

Classifying Malware into families Based on File Content

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Abstract— We present a mechanism to classify a malware file into one of nine families: Rammit, Gatak, Tracur, Vundo, Simda, Kelihos.ver1, Obfuscator.ACY, Lollipop and Kelihos.ver3. The system uses a large training set of disassembled malware executables, both in their binary and assembly forms. We ran two separate experiment processes: the first involved extracting n-grams from the binary files using the kfNgram tool, and the second used a shell script to parse the assembly files for method calls to external API libraries. In both cases, the attributes are merged to form a master list and later reduced by selecting the top 500 with the highest information gain (IG). These 500 attributes are the boolean attributes to determine if they are present or not in each of the malware executables. The training set, using the selected attributes, was transformed into an .arff file required by Weka [Witten and Frank 2005] to run several classifiers, i.e. nave bayes, decision trees and support vector machines (SVM). We then compared the different algorithms using some common measures: accuracy, error rate, true and false positive error rates.

Categories and Subject Descriptors: H.3.3 [Information systems]: Information retrieval—*Information Search and Retrieval*

Additional Key Words and Phrases: malware, classification, n-grams

1. INTRODUCTION

The malware industry continues to evolve in complexity, causing increased personal and commercial damage. Traditional methods of malware detection usually involve matching a piece of malware to a signature that has been predefined in the system. However, malware programmers have learned to evade signature detection by polymorphically obfuscating their code. This means, that, for any given piece of malware, the program itself will be recompiled with randomized variable and string names, rendering standard signature detection near useless in identifying an instance of malware. This has given rise to another goal of both research and industry: given a malware file, can we classify it into a common malware family, such that each instance of that family was morphed from the same original malware program? The ability to categorize a malicious program into a known family provides great importance because it allows for a more focused recovery and repair process. Researchers have developed methods for identifying malware by only considering static portions of the malicious code that are unaffected by polymorphism. In particular, these attributes are the method calls of the external libraries used in the code, and the byte sequence of executable. While the research behind these evaluation processes have shown to have good results, much of this research was performed on small sample size of data, usually less than a few hundred or a thousand examples []. The small data sizes is most likely attributed to the difficulty involved with building a data set of malware. First, a program will need to be trapped and identified as malware. From there, researchers can examine the code either dynamically, or statically. The former involves tracing the program's execution in secure, virtual sandbox environment, while the latter involves run-

ning the program through a disassembler, and outputting its source code. This paper and its referenced work focus on static analysis of programs, which can be generalized into a form of text/document classification, of which there is extensive research in the machine learning community. The purpose of this paper will be to survey and examine previous research in the field, and evaluate how these methods scale and perform on a very large data set. Microsoft has provided a sample data set of 10,838 disassembled malware executables, of which each program is given in both its hexadecimal byte form, and its assembly form. Each of these training examples have been labeled as belonging of one of the aforementioned malware families. The results of our experiment showed similar, and at times, improved classification accuracy compared to previous research. Also, our modified system, designed to handle our 400 GB training performed well and showed its ability to scale with the large data set. Given more time, we would have liked to explore how are system handles classifying both programs that do not belong to one of the 9 origin families, as well as those that are not malware.

2. PROBLEM DEFINITION AND METHODS

2.1 Task Definition

Our approach to feature extraction and classification is based on a combination of the methods from the common text classification techniques developed in previous research []. Where our process differed from these methods is our focus on the design of the complete system architecture, in particular, creating a system that was not only able to replicate the successful results of the referenced research, but to do so on a data set of substantially larger magnitude of size. The size of our training set required us to design the feature extraction process in a MapReduce-styled pattern [], but also to only consider machine learning classifiers that were able to scale with our large input. Thus, classifiers such as k-nearest-neighbors and Hidden Markov Models [] were not considered due to their performance on large data-sets and the impracticality of scaling them in regards to our limited computing resources. For both types of feature-sets, we evaluated the classification performance of three classifiers: Naive Bayes, Decision Trees, and Support Vector Machines. Of these classifiers, Decision Trees and Support Vector Machines performed best, and from there we extended our analysis into the boosted forms of these two algorithms.

2.2 Algorithms and Methods

2.2.1 System Architecture. As shown in figure Fig 1, the architecture of the system is rather simple. The main tasks were the preprocessing of the data which involved extracting the N-grams and transform the training set into a format that Weka [Witten and Frank 2005] accepts as input. And then apply several learning methods.

