UNIVERSITY ALEXANDRU IOAN CUZA

DOCTORAL THESIS

Improving Detection Of Malicious Programs

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Introduction

Starting with the year 2007 malware started to increase exponentially. More malware was produced in 2007 than in all years before that put together. The sudden growth was mainly influenced by the idea that malware could be used to earn money. Almost all possible ways of earning money through malicious code were exploited. From the most obvious ones, like stealing access to bank account or asking for a ransom to give access to some encrypted files, to less obvious ones like simulating user behavior for certain websites in order to increase traffic and with it money income for that web-site.

Trying to detect these samples has created an arm race between antivirus products and malware. As antiviruses and operating systems are getting more and more complex and include more technology in order to protect computers, the malware adapts and brings new methods for evading detection. These methods can be grouped in defensive mechanisms (packers, protectors: anti-debugging techniques, polymorphism, server side polymorphism, metamorphism) and offensive mechanisms (detect antivirus product, terminate antivirus product, disable updates, disable firewall, change dns settings, change permissions for files, avoid writing to disk, install a rootkit).

A machine learning algorithm can be used to filter what malware researchers analyze or it can even be used as a primary detection method. However, this detection mechanism must also undergo some restrictions for it to be used in practice.

1. The training speed must be fast enough to allow the algorithm to finish in a decent amount of time when run on very large datasets.
2. Testing speed is also very important. If we want the method to be included in an antivirus product, it must provide as little overhead as possible.
3. The model produced by the classification algorithm must fit in a very small amount of memory.
4. No false positives, or as close to 0 as possible

Improving Malware Detection By Feature Extraction

Malware detection through the use of machine learning is not new; it has been used by other researchers and is currently used in many av-products. However, the results obtained can be better either in terms of lower false positives or by increasing the detection rate. The way I choose to solve this problem is not by modifying the new algorithms, but rather by extracting new features from existing ones such that the accuracy of the original algorithm will increase. I choose this method because I consider there is an already good algorithm, named One Side Class Perceptron (OSCP) which was tested for malware detection with low false positive rate and achieved good results.

The One Side Class Perceptron (OCSP) works by creating a hyper-plane that is able to separate the two classes of samples (malware and benign) such that no samples from one class will be detected. It is very well suited for our problem and by the way it is constructed it guarantees that, on training phase, there will be no false positives.

Even though this algorithm solves the problem of false positives, it also dramatically reduces the detection rate.

2.1 Feature Creationg Using Genetic Programming

The dataset on which the algorithms will be tested consists of 358.144 records of which 42.940 are malicious and 315.204 are benign. The proportion of malicious and benign files is close to the one found in the wild. The files from the dataset are all PE-files, mainly executable and dll files, which were gathered over a period of two months (april and may 2014). The files were statically and dynamically processed and a total of 300 boolean features were extracted.

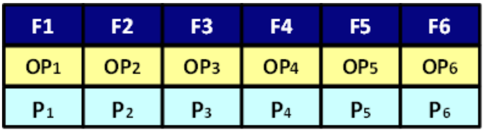
Mapping seems to provide good results. It increases the detection rate while the number of false positive stay low enough to permit the algorithm to be used in practical applications. However, a big disadvantage of this method is the number of features which it needs to create.

In the following paragraphs I will provide a method, based on genetic programming, that will allow us to increase the detection rate of the algorithm. To validate the results, they will be compared to the ones obtained when training with the best features obtained through mapping.In order to not reduce diversity and have records belonging to a different class but with the same set of features, the OSCP algorithm will use 600 features instead of 300: the best 300 features after mapping plus the 300 original ones.

From the results obtained by comparing three boolean operation used for mapping (XOR, AND, OR), the AND operator achieves the best results: 65.35% detection rate, 15 false positives and 95.85% accuracy. For this reasons, these will be used as a threshold to test the features obtained through genetic programming.

We start by defining the chromosome. A chromosome is a set of features (1 to 300) each one connected to other through a boolean operator. Since the order in which the expression is evaluated changes the result, a priority is also given to each boolean operator. The structure can be seen in Figure 2.1.

