On the Effectiveness of Generic Malware Models

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Abstract: Malware detection based on machine learning typically involves training and testing models for each malware family under consideration. While such an approach can generally achieve good accuracy, it requires many classification steps, resulting in a slow, inefficient, and potentially impractical process. In contrast, classifying samples as malware or benign based on more generic "families" would be far more efficient. However, extracting common features from extremely general malware families will likely result in a model that is too generic to be useful. In this research, we perform controlled experiments to determine the tradeoff between generality and accuracy—over a variety of machine learning techniques—based on *n*-gram features.

1 INTRODUCTION

Malware is defined as software that is intended to damage computer systems without the knowledge of the owner (Norton, 2018). According to Symantec (Symantec, 2017), more than 357 million new malware variants were found in 2016. Malware detection is clearly an important research topic

Signature-based malware detection is effective in many cases, but fails to detect advanced forms, such as metamorphic malware. Machine learning techniques including hidden Markov models (HMM), support vector machines (SVM), *k*-Nearest Neighbors (*k*-NN), and random forests have been used to effectively detect metamorphic malware, and other challenging classes of malware (Stamp, 2017). Such models are often trained using static features, such as opcode sequences and byte *n*-grams.

Previous research has shown that a variety of techniques based on byte *n*-grams can achieve relatively high accuracies for the detection problem (Liangboonprakong and Sornil, 2013; Reddy and Pujari, 2006; Shabtai et al., 2009; Tabish et al., 2009). However, a recent study based on *n*-gram analysis rejects this view and argues that *n*-grams promote a gross level of overfitting (Raff et al., 2016).

In this research, we consider a somewhat similar problem as in (Raff et al., 2016), but we take a much different tack. Our goal here is to perform carefully controlled experiments that are designed to expose the relationship between the level of generality of the training data and the accuracy of the resulting model. Intuitively, we expect that as the training data becomes more generic, the models will become less accurate, and our results do indeed support this intuition. We believe that the results that we provide in this paper cast the work presented in (Raff et al., 2016) in a much different light, namely, that the inability to construct a strong model based on the extremely diverse and generic data follows immediately from the generality of the data itself, rather than being an inherent weakness of a particular feature, such as *n*-grams.

The remainder of the paper is organized as follows. In Section 2, we cover relevant background topics, including an overview of selected examples of related work. This background section also includes a brief overview of the classification techniques used in this paper, namely, support vector machines, a statistical χ^2 score, *k*-nearest neighbors, and random forests. Our experiments and results are covered in detail in Section 3. The paper concludes with Section 4, where we also discuss future work.

2 BACKGROUND

In this section we discuss selected examples of related work. Then we also provide a high-level introduction to each of the various machine learning techniques employed in the research presented in this paper..

2.1 Related Work

Wong and Stamp (Wong and Stamp, 2006) show that hidden Markov model (HMM) analysis applied to op-

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codes can effectively distinguish some examples of highly metamorphic malware. The authors trained a model for each of three different metamorphic malware families and they were able to successfully distinguish each family. This malware detection scheme outperformed commercial anti-virus products. These results are not particularly surprising, considering that most commercial products rely on signature based detection methods. This work makes a reasonable case for the use of opcodes as a feature for malware detection.

Singh et al. (Singh et al., 2016) applied three different techniques to obtain malware scores, namely, an HMM score, a distance based on principles from simple substitution cipher cryptanalysis, and an straightforward opcode graph score. These three scores were combined using an SVM to construct a classifier that was shown to be stronger and more robust than any of the component scores. This research demonstrates the strength of an SVM, particularly when used to combine multiple scores into a single classifier.

Reddy and Pujari (Reddy and Pujari, 2006) use a feature selection method that ranks *n*-grams based on frequency and entropy. Their experiments show that performing a class-wise feature selection improves the efficiency of the models. This process involves extracting the *k* most frequent *n*-grams from the benign and malware sets and using a union of the two sets as features. We follow a similar approach in our *n*-gram analysis considered here.

