Towards an Understanding of the Misclassification Rates of Machine Learning-based Malware Detection Systems

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Abstract: A number of machine learning based malware detection systems have been suggested to replace signature based detection methods. These systems have shown that they can provide a high detection rate when recognising non-previously seen malware samples. However, in systems based on behavioural features, some new malware can go undetected as a result of changes in behaviour compared to the training data. In this paper we analysed misclassified malware instances and investigated whether there were recognisable patterns across these misclassifications. Several questions needed to be understood: Can we claim that malware changes over time directly affect the detection rate? Do changes that affect classification occur in malware at the level of families, where all instances that belong to certain families are hard to detect? Alternatively, can such changes be traced back to certain malware variants instead of families? Our experiments showed that these changes are mostly due to behavioural changes at the level of variants across malware families where variants did not behave as expected. This can be due to the adoption of anti-virtualisation techniques, the fact that these variants were looking for a specific argument to be activated or it can be due to the fact that these variants were actually corrupted.

1 INTRODUCTION

Malware is a major concern in most computer sectors. Past research has shown that machine learning based detection systems can detect new malware using the knowledge gained from training a classifier on previously discovered and labeled malware samples (e.g. (Bailey et al., 2007; Firdausi et al., 2010; Pirscoveanu et al., 2015; Hansen et al., 2016)). However, due to the fact that malware are evolving and their behaviour can change, as in the case of exploiting a new vulnerability (Walenstein and Lakhotia, 2007) or an attempt of malware writers to avoid detection, malware can remain undetected and, therefore, be classified incorrectly as benign.

In this paper we investigate the reasons behind the misclassification of malware by using a knowledge-base of malware and benign samples that we have collected from a range of sources. We tracked changes adopted by the misclassified malware instances and we investigated whether there was a recognisable pattern across these misclassified samples. In our first experiment, we grouped malware by year and classified them in order to check whether there was any relation between the passage of time and the malware detection rate. In our second experiment, we checked whether the changes that caused the misclassification occur in malware at the level of families where all instances that belong to specific new families are misclassified, or if these changes can be traced back to individual variants?

In summary, in this paper we have investigated the following research questions:

- Does misclassification increase over a period of time?
- Does misclassification occur in malware at the level of families, where all instances that belong to specific new malware families are misclassified?
- Alternatively, does misclassification occur at the level of variants, and it is not related to malware families?
- When misclassification does occur can we find the reason for it?

In order to answer these questions we used 5410 malware samples, from approximately 400 variants drawn from 200 malware families. Although anti-malware vendors may have different names for the same sample, they usually share a similar naming scheme where malware can be grouped into families

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based on some similarities (code similarity as an example) and then each family can have a number of variants where each variant represent a new strain that is slightly modified. Figure 1 shows an example of the naming scheme followed by the company Symantec; it consists of a prefix, the family name and a suffix (Symantec, 2013a). Throughout this paper Symantec's *Listing of Threats and Risks* (Symantec, 2016a) has been used as a source of malware discovery date, types and malware family and variants names.

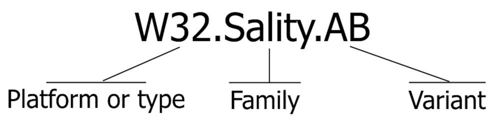


Figure 1: Symantec malware naming scheme.

We first build a classifier based on our malware and benign samples. We have an imbalanced dataset as the malware class is the majority, which is an issue that proposed malware detection systems usually encounter (Miao et al., 2015; Tian et al., 2010). We showed that malware detection systems based on *Bagging* (Breiman, 1996) classifier could be affected by the imbalance problem as the classifier becomes more biased towards the majority class, therefore, we propose to adopt *Exactly Balanced Bagging* (EBBag) (Chang et al., 2003) instead, which is a version of Bagging for dealing with an imbalanced dataset.

We then conducted multiple experiments: in the first experiment we ran the classifier on new malware grouped into their year of discovery. In the second experiment we grouped each new malware family into their available variants. We recorded the detection rate resulting from each group, in each experiment, in order to answer the research questions mentioned above. We used two different classification algorithms: Support Vector Machines (SVM) and Decision trees (DT) as a base for our classifier to make sure that the results produced are not dependent on a specific classification algorithm.

When looking at how the classifier performed on malware released after the training data, we saw a small fall in the detection rate after the first tested year, however we found no significant, long-term correlation between the time since a classifier is built and the misclassification rate of new malware, i.e., after a small initial drop off, the behavioural changes in the new malware did not reduce the accuracy of the classifier. It can be seen, however, that when having access to more training data the classifier tend to perform slightly better overall. Our research also showed that most of the behavioural changes that affect the classification rate of malware can be traced back to particular malware variants, and in most cases these changes are not replicated across malware families. Meaning that we would see a single variant that was hard to detect in a family of malware in which the other variants could be reliably detected.