Notice that in Figure 2.1 each F_i, where $i = \overline{1, 300}$ refers to one of the original features, each OP_i refers to one of the



F1	F2	F3	F4	F5	F6
OP_1	OP_2	OP_3	OP_4	OP_5	OP_6
P_1	P_2	P_3	P_4	P_5	P_6

FIGURE 2.1: Chromosome

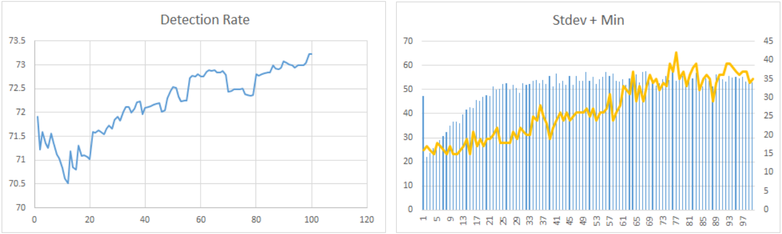
boolean operations $\{and, xor, or\}$ and each P_i is a number that reflects the priority of the boolean operation among the expression. The chromosomes could have also been implemented using binary trees; however I consider this method to be more practical since it allows mutation on every part of the chromosome (priority, operator and feature)

The first generation is constructed by generating 300 chromosomes, of length 1. Each chromosome has one of the original features, each operation is randomly chosen among the set of boolean operators $\{and, or, xor\}$ and each priority is initialized to 0.

The crossover operation is implemented in the following way: 1000 new chromosomes are generated by randomly selecting two parents and performing crossover on a randomly selected point. The mutation operation can be performed on any part of the chromosome. A probability of mutation of 3% is considered. From the new generated set of 1000 chromosomes, three sets of 30 chromosomes are chosen. For the elements in the first set, a feature will be randomly selected and negation will be performed. For the elements in the second set, one of the operators will be switched to a randomly chosen one from the boolean set $\{and,or,xor\}$. Finally, for each chromosomes in the final set, a priority will be chosen, and based on a randomly generated number it will be incremented or decremented.

Based on the F-score, the best 300 chromosomes will be selected. The parents are also included in the selection process in order not to lose the best chromosomes found so far. Doing so, a 71% in detection rate and 17 false positives were obtained

To further improve the results, the current problem is approached as a multi modal optimization problem. A function is defined that gives a very low fitness score (negative) for the individuals that get activated more on the clean records than on the malicious ones and for the others will normalize the difference between the number of malicious and clean records where the feature is being activated based on how important is that feature for all the malicious records. Using this function the detection rate increases to 73.23% while the number of false positives increases with just 2 units, reaching to 19 false positives. The graphic in Fig 2.2 presents how the detection rate modifies with each generation. The yellow line represents the minimum number of features that are activated on every record on each generation, while the vertical bars represent the standard deviation of the number of features activated on every record on each generation.



(a)

(b)

FIGURE 2.2: Evolution on each generation. Detection Rate (a). Nr. of features activated on each record(b).

As it can be seen the detection rate increases as more features are being set on the records with a low number of activated features.

2.2 Feature Creation Using Restricted Boltzmann Machine

The idea of creating features using a mathematical operator can be extended. First of all, the mathematical operator only brings a limited kind of relation between features. Secondly, features could be created from the combination of more than two initial features. In this way the new created features may contain more information and could prove more important in separating the records. To address these ideas the mathematical operator should be replaced with a function that has as arguments all the existing features and the result of this function is a new feature. Since the newly created features will be used as input for a linear classifier it is important that the function used to create them should be a non-linear one. Finding a function that is optimized for this task may seem dificult, however these restrictions are very similar to the ones imposed by a restricted Boltzmann machine.