Raff et al. (Raff et al., 2016) experimented with *n*-grams and elastic-net regularized logistic regression. These experiments were conducted using a large dataset containing over 200,000 malware samples. The detection results obtained from these experiments were poor and, as mentioned above, the authors claim that *n*-grams are not suitable for malware detection. Unfortunately, the authors' data was obtained from an undisclosed "industry partner" and is not available for independent verification of the results.

In this research, we determine the accuracy of *n*-gram based malware models as a function of the generality of the training data. We see that the more generic the training dataset, the less distinguishing and weaker is the resulting model. While this is true in general, we do observe some differences in various machine learning techniques, indicating that some approaches are more robust than others in this respect.

2.2 Classification Techniques

In this section we briefly discuss each of the classification techniques used in this paper. Specifically, we consider support vector machines (SMV), a straightforward χ^2 statistic, *k*-nearest neighbors, and random forests. Then in Section 3, each of these techniques will be used to distinguish between malware and benign samples, based on *n*-gram frequencies.

2.2.1 Support Vector Machines

SVMs are supervised learning algorithm for binary classification. An SVM is trained on a labeled dataset and the resulting model can be used to classify samples. Conceptually, the main ideas behind SVMs are the following (Stamp, 2017).

- Separating hyperplane — A hyperplane is constructed based on the two classes in the training data. Ideally, this hyperplane separates the training data into its two classes.
- Maximize the margin — The separating hyperplane is chosen such that the margin between the two classes of data is maximized. Intuitively, this gives us the maximum margin for error (relative to the training data) when using the model to classify samples.
- Kernel trick — We transform the input data to a higher dimension feature space using a nonlinear kernel function. By doing so, we greatly increase the chance of finding a separating hyperplane. The "trick" here is that in spite of the nonlinear kernel function that we have embedded in the process, training and scoring are highly efficient operations. However, choosing the kernel function is more art than science. Popular kernel functions include polynomial learning machines, Gaussian radial-basis functions (RBF), and two-layer perceptrons.

2.3 Chi-squared Test

The chi-squared test (Plackett, 1983) is a simple and effective statistical technique that can be applied to categorical data to determine whether an observed frequency distribution differs from a specified frequency distribution. This statistical technique was first described by Pearson (Pearson, 1900) in 1900.

Mathematically, the χ^2 statistic is essentially a normalized sum of square deviation between the expected and observed distributions. This statistic is computed as

$$\chi^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i}$$

where

$$\begin{aligned}\chi^2 &= \text{cumulative chi-squared statistic}\\ n &= \text{number of dimensions or features}\\ O_i &= \text{observed value of the } i^{\text{th}} \text{ feature}\\ E_i &= \text{expected value of the } i^{\text{th}} \text{ feature}\end{aligned}$$

2.4 *k*-Nearest Neighbors

The *k*-nearest neighbor (*k*-NN) algorithm is among the simplest machine learning algorithms (Stamp, 2017). The *k*-NN algorithm is a supervised learning technique and hence requires labeled training data. In *k*-NN, we classify a sample based on a majority vote of the *k* nearest samples in the training set. Several variations of *k*-NN are possible, including weighting the training samples based on their relative frequencies and weighting the “votes” based on their distance from the sample we are attempting to classify. One significant advantage of *k*-NN is that it requires no explicit training phase.

2.5 Random Forests

Random forests are a generalization of a very simple concept, namely, decision trees (Stamp, 2017). In a process know as “bagging,” random forests construct multiple decision trees based on subsets of the training data as well as subsets of the available features. A majority vote of the resulting component decision trees is used to determine the classification of a given sample. Bagging reduces the tendency of decision trees to overfit the training data.

3 EXPERIMENTS AND RESULTS

In this section, we discuss the experiments we have performed and the results obtained. As mentioned above, the techniques used are SVM, a χ^2 test, *k*-NN, and random forests, all of which are based on *n*-gram features. Our primary goal is to carefully analyze the strength of each of these various models as we add more malware families into the training set.

