727b5c43.EJIK
TEEEEEEEEEEEEEEEAAAIDCRCRCIIAABIIKAAAEEAAEDECAABEEEEEABBCABE
XXABCECEECPABABCEPPTLPABBAADLD----E----CLTCELTEEEEEEEEEEEEEE
EEEEEEEEEEDECAABEEEEEABBCABEXXPABAAEEAAAEECCCCCCCCCCCCCCCCCC
CCCCCCCCCCCCCCCCCCCCCCCCCEEEKKKKPBKKKKPBABPBPBPBPLTTEEEEEEEEEE
EEEEEEEEEE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

Figure 2: A sample MSA file for EJIK Malware Sequences.

multiple sequences. This multiple sequence alignment represents a family of similar sequences, where some subsequences are conserved in all. While 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(Edgar, 2004). 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. 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

$$A_{uv} = \frac{N^A_{uv}}{\sum_v N^A_{uv}} \tag{2}$$

$$A_{uv} = \frac{N^E_{ut}}{\sum_t N^E_{ut}} \tag{3}$$

Where $N^A_{uv}$ represents the number of transitions from the state $u$ to $v$ and $N^E_{uv}$, the number of emissions of $t$ given a state $u$.(Durbin et al., 1998) After the model $\lambda$ 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

$$y(X) = argmax_k P(X|\lambda_k) \quad (4)$$

*HMMER(Eddy, 2003)* 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.

# 4 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(Trinius, 2009). The malware files in this dataset were annotated by choosing the majority of the labels given independently by six different antivirus 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. 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 some 20 operations are very frequent. A sample MIST instruction for a CWSandox reresentation is shown in Fig 4. 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.

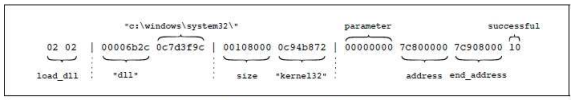
Now for every family of malware, say *Allaple*, we choose few *(typically between 5-20)* files and add their sequence representation to FASTA (*.fa) file. This FASTA file with the sequences is given to the multiple sequence alignment module and the output is an *aligned FASTA (*.afa)*, which has the 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.

| 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: The different malware families and the number of files in each, as in Malheur reference dataset(Trinius, 2009).

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

(a) CWSandbox representation

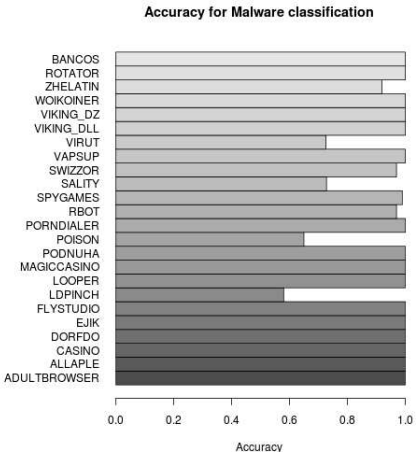



(b) MIST representation

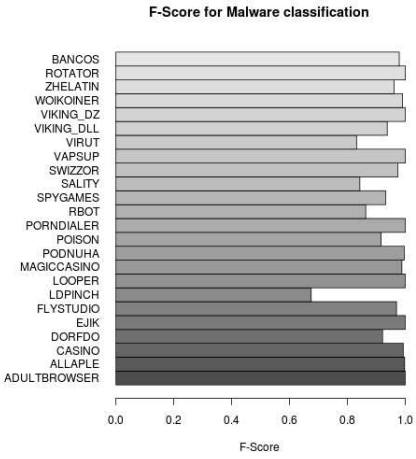
Figure 4: Sample of MIST representation of a portion of CWSandbox report(Trinius et al., 2010).

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.

