IAENG International Journal of Computer Science, 42:2, IJCS_42_2_09

Unknown Metamorphic Malware Detection: Modelling with Fewer Relevant Features and Robust Feature Selection Techniques

Jikku Kuriakose,Vinod P

***Abstract*—Detection of metamorphic malware is a challenging problem as a result of high diversity in the internal code structure between generations. Code morphing/obfuscation when applied, reshapes malware code without compromising the maliciousness. As a result, signature based scanners fail to detect metamorphic malware. Prior research in the domain of metamorphic malware detection utilizes similarity matching techniques. This work focuses on the development of a statistical scanner for metamorphic virus detection by employing feature ranking methods such as *Term Frequency-Inverse Document Frequency (TF-IDF), Term Frequency-Inverse Document Frequency-Class Frequency (TF-IDF-CF), Categorical Proportional Distance (CPD), Galavotti-Sebastiani-Simi Coefficient (GSS), Weight of Evidence of Text (WET), Term Significance (TS), Odds Ratio (OR), Weighted Odds Ratio (WOR) Multi-Class Odds Ratio (MOR) Comprehensive Measurement Feature Selection (CMFS)* and *Accuracy2 (ACC2)*. Malware and benign model for classification are developed by considering top ranked features obtained using individual feature selection methods. The proposed statistical detector detects Metamorphic worm (MWORM) and viruses which are generated using Next Generation Virus Construction Kit (NGVCK) with 100% accuracy and precision. Further, relevance of feature ranking methods at varying lengths are determined using *McNemar test*. Thus, the designed non–signature based scanner can detect sophisticated metamorphic malware, and can be used to support current antivirus products.**

***Index Terms*—metamorphic malware, feature selection, non–signature, code obfuscation, classifiers.**

I. INTRODUCTION

Metamorphism refers to approaches used to transform a piece of software into distinct instances [1]. Traditional antivirus fail to detect metamorphic malware due to variability in the internal structures [2]. A metamorphic engine morphs the base malware by applying code obfuscation techniques without altering the functionality. Application of mutation techniques may either increase/decrease the size of malicious code resulting in variable byte patterns.

Prior research in [2] discusses a statistical method using Hidden Markov Model (HMM) for identifying metamorphic viruses. A comparative analysis with different metamorphic engines demonstrates that those viruses generated by *Next Generation Virus Construction Kits* are found to depict highest degree of metamorphism. Authors in [3] proposed metamorphic malware detection using *Profile Hidden Markov Model* (PHMM). The detector identified variants generated by VCL-32 and PS-MPC, but failed to detect NGVCK viruses.

Metamorphic Worm (MWORM) created in [4] evades HMM based detector, had the malware been padded with benign subroutines. Authors in [5] developed a hybrid model for metamorphic malware detection by combing HMM with Chi–Square Distance (CSD). The hybrid model thus developed was tested with NGVCK viruses padded with different percentage of dead code (precisely benign code segment acting as dead code). The hybrid model based on the combination of HMM and CSD demonstrated better accuracy over independently developed malware scanners.

Authors in [6] widened the research by employing structural entropy in the domain of metamorphic malware detection. The method uses segmentation of malware files to estimate the difference in bytes within a segment. Results depicted higher accuracy using entropy based method in identifying MWORM padded with benign code. However, the entropy based approach identified NGVCK viruses with false alarms.

Thus, the objective of this study has been to develop a non–signature based method for metamorphic virus detection. To ascertain this, feature ranking methods such as *Term Frequency-Inverse Document Frequency (TF-IDF), Term Frequency-Inverse Document Frequency-Class Frequency (TF-IDF-CF), Categorical Proportional Distance (CPD), Galavotti-Sebastiani-Simi Coefficient (GSS), Weight of Evidence of Text (WET), Term Significance (TS), Odds Ratio (OR), Weighted Odds Ratio (WOR) Multi-Class Odds Ratio (MOR) Comprehensive Measurement Feature Selection (CMFS)* and *Accuracy2 (ACC2)* that are predominantly employed in the domain of text mining have been implemented. Bi–gram opcodes are ranked using these feature ranking schemes. Malware and benign models have been prepared by considering variable feature lengths. Moreover, evaluation of feature ranking methods at a given feature length is performed using *McNemar test* [7], in order to ascertain its applicability in real time malware scanner.

This paper has been organized as follows. Section II provides previous research in the domain of metamorphic malware detection. Proposed methodology listing different feature ranking methods have been explained in Section III. Further, steps such as *preprocessing, rank feature, model generation, prediction* and *evaluation of feature selection methods* have been covered in Section III. Experimental results and findings have been discussed in Section IV. Finally, inference and conclusions of work have been presented in

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Manuscript received July 03, 2014; revised April 05, 2015

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(Advance online publication: 24 April 2015)

Section V and VI respectively.

II. RELATED WORKS

In [8], a similarity based approach for metamorphic malware detection was developed. A weighted opcode graph was constructed from disassembled opcodes, where each node of the graph represented individual opcodes. When an opcode is followed by another, then a directed edge was inserted in the graph. Weight of an edge was taken as the probability of occurrence of opcode (successor) with respect to a considered opcode. It was experimentally proved that the graph based approach depicted better result on samples where HMM models failed.

In [9] authors presented a novel method for the detection of metamorphic malware based on face recognition technique known as eigenfaces. The premise was that eigenfaces differ due to change in age, posture of face or conditions of light during image acquisition. These eigenfaces are mathematically represented using *Principal Component Analysis*. For each malware, eigenvectors were determined which have larger variances on eigenspace. An unseen binary sample is projected to eigenspace. Subsequently, the euclidean distance of test specimen is computed with predetermined eigenvectors in the training set. Experiment was performed with 1000 metamorphic malware and 250 benign binaries. Detection rate of 100% was obtained with a false positive of 4%.

Authors in [10], created a normalized control flow graph (CFG) using opcode sequences. Variants of malware families were compared using longest common subsequence. It was reported that variants of malware produced higher intra family similarity. Also, morphed malware copies were differentiated from benign samples.

In [11], a method for detecting unseen malware samples by extracting API using STraceNTx in an emulated environment was proposed. Authors investigated the degree of metamorphism amongst different constructors. Inter constructor similarity was determined by computing proximity index. Results exhibited that NGVCK generated variants depicted less intra and inter proximity.

Vinod et al in [12], developed probabilistic signature for the identification of metamorphic malware inspired by bioinformatics multiple sequence alignment method (MSA). Their study revealed that the signatures generated using sequence alignment method was far superior in comparison to those used by commercial AV. The proposed detector resulted in detection rate of 73.2% and was ranked third best compared to other commercial malware scanners used in the experiment.

Authors in [13], employed code emulation to discover dead code in malware specimens. Subsequently, emulator was tested on the metamorphic worm on existing HMM based scanner. It was reported that if the morphed files were normalized to a base malware, the scanner employing HMM identified unseen samples with higher accuracy. However, to develop a precise program normalizer is again a complex function.

In [14], authors developed a non–signature based metamorphic virus detector using Linear Discriminant Analysis (LDA). Experiment was performed by ranking the bi–gram features extracted from NGVCK and MWORM samples. Results showed an accuracy of 99.7% using 200 prominent ranked LDA features.

The authors in [29] proposed a statistical analysis technique known as Mal-ID based on common segment analysis. Initially, two repositories (a) consisting of common function libraries used in both malware and benign set and (b) threat function libraries includes functions that is only included in malware files were created. The proposed approach employed two stages: setup and detection. The setup phase involved in creating the common function library and the detection phase identifies unseen instances. Comparative analysis was performed with n-gram approach proposed by Kolter and Maloof [28]. The proposed methodology resulted in very high accuracy of 0.986 with FPR of 0.006. Their result suggest that common segment analysis boosted the performance of n-gram methods.

In [30], authors presented the known and unknown malware detection based on control flow graphs based features. A control flow graph (CFG) was constructed from the disassembled code. A CFG constituted number of basic blocks, where each block has sequential instruction that does not alter the flow of execution. The break point of the basic block was considered if a conditional/unconditional branch instruction was encountered. Vector space model was created with CFG features by determining the TFIDF of each features. Classification was performed using J48, Bagging and Random Forest implemented in WEKA. The authors concluded that Random Forest achieved 97% accuracy with 3.2% false rate.

In [31], the authors performed the analysis of opcode density features using SVM. The features were collected by executing samples in controlled environment. Principal Component Analysis was performed for reducing the feature space. Experiments was conducted with 260 benign and 350 malware files. Legitimate samples were Windows XP executables and malignant files were collected from VX Heavens repository. Each sample was executed for three minutes to ensure that the sample exhibited its real behaviour. The study reported that SVM marked features precisely classified executables. Also, highly used opcode such as `mov` did not identify those samples. However, when used along with opcodes such as `ja`, `adc`, `inc`, `add` and `rep` the samples resulted in better performance. Also, `ja`, `adc` and `sub` were identified as strong indicators for malware analysis when the reference model was constructed with support vector machine.

