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Feature Selection and Extraction for Malware Classification

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The explosive amount of malware continues their threats in network and operating systems. Signature-based method is widely used for detecting malware. Unfortunately, it is unable to determine variant malware on-the-fly. On the hand, behavior-based method can effectively characterize the behaviors of malware. However, it is time-consuming to train and predict for each specific family of malware. We propose a generic and efficient algorithm to classify malware. Our method combines the selection and the extraction of features, which significantly reduces the dimensionality of features for training and classification. Based on malware behaviors collected from a sandbox environment, our method proceeds in five steps: (a) extracting n -gram feature space data from behavior logs; (b) building a support vector machine (SVM) classifier for malware classification; (c) selecting a subset of features; (d) transforming high-dimensional feature vectors into low-dimensional feature vectors; and (e) selecting models. Experiments were conducted on a real-world data set with 4,288 samples from 9 families, which demonstrated the effectiveness and the efficiency of our approach.

Keywords: dynamic malware analysis, data classification, dimensionality reduction, term frequency inverse document frequency, principal component analysis, kernel principal component analysis, support vector machine

1. INTRODUCTION

The growth of malicious programs is exponent. Symantec blocked approximately 5.5 billion malware attacks in 2011, yielding an increase greater than 81% compared with 2010. [1] Signature-based antivirus systems are widely used for detecting viruses in real time. However, according to AV-Comparatives statistics [2], commercial products provide a 14%-69% detection rate regarding new malware. Moreover, viruses can be easily manipulated by hackers, producing numerous variants. It is easy to change malware signatures to evade detection by anti-virus software; thus, it is impossible to update the signature database as rapidly as the explosive speed at which malware variants are developed.

The behaviors of two given malware variants remain similar, although their signatures may be distinct. Recent studies have developed tools to monitor and analyze malware behaviors [3-12]. Egele [13] surveyed automated dynamic malware analysis techniques and tools; automated dynamic analysis provides a report for each malware program, describing its run-time behavior. The information yielded by these analysis tools

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elucidates malware program behaviors, facilitating the timely and appropriate implementation of countermeasures. Rieck [14] analyzed malware behavior by using a CW-Sandbox environment [12], identifying typical malware families as classified by standard anti-virus software; after examining single-family models by using the machine learning toolbox, a malware behavior classifier was constructed. The Institute for Information Industry (III) developed a sandbox environment to record malware behavior; the sandbox can collect the activity of a file, registry, or process. Compared with signature-based methods, behavior-based methods can improve the accuracy of malware classification. However, the time cost for training a classifier is higher than that of training a signature-based method. The computational demands of a behavior-based method cannot meet the requirements of a real-world scenario because excessive time is consumed during feature extraction and model adaptation. Bordes [23] proposed a novel online algorithm, namely, LASVM (fast large-scale support vector machine), which can reduce the execution time by 30% when retraining the classifier; however, the time increased in $O(n^2)$ with respect to the number of features.

To reduce the time cost of behavior-based malware detection, we propose a two-stage dimensionality reduction approach, combining feature selection and extraction to substantially reduce the time cost. Malware behavior logs were collected from a sandbox environment, and an n -gram feature data set was generated based on function calls and bag-of-words model. Feature selection and extraction methods were analyzed to reduce the dimensionality of features, and a support vector machine (SVM) method was used to build the classifier. We showed that using term frequency inverse document frequency (TF-IDF), principal component analysis (PCA), and kernel principal component analysis (KPCA) methods can reduce the number of dimensions, maintaining a promising predictive accuracy. In addition, the selected and extracted features reflected the major behaviors of malware families. Moreover, we propose a multigrouping (MG) algorithm to further improve classification in small feature sets. The proposed approach yielded promising performance and efficiency levels.

2. RELATED WORK

Dynamic behavior analysis is an effective method for predicting unknown malware. Sun *et al.* [24] proposed a method for detecting worms and other malware by using sequences of WinAPI calls and depending on fixed API call addresses. Tsyganok *et al.* [25] proposed a measure of similarity by using system calls to classify the malware. The classification error ranged from approximately 18.5% to 21.4%. Wang *et al.* [26] used two – to three API function call sequences to describe eight suspicious behaviors. The experiment involved using a Bayes algorithm to classify whether program was malicious and achieved 93.98% when 80% of the data were used to train in 914 samples with 453 malicious malwares. Hegedus *et al.* [27] proposed random projections and k-nearest neighbor classifiers. By using the proposed methodology as well as the knowledge and experience of an F-Secure Corporation expert, 24 malware candidates were extracted from 2441 original candidates, of which 25% were known to be malicious and 50% were likely to be malicious. Palahan *et al.* [28] collected 2393 executables from 50 malware families to produce 2393 system call dependency graphs, and achieved an 86.77% accuracy result. Nakazato *et al.* [29] proposed a classification method that consists of two

primary techniques, namely N-gram and TF-IDF. The frequency of N-gram Windows sequence API log data was extracted from 2312 malware samples. The characteristics of the malware samples were deduced by using the TF-IDF technique. By using TF-IDF scores and call sequences as the cluster algorithm for classification, the average precision and recall were approximately 55% and 90%, respectively. For analysis of a substantial amount of computing, Liu *et al.* [30] used MapReduce to reduce the overhead time to improve performance by more than 30%. The experimental result regarding accuracy was 45% (from 50% to 90%) for detecting Trojans, viruses, worms, and spyware. The reduction in time cost in this study cannot be achieved if a high number of malwares or features are used in the classifier. Unlike certain studies that have focused on the identification of specific Windows API call sequences, key values, and parameters for malwares, our classifier incorporated a multigrouping (MG) TF-IDF and PCA, and a KPCA algorithm was used to determine the effective API sequences and was combined with the SVM learning algorithm. Determining the most effective API behavior composition for malware families and rebuilding the classifier in a competitive time-saving manner is easy. After conducting feature selection and extraction analysis, we determined the composition and weighting of behavior functions for malware families. Our results were consistent with the general cognition of the major proportion of malware behaviors.

3. METHODOLOGY

To perform online malware analysis, the retraining and forecasting of updated malicious behaviors must be completed as rapidly as possible; thus, the number of features must be reduced in the learning and classification step. We exploited the feature selection and extraction techniques, using a support vector machine (SVM) classifier, proposing a generic dimension reduction method to update the learning model in few seconds. The following basic steps outline the proposed learning approach:

- 1: Behavior monitoring and data preprocessing. A corpus of malware binaries was executed and logs were collected using a sandbox environment based on hardware virtualization technology to avoid anti-malware detection. Regarding the application programming interface (API) function calls, the feature data were generated based on behavior logs by using the bag-of-words model.
- 2: Training and testing. Machine learning techniques were applied to classify malware families and determine the optimal classifiers and parameters to achieve the ideal accuracy and learning times.
- 3: Feature selection analysis. The effective feature set was calculated using the TF-IDF algorithm. The feature weighting was determined based on the TF-IDF value to determine which feature set yields the optimal accuracy and learning times.
- 4: Feature extraction analysis. The reduced feature dataset was converted from term frequency data by using the PCA and KPCA algorithms to determine the optimal reduced feature set that yields the optimal accuracy and learning times.
- 5: Model selection and online extension. Based on the effective and reduced feature sets, machine learning techniques were applied to classify the malware families; the goal was to determine the optimal classifiers and parameters that yielded the ideal accuracy and learning times.

These steps and the corresponding technical details are presented in detail in the subsequent sections.

3.1 Behavior Monitoring and Data Preprocessing

The malware behavioral datasets were collected from a sandbox environment based on the hardware virtualization technology developed by the Institute for Information Industry (III). The malware was executed in a guest operation system (Microsoft OS) that started on a host computer operation system (Xen) and communicated with a virtualization layer. The sandbox recorded the behavior function calls from the guest operation system, which include cross-matching data (hidden files, hidden registry, hidden connection), file Activity, registry activity, process activity, and generating a detailed report.

Table 1 provides an example of the operations observed in the analysis reports. The report collected up to 150 seconds (approximately 30,000 procedures) of data after the malware was executed.

Including the non-malware family programs, 4,288 samples of nine families were executed and recorded. The malware families and numbers of each malware family were shown in Table 2.

Table 1. An example of operations as reported by sandbox during run-time analysis.

No.	Content
1	CALL name: [], cr3: [0xc08e000] pid: [856],tid: [908], NtOpenKey (0x12fc74: 0x0, 0x80000000, 0x12f950: \Registry\Machine\Software\Microsoft\Windows NT\CurrentVersion\Image File Execution Options\Adware.Admedia.exe) ts-2012-02-11_00:23:42;
2	CALL name: [], cr3: [0xc08e000] pid: [856],tid: [908], NtOpenKey (0x12fc74: 0x0, 0x80000000, 0x12f950: \Registry\Machine\Software\Microsoft\Windows NT\CurrentVersion\Image File Execution Options\Adware.Admedia.exe)
3	CALL name: [C:\Adware.Admedia.exe], cr3: [0xc08e000] pid: [856],tid: [908], NtOpenKeyedEvent(0x12fb14: 0x7c99b140, 0x2000000, 0x12faec: \KernelObjects\CritSecOutOfMemoryEvent) ts-2012-02-11_00:23:42;
...	...

Table 2. The malware families and numbers of each malware family.