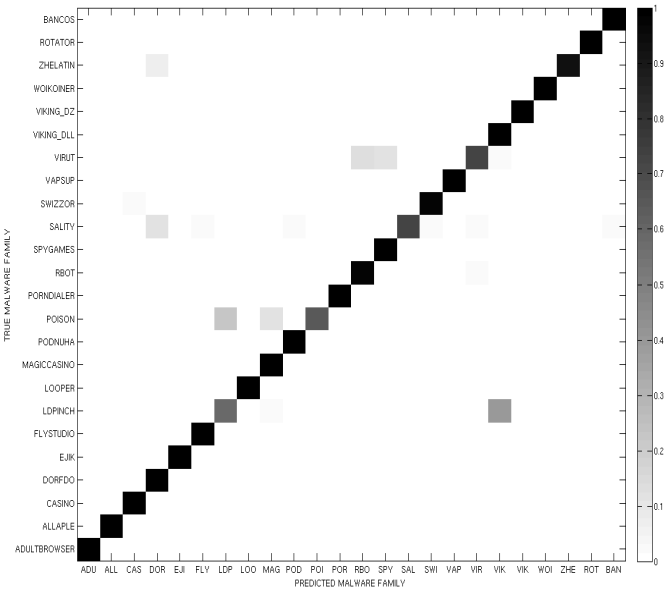
The hmmsearch operation takes longer time for identifying very long sequences with more than 50000 operations in a single report. Multiple sequence alignment and hmmsearch operations were run on a system with quad-core Intel(R) Xeon(R)E5440 @ 2.83GHz processor with 32GB of RAM. Some sequences in the 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.




(a) Histogram of classification accuracy




(b) Histogram of F-scores




(c) Confusion matrix for malware classification

Figure 5.

# 5 RESULTS

## 5.1 On the Reference Dataset

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(Trinius, 2009). 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 5(c). 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*(Rieck et al., 2011), 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 5(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.

The Figure 5b) shows a plot of the F-scores 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 (Rieck et al., 2011) and (Bayer et al., 2010) which give average F-scores of about 0.88 and 0.97 respectively.

The confusion matrix for the multi-class prediction of malware families is presented in the Figure 5(c). 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.

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.

## 5.2 Challenges of the Previous Approaches

We wanted to 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(Trinius, 2009) has close to about 400 different families of malware reports available, on which we wanted to test our approach and do a comprehensive study.

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. 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 (Li et al., 2010) , 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(Bayer et al., 2009). 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 LSH based clustering technique considered in (Bayer et al., 2009) 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.

# 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(Trinius et al., 2010) 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.

## 6.1 Encoding the Behaviour Reports

The behaviour reports of the malware dataset(Trinius, 2009) are encoded using the MIST codes as in the paper(Trinius et al., 2010). 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 encoding gives shorter alphabet code for more frequent instructions and longer codes for the rare ones in the behavior reports. This gave us a nice encoding that will ensure that the sequences are not too long and hence easing the complexity involved in multiple sequence alignment step.

## 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.

## 6.3 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.

## 6.4 Malware Phylogeny from Our Experiments

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 is shown in Figure 6. 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 is shown in Figure 7. Palevo was a worm that surfaced in 2009 and it opens a back door on the compromised computer

Table 1: Malware Clustering Comparision.