III. PROPOSED METHODOLOGY

The proposed scanner contains the following phases (a) Preprocessing (b) Rank feature (c) Model generation and prediction (d) Evaluation of feature selection methods.

A. Preprocessing

Dataset preprocessing is the initial step (refer Figure 1). Malware and benign portable executables are disassembled using Ida-Pro disassembler. Later the bi–gram opcodes are extracted from disassembled files. Dataset is divided into train and test set, such that nearly 50% of samples are used for training and the rest is reserved for testing.

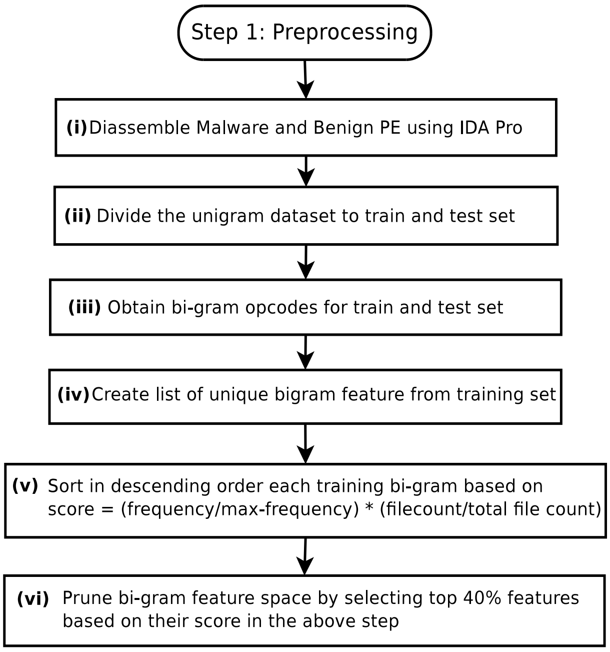


Fig. 1. Preprocessing Phase

Opcode n–gram are overlapping mnemonics of length n collected in a sliding window fashion. An example of generated uni–gram and bi–gram is shown in Table I.

```
push ebx
push esi
push [esp+Length] ; Length
mov ebx, 0C0000001h
push [esp+4+Base] ; Base
push 0 ; MemoryDescriptorList
call ds:MmCreateMdl
```

TABLE I
EXAMPLE OF UNI–GRAM AND BI–GRAM OPCODES

Size of n–gram	Opcode n–gram
uni–gram	push, push, push, mov, push, push, call
bi–gram	pushpush, pushpush, pushmov, movpush, pushpush, pushcall

It is experimentally demonstrated in [10] that for metamorphic malware detection bi–gram feature outperforms uni–gram attributes. Present study showed high variability in frequency of bi–grams in malware and in benign model (refer Figure 2). Thus, bi–gram features generated from uni–gram are extracted from train and test set. From training set 6923 opcodes are obtained. Subsequently, 2769 features are selected based on their prominence in training file (refer Figure 1).

B. Rank Feature

Pruned bi–gram feature space is further ranked using feature selection methods (refer Figure 3) such as *Term Frequency-Inverse Document Frequency (TF-IDF)*, *Term Frequency-Inverse Document Frequency-Class Frequency (TF-IDF-CF)*, *Categorical Proportional Distance (CPD)*, *Galavotti-Sebastiani-Simi Coefficient (GSS)*, *Weight of Evidence of Text (WET)*, *Term Significance (TS)*, *Odds Ratio (OR)*, *Weighted Odds Ratio (WOR) Multi-Class Odds Ratio (MOR) Comprehensive Measurement Feature Selection (CMFS)* and *Accuracy2 (ACC2)*. Feature selection techniques can be broadly categorized as (a) feature search and (b) feature subset evaluation [33]. Feature can be picked using exhaustive, sequential or random searches that improves the classification. Whereas, in feature subset approach a collection of fewer feature is extracted from a larger feature space that enhances the accuracy. Usually, subset methods are segregated into filter and wrapper approaches [32]. Following are the advantages of attribute selection techniques.

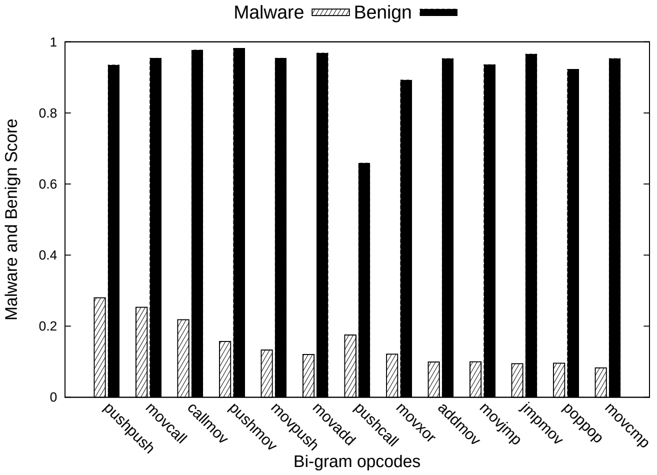


Fig. 2. Frequency Variation of Bi–gram Opcodes in Target Class

- Reduced feature length drastically alleviate classification time and memory requirements.
- Provides better visualization and knowledge of dataset.
- Remove redundant features resulting in maximum discriminant features that contribute towards classification.

1) Term Frequency-Inverse Document Frequency (TF-IDF): TF-IDF score [15] of a bi–gram feature *j* for a sample *i* belonging to a class is computed as,

$$a_{i,j} = log(tf_{i,j} + 1.0) * log\left(\frac{N + 1.0}{n_j}\right) \qquad (1)$$

where,
$tf_{i,j}$: Frequency of opcode j in sample i.

N : Total number of training samples.

n_j : Total occurrences of opcode j in training set.

2) Term Frequency-Inverse Document Frequency-Class Frequency (TF-IDF-CF): TF-IDF-CF [16] score for a bi-gram feature j in i^{th} specimen is calculated as,

$$a_{i,j} = log(tf_{i,j} + 1.0) * log\left(\frac{N + 1.0}{n_j}\right) * \frac{n_{c,i,j}}{n_{c,i}} \qquad (2)$$

where,
$tf_{i,j}$: Frequency of bi–gram j in sample i.

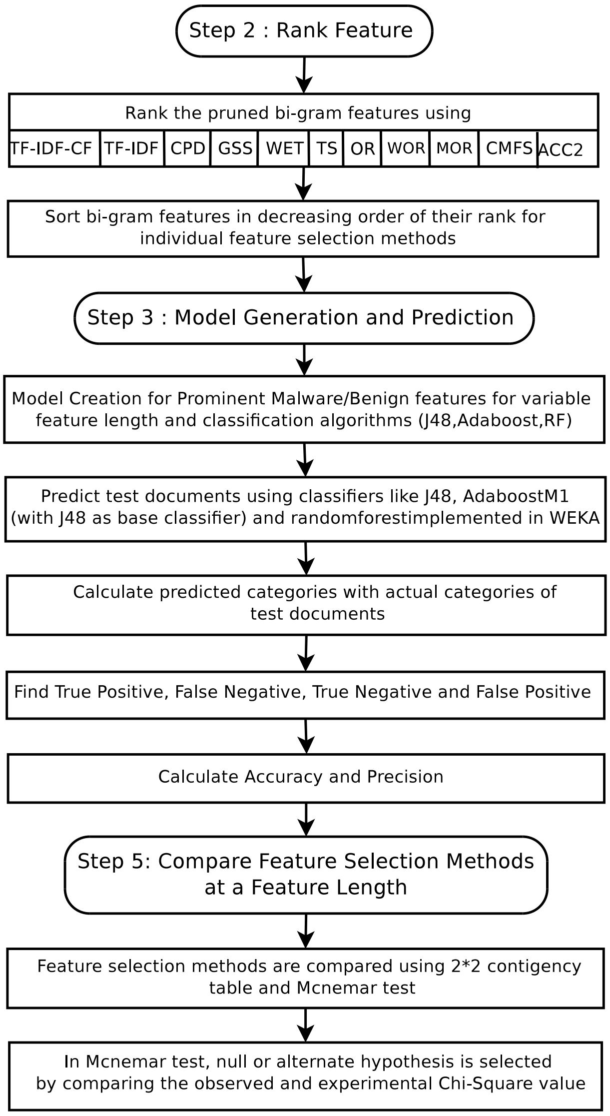


Fig. 3. Feature Ranking and Classification

N : Total number of training specimens.

n_j : Number of occurrences of opcode j in training documents.

