



DEPARTMENT OF INFORMATICS

TECHNISCHE UNIVERSITÄT MÜNCHEN

Master's Thesis in Informatics

**“Botnet Battlefield”: A Structured Study of
Behavioral Interference Between Different
Malware Families.**

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**“Botnet Battlefield”: Eine strukturierte
Fallstudie über Verhaltensinterferenz
zwischen verschiedenen Malware Familien.**

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Submission Date:	February 15, 2016



I confirm that this master's thesis in informatics is my own work and I have documented all sources and material used.

Munich, February 15, 2016

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Acknowledgments

Abstract

We present a novel approach for finding the behavioral interference between malware families at large scale. Driven by monetary profit, malware from different families might try to uninstall each other before infecting a system, to get the larger share on the underground market. This is an interesting case of ‘environment-sensitive malware’ and behavioral interference between malware families. To the best of our knowledge, there is no prior research addressing this problem in systematic way. We explore this scene in the wild, on millions of malware samples, collected over time by *Anubis*, a dynamic full-system-emulation-based malware analysis environment, from its public web interface and a number of feeds from security organizations. Because of the large dataset and Anti-Virus labels being unreliable, we used machine learning to cluster and filter our dataset, without compromising the quality. We clustered our dataset based on the behavioral profile of malware into different malware families. We used heuristics to find the probable malware pair with behavioral interference, based on common resources (files, registries, and others), interactions (modify or delete), and belonging to different clustered families. Our approach could find X number of malware pairs with the true positive rate of $X\%$. This novel research will help better understand the dynamic aspect of malware behavior.

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1 Introduction

Malware, short for malicious software, is a generic term referring to any illegitimate software that can cause damage, disrupt, or steal on a computer, server, or computer network [Cis]. Malware can infect the system by being bundled with some other program or being attached as macros in a file. When a user opens such a program or file, the malware gets installed onto the user's machine. Malware can also install themselves by exploiting some common vulnerabilities in an operating system (OS), a network device, or other common software. A vast majority of malware is installed by some action by the user, such as clicking an e-mail attachment or downloading a file from the Internet [Cis].

Malware can be classified into self-replicating, such as *viruses and worms*, and non-replicating, such as *Trojans* [Che]. Unlike a virus, which needs user action (opening the infected file), worms are capable of automated replication and propagation, through computer networks [Che]. Trojans disguise themselves to be legitimate and harmless, but have hidden malicious functions. A malware can also be categorized into *polymorphic* and *metamorphic*, by its ability to change its code-structure every time it infects a new victim. *Polymorphic* malware uses code obfuscation (e.g. dead-code insertion, subroutine reordering, instruction substitution) and encryption to create a new variant of itself, whereas, *metamorphic* malware uses only code obfuscation to change its code-structure [RMI11; RMI12]. However, the semantics of the program (malware) remains same. We discuss in details about types of malware in section 2.1.

As the Internet increased growth over the last two decades, more and more devices are now connected to the Internet. Many of our daily life activities are now depended on its usage, such as email, banking, bill payment, and social networking. Along with this, the underground Internet economy, illegal trading of valuable data and personal information, has also been on the rise. Malware authors now do not write malware just for fun, to create annoyance or break into some system for bragging rights, but also for profit. Malware authors look for banking credentials, credit cards, and personal information that they can gather and sell in the underground market. In 2006, annual losses caused by malware were estimated to be 2.8 billion dollars in United States and 9.3 billion euros in Europe [MCA09]. Driven by the high profit and rise in easily available tools to create polymorphic and metamorphic malware, there has been rapid

increase in the number of new malware being introduced each day [Tia+10]. According to *AV-Test*, an independent IT-Security Institute based in Germany, about 140 million new malware were introduced in 2015 alone, making the total number of malware recorded so far almost half a billion [AVT].

Malware has become a lucrative business. Malware authors are now vying with each other to take sole control of their victim for larger profit. Many cases have been found, where one malware tries to delete another malware from the victim’s machine. Further, once they have infected the victim, they prevent the host from being infected by other malware. In 2010, *SpyEye*, a Trojan, was found to have a feature *KillZeus* that would remove *Zeus*, which is also another Trojan, making *SpyEye* the only malware to run in the compromised system [Har]. In 2015, *Shifu*, a banking Trojan, was found to have behavior similar to Anti Virus (AV), i.e., preventing the host from further infection by other malware, once it had taken control over the victim’s machine [Lim]. We have discussed in details, about such anecdotal evidence of interaction between malware families, in section 2.2.

The study of aforementioned behavioral interference between the malware family will provide novel knowledge for understanding the dynamic aspect of modern malware and the inter-family relations. This behavior is also a case for environment-sensitive malware, where malware change their behavior depending on different factors of its running environment, such as presence or absence of files, programs, or running services. To the best of our knowledge, there hasn’t been a study of such interference between two malware families so far. We present a systematic way to find out such interferences from a large number of malware samples.

Our dataset consists of 22,154,180 malware samples, collected overtime by *Anubis* [Anu], a dynamic full-system-emulation-based malware analysis environment, from its public web interface and a number of feeds from security organizations. Detailed discussion on *Anubis* and malware analysis is done in section 2.3. Randomly picking a malware pair to analyze from the available dataset would not be a good approach, whereas running all the possible pairs of millions of malware is not scalable. We wanted to filter our data set without losing malware samples exhibiting behavioral interference. In order to minimize our search space for candidate pair selection, and maximize the probability for finding a pair with behavioral interference, we, take into account only those malware which would create a resource successfully and another malware that tries to access or delete that same resource, but with a failure. We call those malware pairs as possible *candidate pairs*. **Resource** refers to any entity, such as Files, Registry, Section, Sync, that can be modified or queried by malware using system

calls. Since *Anubis* emulates the Windows OS, **system calls** refers to the Windows Application Programming Interface (API) functions. The trace of all the resources modified or queried by malware during its execution is referred to as the **Behavioral Profile** of that malware. In subsection 3.1.1 and subsection 3.1.2 we define behavioral profiles and different resource types in detail respectively. If malware makes a failed attempt to access or delete resources created by another malware, there should be some interaction between those malware, as these actions are suspicious. It is trying to detect the presence of other files or registries in the environment it is currently running, and its behavior is affected by the positive or negative detection. This shows the dynamic aspect of malware behavior and its environment-sensitive nature.