2.2.2 Data Preprocessing. The preprocessing part was a process that required a considerable effort because of the size of the

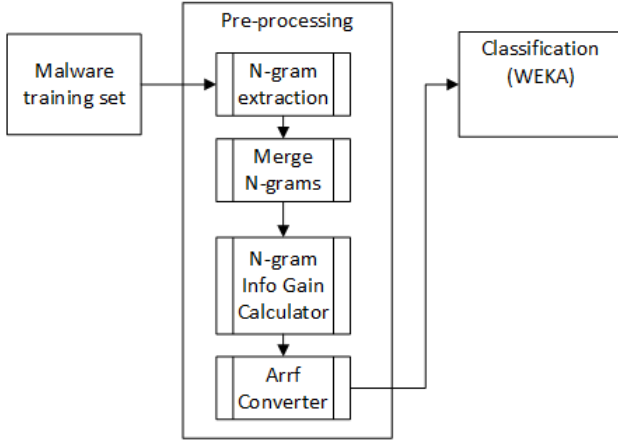


Fig. 1. System architecture.

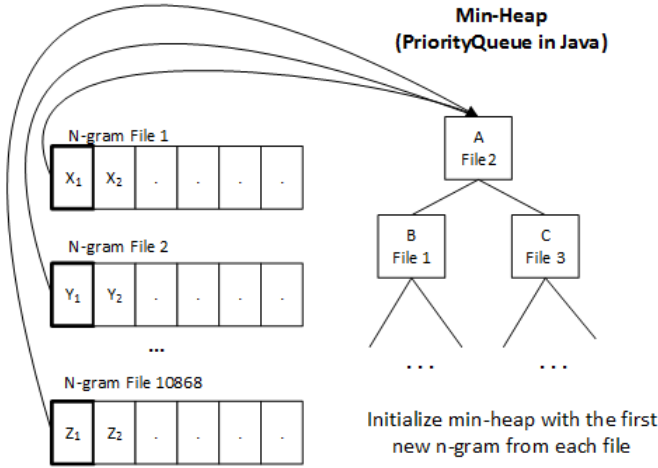


Fig. 2. Initializing PriorityQueue to merge N-grams.

training set, 10,868 files. The first step was to extract the hexadecimal N-grams from the binary files using the kfNgram tool [Fletcher 2012], we used $n=4$.

It was then necessary to merge the resulting sorted N-gram files to effectively calculate the *information gain* (IG) of each N-gram. Because these files were extremely long, we could not use the merge functionality built in the kfNgram tool, and we have to halt the application after running for three days. To optimize this process we merged the files maintaining a min-heap (or *PriorityQueue* in Java) in memory with the first distinct N-gram from each file, as shown in Fig 2. We were also able to keep 10,878 Java scanners in memory to speed up I/O. Then, to merging process would consist in each iteration to perform a `pop()` operation from the *PriorityQueue*, append the element to merged file, and insert the next N-gram from the same file of the element that was popped to the *PriorityQueue*. This process is represented in Fig 3.

Once merging was complete, we obtained a total of N-grams was 255,942,370, therefore we had to reduce them by calculating the *information gain* (IG) of each N-gram and selecting the top 500 (Fig. 5), the same approach used in [Kolter and Maloof 2006]. The *average mutual information* [Yang and Pederson 1997] was used to select the most relevant attributes:

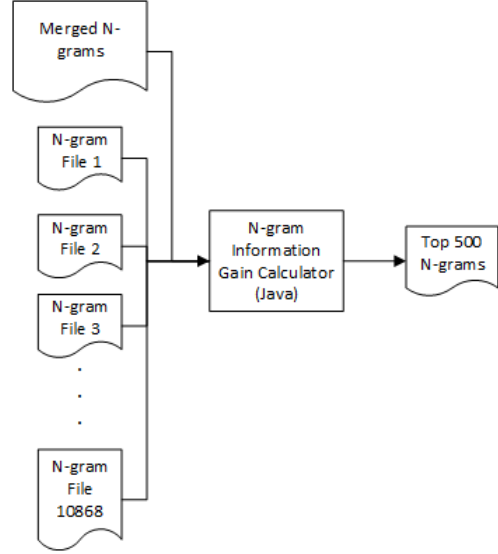


Fig. 4. Process of calculating the information gain of each N-gram.