$n_{c,i,j}$: Number of files in which bi–gram j belonging to class c where file i is a member.

$n_{c,i}$: Total number of files in class c (malware/benign), where i is a member.

3) Categorical Proportional Distance (CPD): Categorical proportional distance [17] of a feature t in class C_k is defined as,

$$CPD(t, C_k) = \frac{N_{t,C_k} - N_{t,\overline{C_k}}}{N_t} \tag{3}$$

where,
N_{t,C_k} : Number of samples in class C_k consisting of bi–gram feature t.

$N_{t,\overline{C_k}}$: Number of specimens in class $\overline{C_k}$ containing bi–gram feature t.

N_t : Total malware and benign samples consisting of bi–gram feature t.

4) Galavotti-Sebastiani-Simi Coefficient (GSS): GSS Coefficient [18] for a bi–gram feature t_k is obtained as,

$$GSS(t_k, C_i) = P(t_k, C_i).P(\overline{t_k}, \overline{C_i}) - P(t_k, \overline{C_i}).P(\overline{t_k}, C_i) \tag{4}$$

where,
$P(t_k, C_i)$: Joint probability of an opcode t_k with respect to class C_i.

$P(\overline{t_k}, \overline{C_i})$: Joint probability of absence of an opcode t_k in class $\overline{C_i}$.

$P(t_k, \overline{C_i})$: Joint probability of an opcode t_k with respect to class $\overline{C_i}$.

$P(\overline{t_k}, C_i)$: Joint probability of absence of opcode t_k with respect to class C_i.

C_i and $\overline{C_i}$: Represent malware (M) and benign (B) class.

5) Weight of Evidence of Text (WET): Weight of evidence of text [15] for a feature f is obtained as,

$$WET(f) = \sum_{i=1}^{m} P(C_i).P(f).log\left(\frac{P(C_i|f).(1 - P(C_i)}{P(C_i).(1 - P(C_i|f)}\right) \tag{5}$$

where,
$P(C_i)$: Prior probability of classes.

$P(f)$:Prior probability of bi–gram feature f.

$P(C_i|f)$: Conditional probability of class C_i given the probability of feature f.

m : Total number of classes

6) Term Significance (TS): Term significance [19] score of a bi–gram feature t with respect to class C is determined as,

$$TS(t, C) = \begin{cases} \frac{log(max\{P(t),P(C)\})}{1-log(min\{P(t),P(C)\})}, if P(t, C) = 0 \\ \\ \frac{log(max\{P(t),P(C)\})-log(P(t,C))}{1-log(min\{P(t),P(C)\})} \end{cases} \tag{6}$$

where,
$P(t)$: Marginal probability of bi–gram t.

$P(C)$: Prior probability of Class C.

$P(t, C)$: Joint probability of opcode t in class C.

7) Odds Ratio (OR): For a bi–gram feature f, Odds Ratio [20] with respect to class C_k is calculated as,

$$OR(f, C_k) = log\left\{\frac{P(f|C_k).(1 - P(f|\overline{C_k}))}{P(f|\overline{C_k}).(1 - P(f|C_k))}\right\} \tag{7}$$

where,
$P(f|C_k)$: Conditional probability of bi–gram f given the probability of class C_k.

$P(f|\overline{C_k})$: Conditional probability of bi–gram f given probability of class $\overline{C_k}$.

8) Weighted Odds Ratio (WOR): Weighted Odds Ratio [21] score for a feature f is determined as

$$WOR(f) = \sum_{k=1}^{C} P(C).OR(f,C) \tag{8}$$

where,
$P(C)$: Prior probability of class C.

$OR(f,C)$: Odds score of bi–gram feature f with reference to class C.

9) Multi-Class Odds Ratio (MOR): Multi-Class Odds Ratio [21] of a feature f is obtained as,

$$MOR(f) = \sum_{j} \left| log \left\{ \frac{P(f|C_j).(1-P(f|\overline{C_j}))}{P(f|\overline{C_j}).(1-P(f|C_j))} \right\} \right| \tag{9}$$

where,
$P(f|C_j)$: Conditional probability of feature f given probability of C_j.

$P(f|\overline{C_j})$: Conditional probability of bi–gram f for known probability of target class $\overline{C_j}$.

10) Comprehensive Measurement Feature Selection (CMFS): Comprehensive Measurement Feature Selection [22] for a bi–gram t_k in class C_i is evaluated as,

$$CMFS(f,C_i) = P(f|C_i).P(C_i|f) \tag{10}$$

where,
$P(f|C_i)$: Conditional probability of feature f given probability of class C_i.

$P(C_i|f)$: Conditional probability of class C_i given probability of bi–gram feature f.

11) Accuracy2 (ACC2): Accuracy2 [23] of a feature f in class C_i is computed as,

$$ACC2(f,C_i) = \left| P(f,C_i) - P(f,\overline{C_i}) \right| \tag{11}$$

where,
$P(f,C_i)$: Joint probability of feature f in class C_i.

$P(f,\overline{C_i})$: Joint probability of feature f in class $\overline{C_i}$.

C. Model Generation and Prediction

Bi–gram feature space is sorted in the decreasing order of their ranks obtained with feature selection methods. Besides *WET, WOR, MOR* and *ACC2*, feature selection methods such as *TF-IDF, TF-IDF-CF, CPD, GSS, TS, OR* and *CMFS* are used to acquire discriminant features pertaining to target classes (malware and benign) as discussed in Algorithm 1. Relevant bi–gram with variable lengths are used for constructing malware/benign model. Further, learning models are prepared using classification algorithms such as J48, AdaboostM1(using J48 as base classifier) and Random forest implemented in WEKA [24] with default settings.

Algorithm 1 Selecting Discriminant Bi–grams of a Class

```
INPUT: (a) $O = \{b_1,b_2......,b_N\}$ // Bi–gram opcodes
       (b) $C = \{M,B\}$ // Malware or Benign class
       (c) $FS = m_1,m_2.......,m_p$ // Ranking methods
OUTPUT: (a) $\{DList^M_{m1},DList^B_{m1},.....,DList^M_{mp},DList^B_{mp}\}$.

for $i \leftarrow 1to|F|$ do
    $DList^M_{m1} \leftarrow 0$        ▷ Initialize the discriminant list
    $DList^B_{m1} \leftarrow 0$
end for
for $p \leftarrow 1to|O|$ do
    for $q \leftarrow 1to|FS|$ do
        for $r \leftarrow 1to|C|$ do ▷ Computing relevancy score
            $index[r] \leftarrow Score(b_p, m_q)$
        end for
        $Cid \leftarrow MaxScore(temp[1], temp[2], .., temp[|C|]$
                    ▷ Return class index with maximum size
        $DList^{Cid}_{mq} \leftarrow DList^{Cid}_{mq} \cup (b_p, temp[Cid])$
    end for
end for
for $p \leftarrow 1to|FS|$ do
    for $q \leftarrow 1to|C|$ do
        $Sort(DList^q_{mp})$     ▷ Sort bi–gram opcodes in
                    ▷ decreasing order of their relevance
    end for
end for
```

Motivated by a prior work in [25], prediction models obtained from tree based classifiers such as Adaboost and Random Forest are given stronger preference. Models are evaluated using metrics such as accuracy, precision, true positive rate and false positive rate by feeding unseen samples (not used in feature selection phase) to the previously constructed models.

D. Comparison of Feature Selection Methods

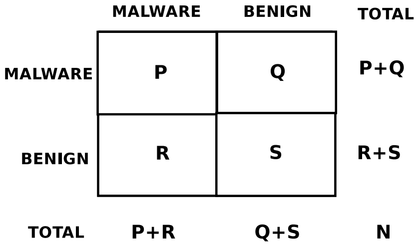
Models generated with feature selection methods perform differently on varying feature length. Therefore, to determine prominent feature selection method at a given feature length *McNemar test* [7] is employed. McNemar test is a non-parametric approach that follows chi–square distribution. Contingency table obtained for feature selection technique at a specific length is supplied as input for statistical testing. The method is based on acceptance or rejection of null or alternate hypothesis based on the computed chi–square value as in Equation 12.

$$\chi^2 = \frac{(|Q-R|-1)^2}{Q+R} \tag{12}$$

where,
Q : Number of malwares misclassified as benign.

R : Number of benigns misclassified as malware.

Computed chi–square value is further compared with tabulated value (i.e. is 3.84 in the present case). If the computed value is less than tabular value, null hypothesis is accepted else alternate hypothesis is considered.