The simple heuristic of finding candidates based on common resource gave us concrete candidate pairs. The candidate pairs were still too large to run in a scalable manner and find substantial results. In order to further study the dataset, we used clustering of malware (based on behavior of malware). **Malware Clustering** is the process of grouping a set of malware in such a way that malware in the same group are more similar, based on the behavioral profile in our case, to each other than to those in other group. Such groups are called **clusters**. Clustering of malware based on behavioral profiles has been used extensively in previous research, which we have listed in details in section 2.4. We treat each cluster as a family, and malware falling in those clusters as variants of that family. Candidate pairs are chosen in such a way that two malware representing a pair, do not belong to the same family. The algorithm for candidate selection based on clustering results and the common resource heuristic is described in subsection 3.2.5. An *unpacker* was designed in order to run a candidate pair inside the *Anubis* system for analysis. The **Unpacker** drops the candidate pair into the analysis system and executes both malware with a set time interval in between two executions [see section 4.2]. We were able to successfully find X pairs of malware with interfering behavior with a true positive rate of X.

Our research will provide the following contributions:

- To the best of our knowledge, we are the first to perform a systematic study of interferences between malware families. Our work is based on a wide variety of a large malware dataset collected over time in the wild. This novel research will help better understand the dynamic aspect of malware behavior.
- A novel approach to malware clustering based on their behavior profiles. We show our clustering approach is good at grouping similar behaving malware in to the same cluster.

- An automated system that detects interfering malware samples on a large scale. Our system was able to find malware pairs with interfering behavior with good accuracy.

We discuss malware types and families, evidence of interaction between malware families, malware analysis system, previous works on the use of malware clustering based on malware behavior generated from dynamic malware analysis, and motivation for our research in chapter 2. In chapter 3, following the motivation, we give an overview, design rationale, and give a technical description of our work flow and system. In chapter 4, we explain how we implemented the system, problems faced during the implementation, and how we solved them. We present the findings of our work in ???. Finally, we conclude with a discussion of our work and possible improvement in future in chapter 6

2 Literature Review

In this chapter we will discuss anecdotal evidence of malware interference, malware analysis systems, and previous research on malware clustering. With the insight from the literature review, we reason the motivation and design rational of our research work; to study the behavioral interference between malware families at a large scale. We first describe commonly known malware types and families.

2.1 Malware Types and Families

Some of the commonly known malware types are viruses, worms, Trojans, and bots. A **Virus** is a piece of malicious code attached to some other executable host program or file, which gets executed when the user runs the host program. It can replicate itself to form multiple copies but cannot propagate on its own. It spreads when it is transferred or copied, by the user, to another computer via the network by file sharing or as an email attachment.

A **Worm**, unlike a virus, is capable of running independently and is self-propagating. It propagates by exploiting some vulnerability in a machine's OS, a device driver or taking the advantage of file-transfer features, such as email or network share.

A **Trojan** is a non-replicating malware which gets its name from the ancient Greek story about the *Trojan Horse*. It is a software that looks legitimate, but is harmful. Trojans are non reproducing and non self-replicating. It spreads only by user actions such as opening infected Internet downloads and email attachments [Cis]

A **Bot** is a malicious software that allows the infected host machine to be accessed and controlled remotely by its author, also called "*botmaster*". The botmaster does this from a central server called the Command and Control (C&C) server. A network of such many Internet-connected bots is called **Botnet**. A bot is capable of logging keystrokes, gathering passwords and financial information, and sending it to the C&C server. A Botnet can also be used to launch *Distributed Denial of Service (DDoS)* attacks, by flooding a single server with many requests, or sending spam at a large scale.

Some malware is able to change their structure and create a new variant of itself each time it infects a new victim. On the basis of how a malware changes its structure, it can be broadly divided into Polymorphic or Metamorphic malware. **Polymorphic** malware

divides its program into two sections of code: a “decryptor” and “encryptor”. The first code section, the “decryptor”, decrypts the second section of the code and hands the execution control to the decrypted section of code. When the second section of the code (encryptor) executes, it creates a new “decryptor” to encrypt itself, and links the new encrypted code section (encryptor) and the new “decryptor” to construct a new variant of the malware. Code obfuscation techniques (e.g. dead-code insertion, subroutine reordering, instruction substitution) are used to mutate the “decryptor” to build the new one for a new victim [RMI11]. **Metamorphic** malware are body-polymorphic malware [SF01]. Instead of generating new “decryptor”, a new instance is created using similar code obfuscation techniques as used in polymorphic malware. Unlike Polymorphic malware, it has no encrypted part [RMI12]. In both cases the new variants may have different syntactic properties, but the real behavior of the malware remains same.

Malware is categorized to different families in accordance to the malware author and similar behavior. In this section, we briefly describe three most common malware families to provide an idea of their behaviors, capabilities, and mode of operation. Even between these three families we can see stark differences in their behavior and approach of infecting a victim’s machine permanently, keeping low presence. Each malware family creates or modifies some specific resource (such as file or registry), which can be used to detect their presence.

2.1.1 Conficker

Conficker is a computer *worm* that targets the *Microsoft Windows* Operating system which was first found in November 2008. According to *Microsoft* the detection of *Conficker* worm increased by more than 225 percent since the start of 2009 [Micn]. It is capable of infecting and spreading across a network without any human interaction. If the user of the compromised machine does not have admin privilege, it is capable of trying different common weak passwords (such as ‘test123’, ‘password123’) in order to gain admin privilege of the network share directory, and drop a copy of itself there. The worm first tries to copy itself into the Windows system folder as a hidden Dynamic Link Library (DLL) using some random name. When unsuccessful it tries to copy itself in %ProgramFiles% directory. In order to run on startup, every time Windows boots, it also changes the registry as in Listing 2.1.

Listing 2.1: Registry key created by Conficker worm for autostart

- 1 In subkey: HKCU\Software\Microsoft\Windows\CurrentVersion\Run
- 2 Sets value: "<random string>"

- 3 With data: "rundll32.exe <system folder>\<malware file name>.dll,<malware parameters>"

2.1.2 Zeus

Zeus is another malware of *Trojan* type, that affects the *Microsoft Windows* OS. It attempts to steal confidential information once it infects the victim's machine. The information may include systems information, banking details, or online credentials of the compromised machine. It is also capable of downloading configuration files and updates from the Internet and change its behavior based on new update. The Trojan is generated by a toolkit which is also available in the underground criminal market, and distributes itself by spam, phishing and drive-by downloads [Sym, Trojan.Zbot].