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

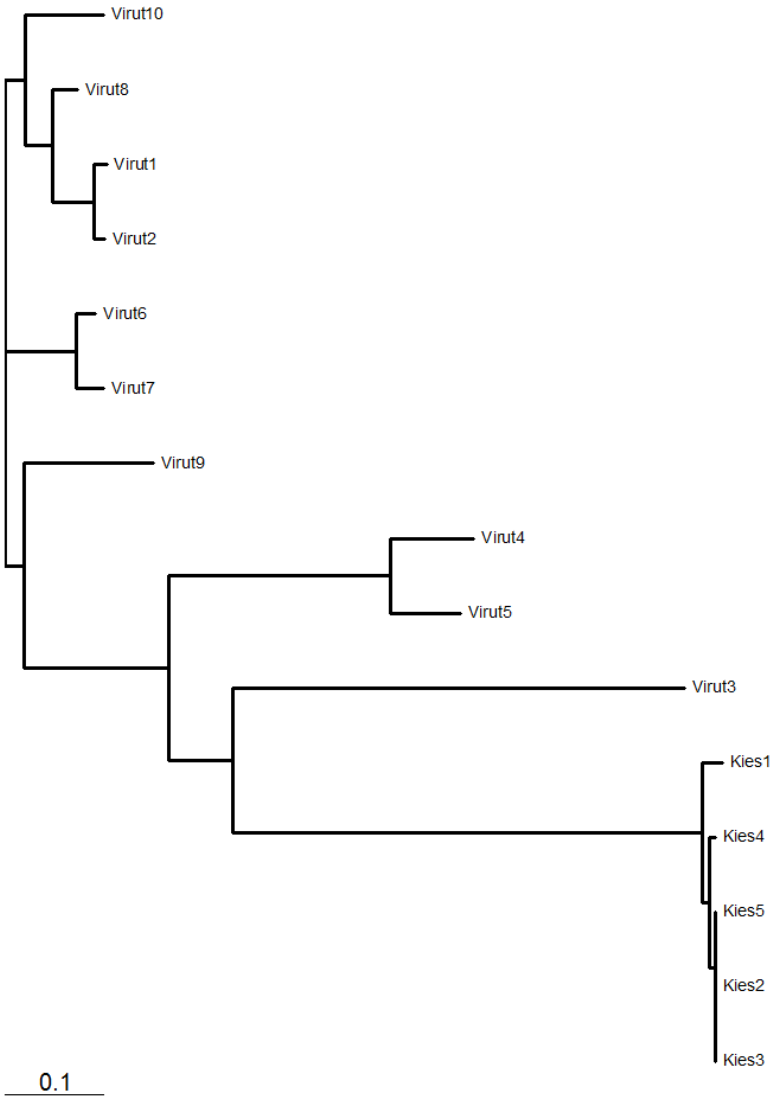



Figure 6: Phylogenetic tree for Virut and Kies.

and attempts to connect to the following IRC server to receive commands and the Buzus shared similar behaviour too. The length of the branches in the tree reflects the genetic distance between aligned sequences. This distance is usually defined as the fraction of mismatches at aligned positions, with gaps either ignored or counted as mismatches.

## 6.5 Analysis of the Results

The distribution of files over the 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