	MALWARE	BENIGN	TOTAL
MALWARE	P	Q	P+Q
BENIGN	R	S	R+S
TOTAL	P+R	Q+S	N

Fig. 4. Contingency Table

IV. EXPERIMENT AND FINDINGS

Experiments have been conducted on a computer system employing an Intel Core i3 processor with a RAM capacity of 4GB on a Linux 12.04 operating system. Extensive experimentation following investigations have been carried out:

- Effect of feature length on classification accuracy.
- Feature selection methods that can produce better accuracy with optimal feature length.
- Bi–gram opcodes that are predominantly used for generating morphed malware copies.
- Suitable classifiers to be used for developing malware scanner.

A. Dataset

Malware data set consisting of 868 samples of NGVCK viruses and metamorphic worm as in [26] have been considered in afore mentioned experiments. Prior studies in [26] reported that highly morphed NGVCK samples could easily bypass strong statistical detector based on HMM. Likewise, 1218 executables including games, web browsers, media players and executables of system 32 (Windows XP operating system) are considered as benign set. Before including the samples in benign set, they were scanned with commercial antivirus scanners to assure that none of the benign samples are infected. Entire data set is divided into two equal portions where training model is prepared from nearly 50% of samples and remaining files are reserved for prediction phase.

B. Evaluation Parameters

Performance for diverse feature length are evaluated using accuracy, precision, true positive and false positive rate. These evaluation parameters are determined from True Positive (TP), True Negative (TN), False Negative (FN) and False Positive (FP) rates (refer Figure 4). TP is the number of correctly identified malware samples, FN is the number of incorrectly classified malware specimens, TN the number of correctly identified benign samples and, FP is the number of benign files misclassified as malware. A brief introduction to the evaluation parameters have been presented as follows(refer Equations 13 through 16)

- Accuracy (Acc) is the ratio of correctly classified instances in the dataset
$$Acc = \frac{TP + TN}{TP + FN + TN + FP} \tag{13}$$
- Precision (P) is the ratio of number of files that are correctly classified as malware to the total number of correctly identified malware samples and benign files misclassified as malware.
$$P = \frac{TP}{TP + FP} \tag{14}$$
- True Positive Rate (TPR) corresponds to the proportion of malware samples correctly predicted by the classification model.
$$TPR = \frac{TP}{TP + FN} \tag{15}$$
- False Positive Rate (FPR) is the proportion of malware samples misclassified as benign.
$$FPR = \frac{FP}{TN + FP} \tag{16}$$

C. Results

Feature ranking methods such as *TF-IDF*, *TF-IDF-CF*, *CPD*, *GSS Coefficient*, *WET*, *TS*, *OR*, *WOR*, *MOR*, *CMFS* and *ACC2* are applied to pruned 2769 bi–gram features. In this article the impact of classification accuracy at variable feature length is researched.

A bi–gram feature is said to be discriminant to a class, if it is prominent in a specific class compared to other. It has been observed that for *TF-IDF, TF-IDF-CF, GSS Coefficient, OR* and *CMFS* model constructed with discriminant malware feature (10 features) furnished 100% accuracy (refer Figure 5 through 9). Likewise, *MOR* features displayed an accuracy of 100% at a reduced feature length of 10 (refer Figure 21). Further reduction of feature space below ten bi–grams drops the classification accuracy. This is because, features that contribute towards classification are eliminated from feature space. However, *TF-IDF-CF* and *TF-IDF* discriminant benign features also yielded 100% accuracy with feature length of 200 and 300 respectively. It is because benign bi–gram samples are diverse and large number of features are required for classification (refer Figure 12 and Figure 13).

GSS discriminant benign features resulted in an accuracy of 99.8% at feature length of 40 and 100 respectively (refer Figure 14). Further increase in feature space does not improve accuracy and at 800 feature length 100% accuracy is obtained. We choose top 40 discriminant benign *GSS* features as optimal feature length because only 0.2% increase in accuracy is achieved by increasing feature space from 40 to 800. Adding extra 760 features increases processing overhead. For *CPD* feature selection, discriminant malware features resulted in 100% accuracy and precision at feature length of 200 bi–grams (refer Figure 10). Moreover *CPD* discriminant benign features resulted in 99.8% accuracy at 800 feature length (refer Figure 17). It is because CPD renders higher rank for features that fall only in a class even present in few samples.

TS discriminant malware depicts an accuracy of 100% at a feature length of 800 (refer Figure 11), whereas *TS*

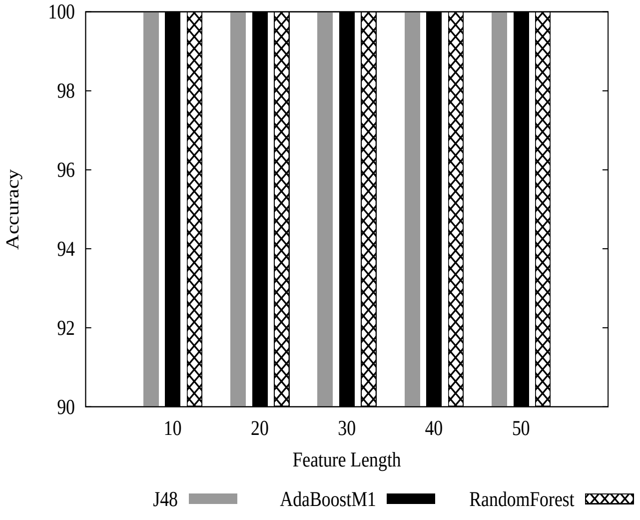


Fig. 5. Evaluation Metrics for TF-IDF(Discriminant Malware Features)

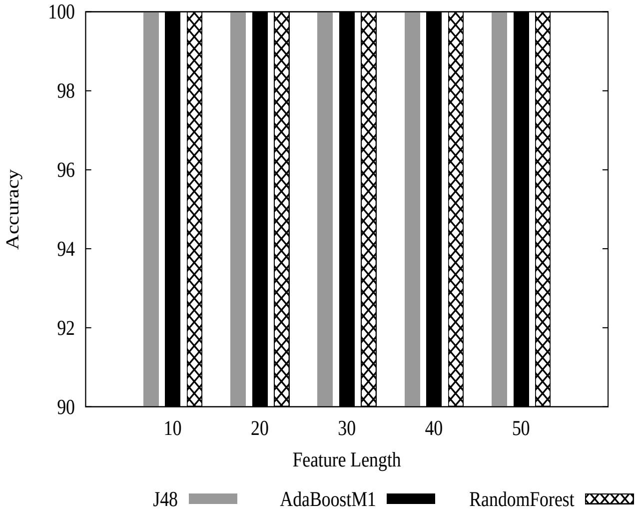


Fig. 6. Evaluation Metrics for TF-IDF-CF(Discriminant Malware Features)

discriminant benign features results in an accuracy of 99.9%, 99.8% at 700 and 400 bi–grams (refer Figure 18). Thus, for *TS* discriminant benign features, optimal feature length is considered as 400 since there is only a marginal increase in accuracy if feature space is substantially increased. *OR* and *WOR* discriminant bi–grams resulted in 99.8% accuracy for 40 feature length (refer Figure 15 and Figure 20). Further increase in bi–gram feature space reduces accuracy and later remains constant. It is also observed that *CMFS* benign features depicts an 100% for 50 bi–gram features (refer Figure 16).

Moreover, *WET* and *ACC2* ranked bi–gram feature resulted in 100% accuracy at 20 and 30 feature length. It is noticed that because of increased false alarms, accuracy drops when feature length is dropped below 10 (refer Figure 19, Figure 22).