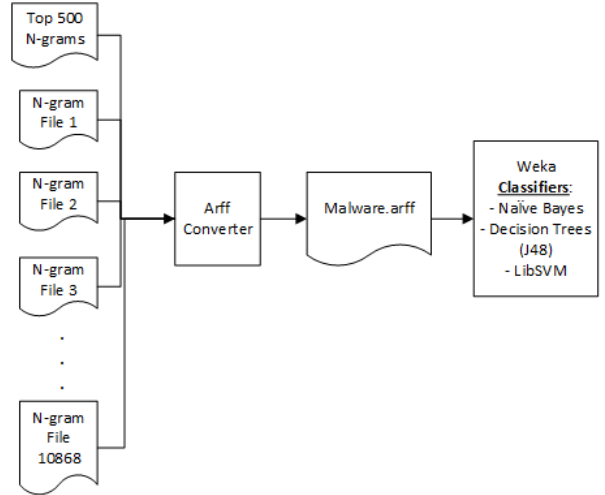


Fig. 5. Transforming training set into .arff format.

$$IG(j) = \sum_{v_j \in \{0,1\}} \sum_{C_i} P(v_j, C_i) \log \frac{P(v_j, C_i)}{P(v_j)P(C_i)} \quad (1)$$

where C_i is the i th class, v_j is the value of the j th attribute, $P(v_j, C_i)$ is the proportion that the j th attribute has the value v_j in the class C_i , $P(v_j)$ is the proportion that the j th n-gram takes the value v_j in the training data, and $P(C_i)$ is the proportion of the training data belonging to the class C_i [Kolter and Maloof 2006].

The final step, as shown in Fig 0??, in the data preprocessing was to transform the training set in .arff format where each example was represented by the presence (or absence) of the top 500 N-grams. This .arff file is one of the formats supported by Weka [Witten and Frank 2005], which facilitated to experiment with different machine learning algorithms.

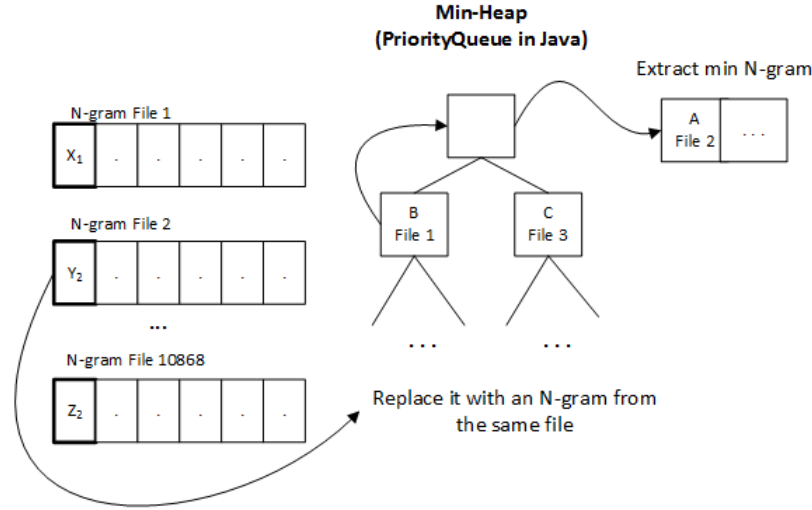


Fig. 3. Process of merging N-grams. The minimum element is extracted and replaced with another N-gram from the same file

2.2.3 Classification algorithms. 1. Naive Bayes The Naive Bayes classifier uses Bayes' Theorem to label examples based on the assumption of conditional independence between features. Given a data set consisting of word counts, the training of this algorithm is very simple, and only requires the computation of the prior probability of each class, $P(C_i)$, and the conditional probability of each word given a class, $P(v_j|C_i)$. For a given instance \mathbf{v} , we aim to classify it into some class, C_i , thus computing $P(C_i|\mathbf{v})$. Using Bayes' Theorem, this can be decomposed into:

$$P(C_i|\mathbf{v}) = \frac{P(C_i) P(\mathbf{v}|C_i)}{P(\mathbf{v})} \quad (2)$$

We can ignore the $P(\mathbf{v})$ term, and estimate the remaining feature probabilities as:

$$P(C_i) = \frac{\text{\# of occurrences of class } i}{\text{\# of total attributes}} \quad (3)$$

$$P(v_j|C_i) = \frac{\text{\# of occurrences of attribute } v_j \text{ with class } C_i}{\text{\# of occurrences of class } i} \quad (4)$$

