Counterfeit Fingerprint Detection of Outbound HTTP Traffic with Graph Edit Distance

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Abstract—

Index Terms—Anomaly Detection, Data Exfiltration, Data Leakage, Application Fingerprinting, Network Security

I. INTRODUCTION

II. RELATED WORK

III. PROPOSED APPROACH

This section gives the details about our proposed method which aims at detecting counterfeit fingerprints from applications' outbound HTTP traffics. Before going further, all PCAP files collected by an enterprise's host is network activities generated by a set of applications such as browsers B = $\{b_1, \ldots, b_n\}$, and which are all installed in hosts. Each browser b_i has several PCAP files which contain specific network characteristics, and our proposed approach possibly create a fingerprint f_{b_i} for each browser. The PCAP files of a host H include union of all browser fingerprints which is defined as $H = \bigcup_{i=1}^{n} f_{b_i}$. The proposed counterfeit fingerprint detection process consists of training and testing phases. In training phase, we assume enterprise hosts aren't compromised. This method mainly arises from the first one that is a data-driven and unsupervised flow responsible for a browser's fingerprint [1] and referrer correlation construction. This step takes the fields of a PCAP file as input and classifies browser traffics, and then construct fingerprints and referrer correlation graphs. In the testing phase, given a browser outbound HTTP traffic reconstructed by fingerprint and referrer correlation graph, and the second step filters benign browser traffics through fingerprint matching. Continuously, compare its and trained referrer correlation graph using Graph Edit Distance (GED) for counterfeit fingerprint detection. The proposed method is depicted in figure 1 and following paragraphs describe the details of each component.

A. Browser Traffic Extractor

For most cases of client-side attacking, hackers whose general goal is to steal valuable data before malware connects to C&C server. As a result, PCAP files, that contain specific network characteristics of an application (e.g., browser) for each host in the enterprise.

TABLE I
FIELDS AND VALUES OF DATABASE IN A PCAP FILE

Field	Value for Instance	
Domain	yahoo.com.tw	
DstIP	140.92.88.140	
User-agent	Mozilla/5.0 (Windows NT 6.1; Win64; x64)	
Accept-Lang	zh-TW	
Len	1253	
Constant	If-Modified-Since, Cookie, Connection,	

To generate fingerprint for each browser, our approach first extracts various entities from PCAP files. Table I shows 6 heterogeneous fields which can be extracted from each one-line log, including domain (*Domain*), destination IP (*DstIP*), useragent (*User-agent*), accept language (*Accept-Lang*), length (*Len*), and constant field (*Constant*). The reason for choosing these 6 fields for browser traffic classification can be summarized as followings and fingerprint construction is represented in next subsection.

In previous research [1], Bortolameotti et al. identified two types of HTTP applications (e.g., browser and background). This subsection aims to filter logs of a PCAP file according to the User-agent, because we focus on counterfeit fingerprints of browser network activities. To identify browser activities, the browser flags we defined are "Mozilla", "Opera", "MQQBrowser", "UCWEB", "NOKIA5700", "Openwave", "Safari", and "Chrome", and which are used for string matching in field User-agent. Furthermore, in both training and testing phase, an implementation time-slot t is a fixed time window of T minutes, and the filtered logs is passed to the next module after t ends.

- B. Fingerprint Constructor
- C. Fingerprint Matching Module
- D. Referrer Correlation Graph Constructor
- E. Graph Similarity Estimator

We denote the graph edit distance between two opcodecomponent graphs g_1 and g_2 as $D(g_1, g_2)$, which is the sum of VertexCost and EdgeCost. In which, VertexCost and EdgeCost indicate the numbers of insertions, deletions and substitutions

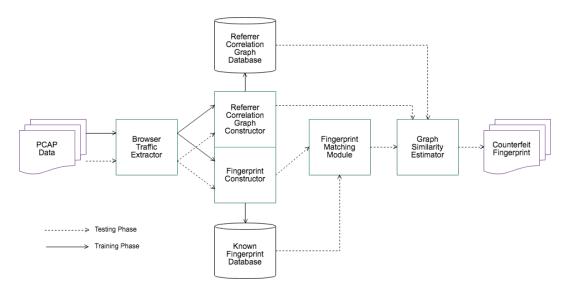


Fig. 1. An overview of our counterfeit fingerprint detection system. Five subsystems are depicted: (1) data preprocessor subsystem, (2) fingerprint constructor subsystem, (3) fingerprint matching subsystem, (4) referrer correlation graph constructor subsystem, and (5) graph similarity estimator subsystem. The system only takes the PCAP files of outbound HTTP traffics as input. In training phase, subsystem (1) and (2) passively extract the benign fingerprint from an application's outbound HTTP traffic, and subsystem (3) could use fingerprints to classify benign traffic in the testing phase. We note that referrer correlation extraction in the subsystem (4) is a key step, in the sense that if it can extract discriminative features for counterfeit fingerprint detection, the detection in the subsystem (5) is relatively straightforward.

of vertices and edges, respectively, where determine the minimum amount of distortion for transforming one graph into another graph [2]. Let $g_1 = (V_1, E_1)$ and $g_2 = (V_2, E_2)$: g_1 is the source graph of malware, and g_2 is the target graph of malware. The graph edit distance between g_1 and g_2 is defined as follows:

$$D(q_1, q_2) = \text{VertexCost} + \text{EdgeCost}$$
 (1)

$$\sigma(g_1, g_2) = \frac{D(g_1, g_2)}{|V(g_1)| + |V(g_2)| + |E(g_1)| + |E(g_2)|}$$
(2)