Label	Malware families	Number	Sample names
1	Adware	377	Adware.Casino, Adware.Downloader,...
2	Virus/Exploit	76	Exploit.DCOM, Backdoor.Agent,...
3	Dialer	210	Dialer.Riprova, Dialer-110,...
4	Heuristic	348	Heuristic.Trojan, Heuristic.W32,...
5	Suspect.Trojan	129	Suspect.Trojan.Generic,...
6	Trojan	1510	Trojan.Agent, Trojan.Downloader,...
7	W32	207	W32.Luder, W32.Virut,...
8	Worm	1042	Worm.Allapple, Worm.Mydoom,...
9	Non-Malware	389	winlogon.exe, smss.exe,...
Total		4288	

Most studies of malware dynamic analysis have attempted to clarify the specific feature function sets of family behaviors. Rieck [14] based on the vector space and bag-of-words models, finding shared behavioral patterns, and yielding implicit feature set and the vector space data to analysis. For generic purposes, we extracted the function call word for each analysis report, using the bag-of-words model to generate a high-dimensional feature space corpus. A document is characterized by the frequencies of the words it contains. We referred to the set of considered words as feature set F and denoted the set of all analysis reports using D . Given a word $\omega \in F$ and a report $d \in D$, we determined the number of occurrences of n in d to calculate the frequency $f = (d, \omega)$.

We derived an extracting function φ that maps analysis reports to an $|F|$ -dimensional vector space by considering the frequencies of all words in F .

$$\varphi: D \rightarrow R^{|F|}, \varphi(D) \mapsto (f = (d, \omega))_{\omega \in F} \quad (1)$$

The 4,288 documents yielded 187 distinct words; that is, F contained 187 dimensions in the resulting vector space that corresponded to the frequencies of these words in the analysis reports. The word ω was encoded with identifiers that ranged from 1 to 187. Table 3 listed the words and identifier of the corpus dictionary.

Table 3. Examples of the words and identifier of the corpus dictionary.

Identifier	Name of words
1	NtOpenKey
2	NtOpen-KeyedEvent
3	NtQuerySystem-Information
4	NtAllocate-VirtualMemory
5	NtOpen-DirectoryObject
6	NtOpenSymbolic-LinkObject
7	NtQuerySymbolic-LinkObject
8	NtClose
9	NtFsControlFile
10	NtQueryVolumeInformationFile
...	...

To analysis the effect of consecutive words, the n -gram model was applied in our corpus. The unigram feature space $f = (d, \omega)$ was equivalent to the bag-of-words model, and the bigram to six-gram feature space were acquired based on the unigram feature space. We assembled the consecutive words ω_N from ω in F to form n -gram feature set F_N . Given a word $\omega_N \in F_N$ and a report $d \in D$, we determined the number of occurrences of n in d and calculated the frequency $f_N = (d, \omega_N)$. We derived an extracting function φ_N that maps the analysis reports to an $|F_N|$ -dimensional vector space by considering the frequencies of all words in F_N :

$$\varphi_N: D \rightarrow R^{|F_N|}, \varphi_N(D) \mapsto (f = (d, \omega_N))_{\omega_N \in F_N, N=1,6}. \quad (2)$$

The number and examples of n -gram words were shown in Table 4.

Table 4. The number and example of n -gram words.

n -gram	Number of distinct word	Sample of Word
unigram	187	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...
bigram	6740	1 1, 1 2, 1 3, 1 4, 1 5, 1 6, 1 7, 1 8, 1 9, 1 10, 1 11, 1 12, 1 13, ...
trigram	46216	1 1 1, 1 1 2, 1 1 3, 1 1 4, 1 1 5, 1 1 6, 1 1 7, 1 1 8, 1 1 9, 1 1 10, ...
four-gram	130671	1 1 1 1, 1 1 1 2, 1 1 1 3, 1 1 1 4, 1 1 1 5, 1 1 1 6, 1 1 1 8, 1 1 1 10, ...
five-gram	242663	1 1 1 1 1, 1 1 1 1 3, 1 1 1 1 4, 1 1 1 1 5, 1 1 1 1 6, 1 1 1 1 10, ...
six-gram	367211	1 1 1 1 1 1, 1 1 1 1 1 2, 1 1 1 1 1 3, 1 1 1 1 1 4, 1 1 1 1 1 8, ...

3.2 Training and Testing

The n -gram feature space data $f_N = (d, \omega_N)$ introduced in the previous section can be applied in various learning algorithms. SVMs [15] were originally designed for use in binary classification. Hsu [16] constructed a multiclass classifier by combining several binary classifiers. The training data from the i th and the j th classes in the one-against-one method is required to solve the following binary classification problem:

$$\begin{aligned}
 & \min_{\varpi^i, b^i, \xi^i} \frac{1}{2} (\varpi^i)^T (\varpi^i) + C \sum_i \xi_i^i \\
 & (\varpi^i)^T \phi(x_i) + b^i \geq 1 - \xi_i^i, \quad \text{if } y_i = i, \\
 & (\varpi^i)^T \phi(x_i) + b^i \leq -1 + \xi_i^i, \quad \text{if } y_i = j, \\
 & \xi_i^i \geq 0
 \end{aligned} \tag{3}$$

where the training data x_i are mapped to a high dimensional space by using the kernel function ϕ , the penalty parameter is C , and the ϖ is the normal vector to the hyperplane. If $\text{sign}((\varpi^i)^T \phi(x_i) + b^i)$ indicates it is in the i th class, one is added to the vote for the i th class. Otherwise, the j th is increased by one. Regarding the k class label, $k(k-1)/2$ classifiers must be constructed. The kernel is related to the transform $\phi(x_i)$ by the equation $k(x_i, x_j) = \phi(x_i) \phi(x_j)$.

The SVM effectiveness depends on the kernel selection, the kernel parameters, and soft margin parameter C . The Gaussian radial basis function $k(x_i, x_j) = \exp(-\gamma \|x_i - x_j\|^2)$ was used to maximize the hyperplane margins. The kernel parameters γ and cost parameters C must be estimated to yield the optimal prediction. The LIBSVM tool [17], which is an established SVM method, was included in the test environment.

Fig. 1 shows the process of data training and classification. The new tuning γ and C values are selected using a grid search, first using exponentially growing sequences, and subsequently using a binary search for precision until the accuracy is less than 10^{-3} .

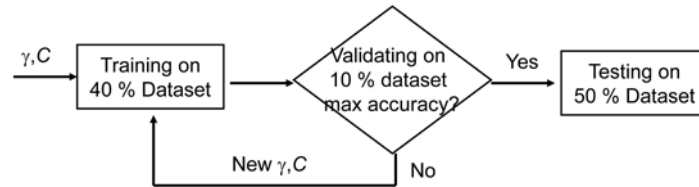


Fig. 1. The process of the data training and classification.

3.3 Feature Selection Analysis

Learning calculation is extremely time-consuming for high-dimensional datasets. The TF-IDF [18] is a numerical statistic that reflects the importance of words in document collections or corpuses. Jing [19] used the TF-IDF feature selection method to process data resources and establish the vector space model, providing a convenient data structure for text categorization. A typical TF-IDF calculation can be expressed as follows:

$$W_i = TF(\omega_i, d) \times IDF(\omega_i) \quad (4)$$

where W_i is the weight of word ω_i in document $d \in D$, $TF(\omega_i, d)$ is the term frequency, or the number of ω_i in d , and

$$IDF(\omega_i) = \log\left(\frac{|D|}{DF(\omega_i)}\right) \quad (5)$$

where IDF is the inverse document frequency and $DF(\omega_i)$ represents the appearance of ω_i in D . The largest value of $IDF(\omega_i)$ occurs when ω_i appears only in one document and its effect is particularly substantial. To sort the weighting of ω_i with all $d \in D$, we normalized the sum of term frequency and modified the TF-IDF model as follows:

$$W_i = \frac{\sum TF(\omega_i, d_l)}{\max\{\sum TF(\omega_i, d_l)\}} \times IDF(\omega_i), \text{ for all } l \text{ in } D. \quad (6)$$

To enhance the accuracy of feature selection, we proposed the following MG TF-IDF method:

$$W_{i,k} = \frac{\sum TF(\omega_i, d_{l,k})}{\max\{\sum TF(\omega_i, d_l)\}} \times IDF_{i,k}, \text{ for all } l \text{ in } D \text{ and } k = 1, 9. \quad (7)$$

The $W_{i,k}$ was calculated by picking the k -family of malware data, using individualized feature selection for each malware family. $\sum TF(\omega_i, d_{l,k})$ is sum of the term frequency of ω_i in the k th class. $IDF_{i,k}$ is the modified inverse document frequency for the k th class:

$$IDF_{i,k} = 10^{(1-IDF'_k) \times IDF_k} \quad (8)$$

where $IDF'_k = (IDF(\omega_i) - IDF(\omega_{i,k})) / (|D| - |D_k|)$, indicates that the exceptive proportion of ω_i in the k th class dataset is as small as possible. $IDF_k = IDF(\omega_{i,k}) / |D_k|$, indicates that the apparent proportion of ω_i in the k th class dataset is as large as possible.

Fig. 2 shows the feature selection process. Regarding data learning and classification using the TF-IDF method, the first m features in the W_i sequence were selected to train and classify. The initial γ and C could be chosen from the same values in the feature domain training. We can determine the optimal accuracy by increasing m in the test. Regarding the MG TF-IDF method, the first m features in the $W_{i,k}$ sequence for all nine families were collected and filtered using the duplicate feature to test.

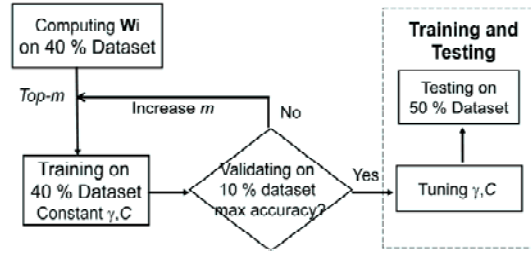


Fig. 2. The process of feature selection.