From here, we can define the classification of training example \mathbf{v} as:

$$\hat{y} = \underset{k}{\operatorname{argmax}} P(C_k) \prod_{i=1}^n p(v_i|C_k) \quad (5)$$

2. Decision Tree Decision trees are a method of classification that use tree-like graphs to model the classification of an example as a path of probabilities from the root node attribute, to one of the leaf (class) attributes. The beauty of decision trees lies in their simplicity and easy interpretation. Likewise, decision trees can be thought of as a "white-box" classification model, because once the tree has been built, the researchers can visualize and analyze each sub-path of an example's classification path. The basic implementation of a decision tree works as follows: for each node of tree, we select the attribute that best splits the our training examples into their respective classes. For our system, we used the J48 decision

tree algorithm in Weka, which is an implementaion of the ID3 decision tree algorithm []. The algorithm is defined as follows: 1. Compute the entropy of each attribute in the data set S 2. Split the set S into subsets using the attribute for which entropy is minumim (or IG is max) 3. Make a decision tree node containing that attribute 4. Recur on subsets of remaining attributes

We define the entropy for a data set S, and its set of attributes V, as:

$$H(S) = - \sum_{v \in V} P(v) \log_2 P(v) \quad (6)$$

Once we obtain the corresponding decision tree, we prune the tree to help minimize over-fitting that may have occurred as a result of tree's greedy construction.

3. SVM Support Vector Machines (SVMs) produced the best classification results of our tested algorithms. The goal of an SVM is to find an optimal hyperplane that separates the training examples by their respective classes, while maximizing the margin between theses classes. The hyperplane is represented by a vector \mathbf{w} and a scalar value b . Thus, the solution of the SVM can be represented by the minimization of:

$$P(\mathbf{w}, b, \xi) = \frac{1}{2} \mathbf{w} \cdot \mathbf{w} + C \sum_{i=1}^n \xi_i \quad (7)$$

such that:

$$\forall_{i=1}^n, \xi_i \geq 0 : y_i(\mathbf{w} \cdot \mathbf{x}_i + b) \geq 1 - \xi_i \quad (8)$$

where ξ_i is the upper bound on the number of training errors and C is the parameter that controls the trade-off between the margin of the hyperplane and the training error. We use the LibSVM [] implementation of this algorithm.

3. EXPERIMENTAL (AND/OR THEORETICAL) EVALUATION

3.1 Methodology

Blah blah

3.2 Results

Blah blah [WebGL 2014].

3.3 Discussion

Blah blah [WebGL 2014].

4. RELATED WORK

Malware detection and classification is a problem being addressed through several angles. In [Christodorescu et al. 2005], the goal is to detect if a program exhibits a specified malicious behavior by determining if a set of templates of sequence of instructions are present in the executable files. This approach requires to have knowledge on semantics of each of the malware families. Although the results are promising, there are several reasons we could not follow this approach, for example, as inferred by the title, it would be necessary to create a set of sequence of instructions for each of the nine families we need to classify the malwares into. This is infeasible due to the length of the course, but also it is outside of the scope of the course. As exhibited in the results, this strategy is resilient to obfuscation and showed improvements when compared to McAfee VirusScan.

Several malware classification algorithms are based on n-grams extracted from the executable files. In [Pekta et al. 2011], instead of byte sequences, the n-grams extracted are formed by machine codes. After obtaining the n-grams from the malwares, a centroid for each family is created by selecting the most frequent n-grams. Then, the strategy to classify a malware into one of the families, is to determine the centroid which the malware is more similar to by counting the number of matching n-grams. When considering this approach, one of the possible limitations analyzed was that selecting the most frequent n-gram could implicate choosing an n-gram irrelevant to the malware family.