We also found that the misclassifications were mostly due: to the adoption of anti-virtualisation techniques, or the fact that particular variants were looking for a specific argument to run, or due to the fact that some variants were actually considered as corrupted files. While removing all examples of misclassified corrupted malware from our dataset would have been possible, we note no other work on malware classification does this, so removing these samples would not reflect other work.

We hope that our results will help the reader to interpret other papers that present the detection rate of a machine learning classification system as their main result, and that our work sheds some light on how these classification rates will perform over time and why some malware avoids detection.

The paper is organised as follows: Section 2 describes related work in this field. Section 3 gives an overview of the methodology followed. Section 4 presents the sample preparation and data collection procedure. The main contribution to this field of research is described in Section 5 and 6 along with the experiments' results. The analysis is presented in Section 7. Section 8 discusses the research outcomes and outlines the conclusion.

2 RELATED WORK

In the following section we review the literature on malware classification and detection systems that is related to our work, and we indicate how this paper differs.

A large number of studies have introduced or evaluated different machine learning-based detection systems; the authors in (Xu et al., 2004; Ye et al., 2008; Wang et al., 2009) have based their detection systems on API calls sequence extracted using static analysis. However, static analysis is known to be questionable when dealing with obfuscation techniques where the sequence of the instructions might be modified or data locations can be hidden (Moser et al., 2007). Motivated by this fact, other researchers have based their detection systems on API call sequence extracted using behavioural analysis (Zhao et al., 2010; Tian et al., 2010; Faruki et al., 2012).

Most of the proposed detection systems have been tested on either a limited, or a current set of malware. Therefore, there was a need to examine the affect of the passage of time on such malware detection systems and explore whether this can affect the systems' detection rate. Islam et al in (Islam et al., 2012) showed that it is possible for current malware detection systems to maintain a high detection rate even when classifying future malware. They considered two sets of malware in order to verify this idea, one collected between 2002 and 2007 and the other collected from 2009 to 2010. In their experiment they dated malware based on the collection date and they used static, behavioural and a combination of both features during their experiment.

In (Shabtai et al., 2012) the OpCode n-gram patterns are used as features. They addressed the question *"How often should a classifier be trained with recent malicious files in order to improve the detection accuracy of new malicious files?"* Their research showed that classifiers can maintain a reliable level of accuracy. However, when testing malware created in 2007, a significant decrease in the accuracy was observed, which might indicate that new types of malware were released during that year.

Our work is different from the research mentioned above in the following respects:

- In addition to looking at malware behaviour over time, we also tracked the misclassification and investigated whether it can be traced back to malware families, or even to variants.
- We also investigated the possible reasons that led to this misclassification and analysed the results.

3 METHODOLOGY

Our work on this paper can be divided into four stages:

1. Collecting malware; described in detail in Section 4.
2. Building a Classifier:
   - Extracting and determining the features that we will be using when classifying the data.
   - Addressing the imbalance class problem on our data where malware samples outnumber the benign samples.
   - Assessing the performance of the proposed method.

   The feature extraction step is described on Section 5.1 while the system architecture is illustrated on Section 5.3.
3. Classifying large grouped datasets: Following the previous step, we will be classifying large datasets which have been grouped into:
   - Years: in order to check whether there is a notable change in malware behaviour over time which might result in a change in the classification rate in one of the years. We chose one year intervals based on the amount of data we have, as it was the minimum period which was able to produce a stable results.
   - Variants: in order to check whether these changes, which affect the detection rate, can be traced back to specific malware families were all their variants are hard to detect, or just to particular variants, without the family membership being a factor.

   The details of these two experiments are described in detail in Section 6.
4. Analysing the misclassified instances, which includes analysis of the misclassification that occurred and identification of its reasons. The analysis is discussed on Section 7.

4 THE KNOWLEDGE-BASE

In order to conduct our experiments we built a knowledge-base, which consisted of information and analysis reports related to all our collected malware and benign samples. The following section provides an overview of the procedure that was followed to collect the data.

Initially, the python-based tools: mwcrawler and maltrieve (Maxwell, 2012; Maxwell, 2015) were used to collect malware samples from a number of sources through parsing multiple malware websites and retrieving the latest malicious samples which have been uploaded to them. These websites include: Malc0de, Malware Black List,Malware Domain List, Malware URLs, VX Vault URLquery, CleanMX and ZeusTracker.