A restricted Boltzmann machine is a stochastic neural network composed of two layers: one made up of visible units (the data) and another one made up of hidden units (the new created features). Every unit from one hidden layer has a symmetrical connection with every unit from the visible layer, however there are no connection between units from the same layer. Each neuron from the network has a binary state: 0 or 1. Figure 2.3 is an example of restricted Boltzmann machine composed of 4 visible units and 3 hidden units and their corresponding biases.

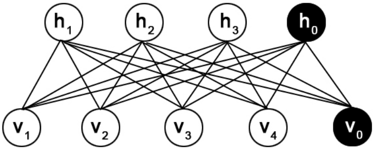


Figure 2.3: A Restricted Boltzmann Machine

The value of each unit is generated according to a probability function computed in regards to the elements from the other layer and the weighs of the connections.

The idea of using a restricted Boltzmann machine and a linear classifier (one side perceptron in this case) is depicted in Figure 2.4. As it can be seen in the figure, the hidden layer will be the new set of features that the perceptron will be trained on.

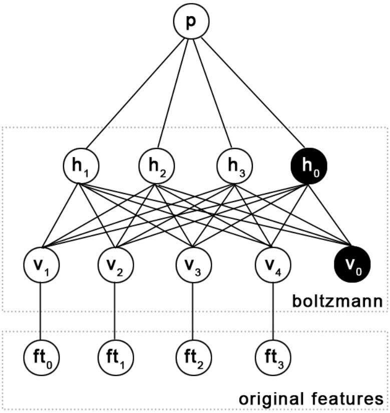


FIGURE 2.4: Restricted Boltzmann machine and Linear Classifier

Besides creating features in a non linear way, this ensemble also has another advantage. Since the restricted Boltzmann machine is a stochastic neural network it means that the units are based on probabilities. After the network has been trained, instead of sampling a binary value for a hidden unit, the probability can be used instead. This means that a continuous value will be used instead of a binary one, thus giving more information to the linear classifier.

Training of this ensemble has to be done in two steps: First train the RBM in an unsupervised manner and then train the OSCP classifier using the features outputted by the RBM.

In order to test how this ensemble performs, a collection of malicious and benign samples was gathered during the months of January and February 2014, containing 3087200 files. This was further processed and only the best 300 features were kept. The results are compared with the OSCP algorithm and its mapped version (OSCP-MAP). The results are displayed in Table 2.1 As it can bee seen, the ensemble (noted with OSCP-RBM in Table 2.1) achieved an increase in detection of 15.72 % compared to the one side class perceptron (OSCP). There is also a decrease in the number of false positives, the ensemble obtaining 6 times less false alarms than the OSCP algorithm. However, when comparing the ensemble to the mapped version of the perceptron the detection rate is smaller with 1.35 %.

Algorithm	Detection	False Positive	Accuracy
OSCP	73.11%	20 (0.00162%)	99.32 %
OSCP-RBM	88.83%	3 (0.00024%)	99.72 %
OSCP-MAP	90.18%	87(0.00707%)	99.72 %

Table 2.1: The results of the 3-fold cross-validation for OSCP, OSCP-MAP, OSCP-RBM algorithms

I consider the small decrease of the detection rate is well compensated by the big difference in the number of false positives obtained by the two algorithms, the OSCP-MAP obtaining 29 times more false positives.

Clustering and Classification of Script based Malware

In contrast to standard documents, where the only actions available are reading and modifying it, there also exists documents that can interact with the user or assist him by doing some automatic actions. This kind of interaction can be very complex and could include sending automatic e-mail, auto-completion of some fields depending of what choices have been previously selected or just automatic parsing of the answers a users may have given to a form. Since the possibilities are unlimited, the only way to implement this kind of feature is to add code to the document that is responsible for the user interaction and add support for the programming language to the software that renders the documents. Some examples of this is the use of JavaScript language for the portable document format (pdf) in the Adobe Reader software, or the use of Javascript for HTML pages. This feature also opened the door for malware creators that can make use of the programming language feature to execute their malicious code. Most of the code is obfuscated in order to avoid detection.