3.1 Experimental Design

In all of our experiments, we use the relative frequencies of *n*-grams as our features, and we conduct experiment based on 2-grams, 3-grams, and 4-grams. The malware and benign datasets used in our experiments are discussed in Section 3.2, below.

For all of our *n*-gram experiments, the feature vector is based on byte *n*-gram frequencies. The total possible number of byte *n*-grams is $256^n = 2^{8n}$, which would be challenging to deal with, even for $n = 2$, and completely impractical for $n > 2$. Consequently, we use a simple feature selection mechanism to reduce the size of the feature vector—the approach employed here is essentially the same as that in (Reddy and Pujari, 2006). Specifically, for each *n*-gram experiment, we select the 10 most frequent *n*-grams present in the malware set and we select the 10 most frequent *n*-grams present in the benign set, and we form the union of these two sets, giving us a feature vector having a maximum length of 20.

For all of our experiments, we use five-fold cross validation. That is, the malware dataset is partitioned into five equal parts, and each of these parts serves as the test set in one experiment, with the four remaining parts used for training. In experiments where we combine multiple malware families, care is taken to ensure that each of the five folds (i.e., subsets) contains a balanced number of samples from each family. Note that cross validation serves to smooth out any bias in the dataset, while also maximizing the number of experimental results for the given amount of data available.

In most of our experiments, we train a model, then classify samples using the resulting model. To measure the success of such experiments, we use the concept of *balanced accuracy*, which is computed as

$$\text{balanced accuracy} = \frac{1}{2}\left(\frac{\text{TP}}{\text{TP}+\text{FN}} + \frac{\text{TN}}{\text{TN}+\text{FP}}\right)$$

where

$$\begin{aligned}\text{TP} &= \text{true positives}\\ \text{TN} &= \text{true negative}\\ \text{FP} &= \text{false positive}\\ \text{FN} &= \text{false negative.}\end{aligned}$$

Note that the balanced accuracy calculation weights all classification errors the same, regardless of any imbalance that might exist between the sizes of the positive and negative sets. This is particularly significant in our experiments, since the size of the benign dataset varies depending on how many malware families we combine in one experiment. Because of this variabillity, a straightforward accuracy calculation, which is of the form

$$\text{accuracy} = \frac{\text{TP+TN}}{\text{TP}+\text{FN}+\text{TN}+\text{FP}},$$

would, in effect, weight false positive cases less as more families are considered. Thus, for our experiments, the balanced accuracy provides a more consistent view of the success of our classifiers than the usual (i.e., unbalanced) accuracy calculation.

The χ^2 experiments discussed below are based on a scoring function rather than a classifier. Consequently, for these experiments, we computer receiver operating characteristic (ROC) curves and use the area under the curve (AUC) as our measure of success. An ROC curve is constructed by plotting the true positive rate (TPR) versus the false positive rate (FPR) as the threshold varies through the range of values. The TPR is given by

$$\text{TPR} = \frac{\text{TP}}{P} = \frac{\text{TP}}{\text{TP}+\text{FN}}$$

while the FPR is computed as

$$\text{FPR} = \frac{\text{FP}}{N} = \frac{\text{FP}}{\text{FP}+\text{TN}}.$$

The area under the ROC curve (AUC) ranges from 0 to 1. An AUC of 1.0 indicates perfect separation, i.e., there exists a threshold for which no false positives and no false negatives occur, while an AUC of 0.5 indicates that the binary classifier is no better than flipping a fair coin. Also, note that if the AUC is, say, $x < 0.5$, then by simply reversing the sense of the classifier, we obtain an AUC of $1 - x > 0.5$. In general, the AUC gives the probability that a randomly selected match case scores higher than a randomly selected non-match case (Bradley, 1997; Stamp, 2017).

3.2 Dataset

The following eight families form the malware dataset used in this research.