To makes sure our dataset reflected the most common types of malware, we have developed a python-based script that collect the most common 10 and 20 malware families recorded by Symantec and Microsoft in their Internet Security Threat reports (Symantec, 2015) and Security Intelligence Reports (Microsoft, 2015), respectively. The script works by pulling all samples resulting from the search request for each malware family, including all the available variants, from an open malware database Open Malware (Offensivecomputing, 2015). In addition, a large number of samples have also been downloaded from VirusTotal website (VirusTotal, 2015) through their *intelligence* service.

We note that this method succeeded in getting more samples from the most common malware families. As a result of the previous step, 5410 malware samples were collected. Our malware samples vary between approximately 400 malware variants with a date of discovery ranging from 08.12.1997 (*Infostealer*) to 22.10.2015 (*W32.Xpiro.I*).

We have also parsed all the information found on Symantecs' *Threats, Risks & Vulnerabilities* (Symantec, 2016a) pages in order to collect some valuable information, such as: malware types, discovery date of each malware family, and the risk level, in addition to the systems affected.

Our benign executables (956 samples) were collected from fresh installations of Windows XP SP3 and several official websites such as Windows and Adobe. Windows XP SP3 was selected to be installed on the virtual machines during the analysis as all the collected malware samples from 08.12.1997 to 22.10.2015 could run on this system according to the Symantec's *systems affected* information for each malware family. In addition, Windows XP SP3 is widely used for the purpose of analysing malware (Ceron et al., 2016; Pektaş et al., 2015) for multiple reasons; one of them is the fact that it *"consumes less memory and CPU power"* (Pektaş et al., 2015). All the executables were sent to Virustotal in order to retrieve the scanning results from multiple vendors such as Symantec, Kaspersky, Avira, ClamAV and others, and to ensure the integrity of the benign applications.

To analyse the malware and benign samples we used Cuckoo Sandbox version 0.2 (Cuckoo Sandbox, 2015), an automated malware analysis system. The sandbox executes samples in a controlled environment (*virtual machines*) for 120 seconds and generates reports with API calls, system traces in addition to network activities in .pcap file. In order to decrease the analysis time, we configured Cuckoo Sandbox to use three virtual machines instead of one where all of them will run simultaneously on a host machine that runs Ubuntu 14.04.

After the analysis was completed, behavioural analysis reports were parsed so that the extracted API calls and the other information included in the report could be added to our knowledge-base, along with the information which was collected from Symantecs' *Threats, Risks & Vulnerabilities* pages.

5 BUILDING A CLASSIFIER

This section discuss the process of extracting the features that will be used and outlines the classification procedure. This section also includes the metrics used to measure performance throughout the paper.

5.1 Feature Extraction

In this paper, we used the API calls as our dynamic features as they have been widely used as behavioural features for such systems, and they also demonstrate that they can offer a good representation of malware behaviour (Fan et al., 2015; Faruki et al., 2012; Tian et al., 2010; Pirscoveanu et al., 2015; Hansen et al., 2016). Additionally, It also worth noting that relying on behavioural analysis helps to avoid problems when dealing with some cases such as malware obfuscation. Based on preliminary tests on 1282 malware samples from our data, we found that the frequency of the APIs did not improve the classification any further, which is similar to the conclusion reached by (Tian et al., 2010), where only information related to the presence of an API is important and not the frequency. Thus we used the binary vector representation of the extracted APIs where 0 refers to the absence of an API call and 1 denotes its presence.

In addition, in our experiments we used an n-gram based method to represent the API call sequence (Alazab et al., 2010) where unigram, bigram, a combination of unigram and bigram, and trigram have been evaluated. Using unigrams means that the sequence of API words is unimportant, where we simply check if a word is present or not (aka 'bag of words' representation). By using bigram and trigram, the feature vector will not only contain a single API word but also will preserve the sequence of two and three words, respectively, which can be considered as taking a snapshot of the malware behaviour.

We also believe that using a hybrid analysis (both static and dynamic features) might boost the detection rate further. However, as we intend to use the classifier in checking malware behaviour in different scenarios such as: over time and with malware grouped into variants, static analysis was beyond the scope of this paper.

5.2 Evaluation Metrics

The following metrics have been used for evaluation purposes throughout the paper:

- True positive (TP): Number of samples correctly identified as malware.
- True negative (TN): Number of samples correctly identified as benign.
- False positive (FP): Number of samples incorrectly identified as malware.

- False negative (FN) Number of samples incorrectly identified as benign.

