MDFRCNN: Malware Detection using Faster Region Proposals Convolution Neural Network

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Abstract

Technological advancement of smart devices has opened up a new trend: Internet of Everything (IoE), where all devices are connected to the web. Large scale networking benefits the community by increasing connectivity and giving control of physical devices. On the other hand, there exists an increased '*Threat*' of an '*Attack*'. Attackers are targeting these devices, as it may provide an easier '*backdoor entry to the users' network*'. **MALicious softWARE** (MalWare) is a major threat to user security. Fast and accurate detection of malware attacks are the sine qua non of IoE, where large scale networking is involved. The paper proposes use of a visualization technique where the disassembled malware code is converted into gray images, as well as use of Image Similarity based Statistical Parameters (ISSP) such as Normalized Cross correlation (NCC), Average difference (AD), Maximum difference (MaxD), Singular Structural Similarity Index Module (SSIM), Laplacian Mean Square Error (LMSE), MSE and PSNR. A vector consisting of gray image with statistical parameters is trained using a Faster Region proposals Convolution Neural Network (F-RCNN) classifier. The experiment results are promising as the proposed method includes ISSP with F-RCNN training. Overall training time of learning the semantics of higher-level malicious behaviors is less. Identification of malware (testing phase) is also performed in less time. The fusion of image and statistical parameter enhances system performance with greater accuracy. The benchmark database from Microsoft Malware Classification challenge has been used to analyze system performance, which is available on the Kaggle website. An overall average classification accuracy of 98.12% is achieved by the proposed method.

Keywords

Malware, CNN, Faster RCNN (F-RCNN), Classification, Malware Static, Dynamic Analysis.

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I. Introduction

MALWARE is a major menace to Internet security today. There are various distinctive sorts of cyber assaults in the current day digital world. A few of these are very renowned like, phishing sites, botnets, denial of service (DoS), malware assaults and so on. Lately malware attacks are being increasingly propagated because of the huge development of internet and web-based products like IoE. A report from Symantec in 2019 announced a new malware technique i.e., FormJacking (FJ). Cyber attackers inject malware code in web page forms (specifically, payment page forms handled by Payment Processors) to steal sensitive information about the payment cards, names, addresses, phone numbers, etc. These types of attacks are called 'Supply Chain Attacks' (SCA), and are written in JAVA. According to the Symantec report, an average of approximately 4800 sites have been compromised by the FJ code and there is a 78% hike in SCA. '***Jacking***' is popular amongst cyber attackers. There are varieties of jackings viz. cyber, crypto, form, page, Brand, I, Wi, page, thread, mouse, paste, Data, side, Bio, Juice, etc.

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Big data Analytics can be defined as the process of lookup, processing, storing enormous data so as to separate important information out of it. With growth in big data analytics, security and protection concerns are additionally amplified.

Big data servers are effectively open to a more extensive population base; consequently, they increase the possibility of malware attacks. To shield users from the hazards of malware, security companies offer a diverse set of antivirus tools. Usually, these tools follow signature-based methodologies. Signature based recognition is inclined to a few difficulties. For example, there has to be a database with patterns of known sets of threats. Also, frequent refresh is required for these signatures in the repositories which requires the intervention of experienced staff in the signature creation process. Thus, antivirus organizations are not able to define, analyze and develop effective signature patterns.

Due to the escalating growth of online transactions, the level and number of cyber-crimes are increasing. In the present situation, where malware assault is massively expanding, it is very troublesome for pattern matching scanners to recognize new variations of existing malicious programs. Therefore, there is a high demand to formulate other strategies to recognize malware.

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This requirement asks for a Malware Detection System (MDS) which can detect malware accurately and act fast enough to quarantine the same. MDS is traditionally feature vector based in which crucial characteristics of the malware are extracted and used to identify the same in real time systems. Behavioral based malware detection can broadly be divided into three categories namely, static, dynamic and hybrid. According to Gandotra [1] in the Static Analysis (SA), malware software is analyzed without being executed. SA typically extracts features like operational code (OPCODE) frequency distribution, control flow graph, syntactic library call, byte-sequence n-grams, string signature etc., after unpacking executable in advance. SA protects the Operating System (OS) from malicious damage but it is vulnerable to code obfuscation techniques. In Dynamic Analysis (DA) malware is executed by making use of a controlled environment viz. sandbox, emulator, simulator, virtual machine and then it is analyzed by monitoring tools like Capture Bat, Process monitor (.pmon), poison IVY, etc. Sandbox generates a detailed and extensive report which requires human interpretation and analysis. The analysis process can be automated to a greater extent but with an addition of extensive computational complexities. Thus, it is time consuming [3]. However, both static and dynamic analyses have some limitations and it is difficult to use either static or dynamic analysis for malware detection. The next approach is the combination of both which is called the hybrid approach. It analyzes the signature of malware in the first phase and combines it with behavioral specifications for a complete analysis.

Malware database is huge. Such systems are largely dependent on Machine Learning (ML) algorithms. To figure out malware patterns in the code successfully, effective solution is - Visual Analytic Technique (VAT), where malware patterns are presented as an image. VAT provides summarized pictures of attacks. These images can be trained using ML for analyzing malware patterns. Malware Detection Developer (MDD) focuses on image patterns due to two reasons. The first reason is, even though the malware developers work in the direction of hiding the code, at the same time, while coming up with variants of the malware, they use the same old code. Therefore, the deviation δ between two images of a single malware family is very small. MDD can take advantage of this mind set and use the similarity mining machine learning method to identify the family of malware. The second reason is an image classification technique which is more mature and faster [4] [5].

This paper presents literature survey in Section III and the Key extract is malware can be packed using different packing methods and with different resolutions. Therefore, for VTA (image) based analysis, research options are still open for providing an improved solution to classify malware. Keeping this as a base, this paper proposes extracting ISSP features for all the malware families taking into consideration all the variants in the binary file. Finally, ISSP features and malware images are trained using fast and robust F-RCNN classifier.

The rest of the paper is organized as follows: related work is presented in Section II. The proposed work model is presented in Section IV. Feature vector formation using perceptual features and the mathematical model of the F-RCNN classifier is described in sections V and VI. Computation of the statistical parameters is described in Section VII. Description of the database is given in Section VIII. Experimental setup and related results are presented in Section IX. Section X discusses the performance analysis of the proposed method. Section XI concludes the paper.

II. Related Work

This section focuses on varieties of features and classification techniques explored by researchers. Related work can be bifurcated in two categories i.e. the work based on image representation and methods other than image representation. As paper proposes image representation of malware, work related to this method is explained first.

A. Image Based Methods

Image is a 2D representation. Key points of 2D representations are as follows

1. Data dimension does not affect processing once similarity space is formed.
2. Equally important clusters are formed.
3. Similar clusters are displayed adjacent for clear visualization [27] [28][29].

Malware analysis using Visualization Technique (VT) was proposed by Yoo [16]. He classified images using Self-Organizing Map. VT is mostly used for document and image analysis where files are huge and data is massive. Therefore, it has wide applications in computer security, as malware attacks are in the thousands at a time. Shiravi [35] and N. Diakopoulos [34] identified Brute Force attack on Secure Shell (SSH) by representing details of Internet Protocol (IP) address, UserIDs and various anomalies using varieties of colors. VT was used to display large network packets and helped security analysts to find similarities by checking minute details using a zoom option. S.Foresti [39] and M. Wagner [40] demonstrated usage of VT to represent information like time ('when'), IP address ('Where'), Data ('what') and estimated distances to other hosts.

Quist [17] proposed the use of an Ether hypervisor framework to track and visually represent execution of malware programs. The dynamic analysis framework was named as VERA. Trinius [18] introduced a new concept i.e., Malware Instruction SeT (MIST) for monitoring malwares. They used a CW Sandbox to collect information regarding API calls and performed action. They visually represented distance matrices of features for five malwares.

To improve malware detection, different sections of the binary executable are now represented as gray scale images. These images provide detailed structure of malware, to the extent that they show even small changes in the code, without altering the remaining code structure. Gray scale texture helps in identifying similar patterns of the binary code [41]. L. Nataraj [42] proposed GIST descriptors to classify obfuscated malware.

The Function Length Frequency (FLF) algorithm proposed by Tian [9] was used to detect Trojan after surveying varieties of techniques. Zolkipli [10] suggested the use of Variable Length Instruction Sequences (VLIS) with machine learning algorithms. Shankarapani [11] proposed two models, namely, Malware Examiner using Disassembled Code (MEDiC) and Static Analyzer for Vicious Executables (SAVE). Results were promising as the model had better detection even if malware is obfuscated. Nataraj [19] presented malware binaries as gray scale images. Using a KNN classifier they achieved good average accuracy along with increased speed of malware detection. On a similar line Kancherla [20] used byte plot (image of executables) and achieved 95% accuracy using the SVM classifier.

Kong and Yan [12] used hex dump n-gram, disassembly code, PE header and selected features using the L1 regularized method. They applied different classifiers viz. NB, SVM, K means Neural Network (KNN), decision tree and analyzed the performance of all the features. They concluded that the PE header feature is more prominent in malware detection. Santos et al., 2013b [13] tried to figure out the relevance of each OPCODE and calculated the frequency of OPCODE sequences. They verified the performance using the same four classifiers used by previous researchers. They stated empirically that the model can detect unknown malware as well.