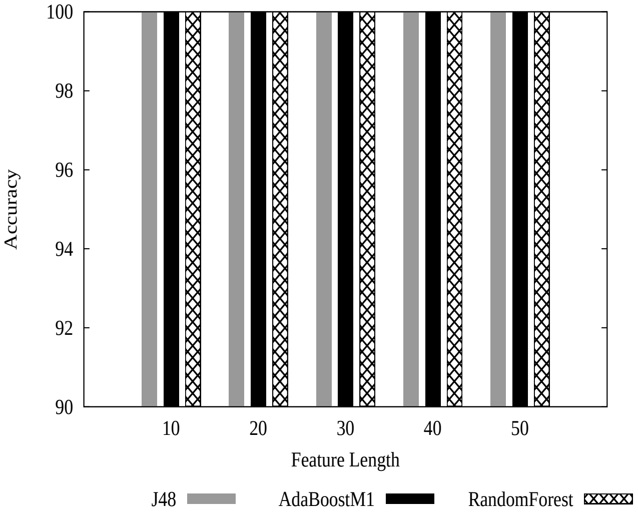


Fig. 7. Evaluation Metrics for GSS(Discriminant Malware Features)

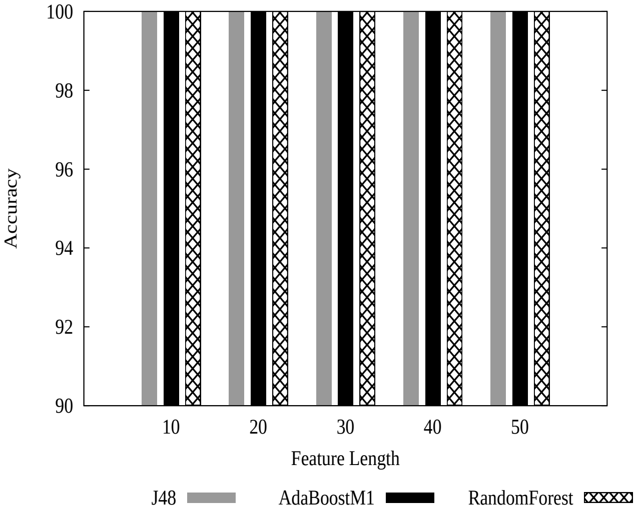


Fig. 8. Evaluation Metrics for OR(Discriminant Malware Features)

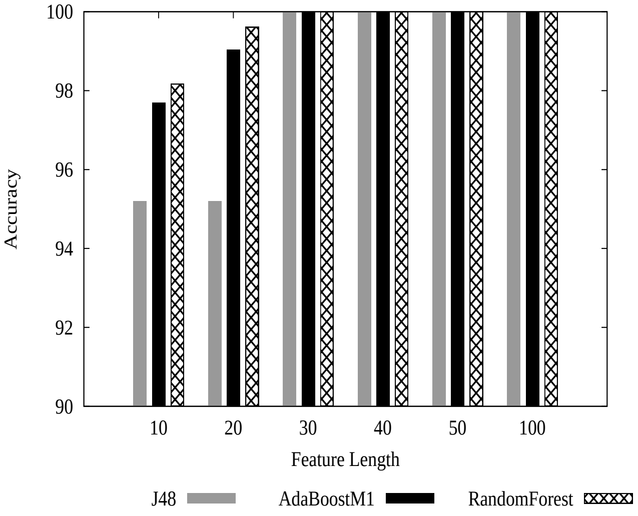


Fig. 22. Evaluation Metrics for ACC2

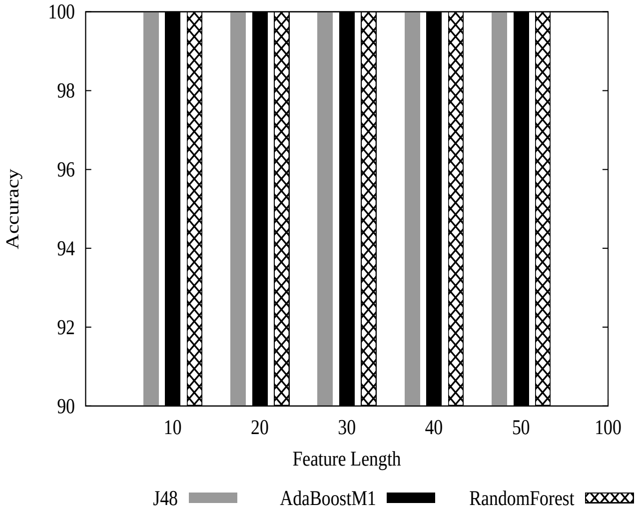


Fig. 9. Evaluation Metrics for CMFS(Discriminant Malware Features)

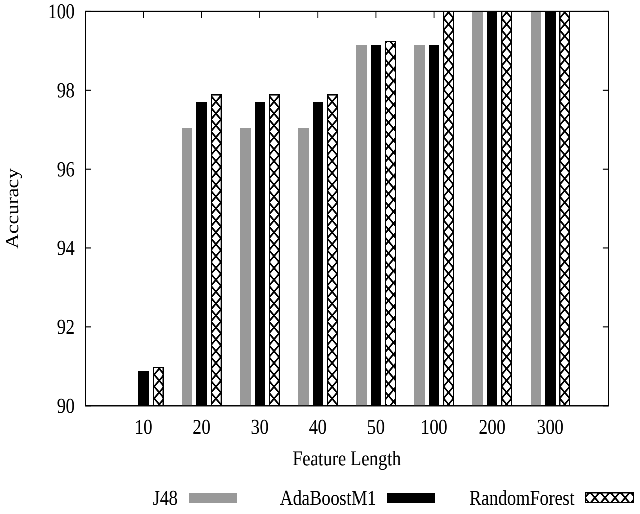


Fig. 10. Evaluation Metrics for CPD(Discriminant Malware Features)

D. Comparative Analysis of Feature Selection Methods

Here, feature selection methods are analysed (refer Table II). From experimental results, it can be argued that discriminant malware features extracted using feature ranking methods are prominent than benign features.

TABLE II
COMPARATIVE ANALYSIS OF FEATURE SELECTION METHOD BASED ON ACCURACY WITH DISCRIMINANT MALWARE FEATURES

Feature Selection	Feature Length	Accuracy with Random forest Classifier	Rank
TF-IDF	10	100	1
TF-IDF-CF	10	100	1
GSS	10	100	1
OR	10	100	1
CMFS	10	100	1
MOR	10	100	1
WET	20	100	2
ACC2	30	100	3
WOR	40	99.80	4
CPD	200	100	5
TS	800	100	6

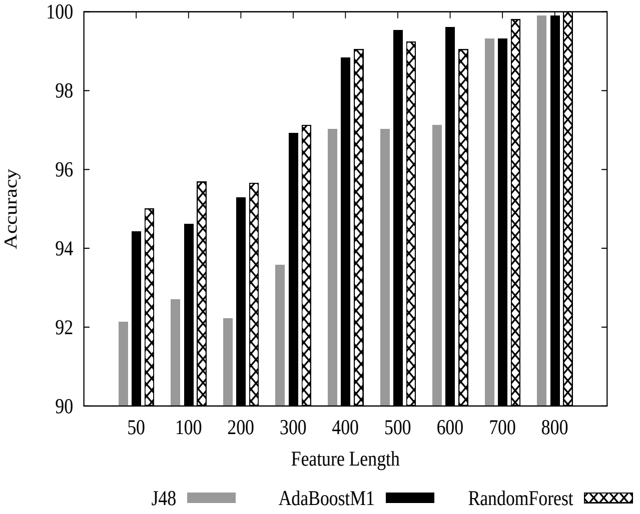


Fig. 11. Evaluation Metrics for TS(Discriminant Malware Features)

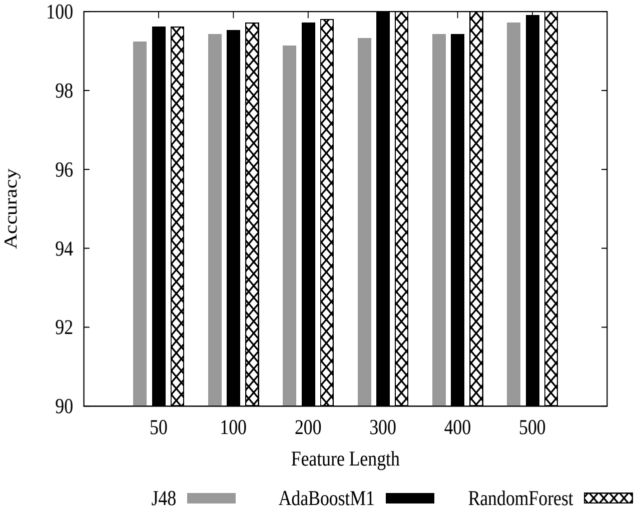


Fig. 12. Evaluation Metrics for TF-IDF(Discriminant Benign Features)

It is observed that for increased feature space using *TF-IDF, TF-IDF-CF, GSS, OR, CMFS* and *MOR* feature selection techniques with malware features, the accuracy remains constant beyond 10 prominent opcodes. However, in case of benign features larger number of attributes are used to develop the model. This is because benign samples are diverse and usually written in high level language. Hence, the common opcodes are rare due to diversification. Whereas, malware programs are author specific (written in low level language) or generated using metamorphic engine. Thus the appearances of common opcodes are more likely to be present in variants of base files. These opcodes are retained by metamorphic engine to preserve maliciousness. Also the complete transformation of x86 assembly code with equivalent sets of opcode is difficult to be implemented. Therefore, it is likely that a malware model may be generated but a generic benign model is difficult to be developed.