Gatak is a trojan that collects information about an infected computer and sends it to a potential attacker. This trojan hides itself as part of a key generator application or an update for a legitimate application (Trojan:Win32/Gatak, 2018).

Kelihos is a family of trojans that send out spam email with links to installers of malware. This malware is a botnet that communicates with remote servers to send spam emails and capture sensitive information (Win32/Kelihos, 2018).

Lollipop is an adware program that displays ads as the user browses the web. This adware can also redirect search engine results, monitor a user's activity and send such information to an attacker (Adware:Win32/Lollipop, 2018).

Obfuscator.ACY is a family of viruses that hide their purpose through various obfuscation techniques. The underlying malware can serve any purpose (VirTool:Win32/Obfuscator.ACY, 2018).

Ramnit is a worm that spreads through infected removable drives. This malware is capable of stealing sensitive information, such as bank credentials (Win32/Ramnit, 2018). Ramnit can give an attacker access to—and control of—an infected machine.

Winwebsec is a trojan that pretends to be an antivirus product. This malware attempts to convince the user to pay for its fake antivirus protection by displaying messages stating that the computer has been infected (Win32/Winwebsec, 2017).

Zbot (aka Zeus) is a trojan horse that infects systems by downloading configuration files or updates. This financial botnet steals confidential information, such as online credentials (Trojan.Zbot, 2010).

Zeroaccess is a trojan that makes use of a rootkit to hide itself. ZeroAccess creates a backdoor on compromised systems and is capable of downloading additional malware (Trojan.Zeroaccess, 2011).

The malware samples used in our experiments were obtained from the Microsoft Malware Classification Challenge (Kaggle, 2015) and the Malicia Project (Malicia Project, 2015; Nappa et al., 2013). Table 1 lists the number of samples used from each malware family. Our representative benign set consists of 300 executables from the System32 folder that were collected from a system running a fresh install of Windows XP.

Table 1: Malware samples per family.

Family	Samples
Gatak	1,013
Kelihos	2,942
Lollipop	2,478
Obfuscator.ACY	1,228
Ramnit	1,541
Winwebsec	5,820
Zbot	2,167
Zeroaccess	1,306
total	18,495

For the bigram experiments discussed below, we consider two cases. First, we use all of the available malware samples in each family. Then, for a second set of experiments, we use a balanced malware dataset, consisting of 1,000 samples from each of the eight malware families. The balanced experiments provide more realistic results in cases where a large malware family (e.g., Winwebsec) is atypical, in the sense of being either unusually easy or unusually difficult to detect. For our 3-gram and 4-gram experiments, we use all of the available malware data.

3.3 SVM Experiments

In this section we discuss our SVM experiments based on bigram in detail. We then give results for the equivalent 3-gram and 4-gram experiments.

For each experiment, we determine the relevant *n*-grams as discussed in Section 3.1. Once we have selected the appropriate *n*-grams, we compute the relative frequencies of each, to yield our feature vectors.

The samples listed in Table 1 were used as our malware dataset and, as mentioned above, we use a set of 300 System32 samples as our representative benign samples. An SVM was trained on these datasets using a radial basis function (RBF) kernel and a soft margin setting of $C = 1$.

First, we tested each of the eight malware families in Table 1 individually. For each family, we performed one experiment using all available samples from the family, and we performed another experiment using a selection of 1,000 samples. The balanced accuracies obtained for all of these experiments are listed in Table 2.

Table 2: SVM balanced accuracy for individual families (bigram models).

Family	Samples per family	
	all	1,000
Gatak	0.9630	0.9803
Kelihos	0.9983	0.9958
Lollipop	0.8409	0.8757
Obfuscator	0.9199	0.9195
Ramnit	0.8402	0.8619
Winwebsec	0.9712	0.9705
Zbot	0.9614	0.9627
Zeroaccess	0.9793	0.9808
Average	0.9342	0.9434

Next, we train SVMs for each of the $\binom{8}{2} = 28$ pairs of the malware families in our dataset. For example, one of these experiments consists of combining the Gatak and Kelihos families into one set, and training a single SVM to detect members of this combined family. As above, we consider both the case where we use all available samples, and the case where only a subset of 1,000 samples from each family is considered.