3.4 Feature Extraction Analysis

Feature extraction is a dimension reduction method that reduces the number of random variables being considered. We introduced PCA and KPCA in the feature extraction algorithms to reduce the time cost of learning calculation for high-dimensional datasets.

3.4.1 Principal component analysis

The central concept of PCA [20] is reducing the dimensionality of a dataset that comprises numerous interrelated variables, retaining as much variation as possible within the dataset. This is achieved by transforming to a new set of variables, the principal components (PCs), which are uncorrelated and ordered so that the first retain most of the variation present in the original variables. Given a dataset comprising m features $(\alpha'_1, \alpha'_2, \dots, \alpha'_m)$, the intent is to transform into a new set of p variables $(\alpha_1, \alpha_2, \dots, \alpha_p)$ of maximal variance. The first step is selecting a linear function $\alpha'_1 \omega$ of the elements of ω that exhibits maximal variance, where α'_1 is a vector of p constants $\alpha_{11}, \alpha_{12}, \dots, \alpha_{1p}$, denoting transpose, where

$$\alpha'_1 \omega = \alpha_{11} \omega_1 + \alpha_{12} \omega_2 + \dots + \alpha_{1p} \omega_p = \sum_{j=1}^p \alpha_{1j} \omega_j. \quad (9)$$

Next, a linear function $\alpha'_2 \omega$ is determined, which is uncorrelated with $\alpha'_1 \omega$ and exhibits maximal variance, and so on, so that at the m th stage a linear function $\alpha'_m \omega$ exhibits a maximal variance subject to being uncorrelated with $\alpha'_1 \omega, \alpha'_2 \omega, \dots, \alpha'_{m-1} \omega$. To derive the form of the PC, first consider $\alpha'_1 \omega_i$; the vector α'_1 maximizes $\alpha'_1 \omega = \alpha'_1 \sum_1 \alpha_1$. To maximize $\alpha'_1 \sum_1 \alpha_1$ subject to $\alpha'_1 \alpha_1 = 1$, the standard approach is using the Lagrange multipliers technique, maximizing as follows:

$$\alpha'_1 \sum_1 \alpha'_1 - \lambda_1 (\alpha'_1 \alpha_1 - 1) \quad (10)$$

where λ_1 is a Lagrange multiplier. Differentiation with respect to α_1 yields

$$\sum_1 \alpha_1 - \lambda_1 \alpha_1 = 0, \quad \sum_1 \alpha_1 = \lambda_1 \alpha_1 \quad (11)$$

or

$$(\sum_1 - \lambda_1 I_p) \alpha_1 = 0, \quad (12)$$

where I_p is the $(p \times p)$ identity matrix. Thus, λ_1 is an eigenvalue of \sum_1 and α_1 is the cor-

responding eigenvector. \sum_1 is the covariance matrix of feature 1,

$$\sum_1 \frac{\sum_{y=1, y \neq q}^T l=1, |D| \text{ observations of documents}}{|D|}, \quad (13)$$

where $y_{1l} = (f(d_1, \omega_1) - (\sum_{l=1}^{|D|} y_{1l}) / (|D|)) / \sigma_1$ is the standard dataset score value as calculated based on the original dataset and σ_1 is the standard deviation of 1st feature. The new feature space dataset g was generated as follows:

$$g_j = y \alpha_j, j = 1, p \quad (14)$$

where the λ value could represent the degree of importance of the new vector, and $\lambda_1 > \lambda_2 > \lambda_3 > \dots > \lambda_p$.

To locate the principal component of each malware family, we proposed a MG PCA method, solving the following problem for each k th family class:

$$(\sum^k - \lambda^k I_p) \alpha^k = 0, k = 1, 9. \quad (15)$$

We picked the k th class data from the training dataset and generated the standard score value dataset y^k . The new transformation vector α^k and λ^k were calculated for each class. We reorganized the new transformation vector α , which was chosen using class-by-class selection and the λ sorted value. A new MG feature dataset g was generated using $g^{new} = y^{old} \alpha$.

Fig. 3 shows PCA feature extraction process; regarding PCA data learning and classification, the first m features in the new dataset g were selected to train and classify. We can determine the optimal accuracy by increasing and testing m . Regarding the MG PCA method, the first m features of g^k in all nine families were collected for testing.

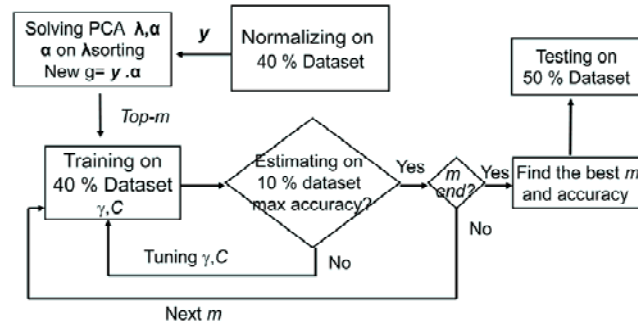


Fig. 3. The process of PCA feature extraction.

3.4.2 Kernel principal component analysis

The KPCA is a non-linear extension of the PCA. [21] Its advantages are nonlinearity of eigenvectors and an increased number of eigenvectors. Karg [22] applied PCA, KPCA and linear discriminant analysis to kinematic parameters and analyzed for feature

extraction. In PCA, the eigenvalue problem is solved as follows:

$$\sum \alpha = \lambda \alpha, \text{ where } \sum = \frac{\sum y y^T}{|D|}. \quad (16)$$

\sum is a covariance matrix. If we nonlinearly map the data into a feature space F by using a non-linear map Φ

$$\Phi: R^N \rightarrow F, y \mapsto Y \quad (17)$$

linear PCA is performed in the high-dimensional space F , corresponding to a non-linear PCA in the original data space. The covariance matrix is calculated as follows:

$$C = \frac{\sum \Phi_i \Phi_i^T}{|D|} = \frac{\sum \Phi \Phi^T}{N}. \quad (18)$$

The eigenvalue problem determines Eigenvalues $\lambda \geq 0$ and Eigenvectors $V \in F$, satisfying $CV = \lambda V$, where $V = \Phi \alpha$. This yields the following:

$$(\Phi^T \Phi) \alpha = (\Phi^T \Phi) N \lambda \alpha \quad (19)$$

thus, the Eigenvalue problem becomes

$$(K - N \lambda) \alpha = 0 \text{ or } K \alpha = (N \lambda) \alpha, \text{ where } K = \Phi^T \Phi. \quad (20)$$

The scalar product of Φ can be substituted with a kernel function K . In this study, a Gaussian kernel $K(x_i, x_j) = \exp(-\gamma_k \|x_i - x_j\|^2)$ was used.

The new feature space dataset g was generated using the following formula:

$$g_j = \frac{\alpha_j^T K}{\sqrt{\lambda_j}}, \quad j = 1, p. \quad (21)$$

Where $\lambda_1 > \lambda_2 > \lambda_3 > \dots > \lambda_p$ and the λ value could represent the degree of importance of the new vector. To focus on finding the principal component of each malware family, we proposed an MG KPCA method. We solved the problem for each k th family class as follows:

$$(K^k - N \lambda^k) = 0, k = 1, 9. \quad (22)$$

We picked the k th class data from training dataset, generated the standard score value dataset y^k , and calculated K^k . The γ^k in Gaussian kernel K must be tuned to yield the optimal transformation. The new transformation vectors α^k and λ^k were calculated for each class. We reorganized the new transformation vector α , which was selected class-by-class, and by the λ sorted value. The new MG feature dataset g was generated using $g^{new} = \alpha^T K / \sqrt{\lambda}$.

Fig. 4 shows the KPCA feature extraction process, involving data learning and classification. The first m features in new dataset g were selected to train and classify. The optimal values of γ^k and m were determined using a grid search method in two loops. Regarding the MG KPCA method, the first m features of g^k in all nine families were collected to test.

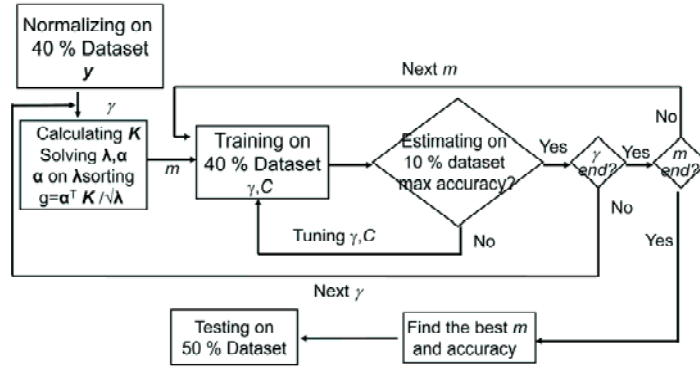


Fig. 4. The process of KPCA feature extraction.

3.5 Model Selection and Online Extension

The numbers and instances of features are the major time consumers in online machine learning. Bordes [23] proposed a novel online algorithm (LASVM) that converged SVM solutions. The experimental evidence for diverse datasets indicates that the LASVM method reliably reaches competitive accuracy levels after performing a single pass of the training set. The effectiveness of LASVM could reduce the execution time by 30% when regenerating classifiers; the time increased in quadratic complexity (n^2 -order) as the number of features increased. We propose a novel dimension reduction algorithm to substantially reduce the number of features used in machine learning. Our two-stage dimension reduction algorithm could save more than 99% of execution time during the re-training process of high feature spaces. The proposed algorithm is described as follows:

$$f(d, \omega) \rightarrow F(f(d, \omega)) \rightarrow f(d, \omega') \rightarrow G(y(d, \omega')) \rightarrow g(d, m) \rightarrow H(g(d, m)) \rightarrow z(d). \quad (23)$$

The first stage $F(f(d, \omega))$ involves using the feature select algorithm detailed in Section 3.3, where $f(d, \omega')$ is the selected subset of the original dataset and y is the standard score value of f . The second stage $G(y(d, \omega'))$ involves using the feature extraction algorithm detailed in Section 3.4, where $g(d, m)$ is the dimension reduction dataset of y and $H(g(d, m))$ is machine learning process that uses the SVM algorithm detailed in Section 3.2, yielding $z(d)$ as the final prediction of document d to evaluate the accuracy. In practical online application, the parameters in this process should be adjusted to reduce the learning time. The optimal parameters could be determined by using initial offline dataset. We used a 40% training dataset and $f(d, \omega) \rightarrow F(f(d, \omega)) \rightarrow f(d, \omega') \rightarrow H(g(d, m)) \rightarrow z(d)$ to determine the optimal feature subset, and then used Equation (4) to calculate the optimal m and γ_k for feature reduction, γ and C for SVM.