Stronger preference for the model generated by Random Forest as well as Adaboost is given. This is because Random Forest [27] is an ensemble of many trees (also known as learners) where, each tree vote for a class. The classifier accumulates votes from entire trees in the forest to categorize new instance. Bagging and boosting properties enhances the

TABLE III
TOP 10 DISCRIMINANT MALWARE BI–GRAM OPCODES WITH TF-IDF, TF-IDF-CF, GSS, OR, CMFS AND MOR

TF-IDF	TF-IDF-CF	GSS	OR	CMFS	MOR
`jemov`	`jemov`	`jemov`	`jemov`	`jemov`	`jemov`
`testje`	`testje`	`cmpjne`	`cmpjne`	`cmpjne`	`cmpjne`
`cmpje`	`cmpje`	`cmpje`	`cmpje`	`cmpje`	`cmpje`
`jnemov`	`jnemov`	`retpush`	`retpush`	`retpush`	`retpush`
`testjne`	`cmpjne`	`jeadd`	`jeadd`	`jeadd`	`jeadd`
`movsxdmov`	`testjne`	`jecmp`	`jecmp`	`jecmp`	`jecmp`
`movmovsxd`	`movsxdmov`	`jnejmp`	`jnejmp`	`jnejmp`	`jnejmp`
`cmpjne`	`movmovsxd`	`testje`	`testje`	`testje`	`testje`
`jmpnop`	`jmpnop`	`jnemov`	`jnemov`	`jnemov`	`jnemov`
`jecmp`	`jecmp`	`testjne`	`testjne`	`testjne`	`testjne`

TABLE IV
MEAN VALUES FOR PROMINENT FEATURES

opcode	Feature Selection Method											
	TF-IDF		TF-IDF-CF		GSS		OR		CMFS		MOR	
	M	B	M	B	M	B	M	B	M	B	M	B
`jemov`	203.10	0	203.10	0	203.10	0	203.10	0	203.10	0	203.10	0
`testje`	199.54	0	199.54	0	199.54	0	199.54	0	199.54	0	199.54	0
`cmpje`	165.49	0	165.49	0	165.49	0	165.49	0	165.49	0	165.49	0
`jmpnop`	121.79	0.05	121.79	0.05	121.79	0.05	121.79	0.05	121.79	0.05	121.79	0.05
`jnemov`	115.57	0	115.57	0	115.57	0	115.57	0	115.57	0	115.57	0
`testjne`	111.40	0	111.40	0	111.40	0	111.40	0	111.40	0	111.40	0
`cmpjne`	101.87	0	101.87	0	101.87	0	101.87	0	101.87	0	101.87	0
`jecmp`	88.84	0	88.84	0	88.84	0	88.84	0	88.84	0	88.84	0
`movmovsxd`	86.73	0.50	86.73	0.50	86.73	0.50	86.73	0.50	86.73	0.50	86.73	0.50
`movsxdmov`	86.18	0.56	86.18	0.56	86.18	0.56	86.18	0.56	86.18	0.56	86.18	0.56
`jnejmp`	27.52	0	27.52	0	27.52	0	27.52	0	27.52	0	27.52	0
`jeadd`	17.67	0	17.67	0	17.67	0	17.67	0	17.67	0	17.67	0
`retpush`	6.97	0	6.97	0	6.97	0	6.97	0	6.97	0	6.97	0

TABLE V
EXPERIMENTAL RESULTS WITH RANDOM FOREST USING TOP 10 SIGNIFICANT FEATURES

Feature Selection Method	TPR(%)	FPR(%)	Accuracy	Time in Microseconds
TF-IDF	100	0	100	0.000579
TF-IDF-CF	100	0	100	0.000593
CPD	78.29	0	90.97	0.000643
GSS	100	0	100	0.000594
WET	100	2.95	98.27	0.000611
TS	97.69	17.40	88.86	0.000748
OR	100	0	100	0.000629
WOR	100	2.95	98.27	0.000642
MOR	100	0	100	0.000614
CMFS	100	0	100	0.000584
ACC2	100	3.11	98.17	0.000627

performance of Random Forest classifier. Performance of decision tree classifiers (J48) is marginally less in comparison to Random Forest and Ababoost. In J48 the decision of splitting a node is performed by gathering information gain determined over all attributes. However, Random Forest picks few attributes in random that have higher probability in identifying a target class. This characteristic of the Random Forest classifier would facilitate in scaling up a model if original feature space is enormous. Moreover, the attributes selected by this classifier are less correlated.

A perfect malware detector should have very high True Positive Rate (TPR) along with less False Positive Rate (FPR). Also, the time to predict test samples using different feature selection methods is closer to those of commercial antiviruses (refer Table V).

V. INFERENCE

1) *What is the effect of feature length on classification accuracy?* It is observed that small feature length has higher classification accuracy and a further increase of features deteriorates the performance. If features discriminant to malware are used for model creation, higher accuracy is obtained at minimal feature space. Thus it characterizes that the dataset used in our study has large number of discriminant features pertaining to malware with less diversification.
2) *Which classifier results in improved performance?* Tree based classifiers like Adaboost and Random Forest resulted in higher preference because they use bagging and boosting approach for classification. Random forest classifier is given higher preference than any other classifiers as reported in prior studies [27].
3) *Which category of feature is better?* Bi–gram features that are discriminant to malware class are used extensively for model preparation. Since malicious code is written in low level language, there exists certain bi–gram features intended to represent malignity which needs to be retained in successive generations. Benign files are written in diverse high level language, the features discriminant to benign samples are distinct and

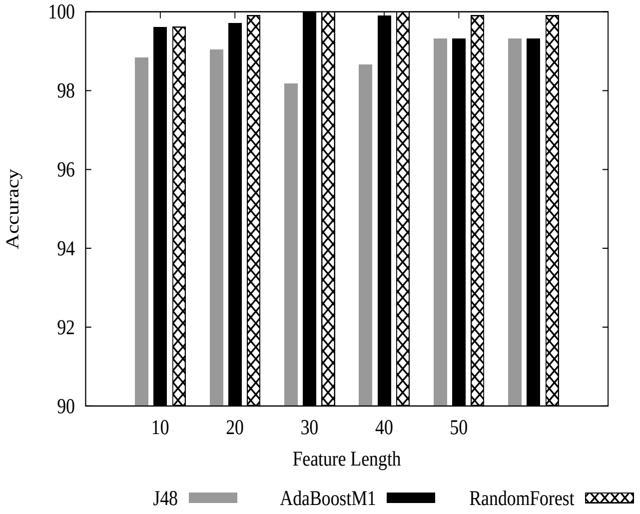


Fig. 13. Evaluation Metrics for TF-IDF-CF(Discriminant Benign Features)

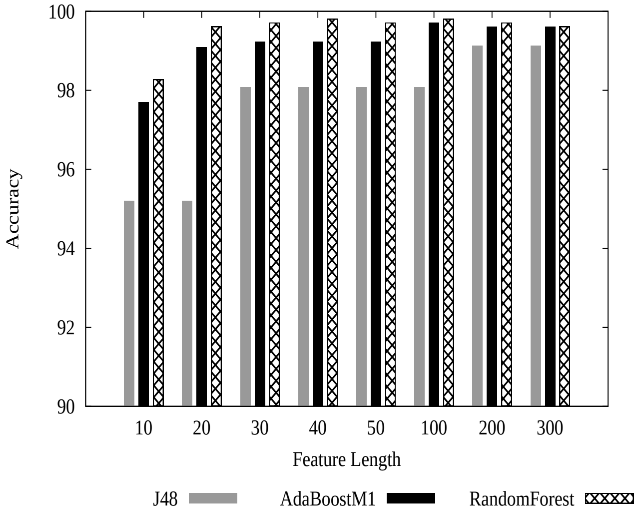


Fig. 14. Evaluation Metrics for GSS(Discriminant Benign Features)

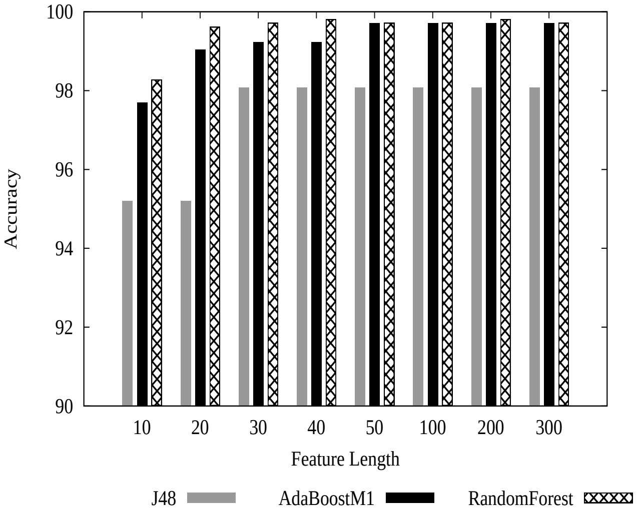


Fig. 15. Evaluation Metrics for OR(Discriminant Benign Features)