3.1 Clustering Document Based Malware

Clustering is very important in malware industry since it reduces the work a malware analyst needs to do. Also, by having many similar files grouped together, generic signatures can be added which in turn, increases productivity and proactivity.

Two methods for clustering are provided: Hierarchical bootom-up clustering (based the distance between every two items) and Hash-Based clustering (based on computing a hash function over every item and clustering together the files for which the function outputs the same value)

3.1.1 Hierarchical Bottom-up Clustering

In order to compute the distance between every malicious document, the files need to be mapped to a coordinate system. To do this, the file needs to be processed, features extracted and stored in an abstract manner. The obtained result will be called PDF fingerprint. In order to create the PDF fingerprint, the following steps must be carried on:

1. Extract the JavaScript code from the PDF file.
2. Tokenize the JavaScript files obtained, by using the grammar from the ECMA scripts [**?**] and for every token extract as tuple its value and its class.
3. Remove unnecessary tokens
4. Emulate simple string operations
5. For each class, count how many times it appears and generate a new set of tuples, that consists of the id of the class and its frequency. The PDF Fingerprint will be the set of tuples generated on this step.

Having the PDF Fingerprint as an abstract representation for the file, it will be used to map the file to a Cartesian coordinate system. For each available token class there will be a coordinate axis, and the frequency present in tuple will serve as the coordinate on that axis. By doing so for every PDF fingerprint, similar files will end up close to each other. A metric is proposed that is based on the Manhattan distance, but changing the subtraction with the division. Secondly, the percentage of similarity between two files is established only using information from the two fingerprints.

$$d(p,\ q) \ = \ \frac{\sum_i^K Dist(i)}{|K|} * 100 \tag{3.1}$$

$$Dist(i) = \frac{\min(tuple_{pi}.frequency, tuple_{qi}.frequency)}{\max(tuple_{pi}.frequency, tuple_{qi}.frequency)} \tag{3.2}$$

$$Dist(i) = 0,\ if\ (i\ \in P_c, i \notin Q_c) \quad or \quad (i\ \notin\ P_c,\ i\ \in Q_c) \tag{3.3}$$

In order to see what kind of clusters could be obtained using this metric, the value of the threshold was set to 80%. The number of clusters obtained is 11, close enough to the number of malware families (12).

Even though this method provides reliable results, its time complexity makes it difficult to use when it comes to large datasets.

3.1.2 Hash Based Clustering

The hash based clustering method tries to address the main problem of the Hierarchical Bottom-up Clustering method, its $O(n^2)$ time complexity. It does this by processing each file only once and applying a hash function (MD5 or SHA256) and clustering together files with the same hash. The algorithm starts with the PDF fingerprint previously described when the Hierarchical Bottom-up Clustering method was introduced. The steps are described bellow:

1. Sort the tuples according to the frequency member. In case of two tuples that have the same frequency, the one which has a higher class-id will come first.
2. Normalize tuples frequency: This means that the frequency member of every tuple will be divided by a factor.
3. Apply a Hash Function:(ie. MD5, SHA256)

For testing both of the clustering methods, a larger database was constructed consisting of 2311035 PDF-files. This dataset consists of 1333420 benign files gathered from the different sources for a period of 12 months and 977615 files gathered from honeypots, spam messages and public sources.

The first comparison between the two clustering methods (Hierarchical Bottom-up Clustering and Hash-Based Clustering) is related to their speed in order too see which one can be used in practical situations. For this reason, a subset of 10000 files from the original dataset was created. The Hash Table clustering finished in 1 second, while the hierarchical bottom-up clustering finished in 1 day 21 hours and 33 minutes. The results clearly state that the Hash Based Clustering method is much time faster than the Hierarchical Bottom-up Clustering.

Going from hash-based clustering method to a way of providing detection for document based malware is very straight forward. The hash outputted by the clustering method will be used as a detection marker.

3.1.3 Classification Of Script Based Malware

In order to achieve good classification results, the scripts will undergo several transformations in order to eliminate as much as possible from the obfuscation techniques. Following this, two classification methods will be used, one relying on the One Side Class Perceptron and the other on Hidden Markov Models.