These terms are used to define four performance metrics which we use throughout the paper:

1. Sensitivity (recall): measures the proportion of true positives: Sensitivity = $\frac{TP}{TP+FN}$
2. Specificity: measures the proportion of true negatives: Specificity =$\frac{TN}{TN+FP}$
3. Geometric mean (G-mean): Also known as the macro-averaged accuracy (Ferri et al., 2009); it is the geometric mean of recall over all classes and it is known in the field of machine learning as a more accurate measure of performance than the normal accuracy in an unbalanced classification scenario as it considers the accuracy of both classes: the majority and the minority (Lin and Chen, 2012; Kang and Cho, 2006). The G-mean can be calculated as follows:
   G-mean=$\sqrt{Sensitivity \cdot Specificity}$
4. Area under the ROC curve (AUC_{ROC}) (Huang and Ling, 2005): The ROC curve is a graphical plot that illustrates the performance of a binary classifier. The curve is created by plotting the true positive rate (sensitivity) against the false positive rate (1-specificity) at various threshold. The value of AUC_{ROC} can vary between 1.0 and 0, where 1 indicates a perfect classifier with an ideal separation of the two classes, and an AUC_{ROC} of 0.5 represents worthless classifier. AUC_{ROC} is insensitive to class imbalance; if the majority labels of the data are positive or negative, a classifier which always outputs 1 or 0, respectively, will have a 0.5 score although it will achieve a very high accuracy. We calculated the AUC_{ROC} score based on the functions provided by *Scikit-learn* library, where the library offers a wide range of machine learning algorithms and tools (Scikit-learn, 2013).

Both metrics, G-mean and AUC_{ROC}, are commonly used to evaluate the imbalanced data classification performance. However as AUC_{ROC} considers all the possible thresholds, it is usually used to assess the performance when choosing the best model that will be used during the classification procedure. Therefore, we used both G-mean and AUC_{ROC} to choose the best model on Section 5.3. Moreover, we used the G-mean, which represents the balanced accuracy, as our main metric when classifying malware based on their year of discovery (Section 6.1). However, in Section 6.2 we used sensitivity as our main metric as it conforms with our goal there, which focused on the classifier's ability to correctly identify those malicious instances without adding any noisy data related to the benign samples.

5.3 Addressing the Imbalance Problem

For our classifiers, we used Support Vector Machine (SVM) and Decision Tree (DT) as they are widely known machine learning algorithms (Cortes and Vapnik, 1995; Kotsiantis et al., 2007). In addition, they have shown State-of-the-Art results in a number of classification problems, including classifying and recognising new malware (Zhang et al., 2006b; Zhang et al., 2006a; Ye et al., 2009; Lu et al., 2010; Alazab et al., 2010; Kruczkowski and Szynkiewicz, 2014) . The SVM and DT classifiers are based on the implementation of *Scikit-learn* library.

As mentioned previously, we have also evaluated the performance of our classifiers with different sizes of n-grams: unigram, bigram, unigram+bigram and trigram as shown in Table 1, and we have chosen the best for each classifier. In the case of SVM, the bigram and the unigram+bigram both gave us the best results, however, as our aim is to test malware discovered on the followed years where a match of an exact sequence might not be found, we thus preferred to use the unigram+bigram which will result in more generalisation, as it tests the occurrence of a single API word, in addition to a sequence of two APIs together.

The class imbalance is a common problem in the area of machine learning in general (Yap et al., 2014) and in malware detection in particular (Moskovitch et al., 2008; Ye et al., 2010). The imbalance problem occurs when the number of instances in each class varies. In malware detection systems, this is due to the fact that malware can be downloaded on large numbers from open access databases, such as Openmalware (Offensivecomputing, 2015), VX-Heaven (VX Heaven, 2016), VirusShare (Virusshare, 2016), whereas it is more difficult to gather large number of benign samples. The imbalance problem can affect the classification process as the classifier becomes more biased towards the majority class which is usually the malicious class, as mentioned in (Miao et al., 2015). Motivated by (Moskovitch et al., 2008), where they stated that the classification is more accurate when we have the same number of malware and benign, we addressed this problem by evaluating a well-known approach in the area of machine learning that is referred to as *Exactly Balanced Bagging* (EBBag) (Chang et al., 2003; Kang and Cho, 2006; Khoshgoftaar et al., 2011). This approach is based on classifying balanced subsets; it is a modified version of *Bagging* (Breiman, 1996), which is a method that have been used extensively in malware detection systems with different base classifiers; it delivers a considerably higher detection rate than the normal classifiers (Ye et al., 2009) even with an

Table 1: Classifiers performance on different n-gram sizes.

	SVM		DT	
Feature set	G-mean	AUC_{ROC}	G-mean	AUC_{ROC}
API_{Uni}	0.93	0.93	0.93	0.93
API_{Bigram}	0.94	0.94	0.92	0.92
$API_{Uni+Bigram}$	0.94	0.94	0.92	0.92
API_{Tigram}	0.92	0.92	0.90	0.90

imbalance dataset (Peiravian and Zhu, 2013). To the best of our knowledge, this paper is the first that uses EBBag for malware detection.