The online training was simulated by initially collecting 40% of a dataset, and the parameters were fixed in the following training and testing. The classifier was rebuilt to accumulate 50% to 90% of the data in increments of 10% and tested for the subsequently incoming 10% of the dataset.

4. EXPERIMENT

We collected 4,288 documents from nine family classes of malware samples, as described in Section 3.1. Cross validation was used to identify effective parameters, allowing the classifier to accurately predict unknown data and prevent overfitting. [18] In v -fold cross-validation, the training set is divided into v subsets of equal size. Sequentially one subset is tested using the classifier trained on the remaining $v-1$ subsets. This is called the holdout method if $v = 2$. We used three-part cross validation, modifying the v -fold cross-validation to yield an estimate. We generated 10-fold data subsets: four subsets were the training set, one subset was the estimate set used for optimal parameter tuning, and the remaining five subsets were used in independent testing. Total 10 runs were tested by random combination of 10-fold subsets data. A confusion matrix is a specific table layout that displays the performance level of a classification system; thus, a confusion matrix table was generated and the accuracy was evaluated for each estimated subset and testing subset.

4.1 Behavior Monitoring and Data Preprocessing

In the first experiment, we examined the general classification performance level of the proposed malware behavior classifier. The learning and classification methods described in Section 3.2 were used to analyze a unigram to six-gram dataset. Various methods were used to evaluate our retrieval system. Table 5 lists the result of families for the first-fold SVM test, using unigram, where TP no. = the number of true positives, FN no. = the number of false negatives, FP no. = the number of false positives, TN no. = the number of true negatives, accuracy $A = (TP + TN)/(TP + FN + FP + TN)$, precision (Sensitivity) $P = TP/(TP + FP)$, recall $R = TP/(TP + FN)$, specificity $S = TN/(TN + FP)$, negative predictive value $N = TN/(TN + FN)$, and F -measure $F = 2PR/(P + R)$.

Table 5. Various measures result of families by 1st run SVM test for unigram.

Label	TP no.	FN no.	FP no.	TN no.	A	P	R	S	N	F
1	184	16	33	1936	0.98	0.85	0.92	0.98	0.99	0.88
2	26	20	12	2111	0.99	0.68	0.57	0.99	0.99	0.62
3	87	11	12	2059	0.99	0.88	0.89	0.99	0.99	0.88
4	123	55	27	1964	0.96	0.82	0.69	0.99	0.97	0.75
5	50	16	23	2080	0.98	0.68	0.76	0.99	0.99	0.72
6	642	90	126	1311	0.9	0.84	0.88	0.91	0.94	0.86
7	57	51	34	2027	0.96	0.63	0.53	0.98	0.98	0.57
8	489	43	44	1593	0.96	0.92	0.92	0.97	0.97	0.92
9	183	26	17	1943	0.98	0.92	0.88	0.99	0.99	0.89

Table 6 lists the results of the 10-run SVM test for the unigram dataset, where

$$\text{Micro Precision} = \sum_{i=1}^9 TP_i / (\sum_{i=1}^9 TP_i + \sum_{i=1}^9 FP_i),$$

$$\text{Micro Recal} = \sum_{i=1}^9 TP_i / (\sum_{i=1}^9 TP_i + \sum_{i=1}^9 FN_i),$$

$$\text{Micro Specificity} = \sum_{i=1}^9 TN_i / (\sum_{i=1}^9 TN_i + \sum_{i=1}^9 FP_i),$$

$$\text{Micro Negative predictive value} = \sum_{i=1}^9 TN_i / (\sum_{i=1}^9 TN_i + \sum_{i=1}^9 FN_i),$$

$$\text{Macro Precision} = \sum_{i=1}^9 P_i / 9,$$

$$\text{Macro Precision} = \sum_{i=1}^9 R_i / 9,$$

$$\text{Macro F} = \sum_{i=1}^9 F_i / 9,$$

Table 6. The further measures result of families by 10-run SVM test for unigram.

<i>n</i> th Run	Micro <i>P</i>	Micro <i>R</i>	Micro <i>S</i>	Micro <i>N</i>	Macro Precision	Macro Recall	Macro <i>F</i>
1	0.8488	0.8488	0.9811	0.9811	0.8012	0.7801	0.7885
2	0.8418	0.8418	0.9802	0.9802	0.7784	0.7634	0.7693
3	0.8387	0.8387	0.9798	0.9798	0.7908	0.7866	0.7847
4	0.8413	0.8413	0.9802	0.9802	0.7856	0.7678	0.7743
5	0.8559	0.8559	0.9820	0.9820	0.7944	0.8047	0.7953
6	0.8583	0.8583	0.9823	0.9823	0.7827	0.7802	0.7803
7	0.835	0.835	0.9794	0.9794	0.7961	0.758	0.7703
8	0.8506	0.8506	0.9813	0.9813	0.8127	0.7888	0.7988
9	0.8555	0.8555	0.9819	0.9819	0.8152	0.8029	0.808
10	0.8398	0.8398	0.9800	0.9800	0.8033	0.7525	0.7744
average	0.8466	0.8466	0.9808	0.9808	0.796	0.7785	0.7844

The microprecision and micro recall values were the same for the multiclass classification, and the microspecificity and micronegative predictive values were the same. We observed that all of the micronegative predictive values were higher than 97.9%. The results revealed a satisfactory prediction for the negative predictive value. Therefore, the experiments focused on overall true positives; in other words, the microprecision (and recall) measure was used for assessing accuracy and optimizing the parameters. Figs. 5

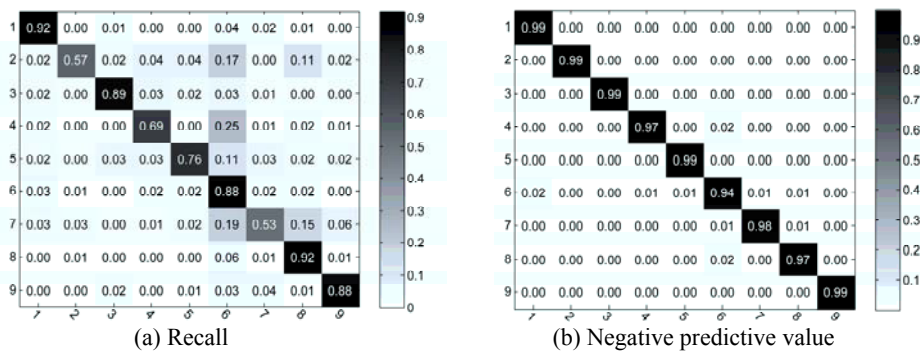


Fig. 5. The confusion result of families for unigram 1st run classify ($C = 500$, $\gamma = 0.00000093$).

and 6 show the confusion matrix results and micro measures results of the families in the first-run SVM test for unigram. The matrix diagonal corresponds to the recall value of each class, and the total accuracy was the micro recall value.

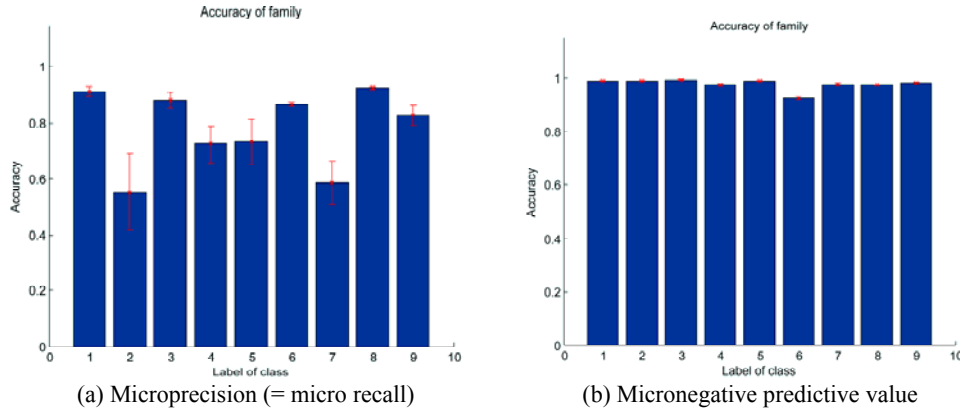


Fig. 6. The micro measures result of each family for unigram classify ($C = 500$, $\gamma = 0.00000093$).