Similarity is calculated based on the distance between each and every pair of points. Minimum distance represents maximum similarity [30] [31]. Projection and semantic orientation are 2D VTs, normally used to check similarity patterns [26] [32] [33].Frequency domain-based feature extraction i.e., Wavelet transforms, was proposed by Gu [14]. Li and Li [15] proposed static features viz. API, classes, functions and packages detecting malware for android APKs. They used different layers of 'Characteristic Tree' containing information of API calls. The method can classify unknown APKs. Han [21] converted a Windows PE binary file into a gray scale image. After that, using an Entropy Graph Generator (EGG), they calculated the entropy of each and every line of an image. Malware detections were done based on similarities of the original binary file.

Arefkhaniet [22] introduced a Local Sensitive Hashing technique specific to image processing, to classify similar input (malware) with high probability. Wu [23] converted disassembled binary executable into opcode sequences into an image. They used PCA to reduce the dimensionality and KNN classifier. Rezaei [24] proposed a similarity measurement algorithm for malware detection which compares the opcode strings of malicious files to improve the detection rate and speed. Venkatraman [36], Zhang [37] and Wylie Shanks [38] explored usage of VT for analyzing malware attack chronology and demonstrated successful system connections with the help of colors.

B. Other Methods

Santos et al., 2013b [13] introduced an OPCODE Executable trace Malware (OPEM) framework. It is a hybrid of statistically obtained frequency of occurrence of OPCODE and dynamically obtained executable traces. Performance was evaluated using Baysine, Decision Tree, SVM and KNN classifiers. Kolosnjaji [25] proposed feature fusion of headers of PE files and convolution of n-grams of an instruction. They achieved a 93% recall rate and accuracy using SVM and ANN (Feed forward) classifier. Ripper Cohen [6] proposed the Repeated Incremental Pruning to Produce Error Reduction (RIPPERk) algorithm that supersedes the learning algorithm, Incremental Reduced Error Pruning (IREP). In RIPPERk, k represents the number of multiple optimization iterations. Schultz [7] made use of three static features (byte sequence, strings and Portable Executable (PE)) and for the first-time used the data mining concept. Kolter [8] proposed a combination of n-gram (instead of non-overlapping byte sequence) features with classifiers viz. Naive-Bayes (NB), Support Vector Machine (SVM), Decision Tree and their boosted versions. They found that the boosted decision tree provides better results.

The following section illustrates an extensive and organized literature summary of innovative techniques proposed by researchers and challenges from state of the art.

III. Literature Survey – Formulating Problem Statement

A research problem should represent the core subject matter and it should be a discovery of new knowledge. This objective not only asks for rigorous literature survey, but also demands interpretation of the surveyed information to achieve a proper research path. Graphical presentation is given by the author which makes it more suitable to extract the required information.

Fig. 1 provides information about three basic analysis techniques like SA, DA and hybrid, explored by researchers. The SA technique is still preferred by most of the researchers [50]. The hybrid approach is not still popular amongst researchers.

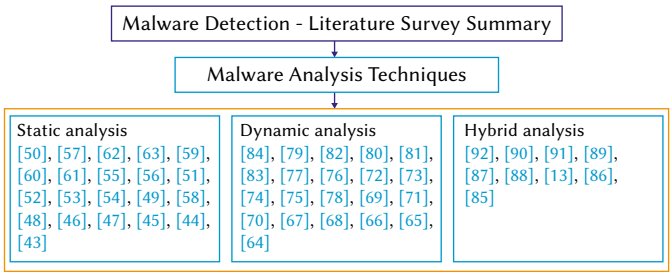


Fig. 1. Survey depicts the type of analysis technique explored by researchers.

Feature extractions and classification techniques are the two pillars of MDS. Fig. 2 is devoted to different feature vectors used by researchers. API calls, system calls, n-gram and OPCODE are still features that are mostly used in MDS. Researchers typically have two paths: the first one is to optimize the feature vector and get a significant limited feature set, and the second one is the selection of a prominent limited set of features manually. Work implemented by researchers in either way is unique itself and uses varieties of byte and hex related features.

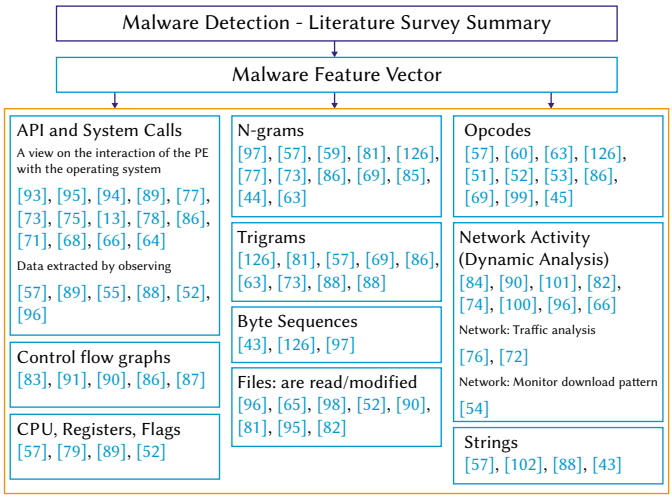


Fig. 2. Survey depicts varieties of feature used by researchers.

A feature vector extracted from malware code should be trained with the help of neural networks. After training, system performance is tested by applying real time malware data. Researchers developed different techniques to extract the feature set. A breakthrough from the survey reveals that researchers using available crawlers, filters etc., end up with a *plethora of* feature vector space which may be redundant. Many times, some features may worsen the accuracy of the system. Thus, feature selection to improve system performance is mandatory but the same should be done without compromising accuracy.

The role of a classifier is important as it defines accuracy and precision. Fig. 3 presents three basic learning process categories i.e., supervised, unsupervised and semi-supervised. Supervised learning is the first choice of researchers where malware annotations are given for training the network.

Fig. 4 presents the wide usage of deep learning techniques like CNN, Deep Neural Network (DNN), Recurrent Neural network (RNN), auto encoders etc. in malware detection. These techniques are well established and provide high performance. CNN and its extensions are preferred for image-based analysis therefore, it is mostly used by researchers. CNN variants viz. Region based CNN (R-CNN), Fast R-CNN, Faster R-CNN are mostly used in image analysis for detecting objects [182].

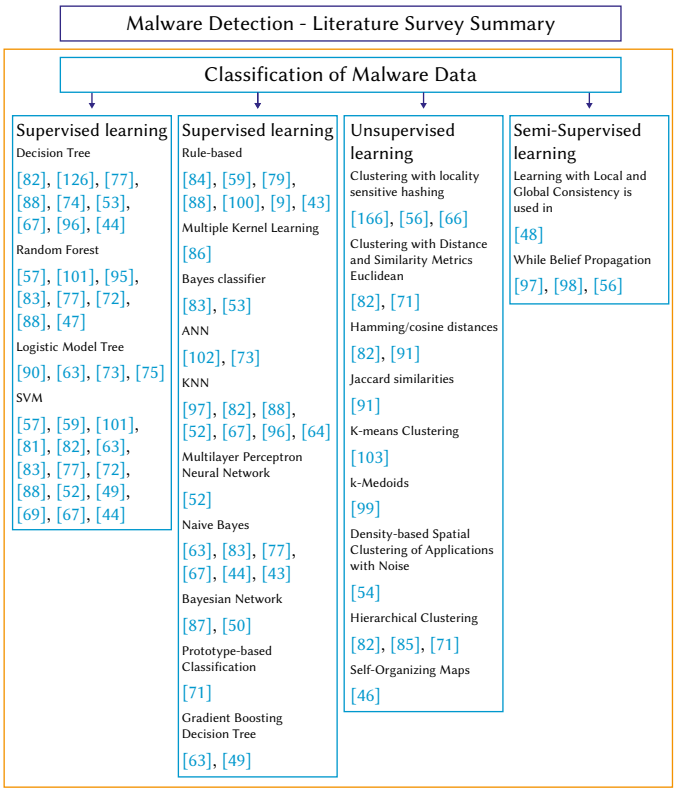


Fig.3. Survey depicts different classifiers explored by researchers.

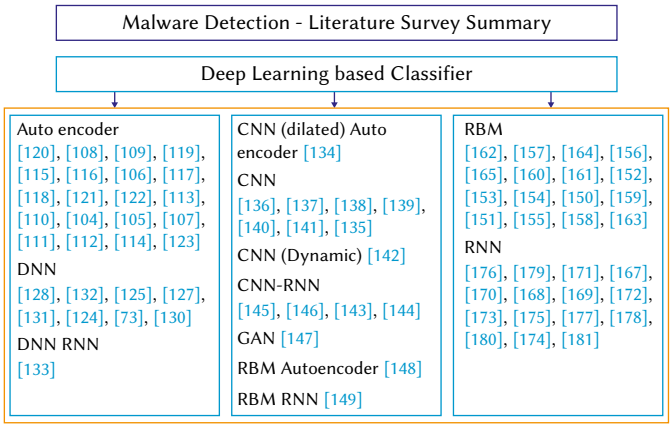


Fig. 4. Literature survey based on Deep Learning Classifier.