Zeus tries to create a copy of itself as any of the names as *ntos.exe*, *sdra64.exe*, *twex.exe* in the <system folder>. In order to make itself run every time the system starts, after reboot or shutdown, it changes the registry as in Listing 2.2 [Micm, Win32/Zbot].

Listing 2.2: Registry key modified by Zeus Trojan to autostart

- 1 In subkey: HKLM\Software\Microsoft\Windows NT\Currentversion\Winlogon
2 Sets value: "userinit"
3 With data: "<system folder>\userinit.exe,<system folder>\<malwar"

2.1.3 Sality

Sality is a family of polymorphic malware that infects files on the *Microsoft Windows* OS with extensions *.EXE* or *.SCR*. It spreads by infecting executable files and replicating itself across network shares and steals sensitive information like cached password and logged keystrokes.

Each infected host becomes the part of peer to peer (p2p) botnet that would create a hard to take down decentralized network of C&C servers. The botnet is also used to relay spam, proxy communications, or achieve DDoS [Nic, Sality].

Sality targets all files in the system drive (usually 'C' drive in Windows) and tries to delete files related to anti-virus. It stops any security (anti-virus) related process and changes Windows registry keys related to AV software in order to lower the computer security. One of the symptoms to diagnose if a machine is infected by the *Sality* family of malware is the presence of files, listed in Listing 2.3, in the system [Micl, Win32/Sality].

Listing 2.3: Files created by Sality in the infected machine

- 1 <system folder>\wmdrtc32.dll

2 <system folder>\wmdrtc32.dl_

2.2 Interference between Malware Families

We discussed malware families and their supposed behavior in the previous section. In this section we show some of the evidence of interference between different malware families. We look upon those incidents to know the families involved, nature of interference, and the reasons behind it. One of our main goals is finding such behavioral interference between the malware families at a large scale. This anecdotal evidence, quite popular among the security related media, will serve as a ground truth for our research work.

2.2.1 Bagle, Netsky, and Mydoom feud

This feud between the malware family dates back to 2004, where there was an exchange of words between the creators of *Bagle*, *Netsky* and *Mydoom*. All three malware families were computer worms spreading through email as an attachment and making victim curious enough to download and open it [Wikd]. The creators inserted their message inside the malware itself, making it visible for the victims too. This also gained much media attention and even appeared in [Bri, BBC]. Message “*don’t ruine (sic) our business, wanna start a war?*” was seen inside the *Bagle.J*, where as *NetSky.F* responded with message “*Bagle you are a loser!!!! (sic)*”. Similar messages with profanity were also seen in variants of *Mydoom.G* families.

The reason for the war between these malware families was *Netsky* trying to remove the other two malware, *Bagle* and *MyDoom*, from the victim’s machine. The creator of *Netsky*, *Sven Jaschan*, admitted that he had written the malware in order to remove the infection with *Mydoom* and *Bagle* worms from the victim’s computer [Wikd].

2.2.2 Kill Zeus

This was another war between the two *Trojan* malware families, *Spy Eye* and *Zeus*. **SpyEye** is a Trojan malware which, like *Zeus*, was created specifically to facilitate online theft from financial institutions, especially targeting the U.S. It infected roughly 1.4 million computers, mainly located in the U.S, and got the personal identification information and financial information of victims in order to transfer money out of victim’s bank accounts [Fed]

SpyEye came with the feature called *Kill Zeus* that was successful in removing large varieties of the *Zeus* family. The battle between these two families were quite dynamic. Many releases of the Trojan toolkit were made from both families in order to negate each others dominance [Har].

2.2.3 Shifu

Shifu, a highly evasive malware family, targeting mainly Japanese (82%), Austrian-German (12%), and European (6%) banks for sensitive data, was detected recently in the year 2015 [Lim]. It is evasive because it terminates itself if it finds out that it is being run inside the virtual machine or is being debugged. It knows if it is being run inside a virtual machine by checking for the presence of files such as *pos.exe*, *vmmouse.sys*, *sanboxstarter.exe* in the system [Diw]. In order to check if it is being debugged, it calls *IsDebuggerPresent* Windows API which detects if program is being debugged [Diw]. *Shifu* also prevented any other malware from infecting its victim. It keeps track of all the files being downloaded from the Internet. For any files that were downloaded from unsecured connections (not HTTPS) or are not signed, it considered those files suspicious, and renamed it to *infected.exe*. It stops those suspicious files from being installed on the system and also sent a copy of the file to its C&C server, probably for further analysis [Lim]. If there was already presence of other malware, it stops any updates to those other malware, by disconnecting them from their botmaster [Lim].

2.3 Malware Analysis

In the previous sections, we discussed malware families and interference between them. We need a malware analysis system to detect such behavioral interference from a large dataset. In this section we describe techniques of malware analysis and *Anbuis*, the dynamic analysis system, we chose for our research.

Malware analysis is the process of dissecting different components of a malware sample in order to study the behavior of the malware when it infects a host or victim's machine. It is done using different analysis tools and reverse engineering the binary. There are two main types of malware analysis techniques, *Static* and *Dynamic*.

Static analysis is done without running the binary, but studying the assembly code of binary to detect the benign or malicious nature of program. One way to perform static analysis is by disassembling the binary with a disassembler, decompiler, and source code analyzer to find the control flow graph (CFG) of all the code segment and path that the program might take under different given conditions. If the analysis result

crosses the preset threshold of malicious activity then it is marked as infected [SS14]. *Static analysis* gives all the possible behavior of program but for large number of huge programs it is hard and time consuming.

Dynamic Analysis is done by running the binary in a closed controlled system such as *Sandbox* and logging all the activities (activity related to Registry, File, Process, Network etc.) of the malware while it runs in host. Detection of malicious activities, such as attempt to open other executables with intent to modify its content, changing Master Boot Record or concealing themselves from the operating system, would label the program as malware [SS14]. The main drawback of dynamic analysis is that only a single execution path is examined. Chipounov, Kuznetsov, and Candea proposed an approach to multi-path execution by triggering and exploring different execution path during run-time [CKC12]. Also, many evasive malware can evade detection by *dynamic analysis* by identifying the presence of analysis environment, and refraining from performing malicious activities [KVK14].