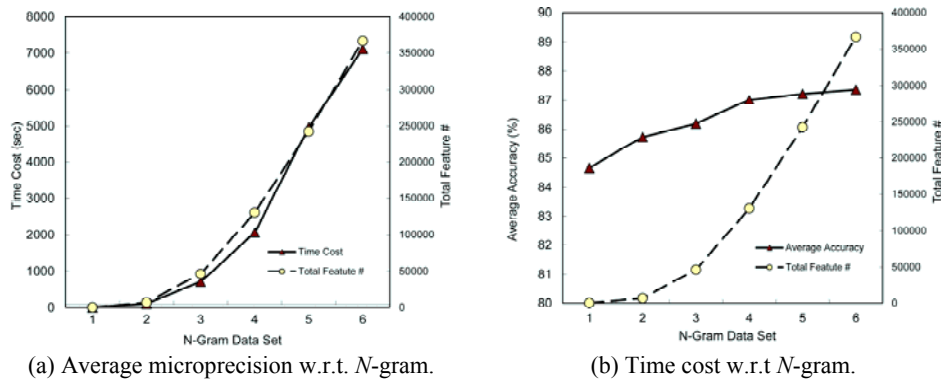


Fig. 7. The microprecision and the time cost of n -gram experiments.

Fig. 7 shows the average microprecision of the used feature numbers and the corresponding time costs of the n -gram experiments. The average values comprised the results of the 10-run experiment. In Fig. 7 (a), the microprecision gradually increased from the unigram to the four-gram experiment, inconspicuously increasing in the five-gram and six-gram experiments; thus, numerous features in the increased five-gram and six-gram experiments were redundant and ineffective. By contrast, in Fig. 7 (b), the time cost continually increased as the size of the feature dimension increased. The time costs of these experiments failed to meet the requirements of online machine learning.

4.2 Feature Selection Analysis

In the first experiment, we determined that the time cost of a machine depended on

the feature dimension size and most features might be redundant and ineffective. Dimension reduction attempts to reduce the time cost of machine learning. In this experiment, we selected the feature subsets of data by using various selection methods, conducting learning and classification testing as described in Section 3.2. Fig. 8 shows the results of the TF-IDF feature selection method (Section 3.3) as compared with those of the random selection method. The MG TF-IDF feature selection method uses the smallest number of

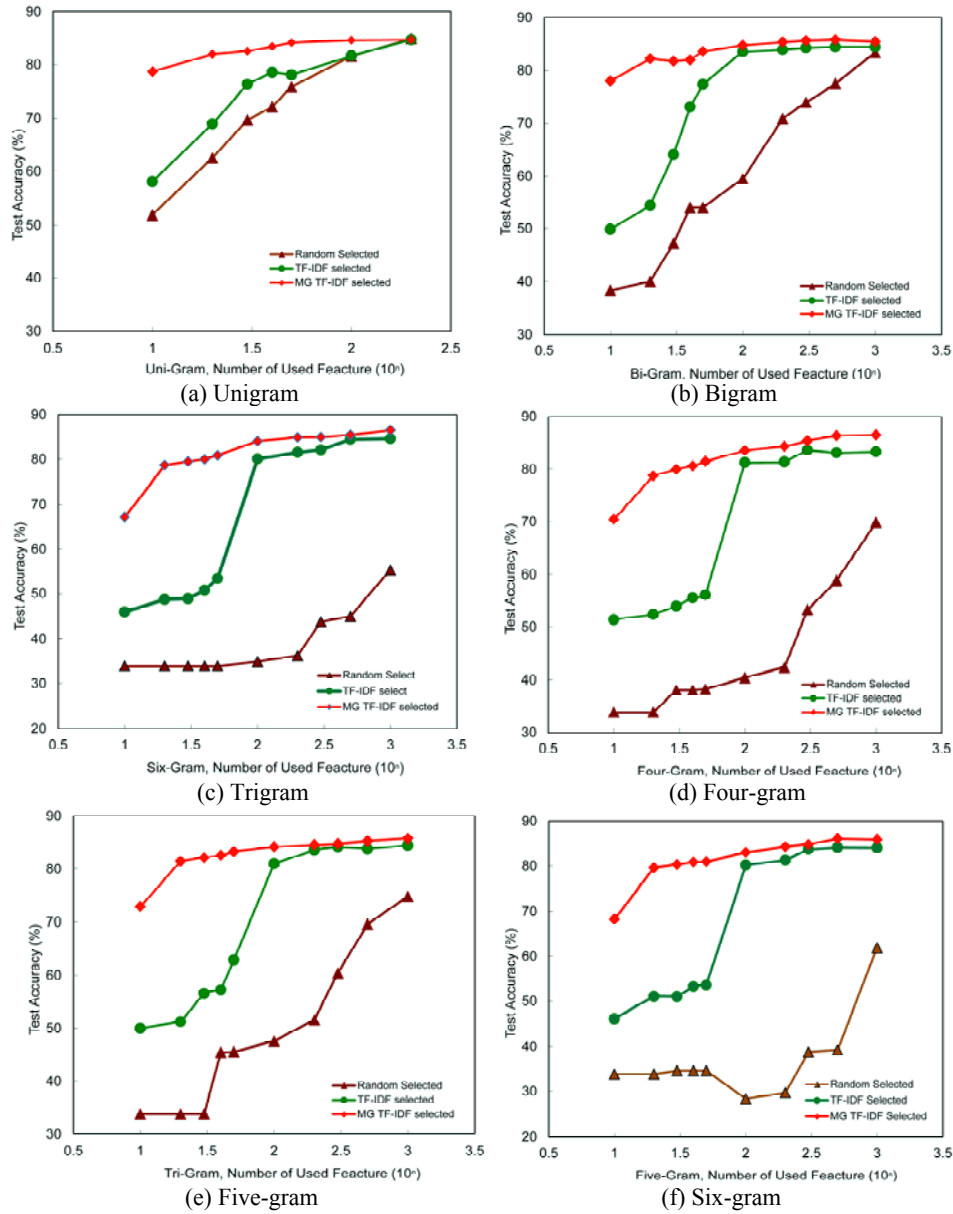


Fig. 8. The microprecision results of diverse feature selection methods.

features, attaining similar microprecision levels; thus, the MG TF-IDF method precisely selects the effective features of individual malware families and is superior to the TF-IDF feature selection method, substantially reducing the required feature dimension, particularly in the proposed MG TF-IDF method, whereby 100-1000 selected features were sufficient to maintain equivalent micro precision. Reducing the feature dimension to less than 1% would allow time cost savings of 99% in high dimensional feature spaces.

As shown in Fig. 8, we observed that the accuracy of four-gram, five-gram, and six-gram MG TF-IDF methods exhibited a similar tendency of increasing to nearly the same final best accuracy.

The MG TF-IDF method effectively selected the major behaviors of each malware family in the unigram test. Table 7 lists the first 10 major words of unigram selected by MG TF-IDF method for malware families.

Table 7. The first 10 selected words of malware families by MG TF-IDF method in unigram test.

	Adware	Virus/Exploit	Dialer
1	NtOpenKey	NtClose	NtWriteFile
2	NtClose	NtOpenKey	NtReadFile
3	NtQueryValueKey	NtQueryValueKey	NtClose
4	NtDelayExecution	NtSetValueKey	NtQueryValueKey
5	NtQueryKey	NtCreateKey	NtOpenKey
6	NtWaitForSingleObject	NtAllocateVirtualMemory	NtAllocateVirtualMemory
7	NtQueryInformationToken	NtMapViewOfSection	NtWaitForSingleObject
8	NtOpenThreadTokenEx	NtQueryAttributesFile	NtMapViewOfSection
9	NtOpenProcessTokenEx	NtProtectVirtualMemory	NtQueryAttributesFile
10	NtQueryInformationProcess	NtReadVirtualMemory	NtRequestWaitReplyPort
	Heuristic	Suspect.Trojan	Trojan
1	NtClose	NtClose	NtClose
2	NtOpenKey	NtOpenKey	NtQueryAttributesFile
3	NtQueryValueKey	NtQueryValueKey	NtOpenKey
4	NtQueryVirtualMemory	NtMapViewOfSection	NtDelayExecution
5	NtOpenFile	NtReadVirtualMemory	NtQueryDirectoryFile
6	NtQueryInformationProcess	NtUnmapViewOfSection	NtYieldExecution
7	NtQueryDirectoryFile	NtQueryKey	NtQueryValueKey
8	NtQueryInformationToken	NtWaitForSingleObject	NtOpenFile
9	NtAllocateVirtualMemory	NtClearEvent	NtQueryInformationProcess
10	NtMapViewOfSection	NtQueryInformationToken	NtMapViewOfSection
	W32	Worm	Non-Malware
1	NtClose	NtClose	NtClose
2	NtOpenKey	NtDelayExecution	NtOpenKey
3	NtQueryValueKey	NtAllocateVirtualMemory	NtQueryValueKey
4	NtMapViewOfSection	NtWaitForSingleObject	NtWaitForSingleObject
5	NtReadVirtualMemory	NtOpenKey	NtQueryInformationToken
6	NtQueryAttributesFile	NtCreateEvent	NtAllocateVirtualMemory
7	NtUnmapViewOfSection	NtDeviceIoControlFile	NtReleaseMutant
8	NtAllocateVirtualMemory	NtQueryValueKey	NtMapViewOfSection
9	NtOpenThreadTokenEx	NtRequestWaitReplyPort	NtQueryDefaultLocale
10	NtOpenProcessTokenEx	NtResumeThread	NtEnumerateValueKey

In addition to the common function, we observed the following:

- The behaviors of peeping user preferences of operation appear in the Adware family. (*e.g.* Query Key Value, Query Information)
- The behaviors of installing and launching program by weaknesses of service appear in the Virus/Exploit family. (*e.g.* SetValueKey, CreateKey, AllocateVirtualMemory)
- The behaviors of sending information or files appear in the Dialer family. (*e.g.* Read/Write File, WaitForSingleObject, RequestWaitReplyPort)
- The behaviors of evading the detection of antivirus system appear in the Heuristic family. (*e.g.* QueryVirtualMemory, QueryInformationProcess, QueryDirectoryFile)
- The behaviors of loading the software into memory appear in the Suspect.Trojan family, *e.g.* MapViewOfSection, ReadVirtualMemory, UnmapViewOfSection.
- The behaviors of launching the task and querying information of files appear in the Trojan family. (*e.g.* QueryAttributesFile, DelayExecution, QueryDirectoryFile, Yield-Execution)
- The behaviors of slowing down the operation of the windows system appear in the W32 family. (*e.g.* QueryValueKey, ReadVirtualMemory, NtOpenThreadTokenEx, NtOpen-ProcessTokenEx)
- The behaviors of continuously copying files, installing and executing softwares appear in the Worm family. (*e.g.* DelayExecution, CreateEvent, DeviceIoControlFile, RequestWaitReplyPort, ResumeThread)
- The less malicious behaviors appear in the Non-Malware family. (*e.g.* no CreateThread, CreateKey, Read/Write File, AllocateVirtualMemory, DelayExecution)

Table A (Appendix A) lists the first 10 major words of further grams that were selected using the MG TF-IDF method for Dialer malware and four-gram tests of Non-malware. A spyware dialer is a malicious program that attempts to create a connection to the Internet or another computer network over the analog telephone, modem, or Integrated Services Digital Network (ISDN) by using WinAPIs. We observed that a serial of NtWriteFile/NtReadFile words were selected in bi-, tri-, and four-gram test, convinced the major behaviors of a spyware dialer. Besides, we observed that most behaviors in the non-malware were key related operation, were significant differences with malware families.

Fig. 9 shows the results of the MG TF-IDF feature selection method from unigram to six-gram. We observed that a high gram yielded favorable accuracy with sufficient words (approximately 1000). If the number of selected features was low (*e.g.*, 10), the accuracy of a high gram was relatively poor. The number of combinations for front ranking function in a high gram was high and accompanied by a low probability. A large number of features caused over-training and resulted in no increase or decrease of test accuracy. In general, the four-gram model demonstrated optimal performance regarding the final accuracy compared with the five-gram model and high gram, and was sufficient for representing the research results of using the most effective selection and parameter tuning method. Besides, five-gram had a 4288×242663 big dataset, maybe need to test in Hadoop platform to solve the resource problem. Considering a large amount of memory and an exponential increase in the time cost of a high gram compared with that of the four-gram model, we focused on investigating unigram to four-gram models in practice.

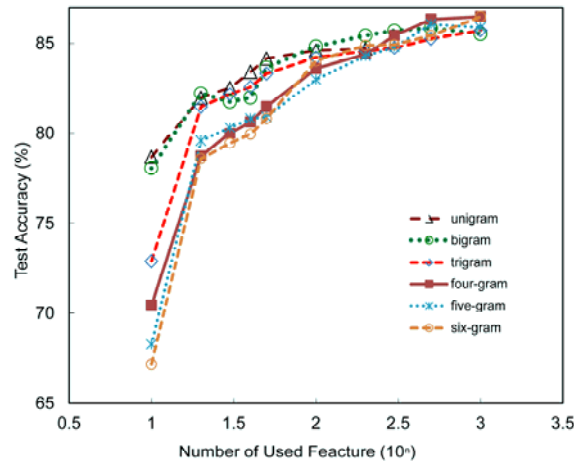


Fig. 9. The microprecision results of diverse grams of MG TF-IDF feature selection.

4.3 Feature Extraction Analysis

Feature selection is a dimension reduction method that reduces the original mass features. In this experiment, we converted the original feature data into new reduced feature space data by using the feature extraction methods described in Section 3.4, conducting learning and classification testing as described in Section 3.2.

The PCA and MG PCA method were used to extract the major behaviors of malware effectively to form few representative components. Table 8 lists the highest five principal component score weightings and the combination of latent functions extracted using the PCA method in the unigram test.

Table 8. The highest five principal component score weightings and the combination of latent functions extracted using the PCA method in the unigram test.

principal component score weighting			
1st		0.242798	
2nd		0.181731	
3rd		0.126186	
4th		0.068949	
5th		0.062883	
1 st principal component		2 nd principal component	
Behavior function	Percent contribution	Behavior function	Percent contribution
NtClose	44.17	NtQueryAttributesFile	25.93
NtQueryAttributesFile	14.61	NtReadFile	24.86
NtOpenKey	14.28	NtClose	19.95
NtQueryValueKey	6.01	NtWriteFile	14.27
NtDelayExecution	4.65	NtDelayExecution	10.14
NtOpenFile	3.47	NtOpenFile	6.30
NtQueryInformationProcess	2.29	NtQueryVirtualMemory	6.21
NtAllocateVirtualMemory	2.21	NtQueryInformationProcess	3.73
NtQueryDirectoryFile	2.04	NtReadVirtualMemory	3.70
NtMapViewOfSection	1.35	NtQueryDirectoryFile	3.51

We observed the increased operation of the registry key and memory in the first principal component, and the increased operation of files in the second principal component, corresponding to the generic cognition of virus attack characteristics.

Table B (Appendix B) lists the first principal component score weighting and the combination of latent functions extracted using the MG PCA method for malware families. The front ranking functions of each family were approaching to the MG TF-IDF observations shown in Table 7.

Table C (Appendix C) lists the first principal component and the combination of latent functions for additional grams that were selected using the MG KPCA method for Dialer malware.

Fig. 10 shows the results of PCA and KPCA as compared with other feature extraction methods. MG KPCA demonstrated a substantial improvement in prediction accuracy. As Kung [31] mentioned, the kernel approach dealt with the relationship and similarity between training set and test set, the bigram test of MG KPCA method demonstrated a substantial improvement (approximate 95% accuracy) in prediction accuracy. When the number of transformed features was small, the MG KPCA method achieved greater microprecision than did the other feature reduction methods. As few as 10-30 transformed features (*i.e.*, 1-3 PCs selected from each malware group) could sufficiently represent individual characteristics, generating an accurate classification. By contrast, increasing the number of transformed features yielded overfitting and reduced the microprecision levels.

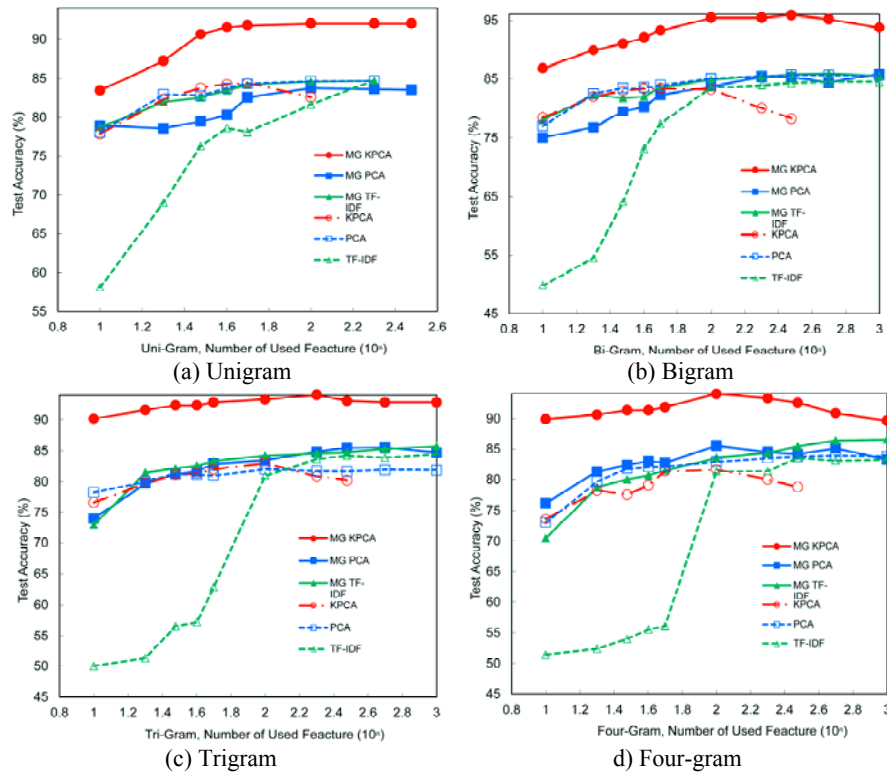


Fig. 10. The microprecision results of diverse feature extraction methods.

Although the PCA and KPCA methods can minimize the time cost of the learning and classification processes, it increases the time cost of the feature extraction process. Table 9 shows the time cost for each estimate method. Compared with the training time for the bag-of-words dataset and PCA methods, the MG PCA method reduced the time cost by approximately 25%. The KPCA and MG KPCA methods doubled the time cost; thus, the PCA and MG PCA methods were the most effective at reducing the time cost of online training.

Table 9. The time cost (seconds) of 40% dataset training for various procedure.

	unigram			bigram			trigram			four-gram		
	F.E.	SVM	Total	F.E.	SVM	Total	F.E.	SVM	Total	F.E.	SVM	Total
Bag of word		5.5	5.5		147	147		942	942		3074	3074
PCA	0.6	1.7	2.3	32	1.7	34	126	2	128	469	1.7	471
MG PCA	1.1	5.3	6.4	175	6.1	181	237	4.6	242	678	3.2	681
KPCA	46	1.9	48	458	3	461	2849	3.1	2852	6356	1.8	6358
MG KPCA	33	2.1	35	312	1.5	314	2452	1.4	2453	5971	1.7	5973

(Test environment: Quad-Core AMD Opteron(tm) Processor 2384, CPU: 800MHz)
(F.E.: The Process of Feature Extraction.)