These techniques are specific to image analysis and provide less training and testing times, which is the need of a malware detection technique, as it has to run in real time and detect malware as fast as possible. This motivates the author to select FR-CNN. It is a technique with a significantly low computational cost and the same has not been investigated for malware detection. This technique achieves more precision and a faster response.

IV. Proposed Model of MDS

The paper proposes MDS architecture comprising of deep learning network to accurately detect and classify malware families using an image-based technique which is described in Fig. 1. The Benchmark database from Kaggle is used to evaluate the performance of a system. The features vector of malware families is presented as gray scale images. These images will be trained using deep learning and facilitate adaptive learning in real time environment to achieve high accuracy.

The Main contribution of this research work is as follows:

1. *Consideration of prominent static features e.g., string signature, byte-sequence, N-grams, OPCODE*
2. *Represent feature vector as a gray scale image reflecting the malware family behavior*
3. *Arrange feature vector sub parts as varieties of 'Regions' of an image*
4. *NOTE: 'Region' is a generic term. Rectangular regions are considered in this paper, as it is common.*
5. *Minimize the training set*
6. *Compute statistical parameters of the image generated in point-2*
7. *Apply the F-RCNN classifier to a matrix having statistical parameters as well as an image.*

To the best of our knowledge, the above combination i.e., a matrix of static features and an image with F-RCNN classifier has not been evaluated by researchers.

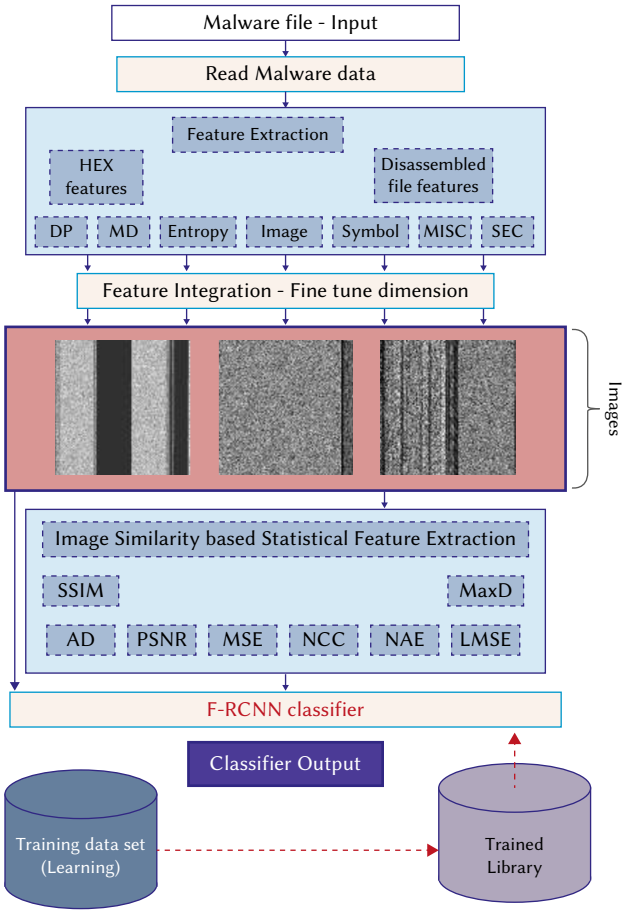


Fig. 5. System Architecture of the proposed MDF-RCNN.

Fig. 5 depicts the system architecture of the proposed MDS. Feature extraction and classification of the malware input file are two major modules of MDS. Each one is described as follows.

V. Feature Extraction Module

A. Features Based on HEX and Disassembled Files

There are basically two major types of features extracted for MDS. These are HEX dump-based features (n-gram, MD1, entropy, image 1(haralick) and Image 2 (lbpfeatures)) and disassembled file features (meta-data, SYM, OPC, MISC, DP and SEC.)

1. Hex Based Features

a) N-gram

An N-gram is a contiguous sequence of n items from a given sequence. The technique is used intensively for characterizing sequences. The sequences may be from a speech or text. Malware samples may be viewed as sequences of HEX value. An N-gram analysis of these HEX values may provide valuable information. The malware sample consists of special symbols viz.??, indicating that the data of that location is not initialized. It also contains byte sequence whose value may range from 0 to 255.

b) Entropy

Entropy (ENT) is basically a measure of randomness or uncertainty or maybe the O amount of disorder. Obfuscation presence can be detected by entropy [183] [184]. In MDS, entropy is calculated based on byte representation. It measures the disarray of the distribution of the bytes in malware code by setting *'order'* and *'randomness factor'*. A sliding window is applied on the malware code and entropy is calculated for each windowed segment. It is represented by:

$$E = e_i, Number\ of\ windowed\ segment\ i = 1, \ldots\ldots, N \quad (1)$$

The Shannon's formula,

$$e_i = -\sum_{k=1}^{m} f(k) * \log_2 f(k) \quad (2)$$

$f(k) =$ *frequency of byte k with window segment.*
$m =$ *number of distinct bytes in the window segment.*

2. Features Extracted From Disassembled Files

Malware executables must first be disassembled to extract features. The PE format is used by Windows OS (WOS). It's basically a data structure encapsulating important information which will be utilized by the WOS loader to manage the wrapped executable code shown in Fig. 6. The PE file contains *Headers* viz. DOS header, Section table, optional header, PE header, and *Sections* viz. code, imports, data. The Dynamic linker uses this information to map the file into memory. The PE information is important as its basic structure manages memory protection based on the code or data region.

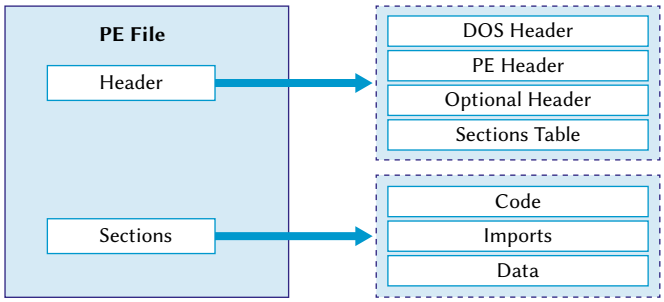


Fig. 6. PE File Structure.

a) Section (SEC)

The '*sections*' consist of code, data and import sections. Further classification includes .data, .idata, .edata, .rdata, .text, .bss, .rsrc, .relocand, .tls. A malware code uses packing techniques where it modifies default sections and may create new sections, to evade Metadata (MD) shown in Fig. 6. An MD program can generate a feature vector by detecting different characteristics of SEC.

b) Metadata

After disassembling, two features viz. the number of lines in the file and file size, are computed and included within the Metadata category (MD2).

c) Symbol:

In malware sample code a set of symbols like [, -, +,], @, ?etc. may be present. Actually, these may correspond to indirect calls or Dynamic Library Loading (DLL), in malware code. In an indirect call, the address of the subroutine is loaded from memory or register. According to [188], the function call depends upon the architecture as well as the optimal decision of a compiler; therefore, such indirect calls may reveal information about data obfuscation. DLL is loaded during runtime by the executable code and executes library functions based on their address. Static analyzers cannot capture such run time events. Therefore, these garbled characters are used specifically by malware developers to evade MD.

d) Operation Code (OPCODE)

OPCODE or mnemonic is a digit and denotes assembly code. The micro-processor executes the OPCODE; therefore, it plays a very important role as it describes the behavioral characteristics of malware as shown in Fig. 7. Machines are x86 based. The instruction set list is complex and large, therefore [189], selected 93 OPCODEs based on frequent use in the malicious application and its commonness. The OPCODE frequency is calculated from the malware code. According to [190], use of Instruction Replacement Technique (IRT) may evade detection. Santos [53] used only OPCODE based features to generate the feature vector and detected malware just by one single class with reasonable amount of accuracy. Thus, it proves that OPCODE based features can contribute more for MD. Researchers also suggested an OPCODE, n-gram based method for MD. The detection is based on the OPCODE frequency feature, calculated by Term Frequency–Inverse Document Frequency (TF-IDF) statistical technique. The OPCODE sequence given vector was used to train the SVM classifier.