We chose dynamic analysis because we can run the candidate malware pair together, to find the behavioral interferences, in live action. Static analysis would be tedious if we were to analyze each candidate of a pair and correlate them for interference, within the time constraint.

2.3.1 Anubis

For our experiment we use **Anubis**, a dynamic malware analysis platform for analyzing Windows PE-executables [Anu]. *Anubis* generates a detailed report about modifications made to the Windows registry or the file system, about interactions with the Windows Service Manager or other processes and logs of all generated network traffic [Anu]. We chose *Anubis* because of the following reasons:

- We had direct access to Anubis and multiple instance of Anubis system to perform our malware analysis.
- Our dataset of malware were those collected by Anubis over time, and we had access to already generated reports of those malware.
- It is one of the well accepted dynamic analysis platforms among security researchers.

2.4 Malware Clustering

We wanted to select pairs that have high probability of behavioral interference and analyze them in *Anubis*, a dynamic analysis system, to confirm. We cluster our large dataset (millions of malware samples) into different clusters (families) based on the malware behavior. This helps us find the candidate pair from smaller candidate set (clusters), malware in a pair belonging to two different clusters, without compromising the quality of the dataset. Anti-virus companies do provide labels to categorize malware into different families (such as listed in *VirusTotal* [Vir] report), but they are not reliable. They do not fulfill the criteria of consistency, completeness, and conciseness [Bai+07].

- **Consistency.** Different AV vendors place the malware into different categories, and these categories also do not hold the same meaning across the vendors. This leads to inconsistency in the AV vendors labels.
- **Completeness.** Not every malware has been labeled by the AV vendors, and many malware go undetected because of this. A month old binary could still be unlabeled, which makes the AV system labeling incomplete.
- **Conciseness.** The label provided by an AV vendor are either too little or too much information with not much substantial meaning. They usually give a general idea of broad term as “trojan” and “worm” and not a concise description of the specific malware or its family.

As malware continue to evolve and rise in numbers [KVK14; AVT], researchers are investigating machine learning techniques such as classification and clustering to analyze malware. **Classification** is an instance of supervised learning where a trained set of correctly identified data is used as a reference to classify new data. Some examples of classification algorithms are *Naive Bayes*, *Random Forests*, and *Neural Networks* [Wikc]. **Clustering**, on other hand, is an instance of unsupervised learning, i.e, grouping unlabeled data object which are similar in some sense, in the same cluster. Some examples of clustering algorithms are *expectation-maximization* and *k-means* [Wika]. A good clustering system would be able to study behavior of a new binary to find, if the new binary is a variant of previously known malware and classify them accordingly.

Because AV label on malware families are not reliable, we look onto different clustering techniques to categorize our dataset into different families. **Pirscoveanu et al.** used *Random Forest* classifier on the behavior data set of 42,068 malware to achieve a high classification rate with a weighted average Area Under Curve (AUC) value of 0.98 [Pir+15]. **Moskovitch, Elovici, and Rokach** used *Naive Bayes* classifier based

on 20 malware-behavior to detect malware with mean detection accuracy of over 90% [MER08]. **Yavvari et al.** used behavioral mapping approach to cluster 1,727 unique malware pair samples [Yav+12]. **Firdausi et al.** in their paper did the measurement of five different classifiers, *k*-Nearest Neighbor, Naive Bayes, J48 decision trees, Support Vector Machine, and Multilayer Perception Neural Network, to classify the malware based on behavioral data, and state that machine learning techniques based on behavioral profile can detect malware quite efficiently and effectively [Fir+10]. Previous research work, showed that clustering and classification yields superior performance in timely detection of malware, against the arms race with malware authors, compared to signature based, dynamic or static analysis [Bai+07; Bay+09; Rie+09].

Bailey et al. introduced the first clustering system based on observed behavior of malware [Bai+07], which was later extended by Bayer et al. [Bay+09], to be scalable [Rie+09]. We studied the work of Bayer et al. in detail, as their work clustered malware in large scale; 75 thousands malware under three hours [Bay+09]. The clustering was done for tens of thousands of malware samples, but the approach still was not scalable to millions of samples we needed to cluster. The approach has a linear bootstrapping phase of Locality-sensitive hashing (LSH), after which the $O(n^2)$ hierarchical clustering starts. The whole premise of faster execution lies within careful tuning of multiple parameters and hash functions (to make the initial phase take care of most of the load), which had not been done by the authors for millions of samples (the biggest execution they had was for 75,000 samples). This means that we would have needed to tune and change the code as we go forward to get the results we hope for. Instead we preferred using something ready to use (not to spend time improving something that would not be considered any novelty for our work).

Another approach was to use a clustering algorithm that is scalable and capable to cluster millions of samples. We decided to map the problem to document clustering, considering each malware as a document, and their behavioral profile as the words in document. As **term frequency-inverse document frequency** (*tf-idf* a statistically measured weight to evaluate the importance of a word in document with respect to the whole corpus [Wike]) approaches have a large memory footprint, $O(\#documents \times \#words)$, we switched to clustering algorithms whose memory footprint does not depend on the number of documents, and decided to use *latent Dirichlet allocation* (**LDA**). *Latent Dirichlet Allocation* (**LDA**) is a generative probabilistic model for collections of discrete data such as text corpora [BNJ03, LDA]. **LDA**, equivalent to dimension-reduction algorithms for high-dimensional clustering, is one such algorithm which does not depend on the number of documents and its memory footprint is $O(\#words \times \#clusters)$. This gives us a more fine grained clustering compared to previously proposed LHS (Locality-sensitive hashing) based approach.

2.5 Summary and Motivation

Motivated by economic profit, there has been an increase in the number of new malware, and fighting between the malware families to control the larger share of the underground economy. To get the larger piece of the economy and show their superiority, malware family try to negate the existence and influence of another family. We showed some evidence of interferences between the malware families where they removed other malware, added a feature to remove other malware, or blocked other malware from infecting its victim. Such behavioral interference between the malware families is an interesting case to study and would provide a novel aspect of dynamic behavior to evolving malware. Our research provides a systematic way to find such behavioral interference of malware families on a large scale.