4.4 Model Selection and Online Extension

Feature selection and extraction were verified to reduce time cost. In this experiment, we combined these methods, forming a two-stage dimension reduction method as described in Section 3.5, and conducting learning and classification testing as described in Section 3.2. Online learning was simulated in accumulating 50% to 90% of the data in increments of 10% to train and collected the subsequently incoming 10% of the dataset to test.

The first online simulation experiment was comparing the effectiveness between all feature selection and MG TF-IDF feature selected methods. Fig. 11 shows the microprecision level and time cost results; the prediction microprecision value of both methods were highly approaching, however, MG TF-IDF methods saved increasingly more time as the n -gram number increased.

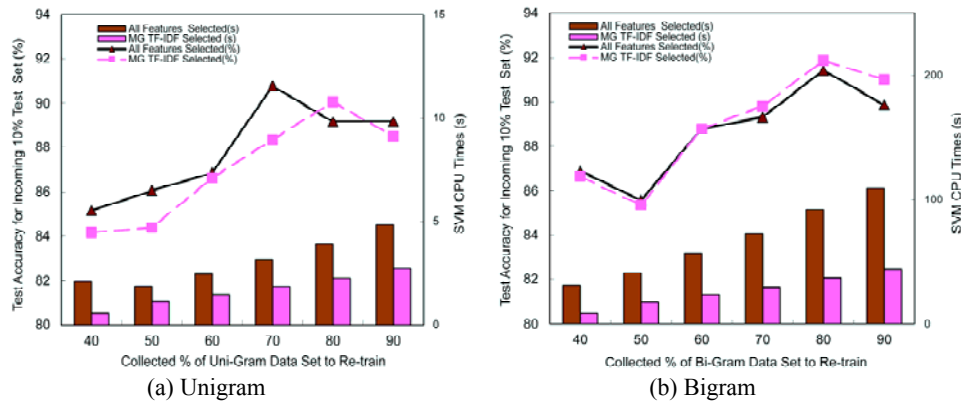


Fig. 11. The microprecision level and time cost results of various combination methods.

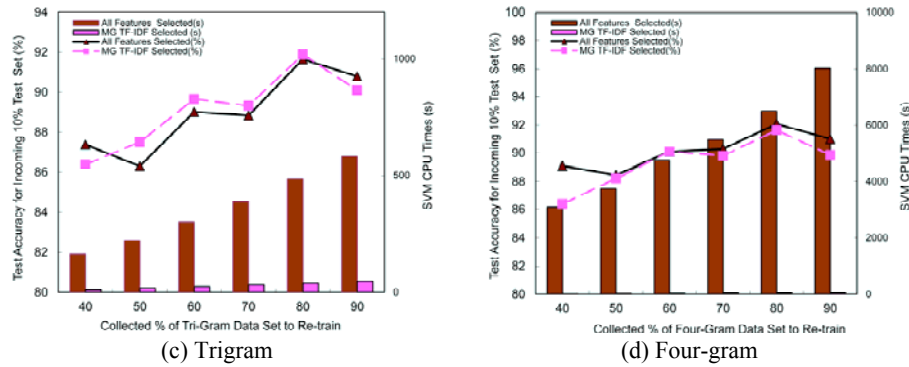


Fig. 11. (Cont'd) The microprecision level and time cost results of various combination methods.

To decrease the time cost, we combined the MG TF-IDF and feature extraction methods, forming a two-stage feature reduction method. Table 10 lists the selected and extracted feature numbers in the experiment.

Table 10. The number of selected features and extracted feature of various experiment.

	unigram		bigram		trigram		four-gram	
	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)
MG TF-IDF + PCA	60	50	1000	50	1000	50	1000	50
MG TF-IDF + MG PCA	60	50	1000	100	1000	100	1000	100
MG TF-IDF + KPCA	60	50	1000	50	1000	50	1000	50
MG TF-IDF + MG KPCA	60	100	1000	100	1000	100	1000	100

(1: no. of selected feature, 2: no. of extracted feature)

Fig. 12 shows the microprecision results of the online training simulation, using various combined methods. With the more data collected, the accuracy had gradually increased. In the bigram to four-gram online simulations, the trends and value of prediction microprecision were highly approaching to the whole selecting features test. The accuracy of our feature selection and reduction approach continued to fit the performance as original whole dataset test.

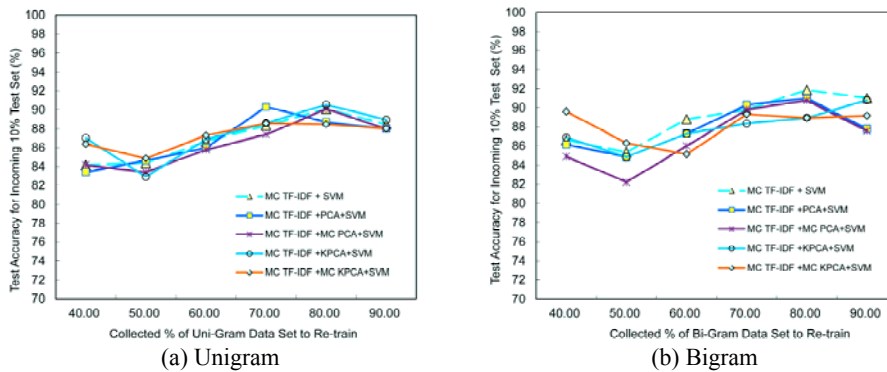


Fig. 12. The microprecision results of various combination methods in online simulation.

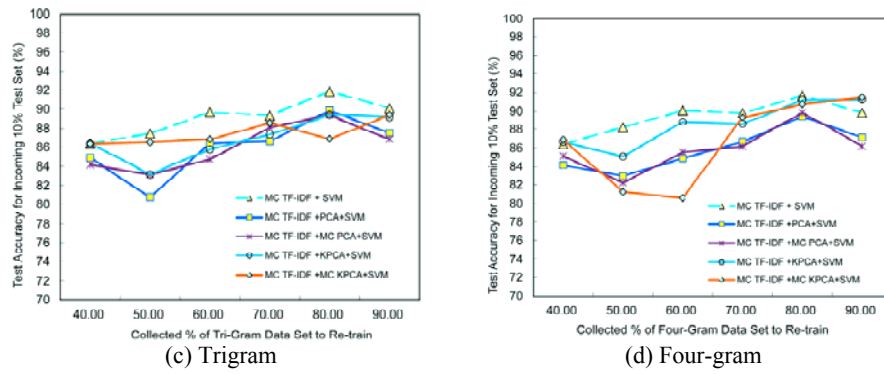


Fig. 12. (Cont'd) The microprecision results of various combination methods in online simulation.

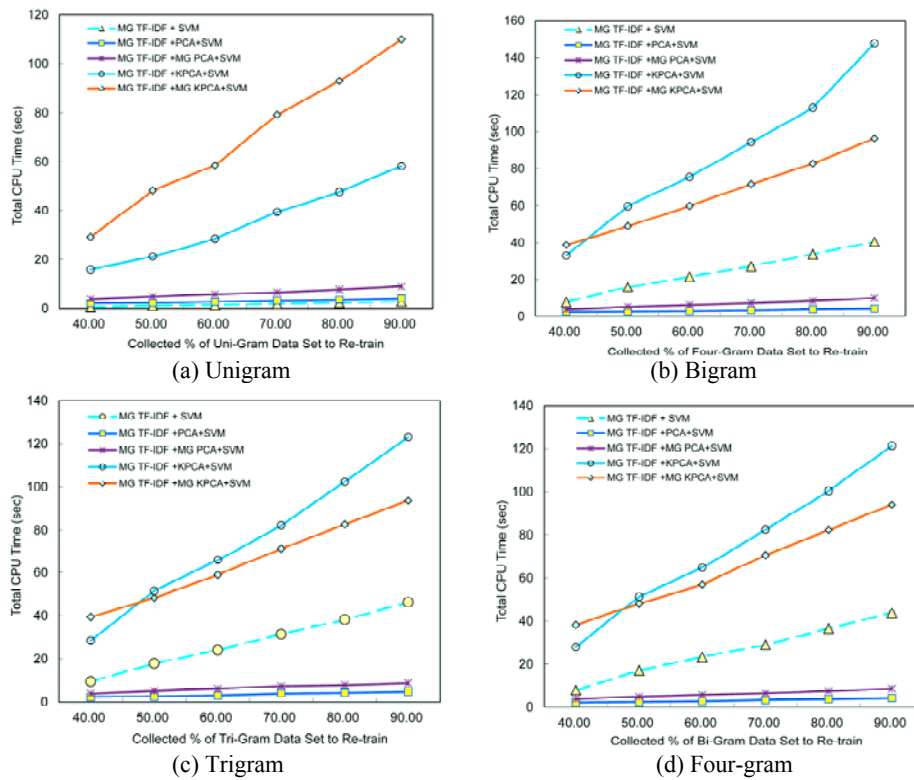


Fig. 13. The total time cost results of the online training simulation.

Regarding the time cost analysis, Fig. 13 shows the total time cost results of the online training simulation, using various combined methods. The MG TF-IDF selection algorithm combined with the PCA or MG PCA extraction algorithms yielded the minimal time cost. The accuracy of our feature selection and reduction approach continued to fit the performance as original whole dataset test. The execute time of the rebuilding the classifier was below 10s, the findings show that the proposed algorithm significantly

reduces the time cost and meets the online learning requirement of collecting malware behavior every minute.