Finally, the similarity $\sigma(g_1,g_2)$ of two graphs g_1 and g_2 is obtained from the graph edit distance $D(g_1, g_2)$. The details are described in Equation 2, which is a real value on the interval [0,1], where 0 indicates that graphs g_1 and g_2 are identical, whereas a value near 1 implies that the pair is highly dissimilar. As mentioned before, finding the minimum graph edit distance, i.e., $min_{D(g_1,g_2)}$, is an NP-hard problem but can be approximated. Riesen et al. and Francesc Serratosa introduced an approximation algorithm with a good trade-off between accuracy and speed [3] [4]. Given two graphs G_1 and G_2 , where $|G_1| = n$ and $|G_2| = m$, their algorithms, respectively, use a $(n+m) \times (n+m)$ cost matrix C_1 and a $n \times m$ cost matrix C_2 , which both give the cost of mapping a vertex $v \in V(G_1)$ to a vertex $v \in V(G_2)$. Next, Munkres algorithm [5], also known as the Hungarian algorithm, which runs in polynomial time, is applied to find an exact one-to-one vertex assignment that minimizes the total mapping cost. Each entry in the cost matrix represents the cost of matching vertex $v \in V(G_1)$ to a vertex $u \in V(G_2)$. The cost of matching a pair of nodes c_{ij} could equal the transformed cost as defined for the graph edit distance in the following subsection.

In this subsection, more accurate cost estimation allows the discovery of better graph matchings and hence more accurate edit distances. The cost of matching a pair of vertices, element c_{ij} of the matrix, could equal the transformed cost as defined for the graph edit distance, which consists three components: Host jaccard similarity, In-degree, jaccard similarity and Outdegree jaccard similarity can be observed developing between vertices v and v but can be presented as v0, v0, v0 and v0 and v1 and their details can be defined as follows:

$$\delta(v, u) = \left| 1 - \frac{Bit_{op}(v) \cap Bit_{op}(u)}{Bit_{op}(v) \cup Bit_{op}(u)} \right|$$
(3)

$$\delta^{-}(v,u) = \left| 1 - \frac{Neighbor^{-}(v) \cap Neighbor^{-}(u)}{Neighbor^{-}(v) \cup Neighbor^{-}(u)} \right|$$
(4)

$$\delta^{+}(v,u) = \left| 1 - \frac{Neighbor^{+}(v) \cap Neighbor^{+}(u)}{Neighbor^{+}(v) \cup Neighbor^{+}(u)} \right| \quad (5)$$

where $Bit_{op}\left(v\right)$ indicates the extraction of vertex v's opcode components, presented by 218 binary bits defined as the above section. Additionally, $Neighbor^{-}\left(v\right)$ and $Neighbor^{+}\left(v\right)$, respectively, present the Neighbor vertices of vertex v, which are defined as follows:

$$Neighbor^{-}(v) = \{z \mid e_{z,v} \in E\}$$
 (6)

$$Neighbor^{+}(v) = \{z \mid e_{v,z} \in E\}$$
(7)

TABLE II
DATASETS USED IN THIS PAPER'S EXPERIMENTS

Datasets	Operation Type	Malware Families	Malware
Ahmadi et al. [?]	API	4	3,829
Ki et al. [?]	Opcode	9	10,867

Clearly, each element c_{ij} of the cost matrix indicates the bijective mapping of the i-th vertex to the j-th vertex that can be defined as follows:

$$c_{ij} = \delta(i,j) + \delta^{-}(i,j) + \delta^{+}(i,j)$$
 (8)

The Munkres algorithm [5] [6] is a known algorithm that solves the bipartite matching problem in polynomial time. After obtaining the conceptual matched matrix, we implement the Munkres algorithm to find the optimal permutation that minimizes the cost as the similarity distance between the two Android malicious samples' graphs g_1 and g_2 . In Algorithm \ref{graphi} , the first three steps determine whether the cost matrix has the specific scenario which means the optimization bipartite match from source sample's vertex to target sample's vertex already exists. Then, we can decide whether the scope of the cost matrix needs to be reduced. Furthermore, we acquire a conceptual match matrix C' from the function $f_{gm}(C)$, which can effectively eliminate the side-effects of each wide variability.

IV. EXPERIMENT RESULTS

Tony, pliz write overview here!!!

A. Experimental Settings

Tony, pliz write like the followings in this subsection!

Malware analyzed in following experiments are malicious behavioral sequences from collected malicious executable files in real world. In proposed method implementation, collected malware were paresed and information of four major fields in table II. Table II also lists the number of malware families, the size of gathered data, and operation types in malicious behavioral sequences.

B. Evaluation Metrics

Tony, pliz replace malware to fingerprint!!!

Essentially, malware clustering is a multiple classification problem aim to identify malware comes from which families. Four well-known metrics for evaluating effectiveness of proposed method are adopted as followings: "true positive" (TP) means the number of malware which belong to same malware families. "False negative" (FN) is the number of malware which's families are wrongly predicted. Similarly, "true negative" (TN) means the number of malware which aren't same families and being viewed as others, while "false positive" (FP) is the number of false alarms that other families' malware being detected as the same ones. Based on accumulation of TP, FN, TN, and FP, one extended metrics (accuracy) popularly used in machine learning problems are

also adopted here to evaluate proposed method and listed in equations below. Note that the optimal *accuracy* of 1.0 means all of malware are successfully classified by proposed approach.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{9}$$

C. Effectiveness Analysis

Tony, pliz show your exp graph and table here!!!

V. CONCLUSION

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