Bagging, in general, is a classifier ensemble technique based on randomly drawn subsets of the training data. Each time a subset is drawn, a classifier is constructed to classify the newly generated subsets. The classification procedure is repeated a number of times (we used 100) and the majority voting over all predictions is calculated as the final prediction to ensure the robustness of the results.

Our framework implemented the EBBag approach which is based on Bagging but with a minor modification to the way the subsets are drawn. In EBBag, the entire minority class is used for each classifier along with randomly generated subsets of the majority class, which are the same size as the minority class, so balancing the data. The procedure of generating smaller subsets is known as "downsampling".

We ran five tests to compare Bagging with EBBag, calculating the classification rate of randomly chosen malware and benign samples, with a malware to benign ratio varying between 2:1 and 10:1. We performed 10-fold cross validation and compared our adopted approach, EBBag, to the Bagging approach, with the same base classifier (SVM) and the best n-gram size. The results of these tests are shown in Figure 2. The figure shows the true positive rate (Sensitivity), true negative rate (Specificity) and AUC_{ROC} recorded for each approach. We note that Bagging becomes increasingly inaccurate as the data becomes more imbalanced. So the figure indicates that imbalanced data will be part of the cause of the misclassification rate in papers that use Bagging alone to classify malware.

By using EBBag, it can be seen that the measures of sensitivity and specificity, which represent the accuracy of the malicious and benign classes, respectively, were not affected by the imbalance problem. Also, the False Positive rate (1-specificity) was significantly decreased from 0.29 to 0.07, where a false positive occurs when a classifier flag a benign file as malicious by mistake; this is usually costly as it consumes a considerable amount of resources and time. As this analysis shows that EBBag outperforms Bagging, we used EBBag for the rest of the paper. Our

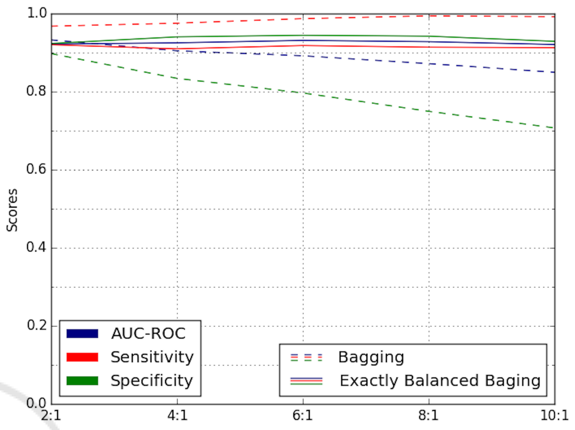


Figure 2: Classification rate with different ratio of malware samples to benign.

implementation of EBBag have been made available on: https://github.com/nalruhaily/EBBag.

6 CLASSIFYING A LARGE GROUPED DATASET

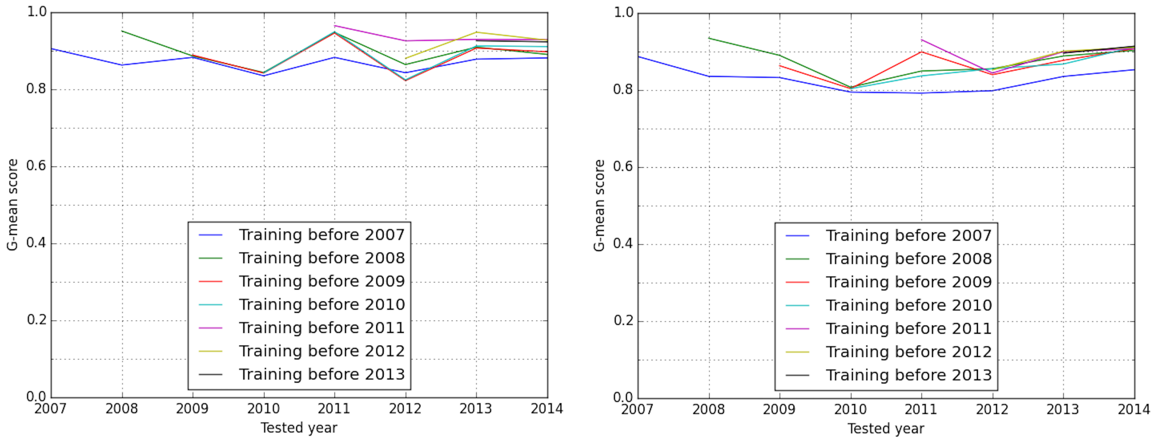
In order to answer the main research questions we have followed two methods to test the data:

1. Classifying all malware based on the year of discovery.
2. Classifying malware based on malware variants.

Section 6.1 and 6.2 describe in detail the process used in these two methods.