5. CONCLUSIONS

Using high-dimensional n -gramor mapping data space can enhance classification predictions; however, such enhancements cost excessive computing time. The primary contribution of this study is the proposed two-stage feature reduction method, which substantially reduces the time cost of classifying malware behavior by using automatic online learning. The key components of the proposed approach comprise (a) using the MG TF-IDF feature selection method to precisely select the effective features of data subsets in the first stage; (b) using PCA or KPCA to convert the original feature space to a low PC feature space in the second stage; (c) automatically tuning the learning and classification by using learning algorithms; and (d) combining feature selection and extraction with learning and classification, and applying these methods to online detection. The malware behavior log data were collected from a sandbox environment based on hardware virtualization technology. The proposed system executed and recorded 4,288 samples from nine malware families. The dimensionality reduction, TF-IDF, PCA, and KPCA methods were analyzed to reduce the time cost of classification. Furthermore, we proposed an MG algorithm for each feature of the reduction method; the findings showed the effectiveness of its feature reduction. Moreover, we evaluated our method by using an online training simulation experiment. Our two-stage dimensionality reduction approach substantially reduced time costs. Combining the MG TF-IDF, PCA, and SVM methods for online training allows the re-training and classifying procedures to be completed in few seconds, meeting the online learning requirements for collecting malware behavior every minute. The proposed sandbox test environment uses a similar concept as hypervisor architecture that is easily applied to cloud environments. The propose approach offers a competitive malware detection procedure.

APPENDIX A

Table A. The first 10 words of Dialer malware selected using the MG TF-IDF method from the bigram to four-gram tests and four-gram tests of Non-malware.

	bigram	trigram
1	NtWriteFile, NtReadFile	NtWriteFile, NtReadFile, NtWriteFile
2	NtReadFile, NtWriteFile	NtReadFile, NtWriteFile, NtReadFile
3	NtQueryValueKey, NtQueryValueKey	NtQueryValueKey, NtQueryValueKey, NtQueryValueKey
4	NtOpenKey, NtOpenKey	NtWriteFile, NtWriteFile, NtWriteFile
5	NtOpenKey, NtQueryValueKey	NtOpenKey, NtQueryValueKey, NtClose
6	NtWriteFile, NtWriteFile	NtQueryInformationToken, NtClose, NtOpenKey
7	NtClose, NtOpenKey	NtOpenProcessTokenEx, NtQueryInformationToken, NtClose
8	NtQueryValueKey, NtClose	NtOpenThreadTokenEx, NtOpenProcessTokenEx, NtQueryInformationToken
9	NtClose, NtClose	NtClose, NtOpenKey, NtQueryValueKey
10	NtFsControlFile, NtWait- ForSingleObject	NtWaitForSingleObject, NtFsControlFile, NtWait- ForSingleObject

four-gram tests of Dialer malware	
1	NtReadFile, NtWriteFile, NtReadFile, NtWriteFile
2	NtWriteFile, NtReadFile, NtWriteFile, NtReadFile
3	NtQueryValueKey, NtQueryValueKey, NtQueryValueKey, NtQueryValueKey
4	NtWriteFile, NtWriteFile, NtWriteFile, NtWriteFile
5	NtOpenThreadTokenEx, NtOpenProcessTokenEx, NtQueryInformationToken, NtClose
6	NtOpenProcessTokenEx, NtQueryInformationToken, NtClose, NtOpenKey
7	NtReadFile, NtReadFile, NtReadFile, NtReadFile
8	NtFsControlFile, NtWaitForSingleObject, NtFsControlFile, NtWaitForSingleObject
9	NtDelayExecution, NtRequestWaitReplyPort, NtDelayExecution, NtRequestWaitReplyPort
10	NtRequestWaitReplyPort, NtDelayExecution, NtRequestWaitReplyPort, NtDelayExecution
four-gram tests of Non-malware	
1	NtEnumerateValueKey, NtEnumerateValueKey, NtEnumerateValueKey, NtEnumerateValueKey
2	NtQueryValueKey, NtQueryValueKey, NtQueryValueKey, NtQueryValueKey
3	NtOpenThreadTokenEx, NtOpenProcessTokenEx, NtQueryInformationToken, NtClose
4	NtOpenProcessTokenEx, NtQueryInformationToken, NtClose, NtOpenKey
5	NtDuplicateObject, NtQueryValueKey, NtQueryValueKey, NtClose
6	NtQueryKey, NtDuplicateObject, NtQueryValueKey, NtQueryValueKey
7	NtEnumerateKey, NtOpenKey, NtEnumerateKey, NtOpenKey
8	NtClose, NtClose, NtQueryKey, NtDuplicateObject
9	NtOpenKey, NtEnumerateKey, NtOpenKey, NtEnumerateKey
10	NtClose, NtQueryKey, NtDuplicateObject, NtQueryValueKey

APPENDIX B

Table B. The first principal component (PC) score weighting and the combination of latent functions extracted using the MG PCA method for malware families.

Malware family	PC score weighting	Malware family	PC score weighting
Adware 1 st PC	0.835169	Virus/Exploit 1 st PC	0.677811
Dialer 1 st PC	0.980597	Heuristic 1 st PC	0.282665
Suspect.Trojan 1 st PC	0.499817	Trojan 1 st PC	0.363542
W32 1 st PC	0.478477	Worm 1 st PC	0.433603
Non-Malware 1 st PC	0.552503		
Adware 1 st principal component		Virus/Exploit 1 st principal component	
function	contribution	function	contribution
NtOpenKey	36.67	NtClose	72.40
NtClose	32.34	NtOpenKey	11.07
NtQueryValueKey	11.64	NtQueryValueKey	9.52
NtQueryKey	3.26	NtSetValueKey	2.74
NtDelayExecution	3.15	NtCreateKey	2.39
Dialer 1 st principal component		Heuristic 1 st principal component	
function	contribution	function	contribution
NtReadFile	84.56	NtClose	31.71
NtWriteFile	33.37	NtOpenKey	27.15
NtRequestWaitReplyPort	1.27	NtQueryVirtualMemory	19.89
NtQueryVirtualMemory	0.66	NtQueryValueKey	11.80
NtEnumerateValueKey	0.52	NtContinue	1.63

Suspect.Trojan 1 st principal component		Trojan 1 st principal component	
function	contribution	function	contribution
NtOpenKey	29.16	NtQueryAttributesFile	33.80
NtClose	20.98	NtClose	29.26
NtQueryValueKey	13.47	NtReadFile	16.07
NtMapViewOfSection	10.27	NtOpenKey	7.97
NtUnmapViewOfSection	5.88	NtDelayExecution	6.92
W32 1 st principal component		Worm 1 st principal component	
function	contribution	function	contribution
NtClose	39.68	NtClose	61.23
NtOpenKey	25.29	NtAllocateVirtualMemory	12.46
NtQueryValueKey	15.83	NtWaitForSingleObject	3.46
NtWriteFile	4.38	NtDeviceIoControlFile	3.27
NtWaitForSingleObject	2.43	NtDelayExecution	3.19
Non-Malware 1 st principal component			
function	contribution		
NtClose	40.74		
NtOpenKey	21.79		
NtQueryValueKey	20.91		
NtWaitForSingleObject	2.23		
NtQueryInformationToken	2.23		

APPENDIX C

Table C. The first principal component (PC) score weighting (SW) and the combination of the highest 10 latent functions extracted using the MG PCA method for Dialer malware in bigram to four-gram tests.

Bigram 1 st PC SW= 0.991028			Trigram 1 st PC SW= 0.993501		
	Functions	Contribution		Functions	Contribution
1	NtWriteFile, NtReadFile	39.34		NtQueryValueKey, NtQueryValueKey, NtQueryValueKey	24.38
2	NtQueryValueKey, NtQueryValueKey	10.69		NtReadFile, NtWriteFile, NtReadFile	15.66
3	NtOpenKey, NtOpenKey	8.97		NtWriteFile, NtReadFile, NtWriteFile	14.33
4	NtClose, NtOpenKey	6.23		NtOpenKey, NtQueryValueKey, NtClose	4.91
5	NtOpenKey, NtQueryValueKey	5.32		NtWriteFile, NtWriteFile, NtWriteFile	4.08
6	NtWriteFile, NtWriteFile	4.93		NtClose, NtOpenKey, NtQueryValueKey	2.55
7	NtQueryValueKey, NtClose	4.70		NtQueryInformationToken, NtClose, NtOpenKey	2.30
8	NtReadFile, NtWriteFile	2.88		NtOpenThreadTokenEx, NtOpenProcessTokenEx, NtQueryInformationToken	2.21
9	NtFsControlFile, NtWaitForSingleObject	2.21		NtOpenProcessTokenEx, NtQueryInformationToken, NtClose	2.21
10	NtQueryInformationToken, NtClose	2.16		NtWaitForSingleObject, NtFsControlFile, NtWaitForSingleObject	1.91
four-gram 1 st PC SW= 0.994641					
	Functions	Contribution		Functions	Contribution
1	NtQueryValueKey, NtQueryValueKey, NtQueryValueKey, NtQueryValueKey	27.11			
2	NtWriteFile, NtReadFile, NtWriteFile, NtReadFile	12.85			
3	NtReadFile, NtWriteFile, NtReadFile, NtWriteFile	10.61			
4	NtWriteFile, NtWriteFile, NtWriteFile, NtWriteFile	5.10			
5	NtOpenThreadTokenEx, NtOpenProcessTokenEx, NtQueryInformationToken, NtClose	4.14			
6	NtOpenProcessTokenEx, NtQueryInformationToken, NtClose, NtOpenKey	4.11			
7	NtFsControlFile, NtWaitForSingleObject, NtFsControlFile, NtWaitForSingleObject	2.64			
8	NtQueryKey, NtOpenThreadTokenEx, NtOpenProcessTokenEx, NtQueryInformationToken	2.00			

9	NtReadFile, NtReadFile, NtReadFile, NtReadFile	1.85
10	NtWaitForSingleObject, NtFsControlFile, NtWaitForSingleObject, NtFsControlFile	1.55

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