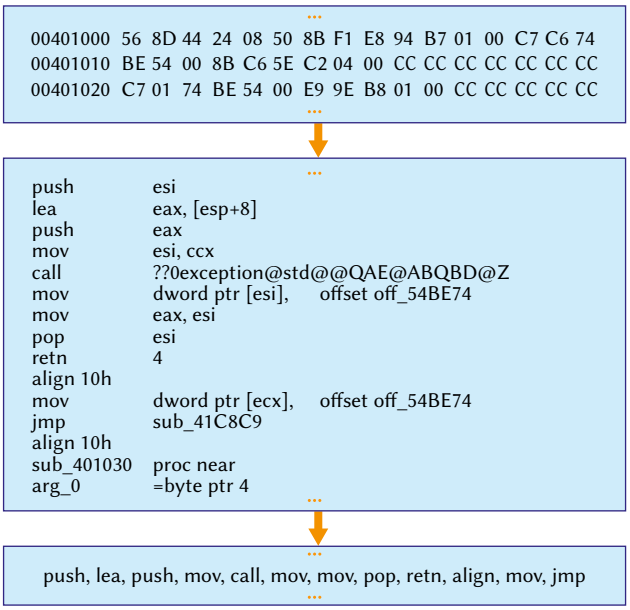


Fig. 7. Disassembly File Structure.

e) Register (REG)

The microprocessor has an internal register set which may be used for a specific task. According to [191], in some situations, registers are renamed to make the MD process more complicated and confusing. This asks for keeping track of REG used and frequency of usage of those registers. This feature is useful and helps in detecting a family of malware.

f) Data Define (DP)

Few malware programs use a packing technique and therefore do not use API calls. Instead they contain a few OPCODEs. Typically, they use data related assembler directives like Define Byte (db), Define Word (dw) and Define Double Word (dd). This feature is key for classifying varieties of malware families.

g) Miscellaneous (MISC)

This feature should be selected manually by identifying keywords from the disassembled code. The Interactive Disassembler (**IDA**) tool may be used for the same. Features extracted will be like the number of imported DLLs, identifying strings viz. **hkey_local_machine**(it specifies access to specific paths of the Windows registry), number of blocks in the PE etc. Thus, it depends upon the experience of the MD software developer engineer.

After extracting these features gray scale image is prepared with the help of feature coefficients. Refer Fig. 8 for the same. Typically, these images of a single family should show similarity as the changes in the malware code is not drastic. Consider this point as a base author motivated to compute image similarity based statistical parameters. The next section describes the same.

B. Features - Image Similarity Based Statistical Parameters

This feature set focuses on similarity between two images. A similarity parameter matrix will be computed based on malware images from the '*x*' family compared with itself as well as the remaining families. Reference image (R_I) and Input image (I_I) are two input images. Suppose R_I is from the '*x*' family then I_I will be the remaining images from the '*x*' family and images from the other families. R_I will be constant throughout the process of computing the similarity parameters. As the number of images per family are in the thousands their mean value will be calculated.

The NCC method is used for template matching which is a process used for finding incidences of a pattern or object within an image. Eq. (1), is used to calculate NCC.

$$NCC(R_I, I_I) = C_{R_I I_I}(\widehat{R_I}, \widehat{I_I}) = \sum_{[m,n]\in R} \widehat{R_I}(m,n)\widehat{I_I}(m,n) \quad (3)$$
$$Where,\ \widehat{R_I} = \frac{R_I - \overline{R_I}}{\sqrt{\sum(R_I - \overline{R_I})^2}},\ \widehat{I_I} = \frac{(I_I - \overline{I_I})}{\sqrt{\sum(I_I - \overline{I_I})^2}}$$

AD provides the average of change concerning the input image and the reference image. AD can be expressed as follows:

$$AD(R_I, I_I) = \frac{1}{mn}\sum_{m=1}^{M}\sum_{n=1}^{N}[R_I(m,n) - I_I(m.n)] \quad (4)$$

MaxD provides the maximum of the error signal (i.e., the difference between the processed and reference image). MD is defined as follows:

$$MaxD(R_I, I_I) = \max\{[R_I(m,n) - I_I(m.n)]\} \quad (5)$$

SSIM is based on three factors i.e., luminance, contrast, and structure to better suit the workings of the human visual system. It is a perceptual metric that quantifies image quality degradation. This parameter is selected as the malware developer makes changes in the old code and comes up with the modified code. The modified code can be thought of as the '*Noise*' element in an image. SSIM is defined as follows:

$$SSIM(R_I, I_I) = \left[l(R_I, I_I)^{\alpha} .\ c(R_I, I_I)^{\beta} .\ s(R_I, I_I)^{\gamma}\right] \quad (6)$$

where l = luminance, c = contrast, s = structure

The Laplacian error map shows spatial error distribution across an image. The overall image quality is given by LMSE as follows:

$$LMSE(R_I, I_I) = \frac{\sum_{m=1}^{M}\sum_{n=1}^{N}[L(R_I(m,n)) - L(I_I(m.n))]^2}{\sum_{m=1}^{M}\sum_{n=1}^{N}[L(R_I(m,n))]^2} \quad (7)$$

where L((m,n)) is the Laplacian operator

NAE measures the numerical variance between the R_I and I_I. Moreover, the results that are near to zero means that the image has a high similarity to the original one and the results near the value one indicate that the image has a very poor quality. NAE is calculated as follows:

$$NAE(R_I, I_I) = \frac{\sum_{m=1}^{M}\sum_{n=1}^{N}|R_I(m,n) - I_I(m.n)|}{\sum_{m=1}^{M}\sum_{n=1}^{N}[R_I(m,n)]} \quad (8)$$

MSE and PSNR are used to compare the quality of the image compression. MSE represents the cumulative squared error between the R_I and I_I, whereas the PSNR represents a measure of the peak error. The lower the value of the MSE, the lower the error.

$$MSE(R_I, I_I) = \frac{1}{mn}\sum_{m=1}^{M}\sum_{n=1}^{N}[L(R_I(m,n)) - L(I_I(m.n))]^2$$
$$PSNR = 10 * \log_{10}\frac{255^2}{MSE} \quad (9)$$

After computing ISSP one more feature vector is produced which will be used to train classifier.

VI. Classifier – F-RCNN

This section describes the reason for selecting the classifier i.e., F-RCNN. In computer vision (CV) object or region detection is a major task. Ross [182] proposed a selective search method to extract *N* number of limited regions from an image. These regions are referred to as *Region Proposals*. Associated training network is referred as *Region Proposal Network* (RPN). The algorithm overrides the problem of selecting a huge number of regions. Region based CNN (R-CNN) is thus a fusion of the *Region Proposals* algorithm with CNN. As the first step, this algorithm selects some proposed regions from the image, puts Bounding Boxes (BB) and labels their categories. The Deep learning algorithm (CNN) extracts varieties of features using forward computation from these proposed regions and then trains the network to classify the categories and BB. Following section describes methodology to represent feature coefficients as an image.

A. Image Representation

Malware samples are represented as an image, where each byte of the malware code corresponds to one pixel of gray scale image [185]. The author proposes use of all the features extracted viz. n-gram, MD1, MD2 etc., to construct an image as shown in Fig. 8. The image is formed in such a way that there are ***'regions'*** of feature vectors. ***Each feature vector (N-gram, MD1, entropy, MD2 etc.) may be viewed as a region of an image. Thus, fundamentally the R-CNN algorithm is more suitable for MDS. R-CNN*** will be more effective and efficient for classifying malware.

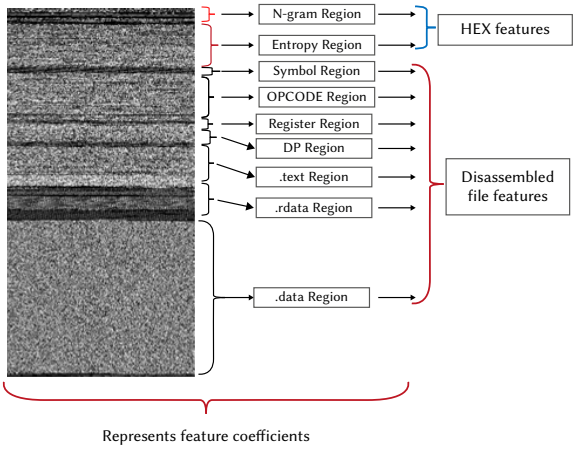


Fig. 8. Gray scale image of malicious code with feature coefficient Regions.