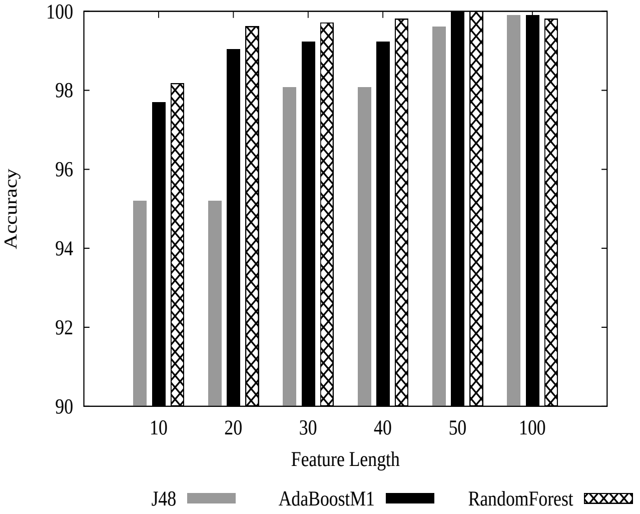


Fig. 16. Evaluation Metrics for CMFS(Discriminant Benign Features)

a universal representation of feature that is required to identify benign files cannot be represented. Thus these features are scarce even after attribute selection algorithm are utilized. Top ten malware bi–gram features for robust feature selection methods that results in 100% accuracy are shown in Table III.

Table IV presents mean values of top ranked bi–gram opcodes obtained from feature selection methods. These features are arranged based on their contribution towards classification. We observe that there is a significant difference in mean values of bi–grams in both the target classes. As a result, these top ranked features could identify unseen samples with better accuracy.

4) *Which feature selection method result in robust feature space?* The appropriateness of feature selection methods (abbreviated as Mi eg: $M1, M2...M11$. $Mi-M$ and $Mi-B$ designate discriminant malware and benign features extracted using method Mi) are evaluated using McNemar Test [7]. McNemar Test is applied to feature selection methods at distinct feature length by determining the Chi–Square value. If the computed Chi–Square value of a give feature selection approach is found to be less in comparison with the tabular value then such methods are considered significant. This indicate acceptance of null hypothesis, i.e. if computed value is less than 3.84 (standard value) otherwise alternate hypothesis is considered. Also, in certain cases optimality of feature selection methods for chi–square value less than 3.84 is discarded considering large feature space. Table VI depict the McNemar Test score for different feature selection methods for variable feature length obtained with a feature selection technique. Each cell in table represents calculated chi–square value. Likewise, Figure 23 shows the feature length and classification accuracy represented using different patterns. In this figure, the cells with diagonal pattern indicate 100% accuracy. It can be observed that for discriminant malware features TF–IDF, TF–IDF-CF, GS, OR and CMFS produces 100% accuracy with 10 bi–grams. However, with benign features better accuracy is achieved at feature length beginning at 100 opcodes (shown in cells with horizontal pattern). Zones

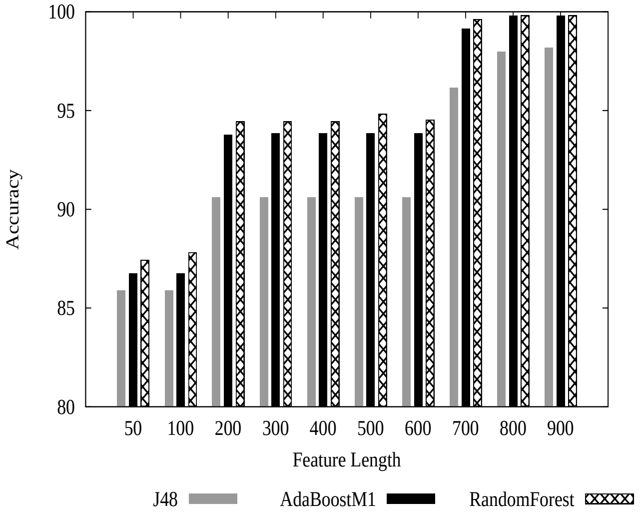


Fig. 17. Evaluation Metrics for CPD(Discriminant Benign Features)

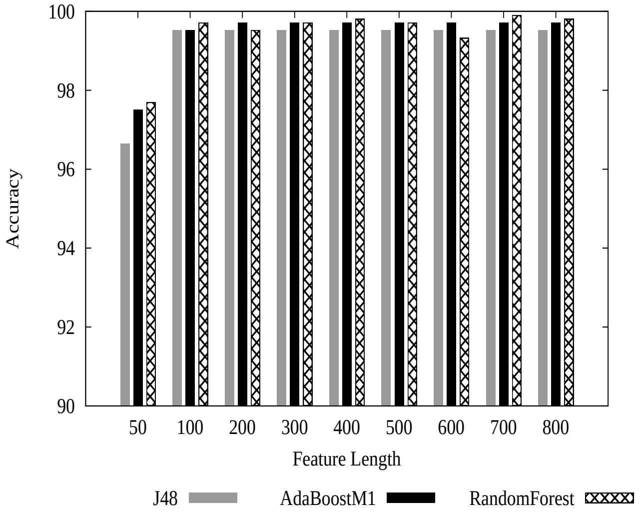


Fig. 18. Evaluation Metrics for TS(Discriminant Benign Features)

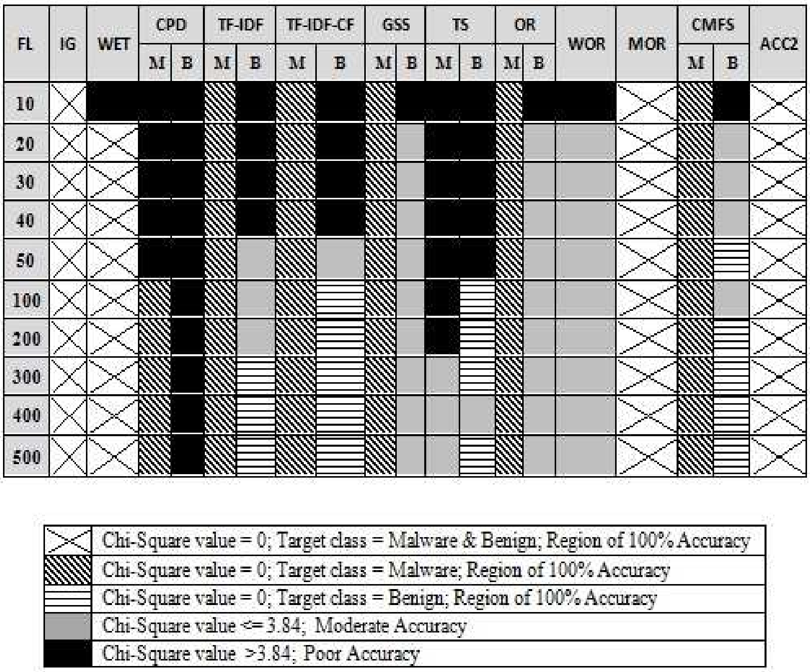
with poor accuracy is indicated with black and light grey color. Also, models constructed with IG, WET, MOR and ACC2 perform well with fewer bi–grams. Thus, from this figure it can be concluded that the models created by pruning features using TF-IDF, TF-IDF-CF, GS, OR, CMGS, IG, WET, MOR and ACC2 accurately identify unseen instances.