6.1 Classifying Malware based on the Year of Discovery

In our first experiment, we tested the classifier on data grouped into years, in order to check whether there was a notable change in malware behaviour over time, which will be represented as a change in the classification rate. We divided the entire test set into years from 2007 to 2014, based on the discovery date recorded by Symantec, thus we ended up with 8 testing sets. We chose one year intervals based on the



(a) Using SVM (b) Using DT

Figure 3: Malware tested yearly.

amount of data we had, as it was the minimum period which was able to produce a stable results. The initial training set included samples until year 2006. Each time, the training set was evaluated separately on each of the followed years, so for the initial training set it was evaluated on malware discovered from 2007 to 2014. We repeated the experiment by extending the training set to include the followed year and test on the remaining years.

Figure 3 shows the averaged accuracy (G-mean) recorded by our framework on data trained on real malware samples. Most of the results showed that the classifier can maintain a score above 80%. It can also be seen that the more the data included in the training phase, the higher the G-mean score for the following year was, except for some cases where a new family was introduced, such as in 2009 and 2010, or where a new variant with a slightly different behaviour was introduced such as in 2012 with W32.Ramnit.B!gen2. In fact, although some variants of the malware family W32.Ramnit were introduced before 2012 and the system was trained on some of them, it failed to identify this variant correctly. It seems that W32.Ramnit.B!gen2 variant implements some anti-sandboxing techniques where the malware tried to unhook Windows functions monitored by the sandbox, causing the Cuckoo monitor to throw 1025 exceptions.

However, overall from Figure 3 we can conclude that the detection rate was not consistently affected by the passage of time; instead, the classifiers, generally, can continue giving a good detection rate. Thus, to analyse the results further, we carried out another experiment which is explained in the next section. The experiment aimed to check whether the misclassification caused by the changes in malware behaviour can be traced back to a number of malware families or even to sub-families (a.k.a variants).

6.2 Classifying Malware based on Malware Variants

In this experiment we tested seven malware families (broken down into variants) in order to check whether the misclassified malware instances were a result of undetected behavioural changes at the malware family level or whether they were caused by other changes in the level of variants.

The experiment was conducted for seven families, namely: W32.Changeup, W32.Pilleuz, W32.Imaut, W32.Sality, Trojan.FakeAV, Trojan.Zbot and Trojan.Gen. The remaining families were not used due to an insufficient amount of samples for each particular variant in the available data set. These seven families correspond to a total of 2737 malware samples. For testing each of these families we trained the classifier on malware data prior to 2007, as we will have after this date a reasonable number of malware families grouped into variants to carry out the testing process.

We used sensitivity here as our main metric in the experiment (referred to in the table as Sens) to measure the detection rate as it conforms with our goal, which is focusing on the classifier's ability to correctly identify those malicious instances without adding any noisy data related to the benign samples.

Table 2 shows the results of classifying each of the malware families, including their available variants. It appears, mostly, that there is no absolute pattern between the misclassification and the malware family, nor with the discovered year of each of the variants. Therefore, it can be concluded that most of the misclassification can be traced back to several malware variants and it cannot be traced back to the discovery date of each of the tested variants, nor to changes at

Table 2: Tested by classifiers trained before 2007.