Next, we trained SVMs for all $\binom{8}{3} = 56$ combined sets of three families, and all $\binom{8}{4} = 70$ sets of four families and so on, up to one super-family that includes all 8 families. In each case, we compute the average balanced accuracy over all cases for a given number of combined families. Table 3 lists these average results for all possible combinations of the eight malware families, where the "Families" column refers to the number of families that were combined.

Table 3: SVM average balanced accuracy (bigram models).

Families	Samples per family	
	all	1,000
1	0.9342	0.9434
2	0.8806	0.9010
3	0.8402	0.8605
4	0.8081	0.8310
5	0.7827	0.8077
6	0.7603	0.7890
7	0.7384	0.7738
8	0.7265	0.7678

Analogous SVM experiments were conducted based on 3-grams and 4-grams, using all of the available malware samples. The results of our SVM experiments based on bigrams, 3-grams, and 4-grams are summarized in the line graphs in Figure 1. Qualitatively, we observe that the SVM results for 3-gram and 4-gram models are similar to those for the bigram case.

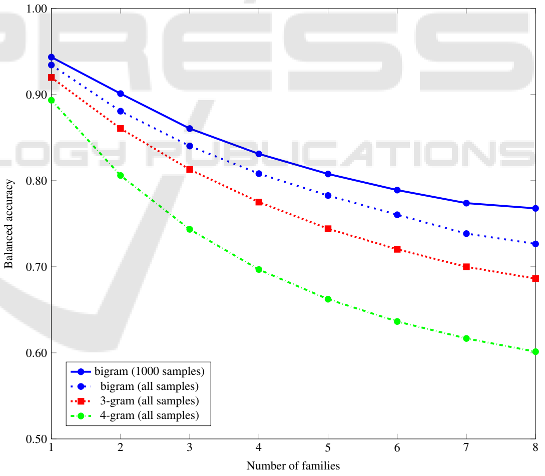

Figure 1: SVM accuracy vs number of families.

3.4 Chi-squared Experiments

In this section we discuss our experiments and results using a χ^2 statistic. The experiments here are essentially the same as those discussed in Section 3.3, except that we use a χ^2 statistic to compute a score, as opposed to an SVM classifier. Since we have a score instead of a classifier, we use the area under the ROC curve as our measure of success, rather than the balanced accuracy.

For the bigram case, we compute the relative bigram distribution (for the most common bigrams) over the entire training set. Then to score any sample, we determine its relative bigram distribution and find the χ^2 distance from the distribution of the training set. This is interpreted as a score, where a smaller value indicates a sample that is closer to the training set.

When testing each of the eight families individually, we obtain the AUC values in Table 4. We note that the range of these results is much greater than the SVM balanced accuracy discussed above. Here, the score range from a near-perfect 0.9943 for Winwebsec, to a near coin flip of 0.6541 for Lollipop.

Table 4: AUC of χ^2 score for individual families (bigram models).

Family	Samples per family	
	all	1,000
Gatak	0.8784	0.9921
Kelihos	0.9943	0.9930
Lollipop	0.6541	0.6876
Obfuscator	0.8750	0.8712
Ramnit	0.8772	0.8748
Winwebsec	0.9450	0.9384
Zbot	0.8709	0.8646
Zeroaccess	0.9502	0.9472

As with the SVM experiments above, we also consider all combinations of families, and we perform analogous experiments using 3-gram and 4-grams. The results of these experiments are summarized in the form of line graphs in Figure 2.