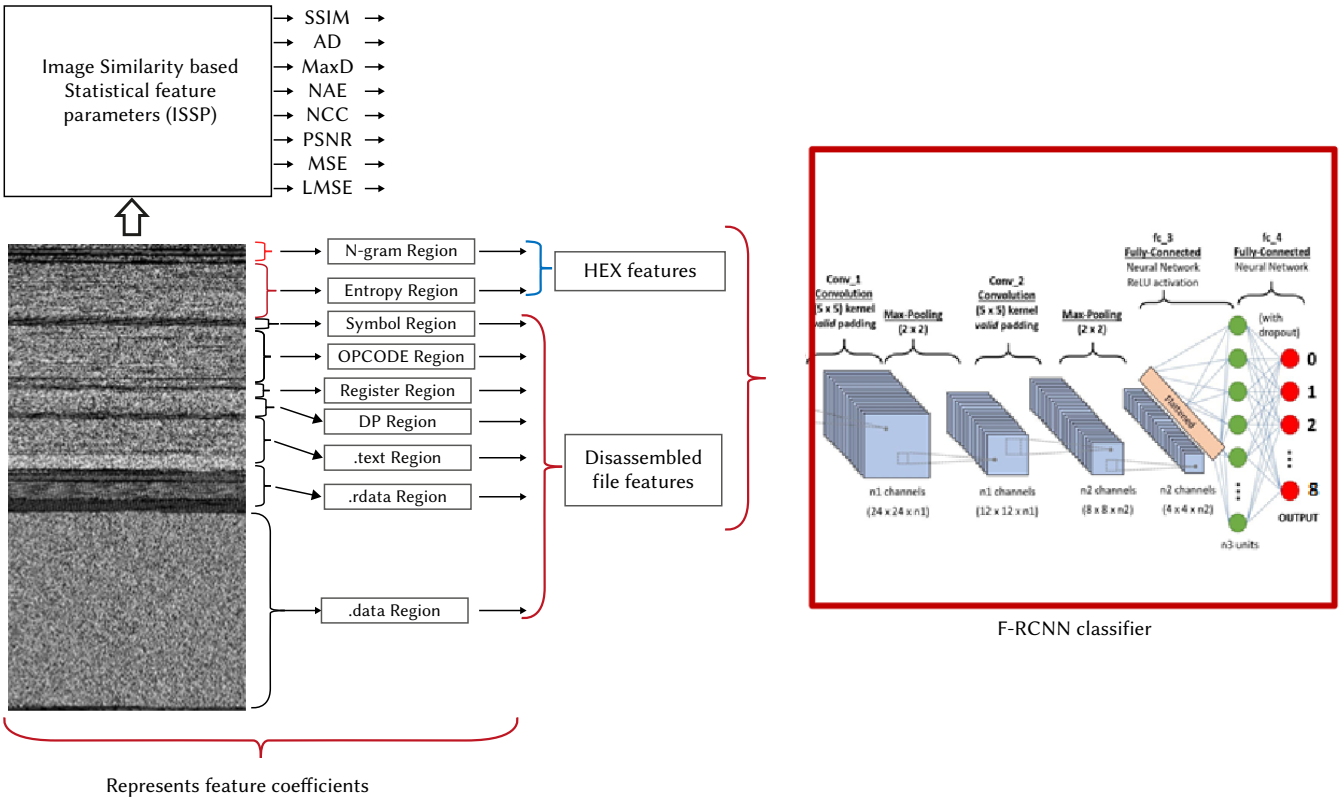


Fig. 9. F-RCNN Architecture for MDS.

Fig. 11 represents a sample of nine malware categories. The image has very fine and typical texture patterns and the same may be used to visualize the malware family. It has been observed that malware of the same family has similar signatures or fingerprints in some area of an image [187]. This information may be used as knowledge to identify the malware family. Zhang [186] represented information gains and the probability of the OPCODE to construct an image. M. Ahmadi [57] used Local Binary Pattern features and Haralick features to construct an image.

As R-CNN extracts features from each block, features from the same block will be repeatedly extracted, leading to a greater number of repetitive computations as shown in Fig. 9. **Therefore, the author proposes F-R-CNN, which is an improved version of R-CNN where CNN performs forward computation on the whole image**.

The entire image with a set of proposed regions (*K* object) with similarity based statistical parameters is input for an F-RCNN network. The network performs several convolution operations *(conv)* and maximum pooling layers on the entire input feature vector, and produces *conv* feature map. Next step it performs is to generate a feature map, by extracting a fixed length feature vector generated from the Region of Interest (RoI) pooling layer operation on the proposed objects. Each and every generated feature vector is input to a sequence of fully connected (f_c) layers. f_c layer provides two outputs. The first output is Softmax Probability Estimation (SPE) over *K* object classes plus a catch-all "background" class. The second output is 4 real valued numbers for every *K* object class. One of the *K* object classes has a set of four values which provides updated bounding box positions, calculated to reduce overlaps shown in Fig. 10.

Faster R-CNN consists of two major modules. The first module i.e., Region Proposal Network (RPN) is a deep fully convolutional network which proposes regions. The second module uses F-RCNN detector which uses the regions proposed by first module and learns about region positions from the same module due to attention-based CNN. The first module is presented in Table I. Table II presents the algorithm for generating the unified network for the overall system.

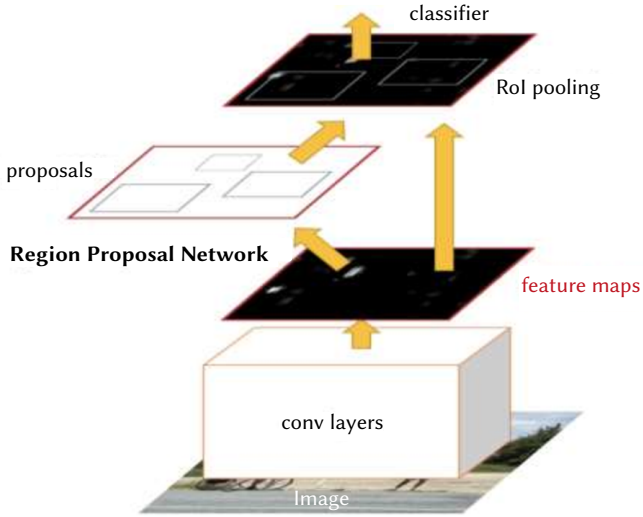


Fig. 10. F-RCNN Architecture.

VII. Statistical Parameters

To compute different statistical parameters, initially all the malware families are segregated in different folders. Nine folders are created as there are nine malware families. Malware files are processed and gray images are produced. These images are used to compute parameters. Table III presents the algorithmic steps.

TABLE I. Region Proposal Generation Algorithm

Region Proposal Network

Input: Image of any size

Output: 1. Set of rectangular object proposals
2. Each object with abjectness score

Convolutional model used: Zeiler and Fergus(ZF) (five sharable convolutional layers)

1 Generate convolutional feature map.

2 $n * n$ Sliding spatial window generated for small network. Sliding window is mapped to feature map of low dimension ($256 d for ZF$).

3 **Anchors**
- a. Each sliding window predicts multiple region proposals, simultaneously.
- b. k = Maximum region proposals for each location (k anchor boxes)
- c. Feature map size = $W * H$
- d. In the sliding window the question and an anchor, both are centered. Aspect ratio and scale is associated. Aspect ratio = 3 and scale = 3, provides $k = 9$ anchors [204].
- e. 'cls' layer is a two class Softmax layer. It estimates the probability of the object or non-object for each region proposal. Logistic regression will be used to produce of $2 * k$ scores.
- f. Regression ***(reg)*** layer has coordinates of k boxes. It will generate $4 * k$ outputs.
- g. The total number of anchors will be $W * H * k$
- h. Anchors are ***translation-invariant which reduces the model size***. As per the case of Fully Convolutional Network (FCN) [204]

4 **Multi-Scale Anchors**
- a. Compute multi-scale anchors by selecting multiple scale sliding window.
- b. Apply multi-scale sliding window to image and feature map of single scale.
- c. Generated structure may be viewed as 'pyramid of filters'

5 **Loss Function**
- a. Apply binary label to each and every bounding box.
- b. ***If*** (*Intersection over Union* (*IoU*) ∩ *Ground Truth*(*GT*) *box*) ≥ 0.7) ***then*** assign positive label
- c. If $(Intersection\ over\ Union\ (IoU) \cap GTbox) \leq 0.3$) ***then*** assign negative label ***else*** discard anchor
- d. Multiple anchors may be marked as positive by a single GT box.
- e. Compute Loss function

$$L(\{p_i\},\{t_i\}) = \frac{1}{N_{cls}}\sum_i L_{cls}(p_i, p_i^*) + \lambda * \frac{1}{N_{reg}}\sum_i P_i^* * L_{reg}(t_i, t_i^*) \quad (10)$$

where, i = anchor index in mini batch
P_i = Predicted probability of anchor being an object
P_i^* = Binary GTlabel
t_i = four parameteroised co-ordinates of Bounding Box (BB)
t_i^* = four parameteroised co-ordinates of GT Box of positive anchor
L_{cls} = log loss over object versus non-object classes
L_{reg} = regression Loss calculated only when $P_i^* = 1$ cls layer has $\{P_i\}$ and reg layer has $\{t_i\}$

- f. Compute Robust Loss

$$L_{reg}(t_i, t_i^*) = R(t_i - t_i^*) \quad (11)$$

- g. Normalize L_{cls} and L_{reg}

N_{cls} = Normalisation of L_{res} by mini batchsize
N_{reg} = Normalisation of L_{reg} by the number of anchor locations

- h. *Apply weight factor λ*
- i. BB regression from an anchor box to GT box

$$t_x = \frac{(x-x_a)}{w_a}, t_y = \frac{(y-y_a)}{h_a}, t_w = \log\frac{(w)}{w_a}, t_h = \log\frac{(h)}{h_a},$$
$$t_x^* = \frac{(x^*-x_a)}{w_a}, t_y^* = \frac{(y^*-y_a)}{h_a}, t_w^* = \log\frac{(w^*)}{w_a}, t_h^* = \log\frac{(h^*)}{h_a} \quad (12)$$

where,
x, y = centre co-ordinates of box
w and h = width and height of box
x, y, w and hare variables for predicted box
x_a, y_a, w_a and h_a are variablesfor anchor box
x^*, y^*, w^* and h^* are variables for GTbox

6 **RoI pooling layer algorithm**
1. Input RoI window of size $h * w$ with $r\,(row)$ *and* $c\,(column)$ information.
2. Divide ROI window into sub windows of size $H * W$

$$window\ size_{approximate} = \frac{h}{H} * \frac{w}{W}$$

3. Generate output grid cell by maximum pooling values from each sub window
4. Apply independent pooling to each feature map channel, on a similar line to the standard maximum pooling.