We also explored sequential pattern extraction of n-grams. The proposed methodology in [Sornil and Liangboonprakong 2013] outlines a procedure to use the n-grams patterns to classify the malware by family. The kfNgram tool [Fletcher 2012] was used to extract the n-grams from the disassembled files with $n=1$, $n=2$, $n=3$ and $n=4$, obtaining the best results with $n=4$. In [Kolter and Maloof 2006] the accuracy achieved was higher with $n=4$, therefore we skipped this evaluation and use only n-grams with $n=4$. The sequential pattern extraction technique in [Zhong et al. 2012] was used to generate frequently occurred sequences of n-grams to represent the data [Sornil and Liangboonprakong 2013]. Then the patterns significance was calculated using the term frequency-inverse document frequency (TF-IDF) where the term refers to the n-gram pattern and a document to the malware file. Since the number of patterns was too large, the sequential floating forward selection (SFFS) procedure was applied to reduce the number of features, in this case, n-gram sequential patterns. With all the features extracted, three classification algorithms were used, C4.5, multilayer perceptron and support vector machine. The training set was randomly split into two partitions using 80% for training and 20% for testing achieving a 96.64% of accuracy [Sornil and Liangboonprakong 2013]. Because of the duration of the course and the complexity of sequential pattern extraction, we were not able to experiment with this approach.

Following Occam's razor, suggesting that the simplest hypothesis is the best, we applied an approach similar to the one described in [Kolter and Maloof 2006]. The n-grams extracted from the executable files represented boolean features, present (i.e., 1) or absent (i.e., 0). Since the n-grams list was too large, it was necessary to

select the most relevant attributes (i.e., n-grams) by computing the *information gain (IG)* described in [Yang and Pederson 1997] for each, also called *average mutual information*. Through pilot studies, it was determined to use the top 500 n-grams, and then applied classifiers implemented in the Wakaito Environment for Knowledge Acquisition (WEKA) [Witten and Frank 2005]: IBk, Naive Bayes, SVM, and J48 (decision tree), and also *boosted* the last three of these learners [Kolter and Maloof 2006]. The results indicated 98% the highest accuracy using boosted decision trees.

```
// Using ThreeJS , load character and
// hair into mesh1 and mesh2 respectively
```

```
var hapgl = HapGL.init({
  ttsUrl: 'http://localhost:88/',
  character: mesh1,
  hair: mesh2
});
```

Generating emotions in HapGL was done also in the same manner as in HapFACS. Emotion FACS (EmFACS) introduces a mapping of subsets of action units to universal emotion identified by Ekman [P. Ekman and Freisen 1983] namely fear, anger, surprise, disgust, sadness, and happiness. The emotions implemented in HapGL were:

- Happiness, combining AU6, AU12, and AU25
- Sadness, combining AU1, AU4, and AU15
- Surprise, combining AU1, AU2, AU26, and AU5
- Anger, combining AU4, AU5, AU7, AU23, and AU24
- Disgust, combining AU9, AU15, and AU16

`getVoices(function getVoicesCallback)` returns a JSON object with an array of voices and will immediately call the `getVoicesCallback` function with the result. Since the HapGLService uses Microsoft Speech API (SAPI), the voices are SAPI-compatible installed on the web-server. More sophisticated voices can be purchased and installed separately. The following is an example of the result of calling `getVoices`:

```
hapgl.getVoices(function(output) {...});
```

```
// Example of voices returned
{
  voices : [{
    id : "MS-Anna-1033-20-DSK",
    age : "Adult",
    name : "Microsoft Anna",
    gender : "Female",
    culture : "en-US"
  }]
}
```

`speak` and `speakssml` are similar, the only difference is that `speak` will only accept a plain string, whereas `speakssml` can accept a string in SSML format as input [SSML 2014]. The voice parameter corresponds to the *name* attribute of the voices returned by `getVoices`, if no voice is passed in then the HapGLService will synthesize using the default voice in the TTS Server. The *ssml* string argument for the `speakssml()` function should be a well-formed SSML Version 1.0 [SSML 2014]. SSML allows to manipulate the voices by modifying parameters such as: *volume*, *rate*, and *pitch* in the `<prosody>` elements. Several `<prosody>` elements can be combined to produce the desired pronunciation of sentences.