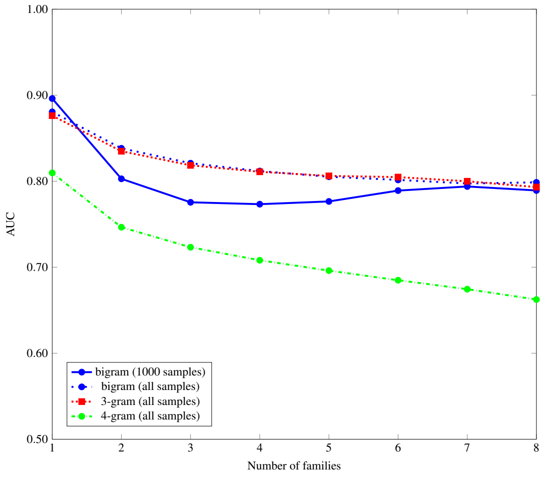

Figure 2: χ^2 score AUC vs number of families.

The bigram (all samples) and 3-gram cases are virtually indistinguishable in these experiments. Also, we see that the low score for the Lollipop family drags down the balanced bigram scores for two families, but has no appreciable effect on the imbalanced datasets, as the larger (and easier to detect) families more than make up for Lollipop.

The results for the χ^2 score are generally similar to those for the SVM classifier, in the sense that the more families we group together, the weaker the results become, on average. However, due to the extremely poor χ^2 score for the Lollipop family, the combined score never falls below that of the weakest individual score.

3.5 k Nearest Neighbor Experiments

In this section we give our experimental results for a k-NN classifier, based on n-gram features. Note that no explicit training is required when using the k-NN technique—after the n-grams are selected, the (labeled) points from the training set form the model. Also, we need to specify the number of nearest neighbors to use, i.e., the value of k in k-NN. In all other respects, the experimental design here is analogous to the SVM case in Section 3.3, above.

To determine value for k, we performed a set of experiments on the Gatak family. Specifically, we tested each $k \in \{2,3,4,\ldots,10\}$ and computed the balanced accuracy for each case. Figure 3 depicts the results of these experiments in the form of a line graph. Although the differences are relatively small, we see that $k = 5$ gives the best results, and hence we have selected $k = 5$ for all of our subsequent k-NN experiments.

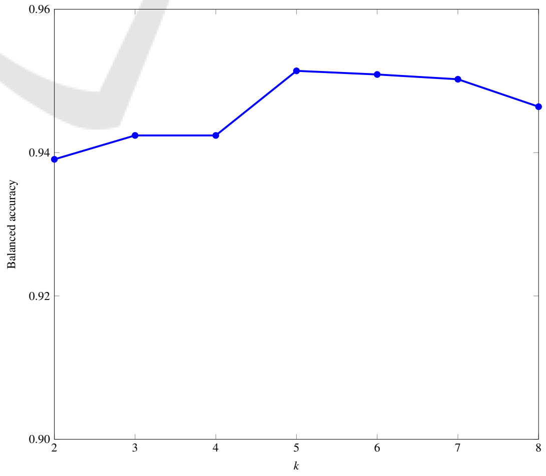

Figure 3: k-NN results for various values of k.

In Table 5, we give our experimental results—in the form of the balanced accuracy—for each of the individual malware families in our dataset. We see that all families score very high, except Ramnit, which at 86% accuracy (for the “all” case) is significantly below the results obtained for any of the other families.

Table 5: *k*-NN balanced accuracy for individual families (bigram models).

Family	Samples per family	
	all	1,000
Gatak	0.9514	1.0000
Kelihos	0.9765	0.9852
Lollipop	0.9334	0.9438
Obfuscator	0.9211	0.9267
Ramnit	0.8632	0.8752
Winwebsec	0.9481	0.9487
Zbot	0.9525	0.9600
Zeroaccess	0.9799	0.9827

We also conducted bigram, 3-gram, and 4-gram experiments with combined families. The results obtained for these cases are summarized here in Figure 4. Qualitatively and quantitatively, our *k*-NN results are very similar to those we obtained for the SVM classifier.