7 **Optimization of Loss function**
1. From a single image mini-batch of many +/- anchors are identified.
2. Sample size of 256 anchors from an image is randomly selected to compute loss function of a mini batch.
3. Equal number of positive and negative anchors are selected i.e., 128 each, if sample size is 256.
4. In case of a low number of either of the anchors (≤ 128), then the mini batch will be padded in such a way to get equal numbers of both the anchors.
5. All new layers are randomly initialized by computing weights from zero mean Gaussian distribution with 0.01 standard deviation.
6. Shared convolutional layers are initialized by standard practice i.e. pre-training model a model for ImageNet classification.

8 **Training RPN**
RPN is trained by back propagation (BP) and stochastic gradient descent (SGD) using 'image centric' sampling strategy.

TABLE II. Approach to Unified Network of RPN and F-RCNN

Problem: Independently trained F-RCNN and RPN networks will modify their convolutional layer differently. The algorithm is required so that both can '*share*' the convolutional layer

Generating Unified system Network

Input: RPN generated regions
Output: Trained model of overall system

1 Train RPN network as per algorithm described in Table I

2
- a. Initialized the ImageNet-pre-trained model
- b. Input region proposals generated by step -1
- c. Train detection network by Fast R-CNN using.

Note: convolutional layer is yet not shared by both the training model

3 *Shared* convolutional layers are finalized.

4 Layers unique to RPN will be fine-tuned.

5 RPN training network is initialized by detector network and the system is trained.

5 Fine tune layers from ***Shared*** convolutional layers unique to F-RCNN.

6 F-RCNN network is trained.

VIII. Database Description

This section describes the publicly available datasets for malware. System performance is analyzed on the benchmark database from Kaggle (https://www.kaggle.com/c/malware-classification/data).It was a Microsoft malware classification challenge. The database contained known malware files representing a mix of 9 different families viz. Gatak, Obfuscator.ACY, Kelihos_ver1, Tracur, Simda, Vundo, Kelihos_ver3, Lollipop and Ramnit. The file structure of the database is shown in Table IV and Table V.

TABLE III. STATISTICAL PARAMETER COMPUTATION

Input Folder structure is as follows
Main folder – contains sub folders equal to number of malware families ($i = 9$ for this case)
- Sub-folders (9 malware families)
- Each sub-folder has different number of images j

R_I = *Reference image*

I_I = *Input image*

i = *Number of malware families* in main directory (folder)

j = *Number of malware variants (images) of specific malware family in a subfolder*

// Initialize empty array

Parameter Array = $\{\emptyset\}$

for $(\beta = 0 ; \beta < i ; \beta ++)$

// Load reference image – first image of malware family

$R_I = \beta[0]$

***for*// select malware families one by one**

$(k = 0 ; k < i ; k ++)$

// Get number of images present of a specific malware family

$j = size\ (k_{sub\text{-}folder})$

for $(local_{cnt} = 0; local_{cnt} < j ; local_{cnt} ++)$

// Load Input image from malware family

$I_i = (k)[local_{cnt}]$

// calculate SSIM

$SSIM(R_i, I_i) = [l(R_i, I_i)^{\alpha} . c(R_i, I_i)^{\beta} . s(R_i, I_i)^{\gamma}]$

where l = *luminance*, c = *contrast*, s = *structure*

// Calculate MSE

$$MSE(R_I, I_I) = \frac{1}{mn} \sum_{m=1}^{M} \sum_{n=1}^{N} [L(R_I(m,n)) - L(I_I(m.n))]^2$$

// calculate PSNR

$$PSNR = 10 * \log_{10} \frac{255^2}{MSE}$$

// calculate Normalized Cross-Correlation (NK)

$$NCC(R_I, I_I) = C_{R_I I_I}(\widehat{R_I}, \widehat{I_I}) = \sum_{[m,n] \in R} \widehat{R_I}(m,n)\widehat{I_I}(m,n)$$

$$\widehat{R_I} = \frac{R_I - \overline{R_I}}{\sqrt{\sum (R_I - \overline{R_I})^2}} \ , \ \widehat{I_I} = \frac{(I_I - \overline{I_I})}{\sqrt{\sum (I_I - \overline{I_I})^2}}$$

// calculate Normalized Absolute-error (NAE)

$$NAE(R_I, I_I) = \frac{\sum_{m=1}^{M} \sum_{n=1}^{N} |R_I(m,n) - I_I(m.n)|}{\sum_{m=1}^{M} \sum_{n=1}^{N} [R_I(m,n)]}$$

// calculate Maximum difference

$MD(R_I, I_I) = \max\{[R_I(m,n) - I_I(m,n)]\}$

// calculate Laplacian Mean Square Error (LMSE)

$$LMSE(R_I, I_I) = \frac{\sum_{m=1}^{M} \sum_{n=1}^{N} [L(R_I(m,n)) - L(I_I(m.n))]^2}{\sum_{m=1}^{M} \sum_{n=1}^{N} [L(R_I(m,n))]^2}$$

where $L(m, n)$ *is Laplacian operator*

// Store all the values in an array

end

// Take average of an array an obtain single value

Parameter_array(k)=[mean(SSIM); mean(MSE); mean(PSNR); mean(NCC); mean(NAE); mean(MaxD); mean(LMSE)]

end

end

TABLE IV. KAGGLE DATASET BASIC INFORMATION

Header	Description
ID	Twenty-character hash value for unique identification of file
Class	Integer representing family of malware
RAW data	HEX representation of the file's binary content
Metadata manifest	Log of various metadata information e.g. Function calls, Strings etc. extracted from the binary using IDA disassembler tool.
Size	0.5 Tera byte uncompressed

TABLE V. DATASET DESCRIPTION

Malware Family	Malware category	Sample Size
Gatak	Backdoor	1013
Obfuscator. ACY	obfuscated malware	1228
Kelihos_ver1	Backdoor	398
Tracur	Trojan Downloader	751
Simda	Backdoor	42
Vundo	Trojan	475
Kelihos_ver3	Backdoor	2942
Lollipop	Adware	2478
RAmnit	Worm	1541

IX. EXPERIMENTAL RESULTS AND DISCUSSION

The gray scale images of the feature vector for the malware family listed in Table V are shown in Fig. 11. It can be clearly observed that the image for each family is unique in itself. Identification becomes simpler. Feature vector 'Regions' are also clearly visible.

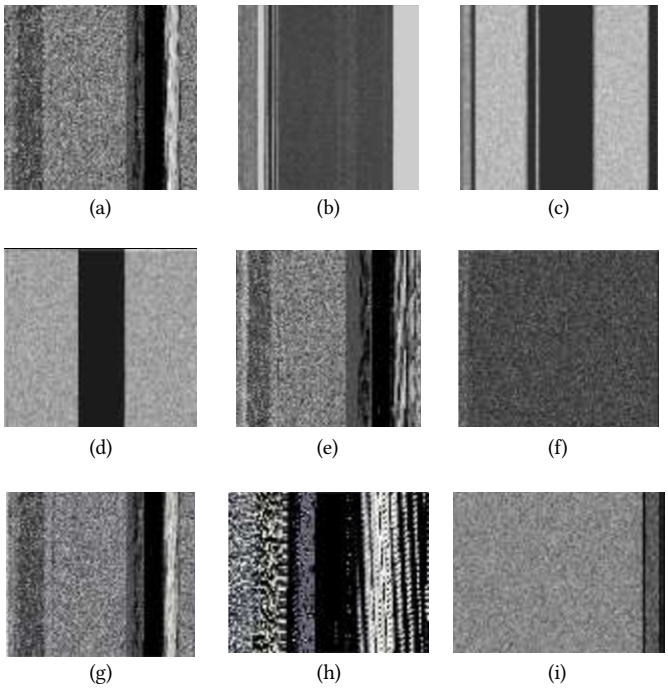
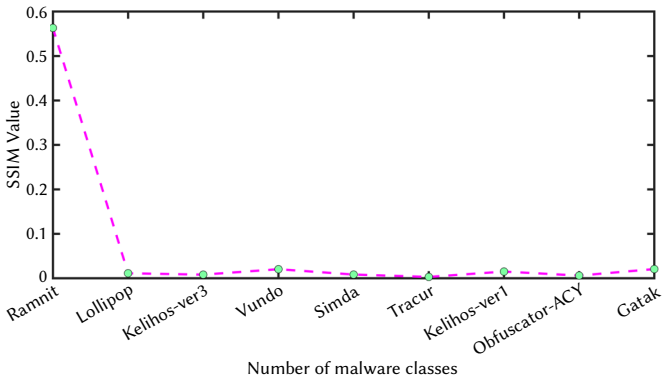


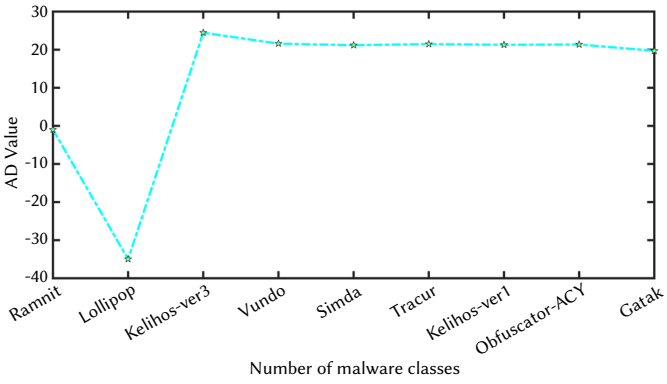
Fig. 11. Malware images of different malware families.
(a) Ramnit (b) Lollipop (c) Kelihos_ver3 (d) Vundo (e) Simda (f) Tracur (g) Kelihos_ver1 (h) Obfuscator. ACY (i) Gatak

As seen, initially one image from the first malware family is taken as a '*reference image*'. The remaining images from the first malware family and all the images of all eight malware families are used as '*Input image*'. Reference image and Input images are used to compute all the parameters. All the parameters per '*Input image*' are stored in the respective arrays (e.g.SSIM_array, MSE_array and so on). After iterating through all the images of one family, the mean value of an array is calculated. Thus, per family there is a single mean value. The mean value matrix is plotted. The same is depicted in Fig. 12.