We gave an overview on two common malware analysis systems and reason for choosing *Anbuis*, a dynamic malware analysis platform, as we could run our candidate pairs in real time to check for behavioral interference. We see that different malware families have different techniques to inject themselves and keep themselves alive even after the system reboot. As described in section 2.1, they copy themselves in certain system paths, disguise themselves with benign filenames and register themselves to autostart services. The names of different resources created by malware can be random or peculiar. These patterns related to each family can be used to check the presence of particular family. We use this rationale in our heuristics to find probable malware candidates with behavioral interference. To select the sample candidate pair, we look for the malware that tries to access or delete certain resources, which was created by another malware, from another family. The detailed approach of selections of pair is described in subsection 3.2.5. We believe such behavior of malware is suspicious and interesting case of interference between two malware family.

We discussed why AV Vendors labeling of malware family are unreliable and how we will be using machine learning to achieve the clustering of malware to families. We discussed the use of machine learning techniques in previous research for clustering and classification of malware based on their behavioral profiles. The results of the work so far on classification and clustering of malware were good in order to improve efficiency and detection rate of the malware analysis system. However, the clustering of malware performed so far are on a small number of samples, consisting of tens of thousands of malware samples, and are not scalable. We present a different approach for large scale malware clustering, using LDA for document clustering and python

library *Gemsim* for the implementation.

Our working dataset consists of 22,154,180 malware samples. The study of behavioral interference between the malware families in this of a large scale is new research in the field of malware study. Our work will be a cornerstone in that topic. It will help to understand dynamic behavior of environment sensitive malware.

3 Methodology

In this chapter we will give overview of our system design and work flow. First, in section 3.1, we will give technical descriptions of terms we will be using to describe our work flow. In section 3.2, we will describe the overall procedure of our research work.

3.1 Terminology

In this section we give a detailed description of different terms we will be using throughout the report.

3.1.1 Behavioral Profile

Bayer et al. define **behavioral profile** as, “the abstraction of a program’s execution trace that provides information on the OS objects that the program operated on, along with the operations”. OS Object refers to resource type such as file, registry or section, that could be modified or queried with the system calls. System calls consisted of Windows NT, native API and the Windows API functions.

The behavioral profile was based on the execution traces of programs irrespective of order execution as reordering system calls could be done without changing the semantics of program [Bay+09]. It consisted of a list of different operations operated on the different OS objects during the execution of binary. The system calls that had same purpose as resultant output but different calling API name were generalized under single name—*NtCreateProcess* and *NtCreateProcessEx* would be generalized as, ‘*create*’ OS Operation for, ‘*process*’ OS object [Bay+09].

OS Objects

OS Object were primarily the resource that were created, delete, modified during the program execution. Bayer et al. define *OS Objects* as:

```
OS Object ::= (type, object-name)
type ::= file|registry|process|job|
        network|thread|section|
        driver|sync|service|random|
        time|info
```

An OS Object consists of its type and object-name. The type of OS Object are file, registry, process, job, network, thread, section, driver, sync, service, random, time, and info. An object-name is the name of the OS object. For an instance, 'c:\ntlos.exe' is an object-name for object type *file*.

OS Operations

Broadly, OS Operation is the generalization of a system call. Bayer et al. define *OS Operations* as:

```
OS operation ::= (operation-name,
                  operation-attributes?,
                  successful?)
```

An OS operation object consists of name of the operation, any additional attributes, and the status of the operation whether it was successful or not.

A snippet of behavioral profile is shown in Listing 3.1 with sample of operations executed on OS Objects file, registry, and section.

Listing 3.1: Behavioral Profile sample

```
op|file|'C:\\Program Files\\Common Files\\sumbh.exe'
  create:1
  open:1
  query:1
  write:1

op|registry|'HKLM\\SOFTWARE\\CLASSES\\CLSID\\{00021401-0000000000046}'
  open:1
  query:1
  query_value(''):1
  query_value('InprocServer32'):0

op|section|'BaseNamedObjects\\MSCTF.MarshalInterface.FileMap.ELE.B.FLKMG'
  create:1
  map:1
```

```
mem_read:1  
mem_write:1
```

To explain the behavioral profile shown in Listing 3.1, ‘*create*’ operation for file OS object ‘C:\ProgramFiles\CommonFiles\sumbh.exe’ was successful with success value 1, whereas ‘*query_value*’ operation with operation-attribute value ‘*InprocServer32*’ for registry OS Object ‘HKLM\SOFTWARE\CLASSES\CLSID\{00021401-00000000000046}’ failed with success value 0.

We had the “behavioral profiles” of the malware samples that we used to create new database which is described in section 4.4. Informations from *OS Objects* and *Operations* were used to extract resource activities (execution traces) of the malware (program).

3.1.2 Resource Type and Activities

As discussed before in section 3.1.1, an OS Object, are representation of resource types. For our research, we considered following 8 resource types into consideration, that could best determine the behavioral interference between malware. We will give a short description of each resource type according to Microsoft Developers Network documentation [Mice, MSDN].

File

A *file* is a means of storing resourceful information which can be retrieved or modified in future. File objects function as the logical interface between kernel and user-mode processes and the file data that resides on the physical disk. It not only holds the data written on the file but also a set of attributes maintained by the kernel for system purposes such as *File name*, *Current byte offset*, *Share mode*, *I/O mode* [Micb].

File type in the behavioral profile encompasses not only general file, but named pipe and mailslot resources. File is an important resource type as many malware creates or deletes file in order to infect the system or remove another malware from the system. These file activities will be important behavior to find the interference between malware families.

Registry

A *Registry* is a database defined by a system where different applications and system components store and retrieve data such as configurations settings for its use. The data stored in the registry varies according to the version of Microsoft Windows. Application performs the basic add, modify, retrieve, or delete operation in the registry through the

registry API [Micg].

Registry keys provide vital information on malware type and behavior as we have seen in section 2.1 that different malware families create different registry keys when they infect a system. Malware from same family modify specific registry key, which is used to detect their presence.