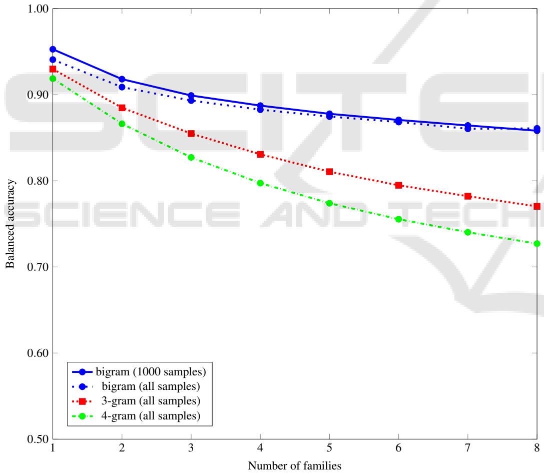

Figure 4: *k*-NN balanced accuracy as a function of the number of families.

3.6 Random Forest Experiments

In this section, we discuss our experiments and results for random forest classifiers. The experimental setup here is analogous to that used for the SVM and *k*-NN experiments considered above. For random forests, there are many parameters, and we experimented with a variety of values. For all of the random forest results presented here, we use the following selection of parameters.

- The number of trees in each forest is 10.
- Entropy is used to measure the quality of a split.
- We use $\sqrt{N}$ features—where N is the total number of features available in the tree—when determining the best split. Note that the value of N is tree-specific.
- No maximum depth, i.e., nodes are expanded until all leaves are pure or until all leaves contain less than 2 samples.
- A minimum of 2 samples is required to split an existing node.

For each individual family, using random forest classifiers with the parameters listed above, we have obtained the balanced accuracy results given in Table 6. From these results, it is clear that random forests perform significantly better on these individual families than any of the techniques considered previously in this paper.

Table 6: Random forest balanced accuracy for individual families.

Family	Samples per family	
	all	1,000
Gatak	0.9882	1.0000
Kelihos	0.9982	0.9962
Lollipop	0.9736	0.9750
Obfuscator	0.9505	0.9407
Ramnit	0.9049	0.9079
Winwebsec	0.9897	0.9882
Zbot	0.9894	0.9765
Zeroaccess	0.9887	0.9922

We also conducted bigram, 3-gram, and 4-gram experiments for random forests. The results for these cases are summarized in Figure 5. Note that the two bigram experiments—using all samples versus using 1,000 samples per family—are virtually indistinguishable in this case.

For our random forest classifiers, the average accuracy drops gradually as we increase the number of families being modeled. However, the magnitude of the decline is even smaller than we observed with *k*-NN. These results indicate that a random forest is, in some sense, the most robust of the classifiers we have considered in this paper. Nevertheless, the average accuracy of our random forest classifier does drop to 88% in the bigram case when we construct a model based on all 8 families, which is significantly below the lowest accuracy of any of the individual classifiers. Similar statements hold for the 3-gram and 4-gram experiments.

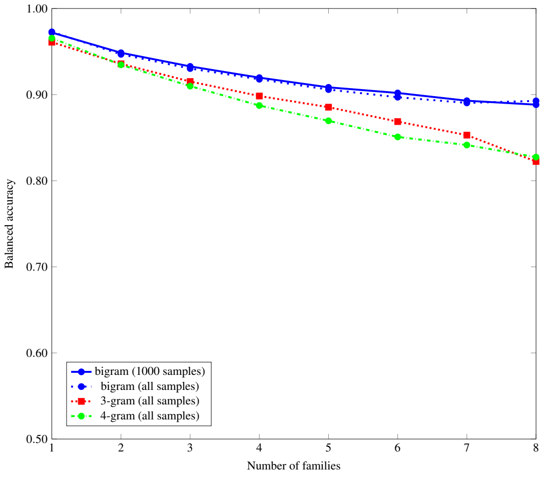

Figure 5: Random forest balanced accuracy as a function of the number of families.