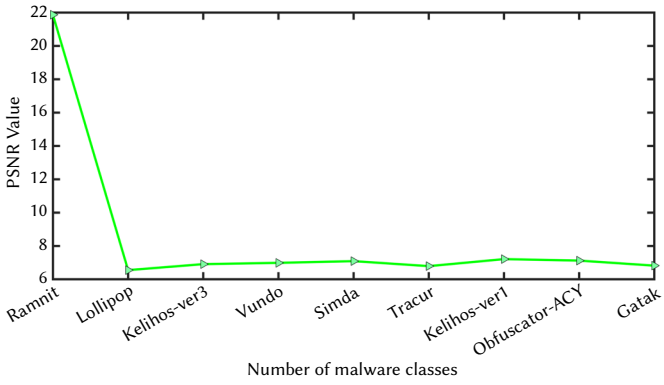
Fig. 12(a) shows the SSIM value. It is 0.56 for the Ramint malware. For the remaining families the value ranges between 0 to 0.02. Thus, there is high structural similarity with self-family, but with other families less SSIM value reflects very little similarity. On a similar line, the NAE parameter for the same family is 0.4 and for other families it is more than 0.7. Refer Fig. 12 (b) – (h). It depicts plots for PSNR, MD, MSE, LMSE, NK. It has been observed that, there is clear bifurcation in



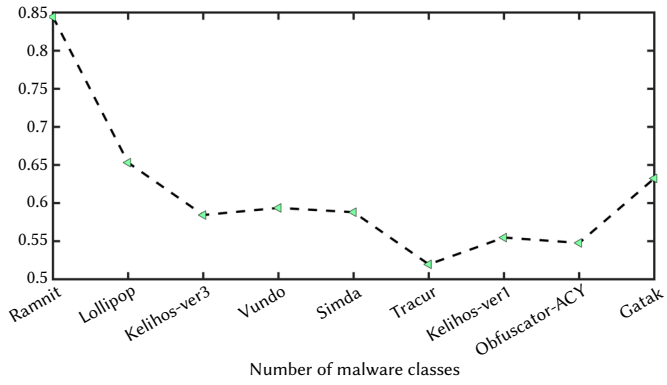
(a)



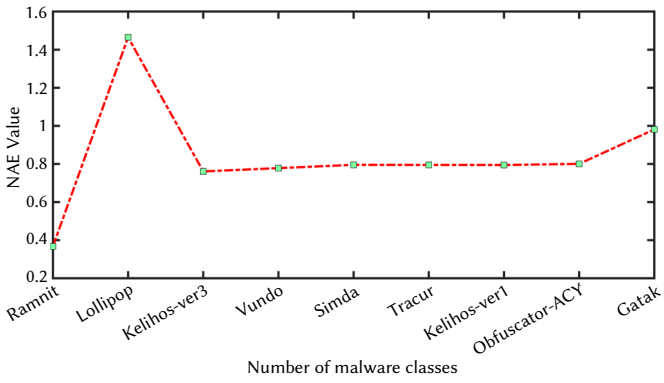
(b)



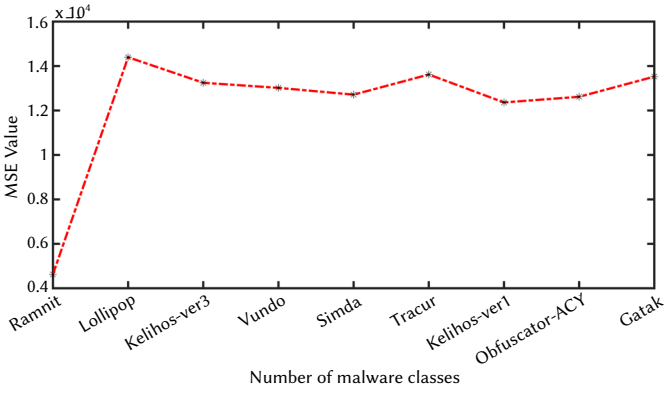
(c)



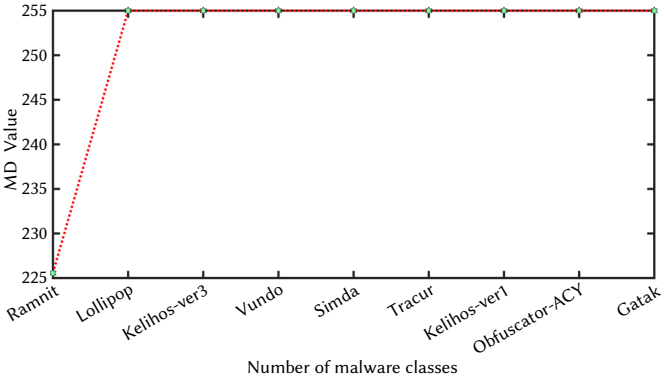
(d)



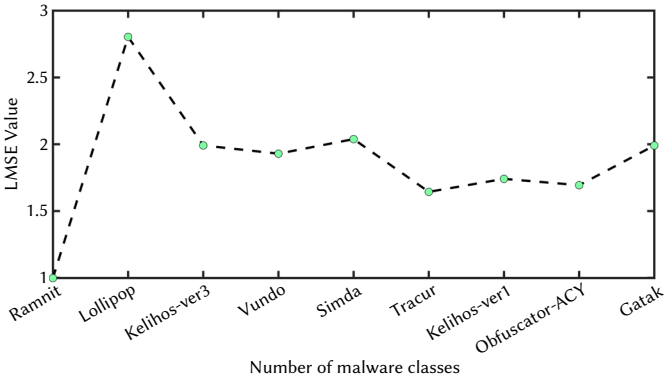
(e)



(f)



(g)



(h)

Fig. 12. Parameter plots - (a)SSIM (b) AD (c) PSNR (d) NK (NCC) (e) NAE (f) MSE (g) MD (h) LMSE.

the statistical parameter values to the same family class and a different family class. But in case of AD for the same class of family the value is approximately -1, but for the remaining families the value is either positive or negative with appropriate value difference. One can define a threshold range (0.95 to 1.1) for the AD. All these parameters can be used to train the F-RCNN classifier.

In Fig. 13 When the SC values were plotted for the same scenario then the results were not so promising. Range or proper threshold was difficult; therefore, this parameter was not taken into consideration by the author.

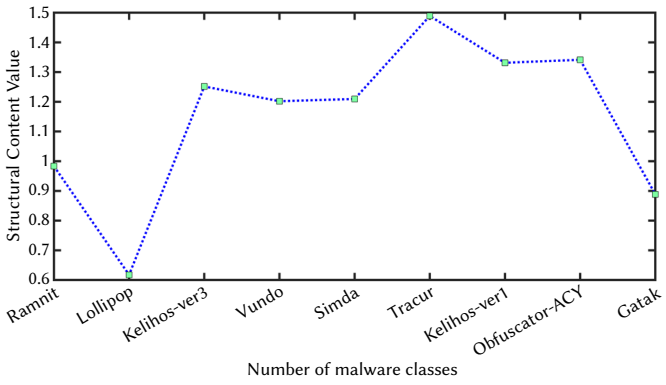


Fig. 13. SC plot.

Generated images are used to train the F-RCNN network. Annotations about regions are marked. In the experiment, the malware image set is randomly divided into a training set (60%) and a testing set (40%). This ratio of 60:40 has been selected to check the robustness of the model. The *training* data is less as compared to standard training data, i.e., 70:30. A trained library or network is created after the training process. After the training model is completed, the error and loss function of the model is used for judgment and evaluation. While training the system 30,000 epochs are selected. But while plotting the graph it is represented in percentage of the total value. Fig. 14 and Fig. 15 represent the error and loss plots in the training process. As the training iteration increases, the total error as well as loss value decreases and gradually stabilizes.

When the iterations reach 100%, the total loss value becomes flat and achieves the possible minimum value. The result shows that the training model based on F-RCNN with ISSP fusion with gray scale image is successful.