VI. CONCLUSIONS

The research carried out here in the domain of metamorphic malware detection to develop a non–signature based scanner using feature ranking methods has been highly successful. Feature selection methods such as TF-IDF, TF-IDF-CF, GSS, OR, CMFS and MOR resulted in the detection of MWORM and NGVCK viruses with 100% accuracy using top ten discriminant malware bi–grams. The significance of the feature selection methods using McNemar Test has been experimentally justified. Through the extensive experiments it can be argued that degree of metamorphism exhibited by MWORM and NGVCK is weak. Dead code added to the viruses can defeat any technique based on sequence

TABLE VI
MCNEMAR TEST SCORE FOR FEATURE SELECTION METHODS AT DIFFERENT FEATURE LENGTH (CELLS SHADED DEPICT LOW ACCURACY I.E. HIGH CHI–SQUARE VALUE)

Feature Length	WET (M1)	CPD (M2)		TF-IDF (M3)		TF-IDF-CF (M4)		GSS (M5)		TS (M6)		OR (M7)		WOR (M8)	MOR (M9)	CMFS (M10)		ACC2 (M11)	Significant Feature Selection Method
		M2-M	M2-B	M3-M	M3-B	M4-M	M4-B	M5-M	M5-B	M6-M	M6-B	M7-M	M7-B			M10-M	M10-B		
10	16.05	92.01	-	0	-	0	-	0	16.05	-	-	0	16.05	16.05	0	0	17.05	17.05	M3-M, M4-M, M5-M, M7-M, M9, M10-M
20	0	20.04	-	0	-	0	-	0	2.25	-	-	0	2.25	2.25	0	0	2.25	2.25	M1, M3-M, M4-M, M5-M, M7-M, M9, M10-M
30	0	20.04	-	0	-	0	-	0	1.33	-	-	0	1.33	1.33	0	0	1.33	0	M1, M3-M, M4-M, M5-M, M7-M, M9, M10-M, M11
40	0	20.04	-	0	-	0	-	0	0.50	-	-	0	0.50	0.50	0	0	0.50	0	M1, M3-M, M4-M, M5-M, M7-M, M9, M10-M, M11
50	0	6.12	117.37	0	2.25	0	2.25	0	1.33	46.17	22.04	0	1.33	1.33	0	0	0	0	M1, M3-M, M4-M, M5-M, M7-M, M9, M10-M, M10-B, M11
100	0	0	113.38	0	1.33	0	0	0	0.50	35.55	0	0	1.33	1.33	0	0	0.50	0	M1, M2-M, M3-M, M4-M, M4-B, M5-M, M6-B, M7-M, M9, M10-M, M11
200	0	0	44.84	0	0.50	0	0	0	1.33	28.86	0	0	0.50	0.50	0	0	0	0	M1, M2-M, M3-M, M4-M, M4-B, M5-M, M6-B, M7-M, M9, M10-M, M10-B, M11
300	0	0	44.84	0	0	0	0	0	2.25	2.70	0	0	1.33	1.33	0	0	0	0	M1, M2-M, M3-M, M3-B, M4-M, M4-B, M5-M, M6-B, M7-M, M9, M10-M, M10-B, M11
400	0	0	44.84	0	0	0	0	0	1.33	0.10	0.50	0	0.50	0.50	0	0	0	0	M1, M2-M, M3-M, M3-B, M4-M, M4-B, M5-M, M7-M, M9, M10-M, M10-B, M11
500	0	0	44.46	0	0	0	0	0	0.50	0.12	0	0	1.33	1.33	0	0	0	0	M1, M2-M, M3-M, M3-B, M4-M, M4-B, M5-M, M6-B, M7-M, M9, M10-M, M10-B, M11



FL	IG	WET	CPD		TF-IDF		TF-IDF-CF		GSS		TS		OR		WOR	MOR	CMFS		ACC2
			M	B	M	B	M	B	M	B	M	B	M	B			M	B	
10	☒	■	■	■	▨	■	▨	■	▨	■	■	■	▨	■	■	☒	▨	■	☒
20	☒	☒	■	■	▨	■	▨	■	▨	▒	■	■	▨	▒	▒	☒	▨	▒	☒
30	☒	☒	■	■	▨	■	▨	■	▨	▒	■	■	▨	▒	▒	☒	▨	▒	☒
40	☒	☒	■	■	▨	■	▨	■	▨	▒	■	■	▨	▒	▒	☒	▨	▒	☒
50	☒	☒	■	■	▨	▒	▨	▒	▨	▒	■	■	▨	▒	▒	☒	▨	☰	☒
100	☒	☒	▨	■	▨	▒	▨	☰	▨	▒	■	☰	▨	▒	▒	☒	▨	▒	☒
200	☒	☒	▨	■	▨	▒	▨	☰	▨	▒	■	☰	▨	▒	▒	☒	▨	☰	☒
300	☒	☒	▨	■	▨	☰	▨	☰	▨	▒	▒	☰	▨	▒	▒	☒	▨	☰	☒
400	☒	☒	▨	■	▨	☰	▨	☰	▨	▒	▒	▒	▨	▒	▒	☒	▨	☰	☒
500	☒	☒	▨	■	▨	☰	▨	☰	▨	▒	▒	☰	▨	▒	▒	☒	▨	☰	☒

☒	Chi-Square value = 0; Target class = Malware & Benign; Region of 100% Accuracy
▨	Chi-Square value = 0; Target class = Malware; Region of 100% Accuracy
☰	Chi-Square value = 0; Target class = Benign; Region of 100% Accuracy
▒	Chi-Square value <= 3.84; Moderate Accuracy
■	Chi-Square value >3.84; Poor Accuracy

Fig. 23. McNemar Test at Varying Feature Length

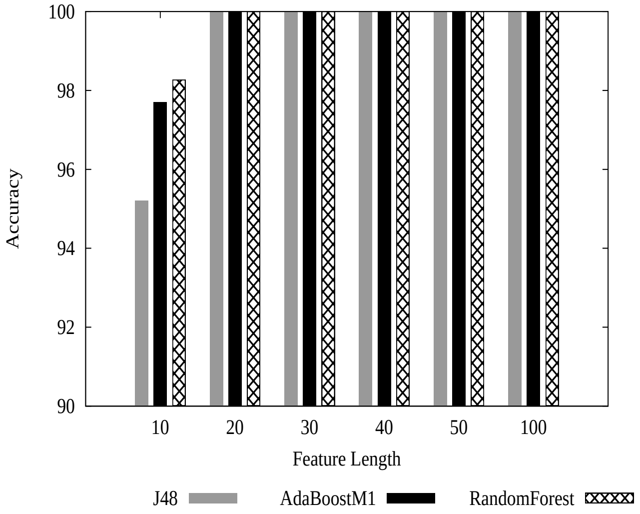


Fig. 19. Evaluation Metrics for WET

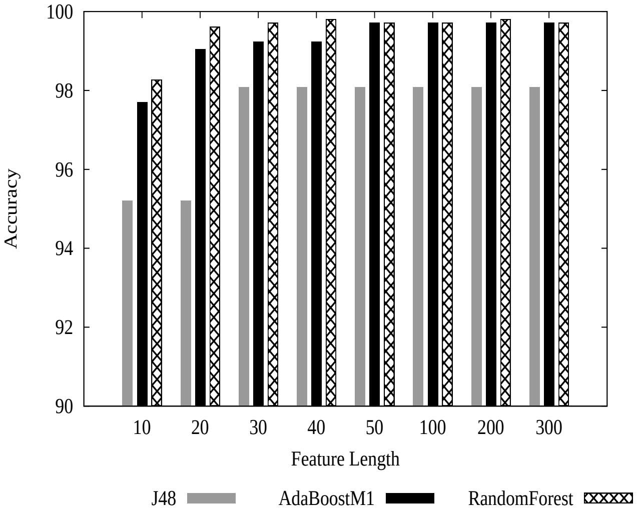


Fig. 20. Evaluation Metrics for WOR

alignment, but approach similar to one presented here can capture such opcodes as they are effectively synthesized during feature selection phase. Thus, the statistical scanner developed can be used for detecting complex metamorphic malware. In future, experiments are likely to be extended on a larger dataset and real metamorphic samples in wild. Moreover, other robust feature selection methods along with their combinations will also be explored.

ACKNOWLEDGMENT

We would like to thank **Professor Mark Stamp** of **SJSU California** for sharing the metamorphic malware dataset for conducting this study.

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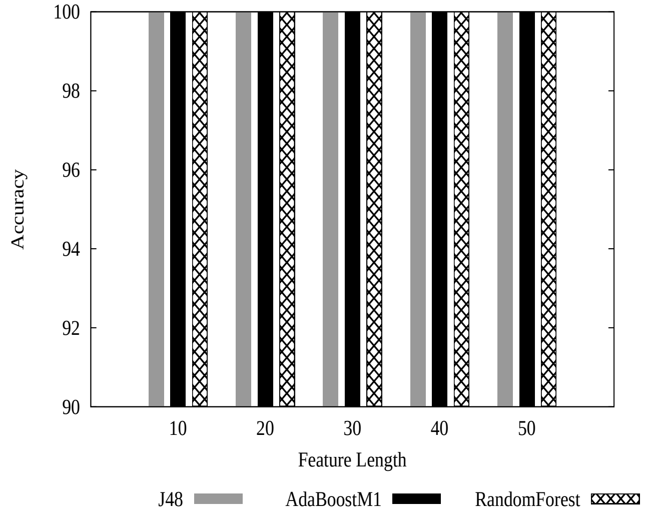

Fig. 21. Evaluation Metrics for MOR

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