	Variants	#	Date	SVM-Sens	DT-Sens
Changeup	W32.Changeup	41	18/08/09	0.98	0.98
	W32.Changeup!gen9	48	02/09/10	1.0	1.0
	W32.Changeup!gen10	47	02/02/11	1.0	1.0
	W32.Changeup!gen12	47	11/08/11	1.0	1.0
	W32.Changeup!gen16	51	20/07/12	1.0	1.0
	W32.Changeup!gen44	76	01/08/13	0.99	1.0
	W32.Changeup!gen46	67	28/05/14	1.0	1.0
	W32.Changeup!gen49	64	20/08/14	0.94	1.0
Pilleuz	W32.Pilleuz!gen1	47	19/01/10	0.77	0.68
	W32.Pilleuz!gen6	138	29/09/10	0.88	0.86
	W32.Pilleuz!gen19	70	17/01/11	0.97	0.79
	W32.Pilleuz!gen21	64	29/03/11	0.28	0.03
	W32.Pilleuz!gen30	46	01/02/12	1.0	1.0
	W32.Pilleuz!gen36	60	07/02/13	1.0	1.0
	W32.Pilleuz!gen40	98	22/08/13	1.0	1.0
Imaut	W32.Imaut.AA	68	07/06/07	0.97	0.80
	W32.Imaut.AS	45	01/08/07	0.84	0.84
	W32.Imaut.CN	73	20/02/08	0.85	0.92
	W32.Imaut.E	64	23/12/08	0.88	0.83
	W32.Imaut!gen1	46	20/09/10	0.24	0.04
Sality	W32.Sality.X	46	12/01/07	0.96	0.93
	W32.Sality.Y!inf	91	16/03/07	0.98	0.98
	W32.Sality.AB	55	11/01/08	0.02	0.02
	W32.Sality.AE	71	20/04/08	0.93	0.87
	W32.Sality.AM	51	18/04/09	0.80	0.75
	W32.Sality!dr	71	31/08/10	0.80	0.80
	W32.Sality!dam	54	30/04/13	0.15	0.15
	W32.Sality.AF	93	02/01/14	0.90	0.77
FakeAV	Trojan.FakeAV	41	10/10/07	0.68	0.85
	Trojan.FakeAV!gen29	70	07/05/10	0.99	0.93
	Trojan.FakeAV!gen99	38	08/03/13	1.0	1.0
	Trojan.FakeAV!gen119	42	01/04/14	0.29	0.12
Zbot	Trojan.Zbot	40	10/01/10	0.98	0.28
	Trojan.Zbot!gen9	48	16/08/10	1.0	0.94
	Trojan.Zbot!gen43	48	26/05/13	0.85	0.88
	Trojan.Zbot!gen71	44	23/12/13	1.0	0.11
	Trojan.Zbot!gen75	32	05/06/14	0.69	0.97
Gen	Trojan.Gen	202	19/02/10	0.48	0.77
	Trojan.Gen.2	137	20/08/10	0.45	0.45
	Trojan.Gen.X	52	12/01/12	0.42	0.42
	Trojan.Gen.SMH	52	26/10/12	0.62	0.40
	Trojan.Gen.3	99	06/08/13	0.61	0.60

the level of the malware family (which would affect all of that families' future variants).

7 REASONS FOR MISCLASSIFICATION

Our aim in this section is to analyse the classification results. This also includes outlining the differences between the correctly classified and the misclassified variants and explaining the reasons that may have led to the misclassification. Generally, From Table 2 we can identify three misclassification cases although most of the misclassifications occurred at the level of variants. We can summarise the different misclassification cases as follows:

- Variants misclassified by both classifiers.
- Variants misclassified by only one classifier.
- Misclassification which occurred on the family level instead of variants.

7.1 Variants Misclassified by Both Classifiers

Table 2 shows malware variants misclassified by both classifiers: SVM and DT. These variants are: W32.Pilleuze!gen21, W32.Sality.AB , W32.Sality !dam, W32.Imaut!gen1 and Trojan.FakeAV! gen119.

In the case of the W32.Pilleuze!gen21, W32.Sality !dam and W32.Sality.AB variants, it seems that they have not performed any behavioural action when being analysed. This can happens because the samples implemented some anti-virtualisation techniques, or they were looking for a specific argument, or because they were corrupted files. All three mentioned variants terminated the process by calling NtTerminateProcess. In case of W32. Sality.AB and W32.Sality!dam they also adopted a stealthiness technique, where they disabled the error messages through calling SetErrorMode API with the arguments SEM_NOGPFAULTERRORBOX — SEM_NOOPENFILEERRORBOX. After looking at W32.Sality!dam page on Symantec (Symantec, 2013b) it seems that this variant is considered as a corrupted file where it can no longer be executed or infect other files. As stated previously, while removing all examples of misclassified corrupted malware from our dataset would have been possible, we note no other work on malware classification do this, so removing these samples would not reflect other work.

The W32.Imaut!gen1 worm, on the other hand, did not terminate the process, however, it did not perform any network activity which might led to being misclassified. In fact only 2 samples out of the 46 carried out some network activities and both of them were classified correctly.

In the case of Trojan.FakeAV!gen119, the malware variant used an uncommon API, (compared to others in our database), to connect to the Internet: InternetOpenW, InternetOpenUrlW which are the Unicode based API of the high-level Internet API: Windows Internet (WinINet). The calls used by this variant takes arguments in Unicode format, while the older variants of this malware family used the ASCII based API calls instead: InternetOpenA, InternetOpenUrlA. This raises the question: would normalising the API by removing the appended characters such as A, W, ExW, and ExA when processing the features, such as having only InternetOpen in the features set instead of multiple entries will increase the overall accuracy of API based classifiers?