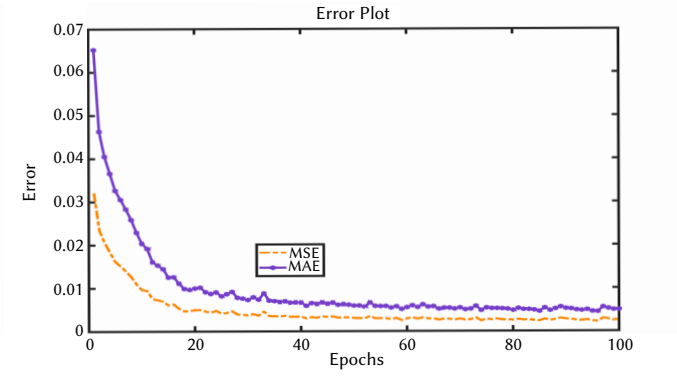


Fig. 14. MSE and MAE plot.

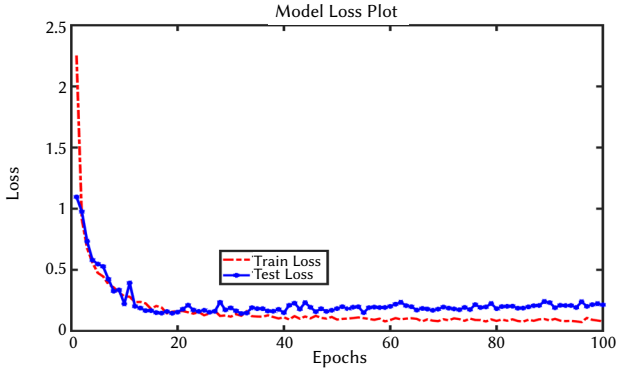


Fig. 15. Loss plot.

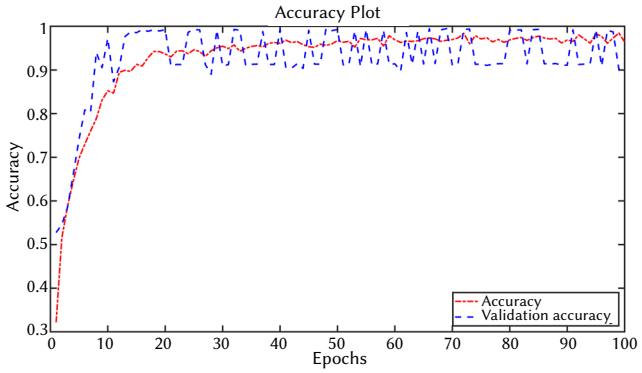


Fig. 16. Training model accuracy plot.

The network keeps a history of the trained data with error, loss and accuracy achieved while training the model. Fig. 16 represents the overall accuracy of the model with validation accuracy which approximates to 98.12%. In the testing phase, the remaining 30% of the malware files will be used. For each file a feature vector will be presented as a gray scale image will be generated and ISSP will be computed. The total matrix will be input to the trained network. The output generated from the trained network will be analyzed with the help of the statistical method where different parameters like True Positive (TP), True Negative (TN), False Positive (FP) and False Negative (FN) will be computed.

X. Performance Analysis

A. Performance Metrics

This section compares results obtained from the proposed work and state-of-the art methods. The proposed method opted the Kaggle benchmark dataset therefore results are compared with those research techniques that opted for the same dataset. Similarly, a comparison of the proposed algorithm for various performance metrics is stated in Table VI and Table VII respectively. Graphical plots for all comparisons are illustrated in Fig. 17.

Accuracy is the major performance parameter for the MD system, which specifies how accurately malwares are classified. Accuracy is calculated based on the following equation:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} X\ 100$$

Table VI depicts the confusion matrix of the proposed scheme for the MDS using Kaggle database.

TABLE VI. Confusion Matrix

Malware	Malware Detection %								
	Ramnit	Lollipop	Kelihos_ver3	Vundo	Simda	Tracur	Kelihos_ver1	Obfuscator.ACY	Gatak
RAmnit	98.57	0.19	0.19	0	0	0.06	0.45	0.45	0.06
Lollipop	0.36	98.82	0	0.40	0	0	0	0.40	0
Kelihos_ver3	0.03	0	99.66	0	0	0	0	0.30	0
Vundo	0	0	0	96.42	0.21	0.84	0	2.52	0
Simda	0	0	0	0	95.12	2.43	2.43	2.43	0
Tracur	0	0	0	0	0	99.73	0.13	0.13	0
Kelihos_ver1	0	0	0	0	0	0	100	0	0
Obfuscator.ACY	0.97	0.40	0.40	0.40	0.65	1.30	3.50	91.36	0.97
Gatak	0	0	0	0	0	0.09	0	0.19	99.70

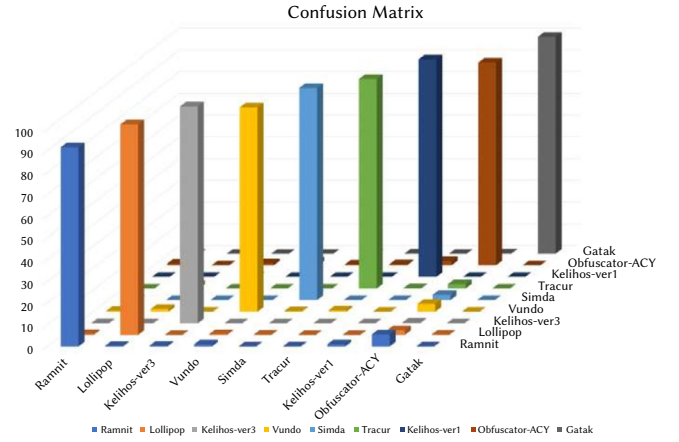


Fig. 17. Confusion Matrix Plot.

As the FRCNN classifier is not used by other researchers, the author compared the results with learning algorithms presented by researchers, as shown in Table VII.

TABLE VII. Comparative Performance of the Proposed System

Author/ Year	Dataset Used	Classifier	Accuracy (%)
Rao et al., 2017 [192]	NSL-KDD	IPDS-KNN	99.6
Shapoorifard et al., 2017 [193]	NSL-KDD	KFN-KNN	99
Vishwakarma et al., 2017 [194]	KDD cup 99	ACO-KNN	94.7
Dada et al., 2017 [195]	KDD cup 99	MIX-KNN	98.55
Ingre et al., 2017 [196]	NSL-KDD	CFS-DT	90.3
Malik et al., 2017 [197]	KDD cup 99	MULTI-DTs	91.94
Moon et al., 2017 [198]	Netflow	DT	84.7
Zhao et al., 2017 [199]	KDD cup 99	DBN-PNN	99.14
Tan et al., 2017 [200]	NETFLOW	DBN	97.6
Le et al., 2017 [201]	KDD cup 99	LSTM	97.54
Agarap et al., 2017 [202]	NETFLOW	GRU	84.15
Saxe et al., 2017 [203]	NETFLOW	CNN	92
Ding et al., 2016 [165]	Netflow	DBN	96.1
Nadeem et al., 2016 [120]	KDD cup 99	DBN	99.18
Alom et al., 2016 [159]	NSL-KDD	DBN	97.5
Krishnan et al., 2016 [180]	KDD cup 99	RNN	77.55
Kim et al., 2016 [173]	KDD cup 99	LSTM	96.93
MDFRCNN	**Kaggle dataset**	**F-RCNN**	**98.12**

XI. Conclusion

The paper proposes a state-of-the-art technique at feature extraction as well at classification level. The paper analyses different features viz. n-gram, MD1, MD2, entropy, OPCODE, Register, symbols, data define and sections of malware file for generating the feature vector. The feature vector is converted to a gray level image for visual analysis, where typical behavioral patterns can be observed for a particular malware family. Gray-scale image conversion widely opens up the scope for using state of the art image processing techniques, which have been more mature and proven.

Feature vectors have been presented in an image as different '*Regions*' which allows the use of Region Proposed Network (RPN). Exhaustive work done in the region-based analysis in an image, motivated the author to opt for the proposed methodology.

Malware codes are normally 75% to 80% identical. The image constructed from this code after extracting features should show similarity. Considering this point the author is motivated to introduce different image similarity based statistical parameters (ISSP) such as NCC, AD, MD, SSIM, LMSE, MMSE and PSNR as a feature set to improve system performance. The feature plot shown in Fig. 14, concludes that the features are distinctive. Thus, fusion of gray scale image with similarity parameters is used to train the classifier.

The development of region-based analysis with CNN as a base classifier offers R-CNN. The next modified versions of the basic R-CNN are Fast RCNN and Faster R-CNN (F-RCNN) techniques which have been proven for less training and testing time as shown in Fig. 5. This type of deep learning technique is more suitable for MDS where not only real time learning can be implemented with less time, but testing or producing output in the form of malware detection is desideratum. The system performance is analyzed using the benchmark database from Kaggle. This dataset is publicly available and results can be compared with the baseline. The database consists of nine malware families listed in Table V with details of malware families, malware categories and the number of sample files.

F-RCNN classifier with image-based visualization of the feature vector and ISSP as an additional feature resulted in better performance for classifying nine classes of malware. The proposed model offered an overall accuracy of 98.12% with improved rate of MD.

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