In order to create the dataset that is suitable for training and testing the algorithms, several steps were taken. First, in order to find benign script samples, the top 1 million websites from Alexa ranking were visited and scripts that were used in their index page were extracted. The malicious samples were collected during a period of one year from different sources. In doing so, a dataset that contains 1296962 benign samples and 25357 malicious scripts was created. The ratio between malicious and clean files is similar to the one we would find in the wild.

The first approach for classifying JavaScript files was to use the One Side Class Perceptron (OSCP) algorithm. Two variations were tested. The first one (OSCP-simple) uses boolean features (the presence of a javascript token) and achieved only 57.5% detection rate). The second one (OSCP-frequency), that uses the frequency of the tokens in each script achieved 65.59% detection rate.

Finally, a hybrid approach is used. The records are first split using a binary decision tree. For each of the resulted cluster, an OSCP algorithm is used in order to classify the samples. This method will be called BT-OSCP-xxx where xxx defines the depth of the decision tree.The method of grouping the samples is straight forward. It chooses a feature that best separates the dataset and puts all the elements containing the feature in one branch of the tree and the rest in the other branch. Choosing the feature is done according to a score function which promotes the feature that is present in a number of records close to the half of the dataset size.

The final approach was to use a Hidden Markov Model (HMM). In order to train it, several notations must first be established. Since, HMM works with observation and states, the tokens from each tokenized JavaScript file will be considered as a list of observations and the states in which each file can be malicious or clean: $S = S_{clean}, S_{infected}$ where S_{clean} defines the state in which the file performs a genuine action while $S_{infected}$ represent the state where a malicious action is being performed.

To train the model, two HMM were constructed: one for malicious files(M_{clean}) and one for infected files ($M_{infected}$). Each time a script must be classified it is first compared to each of the models and it will be assigned to the group that resembles the most:

- $P(X|M_{clean}) = \sum\limits_{Z} P(X|Z, M_{clean})P(Z|M_{clean})$ - the probability that the observation sequence was generated by M_{clean}
- $P(X|M_{infected}) = \sum\limits_{Z} P(X|Z, M_{infected})P(Z|M_{infected})$ - the probability that the observation sequence was generated by $M_{infected}$
- $S(X) = max(P(X|M_{clean}), P(X|M_{infected}))$

The training of each HMM was done using the Baum-Welch algorithm which is based on the forward-backward algorithm and works in an unsupervised manner.

For the BT-OSCP-xxx two configurations were used, one where the depth of the decision tree was set to 4, BT-OSCP-4, thus 16 clusters resulted and one where the depth was set to 5, BT-OSCP-5, thus 32 clusters resulted. The results can be seen in Table 3.1.

Algorithm	Detection Rate	False Positive rate
OSCP	57.51%	0.02%
OSCP-frequency	65.59%	0.01%
BT-OSCP-4	81.65%	0.22%
BT-OSCP-5	89.75%	0.31%
HMM	76.23%	2.29%

Table 3.1: 3-fold cross validation results for OSCP, OSCP-frequency BT-OSCP-xxx and HMM

The BT-OSCP-5 provides the best detection rate but with a higher rate of false positives. It also takes more time to train due to the need of building the decision tree and training of 32 OSCP algorithms. As for the HMM, its detection rate is in the middle and has the highest number of false positives. It also took the most time to train.

Mobile Privacy Issues

Due to security restrictions imposed by mobile operating systems, malware almost disapeared from official application markets. However, this doesn't mean a user is risk free when using his smartphone. Nowadays, most of the smartphones include many sensors and features (GPS location) and are created with the scope of easing ones life.

However, this also may come with privacy risks. For example, the GPS, can be used by an application to get the user location that will be further used in delivering targeted ads. Even if the GPS is turned off, the device could be geolocated by its ip address.