3.7 Summary of Results

Figure 6 depicts the variation in average accuracy with increasing generality of the data for each of the four techniques considered in this paper. For the χ^2 experiments, the *y*-axis represents the area under the ROC curve (AUC), while for the other three techniques, the *y*-axis is given in terms of the balanced accuracy.

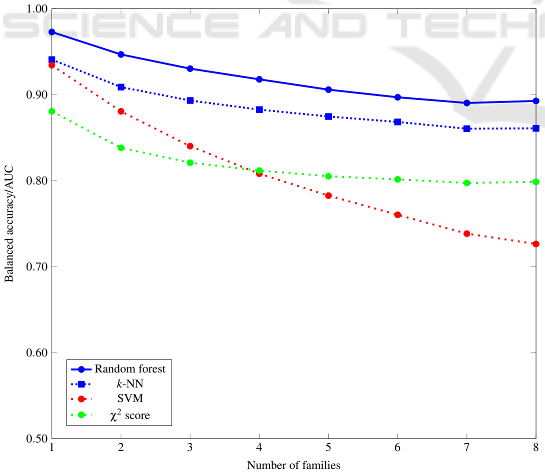

Figure 6: Comparison of average accuracy (bigrams using all samples).

The results in Figure 6 show that a random forest is the strongest and most robust technique considered here, followed closely by *k*-NN, while SVM has the most significant drop off as additional families are included. But perhaps the most pertinent observation is that in every case, a clear trend is apparent—the more generic the training dataset, the weaker the resulting model.

4 CONCLUSION

In this paper, we considered four different learning techniques—SVM, a χ^2 score, *k*-NN, and random forests—and tested the strength of each when faced with increasingly generic malware "families." In each case, we experimented with bigram, 3-gram, and 4-gram features.

Overall, we found that bigrams gave us the best results. In addition, the neighborhood based techniques (i.e., random forest and *k*-NN) proved to be the strongest, with random forest being the best. In all cases, we observed that accuracy generally suffers as the models become more generic.

In our experiments, we considered eight malware families. Even with this fairly small number of families, the effect of an increasingly generic dataset are readily apparent. Of course, the fewer models we have to deal with, the better in terms of efficiency. However, our results show that we are likely to suffer a significant penalty with respect to classification accuracy when multiple families are combined into a single model, except perhaps in cases where the underlying families are closely related. Note that this does not imply any flaw in the classification techniques or the features used. Indeed, our results show that a simple bigram feature, for example, can be quite strong when constructing models within reasonable bounds.

It is also worth noting that the experiments considered in this paper are, in a sense, a relatively easy case, as our dataset only has eight well-defined families. An extremely large and diverse malware dataset is likely to contain a vast number of families, as well as significant numbers of sporadic (i.e., non-family) malware examples. We would expect any model trained on such a generic dataset to learn only the most generic of features. When viewed from this perspective, the results given in (Raff et al., 2016) can be seen to be a natural artifact of the dataset itself, as opposed to an inherent limitation of the particular features (i.e., *n*-grams) under consideration.

For future work, additional features can be considered. For example, we plan to develop models that include *n*-grams, opcodes, and various dynamic features, with the goal of analyzing the robustness of such models in the face of ever more generic datasets. While we would certainly expect any model to deteriorate as the training data becomes more generic, as a practical matter, anything that can be done to effectively group more families together—thus reducing the number of models required for detection—while still retaining a usable degree of accuracy would be a worthy result.

It would also be interesting to study this problem from the perspective of malware type. That is, can we achieve greater success if we restrict our attention to a specific class of malware, such as botnets, trojans, or worrms, for example? It seems plausible that there will be more similarity between families that all belong to the same class than families that span different classes. If so, we would expect to effectively deal with larger numbers of families within a single model.

Another basic problem is the need for an extremely large, labeled, and publicly available malware dataset. While the dataset used here is quite substantial, with 18,495 samples, a dataset with a much larger number of families (as well as sporadic non-family malware samples) would be invaluable for research of the type considered here, as well as for many other research problems. We are currently in the process of assembling just such a dataset.

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