Service

A *Service* is a computer program that operates in system background, similar to UNIX daemon [Micj]. A *service* can be started at system boot through the Service Control Panel, or an application can also use service functions such as *StartService*, *OpenService*, *DeleteService* to configure services. However, it must conform to the interface rules of Service Control Manager (SCM) [Mici].

Malware can stop other services related to security or other malware, create a new service, or hook itself into autostart services. These service related activity are thus interesting to study malware behavior and interaction with other malware.

Section

A *section* object is sharable memory which is used by process to share its memory address space (memory sections) with other processes. It is also used by process to map a file into its memory address space [Mich].

In case of behavioral profile, it broadly represents memory mapped files—file with content in virtual memory, enabling application and multiple processes to modify the file by reading and writing directly to the memory [Micd].

Process

A binary can spawn one or more *processes*. A *process* is simply an instance of a computer program being executed that consists of instructions and current activity of program [Micf].

Malware trying to detect and kill the process created by another malware is interesting case of behavioral interference.

Job

A *Job* object makes grouping of process as single unit to manage possible. It can be named and shared securely to control attributes of processes grouped together and operation on a job makes the affect on all the process in its group [Micc].

Sync

A *sync object* is used to coordinate the execution of multiple threads as more than one process could share the handle of single synchronization object which helps for the interprocess synchronization between these processes [Mick].

The sync object type covers all the synchronization activities. [Mick].

Driver

A *device driver* is a program that is associated with certain device for its operation and control. It is used as an software interface to communicate between the hardware device and the operating system and other software [Wikb, Device Driver]

Windows represent devices with device objects, and one device could be represented by more than one device objects. All operation on device is conducted via device object [Mica].

We capture those loading and unloading of Windows Device Driver recorded in the behavioral profile.

Resource activities in our work refers to operations, such as *create, delete, modify, or access*, performed by a malware (program), on the resource types *File, Registry, Service, Section, Process, Job, Sync, or Driver*, during its execution. **Resource name** is same as object-name in *OS-Objects*[section 3.1.1]—name of the resource created, modified, deleted, or accessed. We use resource activities of malware samples to select the malware candidates that could exhibit behavioral interference [section 4.3]. Further, resource activities related to malware were represented as “*words*” related to “*document*” (malware) to create a text corpora for document clustering [section 4.5]. We describe the terms “*words*”, “*document*”, and “*corpora*” in subsection 3.1.3.

3.1.3 Words, Document, Corpora

In this section, we describe the terms “*words*”, “*document*”, and “*corpora*” and how we associate, malware samples and resource activities, with those terms in our work. The terms will be used extensively when describing clustering [section 3.2.4] and its implementation [section 4.5].

Words

In their work, Blei, Ng, and Jordan, describe word as, ‘A *word* is a basic unit of discrete data, defined to be item from a vocabulary indexed by $\{1, \dots, V\}$ ’ [BNJ03].

We represent a single resource activity of a malware as single word. For an instance,

a file creation activity will be a single distinct word and a file deletion activity will be another distinct word. Same resource activity—with same resource type, resource name and operations—will be considered as repetition of same word. For example, multiple registry keys created with same name by same or different malware.

Document

According to Blei, Ng, and Jordan, “a *document* is a sequence of N words denoted by $\mathbf{w} = (w_1, w_2, \dots, w_N)$, where w_N is the n th word in the sequence” [BNJ03].

A single malware sample will be represented as a single document and all the resource activities related to that malware will be the words in that document.

Corpora

“A *corpus* is a collection of M documents denoted by $D = \{w_1, w_2, \dots, w_M\}$ ” [BNJ03]. The total resource activities (words) related to all the malware samples (documents), in our dataset, will be our corpus.

3.2 Work Flow

In this section we outline an overview of our work flow. Figure 3.1 depicts the overall structure of our system.

3.2.1 Database

We required resource activities of the malware samples, to process and find malware with behavioral interference. We had access to the database that saved the analysis result of malware samples submitted to *Anubis*. It had resource activity of *File*, *Registry*, *Mutex* for operations *create*, *delete*, *modify*, *read*.

However, the old database was missing the resource activities that were not successful, for an e.g., failed attempt to delete a file. *Anubis* analyzed malware one at a time in total new OS environment; so the resources created during one analysis run were not present during the analysis run of another malware. Because of this, malware trying to detect or delete the resource created by another malware would be unsuccessful. A new database with record of such failed attempts was essential.

We used “behavioral profile” of malware sample, described in subsection 3.1.1, to get both the successful and failed resource activities. The “behavioral profile” of malware sample were parsed to get the resource name (object-name) and operations (operation-name) along with successful status, and was used to create new database. The new database was created for the above discussed 8 types of resource (*File, Registry, Service, Section, Job, Process, Job, Sync, and Driver*) and operations were generalized to *modify, read, delete*. The implementation is described in section 4.4.

3.2.2 Reverse Indexing

After we created the database, we created reverse index of the resource activities. The database had all the resource activities (failed and success) of the resource types: such as file created, file deleted, registry modified, registry accessed and so on. We mapped ‘resource name’, with all the malware, that had operations on that ‘resource name’. For instance, we mapped the resource name of the *files*, with all the malware that modified it. Same reverse index was generated for read and delete operations, and for other resource types, *registry* and *mutex*. With the reverse index, for each resource, we have a list of all the malware that modified, accessed, or deleted that resource. We used the reverse index in our heuristics to select candidate malware pairs.

3.2.3 Heuristics

We mapped reverse indexes, based on common resource name, to get malware set, say set ‘A’, that created a resource ‘r’ with another malware set, say set ‘B’, that tried to delete or read the same resource ‘r’. As described in section 2.1, malware families have different ways of infecting and taking control of system, peculiar to themselves. One can detect the presence of malware in the system, by checking the presence of unique resource (files, registries, and others) associated with that malware, in the system. Thus, when a malware tries to access or delete some resource created by another malware (with a failed attempt because each malware was analyzed by Anubis in new OS environment), that activity is interesting for our candidate selection.

We selected malware sample from each of those set ‘A’ and ‘B’, to get a candidate pair, with interference based on resource ‘r’. Large number of malware were present in each candidate set. A single resource name was created by tens of thousands of malware and being accessed by tens of thousands of another malware. We had to lower the number of candidate set to get substantial number of good candidate pair.