The risk that a user downloads such an application are higher when advertising SDKs are also being taken into consideration. In order to make a profit from their application but still make it available for everyone, many programmers use advertising SDKs. These are bundled in the application and at different moments when the application is being run, they contact a server in order to display some marketing ads to the user. However, these sdks come with their set of permissions and they usually collect information that the programmer nor the user is aware of.

Since more than 80% of the applications from the Google Play and more than two thirds of the applications in Apple store are free, the ad-monetization method is dominant. Many of the advertising frameworks collect private information from the user and send them to their servers.

Adware specific behavior	Percent of Apps
Sends location	9.80%
Sends the e-mail address	5.73%
Sends the device ID	14.58%
Sends the phone number	8.82%
Generate spam in notification bar	8.48 %
Greates spam icons on home screen	9.17 %

Table 4.1: Actions Performed by TOP5 3rd Party SDKs

There are even situations where the private data is being sent unencrypted, thus an attacker could intercept the traffic. There are even sdks that allow receiving and execution of JavaScript code from an external server without verifying the server's identity. This allows an attacker to execute code on the device.

In order to highlight the data that is most often being sent by third party sdks, 314.000 application from Google Play were collected and the top 5 third party advertising frameworks were analyzed. The results can be seen in Table 4.1

Since the number of application on Google Play and Apple Store increased by more than 200.000 only in 2014, the only way to analyze their privacy risks is to use an automatic system.

In order to give a verdict for an applications, two stages are needed. In the first one, the features are extracted and stored in a parsable format while in the second one the features will be processed and a verdict will be given. The two stages must be performed separately since verdicts can change from time to time as heuristics are added while the extraction phase changes rarely. Feature extraction is also done in two steps: First there is a static method that parses the code and all meta information contained in the file and then there is a dynamic method that tries to execute the file and collect behavior features. As execution take time, it is easy to understand why feature extraction needs to be separated.

The static extraction method parses the Android executable file (Dalvik Executable), the iOS executable code found in application packages (IPA) and as well as other files that can be found in the application container (i.e. Manifest

File for the Android and the info.plist for the iOS). Features that may be extracted are URL, Classes, Method Names, service names, strings, etc. Using this information, it is easy to detect if the application uses a known adware sdk.

The Dynamic extraction method is the best solution against obfuscation methods. This involves running the application in a controlled environment and observing its behavior as well as the data transmitted over the network. Using Cycript for the iOS platform and Robotium for the Android OS, real user scenarios are simulated.

After analysing over 310,000 applications from Google Pay, the following privacy issues were discovered: 1.13% of the application send the precise location of the device (GPS coordinated), 0.64% send the e-mail address and 12.66% send the device ID, using an unencrypted connection. Besides that, 0.51% of the applications send the username and password required in login or registration forms in plain text.

A simillar study was carried on 207,000 application from the Apple Market. 14.43% send the device ID and 0.56%

send the credentials required in login or registration forms in plain text.

Conclusion and Future Work

This paper analyzed three main problems and solutions regarding security and privacy that people using computers or mobile devices are currently facing.

The first one, which is the oldest, refers to detection of malicious executables that run on the Windows operating system. Here, the accuracy obtained by using the OSCP algorithm was improved by extracting new features from the original ones through the use of a neural network (Restricted Boltzmann Machine) or through the use of Genetic Programming.

The second problem addressed, which is mainly used in targeted attacks, is detection of scripts found in document files. To achieve a good detection rate a Hidden Markov Model was tested as well as hybrid method consisting of a decision tree and the OSCP algorithm.

The final problem presented in this paper is also the newest one present among users. It reefers to the privacy of the user's personal data that is used by applications in mobile devices. An analysis of privacy risks associated with each well known application market was done. The current work also focused on how a framework can be created that is able to analyze these applications both statically and dynamically and provides feedback to the users regarding to the danger they are exposing themselves.

Since using these methods good practical results were achieved, in the near future more attention will be attributed to improving them. Mainly, I am interested on how features can be created using many stacked hidden layers in a neural network and how genetically evolved features can be created using non-linear functions.