The output of `speak(...)` and `speakssml(...)` contains the necessary information to render the sequence of viseme transitions synchronized with the audio stream to produce a realistic talking virtual human. The following example shows the output when speaking the word “Hello”.

```
hapgl.speak('Hello');

// The output of speaking "Hello"
{
  audioFormat: 'data:audio/wav;base64',
  audioStream: '...',
  visemes: [{
    number: 0, // silence
    audioPosition: 0.0,
    duration: 3.0,
    emphasis: 0
  }]
}
```

The sequence of visemes is already sorted in the correct order to be animated. All this information is sufficient for the lip-synchronization algorithm to render each viseme at the correct time. The viseme transitions are done smoothly, otherwise, just displaying the viseme in its maximum intensity would create an undesired illusion. Each viseme transition takes a pair of visemes V_0 and V_1 , where V_0 is the starting viseme and V_1 is the ending viseme. To do the transformation $V_0 \rightarrow V_1$ we consider the duration d_0 of V_0 . In d_0 time, V_0 “fades out” and V_1 “fades in”. By “fade out” we mean interpolating from V_0 by setting the value of the corresponding morph gradually from 1 to 0 in d_0 time. Conversely, “fade in” means interpolating to V_1 by setting the value from 0 to 1. Each viseme maps to a corresponding phoneme, we use the mapping provided by the Microsoft Speech API as seen in Table 0??.

Table I. Viseme to phonemes mapping in Microsoft Speech API

Viseme	Phoneme(s)	Viseme	Phoneme(s)
0	silence	11	ay
1	ae, ax, ah	12	h
2	aa	13	r
3	ao	14	l
4	ey, eh, uh	15	s, z
5	er	16	sh, ch, jh, zh
6	y, iy, ih, ix	17	th, dh
7	w, uw	18	f, v
8	ow	19	d, t, n
9	aw	20	k, g, ng
10	oy	21	p, b, m

Since not all the phonemes have its corresponding Haptex morph register, we choose the most similar morph. We used the following viseme to morph mapping in HapGL:



```
var visemeMorphMapping = {
  '0': {name: 'neutral'}, '11': {name: 'aa'},
  '1': {name: 'aa'}, '12': {name: 'ih'},
  '2': {name: 'aa'}, '13': {name: 'n'},
  '3': {name: 'aa'}, '14': {name: 'n'},
  '4': {name: 'ey'}, '15': {name: 's'},
  '5': {name: 'er'}, '16': {name: 'ch'},
  '6': {name: 'ih'}, '17': {name: 'th'},
}
```

```
'7': {name: 'uw'}, '18': {name: 'f'},
'8': {name: 'ow'}, '19': {name: 'd'},
'9': {name: 'aa'}, '20': {name: 'g'},
'10': {name: 'ow'}, '21': {name: 'm'}
};
```

Table II. AUs with recognition rate of less than 100%. Taken from HapFACS [Amini and Lisetti 2013].

AU	Recognition Rate	AU	Recognition Rate
10	66.67%	16	33.33%
11	66.67%	20	66.67%
12	66.67%	23	33.33%
13	66.67%	25	33.33%
14	66.67%	28	33.33%

Table III. AUs comparison between HapGL and HapFACS.

AU	HapGL	HapFACS
AU1		

5. FUTURE WORK

Malware classification is a topic that is always evolving because viruses’ authors are constantly developing techniques to avoid been detected, for example by obfuscating the code or by designing polymorphic behaviours. The proposed approach is agnostic of these techniques, therefore, we assume intuitively that a set of the extracted N-grams are product of this ingenious methods. Mutation engines are capable of generating millions of variations of the same virus, therefore, to overcome this problem, it would be necessary to have knowledge of the malware behaviors to develop heuristics or detect specific sequence of instructions to find in the malicious files.

For time reasons, we could not research on the possibilities of removing the irrelevant computations in the malware files created to evade anti-viruses. This would help, if using sequential N-gram patterns extraction, to detect patterns that are truly correlated to the malware family. These patterns could, somewhat, describe the common semantics present in each class of malwares.

6. CONCLUSION

Nevertheless, HapGL is still far from being used in production systems as it lacks of other necessary functionalities which could be part of future works. To name some, and not intended to be a comprehensive list, we suggest the following:

—*Detailed Evaluation*, due to time constraints, a thorough evaluation could not be performed. We suggest to measure the *believability* of the system by surveying a random sample of users, preferably greater than 20. Although this is a subjective measure, a user study is still a good indication about the quality of the system.

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