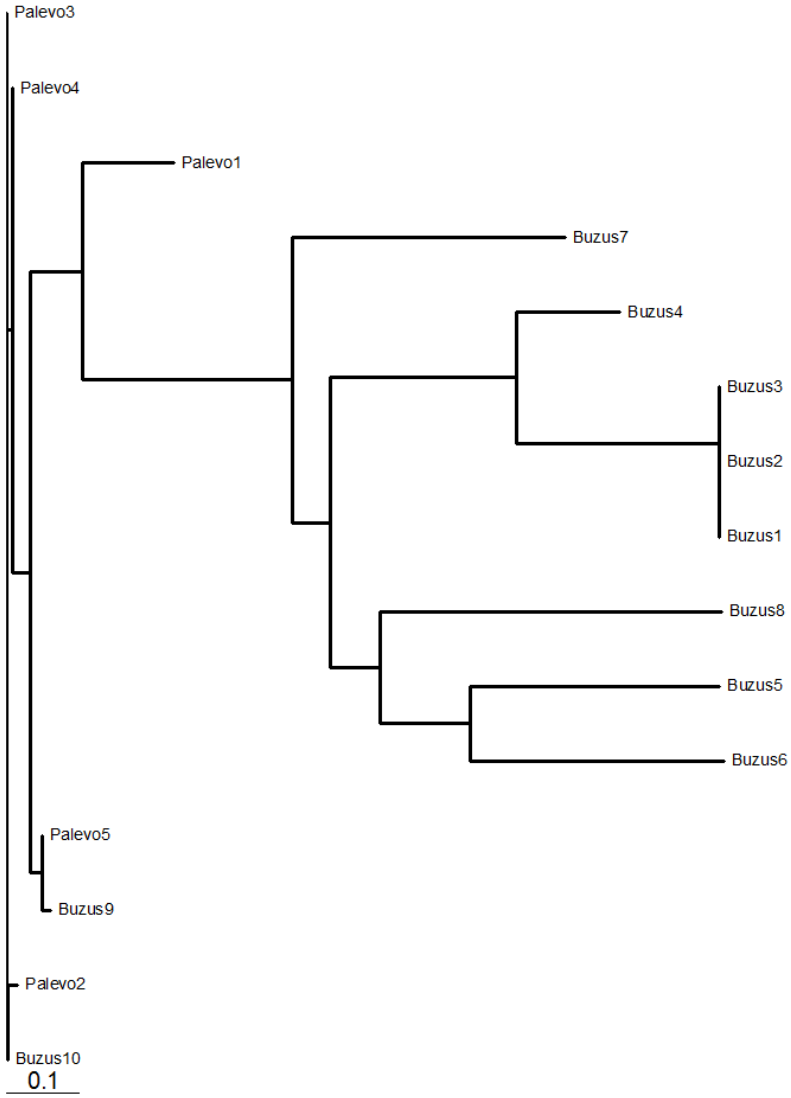



Figure 7: Phylogenetic tree for Palevo and Buzus.

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 Fig.8. It is seen that the clusters are pure and that the cluster size distribution obtained is not very skewed. The results show that the performance of our methodology is comparable with the state-of-the-art, even when using very few sequences to actually model a behaviour profile. PHMM also gives the advantage of lesser complexity in merging profiles or aligning extra sequences to an existing profile, when new variants appear or taxonomy changes.

# 7 FUTURE WORK AND CONCLUSIONS

We have explored the approach of using *profile hidden markov model* for the problem of malware clas-

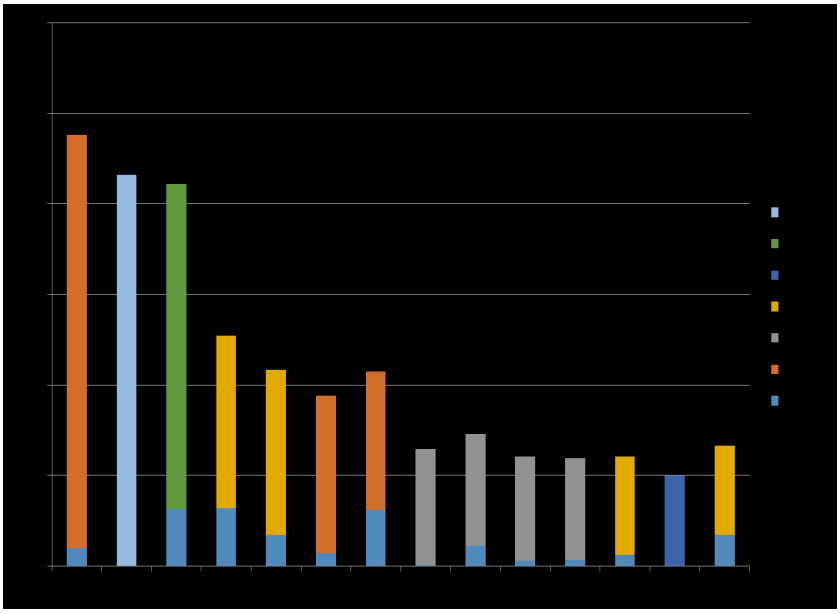


Figure 8: Clustering Results - Top 15 clusters.

sification based on behavior reports. This approach was considered because of the inherent similarity of the metamorphism in malware to that of the mutations in gene or protein sequences. The results are quite assuring of a high classification and clustering performance, even when very few training instances available for building models. We would like to extend this approach for identifying new unseen malware families and to distinguish benign files in our future work that would empower us to design a complete malware triage system. The methods of speeding up the algorithms in the profile HMMs can also be explored,when employing in large scale malware analysis.

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