Table 3: Performance on stemmed and un-stemmed features set.

	un-stemmed 280 API		stemmed 230 API	
	G-mean	AUC	G-mean	AUC
SVM	0.95	0.95	0.94	0.94
DT	0.92	0.92	0.92	0.92

To answer this question we carried out another experiment, using all of our data and normalising the Win32 API by removing the appended characters, such as A, W, ExA and ExW. We then performed 10-fold cross validation to assess the performance of the classifier using the stemmed and un-stemmed features set. The results are shown in Table 3.

It can be seen from Table 3 that removing the appended letters did not have a considerable impact on the classification rate. However, by removing the appended characters we ended up with approximately 230 features instead of 280, without significantly affecting the detection rate. Such an option can be considered to improve the efficiency of the classifier and minimise the time needed for the classification. We note that other papers (Sami et al., 2010; Veeramani and Rai, 2012; Salehi et al., 2014) use feature selection methods to reduce the number of features in their datasets, however, they do not use API stemming, which Table 3 suggests might be a helpful addition.

7.2 Variants Misclassified by Only One Classifier

Another case which we have investigated can be seen in Trojan.Zbot and Trojan.Zbot!gen71, where most of their instances have been correctly classified by the SVM classifier. However, DT failed to classify these samples correctly. We analysed random trees constructed by the classifier to be able to determine the reasons for the misclassification. In the case of Trojan.Zbot, it seems that the absence of the call: SetWindowsHookExA was the reason for the misclassification on almost all the variant's samples. While in case of Trojan.Zbot!gen71 variant, the correctly classified malware called the NtProtectVirtualMemory API to allocates a read-write-execute memory. This API is usually called by malware binaries during the unpacking process, and the absence of this call might indicate that the malware sample was not packed, which, on our case, led to the misclassification of the incorrectly classified instances.

7.3 Misclassification on Malware Family Level

Although most of the misclassification seen occurred at the variant level, there is a single case where the misclassification can be linked to the family instead, as can be seen in Table 2 in the case of Trojan.Gen family. The reason that this family is different from the others seems to be due to the fact that this family is actually a category *" for many individual but varied Trojans for which specific definitions have not been created "* as stated by Symantec on the Trojan.Gen family page (Symantec, 2016b). By checking the misclassified samples and the paths taking by samples belonging to this family, it can be seen that although the samples may share some general characteristics, they adopt different techniques and thus the samples can behave in various ways and take different paths on trees generated by DT classifier (approximately 15 different behavioural paths), unlike other families where their behaviour was very uniform (2 or 3 paths).

As we have explained, the behavioural profiles and definitions that resulted from this family were varied and thus we only giving examples for some of the misclassification cases here, as identifying all the reasons for the misclassification for this family would not be possible. Many of the misclassified instances did not connect to the Internet either, because the malware were applying some anti-virtualisation techniques, an example of this case is: Trojan.Gen.X; or they were terminating the process as a specific argument had not been found, as in Trojan.Gen.3. In the case of Trojan.Gen.X, nearly half of the misclassified samples belonging to this variant were monitoring the user window by calling GetForegroundWindow and checking the mouse movement through calling theGetCursorPos API. They also followed these calls by calling GetKeyState to monitor the following keys constantly: the mouse keys, Alt, Ctrl, and shift key. The execution was then delayed through going on a loop when monitoring these actions and NtDelayExecution also have been called. These techniques have been noticed when analysing recent malware, as reported by malware researchers (SCHICK, 2016) in order to evade sandbox detection, and this could be the reason why all the variants that used that technique have been misclassified.

8 CONCLUSION

In this paper, we classified malware grouped into their year of discovery, in addition to grouping them into malware variants. We have tracked the misclassified malware instances and we investigated whether there were recognisable patterns across these misclassified samples. From our first experiment we found that classifiers can continue to give a high detection rate even after a period of time which means that there is no correlation between the passage of time and the misclassification that occurred, despite a minor rise of the detection rate on the following year. We then concluded from our second experiment that, mostly, there were little recognisable patterns between the misclassification and malware families, as with the discovered year of malware variants. Instead, most of the misclassifications can be traced back to several malware variants. This variation which occurred on the variant level is due to the fact that some variants apply some anti-sandboxing techniques, or because some samples are looking for a specific argument to run, or due to the fact that some variants are actually considered as bad data. This conclusion can help in interpreting the successful rate achieved when proposing a machine learning based detection system.

Also, the situation where only some variants are unrecognisable might be due to the fact that malware writers are not trying to evade, yet, machine learning techniques as they are still considered as new techniques to detect malware, and have not been used as widely as the signature based ones. If these recognition systems became more common, it might be the case that we would see more of these techniques used to evade the detection by such systems.

For future work, we are aiming to investigate whether using hybrid features with our proposed detection system, instead of only using behavioural features, outperform the State-of-the-Art detection systems.

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