3.2.4 Clustering

We wanted to lower the size of candidate sets without losing the quality of our dataset. Malware variants belonging to same family, will have similar behavior pattern (code semantics) despite of code obfuscation. We divide our dataset into different clusters (families), based on the similar resource activities. Candidate pairs, with each malware in the pair from different family, trying to create/delete same resource has higher probability of behavioral interference than the previous heuristics.

Many previous research based on malware clustering were done for small number of malware samples [see section 2.4]. We needed an approach to cluster millions of malware samples. We modeled malware clustering to *document clustering* and used *LDA* for its low memory footprint, $O(\#words \times \#clusters)$, compared to *tf-idf*, $O(\#documents \times \#words)$.

Latent Dirichlet Allocation

A single resource activity—such as ‘file read’, ‘registry delete’ or ‘service modify’—would count as single ‘word’. All such resource activities of a single malware sample, is the total ‘words’ in the single document (malware). We created the corpus for document clustering with all the resource activities of all the malware dataset. We gave each resource type, operation name, and resource name a unique numeric code to represent the resource activity as a word. The number coding is given in Listing 3.2

Listing 3.2: Numeric codes given to resource and operation

```
RESOURCE_CODE = {"file" : "1", "registry" : "2", "section" : "3", "
    service" : "4", "driver" : "5", "sync" : "6", "process" : "7", "job" :
    "8"}
OPERATION_CODE = {"access" : "1", "delete" : "2", "modify" : "3"}
```

So a file delete activity of filename, ‘c:\gbot.exe’, with *file_name_id*, “4986” in our database, by some malware “A”, would be represented as single word “1_2_4986”.

Gensim

“Gensim” [RS10] is an efficient python library. We preferred using it because of its simplicity, well documented API, and ability to work on large corpus. We use the *multicore[Genb]* models for scalability. Some of the benefits of using the *ldamulticore* model were [Genb]:

- The model utilized the multi cores processor of the machine efficiently with parallelization making the clustering process faster.

- The training algorithm is streamed and we could feed the input documents sequentially even for large data.
- The training algorithm runs in constant memory with respect to number of documents. This made possible for us to process corpora that was larger than the memory size of our machine, as size of training corpus did not affect the memory footprint. The maximum size of our corpus was 81 Gigabytes.

3.2.5 Candidate Selection

The candidate selection steps, based on malware clustering, are summarized as follows:

- Let, R , be a set of candidate resources such that each resource “ r ” in R have some malware set that create it (say set A_r) and some other set of malware that try to (unsuccessfully) access/delete it (say set B_r).
- Combine all such sets A_r and B_r corresponding to “ r ” in R to sets A and B , respectively.
- Combine ‘ A ’ and ‘ B ’ and cluster them to cluster ids $[c_1, c_2, \dots, c_n]$ (n is number of family) such that any malware sample x in (A union B) can be tagged/mapped to cluster id $C(x)$, where $C(x)$ belongs to $[c_1, c_2, \dots, c_n]$.
- For each “ r ” in R , generate a set of candidate pairs P_r for experiment. P_r is a set of malware pairs (x_r, y_r) such that x_r belongs to A_r and y_r belongs to B_r and $C(x_r) \neq C(y_r)$, not belonging to same cluster.
- Generate such (x_r, y_r) pairs for all possible cluster pairs $(C(x_r), C(y_r))$ corresponding to a resource “ r ”.
- The final experiment set E is a set of such (x_r, y_r) for all resources r in R .
- Finally for any resource “ r ”, if the size of the set $|C(x) : x \in A_r| > n$ or $|C(x) : x \in B_r| > n$, we discard r and its corresponding experiment pairs from E . The resource modified/deleted by too many families is less interesting. We choose ‘ n ’ accordingly to filter resource associated with too many families.

3.2.6 Running the Candidate

Our chosen dynamic analysis system [see subsection 2.3.1], *Anubis*, analyzes only one binary at a time. We created ‘*packer*’ and ‘*unpacker*’ to execute both malware of a candidate pair, packed together as single binary, with time interval in between two

execution. We used the fact that Windows PE executable loader works fine even with extraneous concatenated data at the end of valid executable file. The **unpacker** is a self reading dropper binary. With **Packer**, we attach the append binary of the candidate pair, to the back of *unpacker* binary, one after another in sequence. Followed by the binary, meta-information, such as size of both binary and preferred time delay, was appended to the end of the *unpacker*. We analyze the packed *unpacker* binary in the *Anubis*. When executed, the *unpacker*, would read itself from the behind to get the meta-information, and recreate the packed binaries, and drop them inside the *Anubis* OS environment. After both the binaries are dropped, it execute the first binary, waits for time delay specified, and runs another binary. In the end, both the binary runs in the *Anubis*, and we analyze the result. In section 4.2, we implement the *packer* and *unpacker*.

3.2.7 Analyze the result

Anubis, generates result of analysis as *Extensible Markup Language* (XML) format. Every binary submitted to *anubis* is renamed into '*sample.exe*', and is considered as the primary analysis subject. All the binaries created and executed, after the execution of primary analysis subject, is tracked for its malicious activities. The XML report has the resource activities of each binaries presented under different XML node.

We are interested in 'access/delete' activity of the 'resource', based on which the candidate pair was chosen—'resource' created successfully by one malware, and failed attempt to access/delete the same resource by another. Any successful access/delete of that resource (files or registries or others) will be the change in behavior of one malware caused by the presence of another malware.

3.3 Summary

In this chapter, we described different terms used in our work in details and also gave an overview of our work flow. In next chapter, we will show how we implemented the work flow in our system.

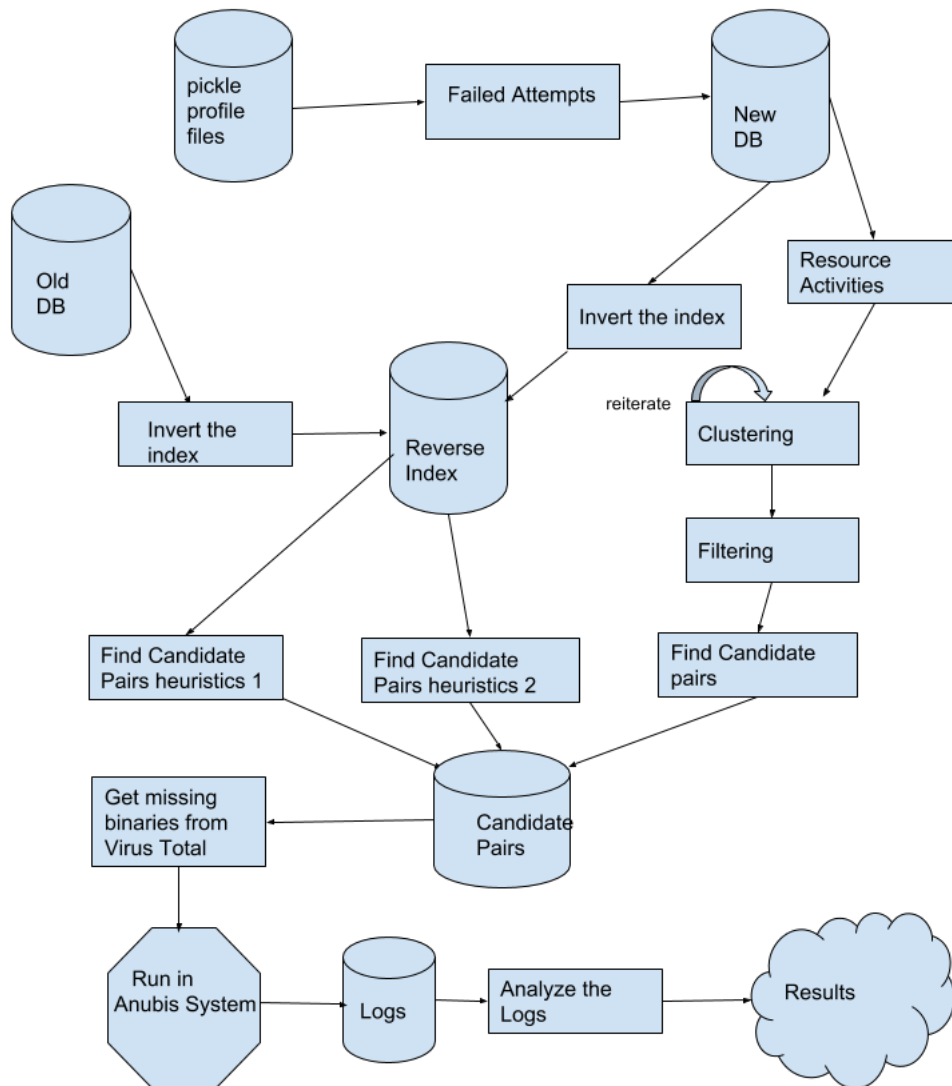


Figure 3.1: Overview of the research and experiment

4 Implementation

In this chapter we give a detail explanation of how we implemented and conducted our research as described in chapter 3.

4.1 Old Database and Reverse Index

Our work was based on wide variety of millions of malware samples, collected over the years, by *Anubis*. We had to effectively and efficiently analyze those to find the behavioral interference between malware families.

We started with studying the Anubis system and its database. We primarily dealt with two database of Anubis backend, the **'db_report'** and **'web_analysis'**. The *'web_analysis'* database was hit first for any binary submitted for analysis from public web interface. Some of the important tables to our work were *'result'*, *'file'*, and *'file_task'*. Each submission is a unique row data in *'result'* table. A new row is also created in *'file'* table with the *'md5'* and *'sha'* hash of the submitted binary. We refer the unique primary key of the *'file'* table as **malware id**. The *file* and *'result'* tables are associated through *'file_task'* table. The analysis of the sample would be done for different behavioral activities related to resources such as File, Registry and Mutex activities. These activities were saved in *'db_report'* database. The resource activities of the malware in **'db_report'** database was associated with the **'web_analysis'** database by the constraint key *'result_id'* of the *'result'* table. In Listing 4.1, in the first line, we show a simple *sql* statement to the *result_id* and *md5* of the binaries submitted to Anubis from the *'web_analysis'* database. In the second line, we get the names of the files created by the binary whose *result_id* is *'12345'* from the *'db_report'* database.

Listing 4.1: *sql* showing database structure to get file created activities of a malware sample

```
1 SELECT result_id, md5 FROM web_analysis.result join web_analysis.  
    file_task using (task_id) join web_analysis.file using (file_id) WHERE  
    task_id = result_id;  
2 SELECT name from db_report.file_created join db_report.file_name using (  
    file_name_id) where result_id = '12345';
```

The total number of malware samples that we had in our test database were **22,154,180**. Initially we considered 3 resource types *File*, *Registry*, *Mutex*, and queried the database for *create*, *read*, *delete* resource activities. For each resource type, their *create*, *read*, *delete* resource activities were queried. Our first step was to create a reverse index from the database so that we could get the list of malware that created/deleted/read the resource. Since, the number of malware to process were in millions, trying to save all their activities in a data structure would cause our machine to run out of memory and crash. We approached this problem with map reduce technique.

We worked on a batch of 50,000 malware at a time, and saved the reverse index of activity to the file with a numbering for each batch. The resultant numbered files were in the format where resource name and list of unique malware ids were separated by commas (,) as delimiter. The numbered files of each resource types were sorted, and then joined, to get the final reverse index. The sort and join operation is shown in Listing 4.2 and was fast as it was a merge sort $O(n \times \log(n))$. Comma is the field separator for both commands and was done on first field which is the resource name.

Listing 4.2: Sort and join the reverse index

```
LANG=en_EN sort -t, -k 1,1 $file_name
LANG=en_EN join -t , -a1 -a2 $file_name1 $file_name2
```

A snippet of reverse index of file created activity is shown in Listing 4.3, where resource type '*file*', with resource name '*mbr.exe*', is created by malware with ids 189524063, 184501719, 87504631, and 86763863.

Listing 4.3: Sample of reverse index created for File activity

```
C:\mbr.exe,189524063,184501719,87504631,86763863
Buttons,111448211
C:/DOCUME~1/ADMINI~1/LOCALS~1/Temp/telnet.exe
,178046895,174206059,183601891,89650247
C:/DOCUME~1/ADMINI~1/LOCALS~1/Temp/1.jpg,161552035,116241803
```

From the reverse index of the resource activities of the Malware, we mapped created activities against the deleted or read activities. We started looking for one to one interaction of malware to a single resource. We looked for a set (a, b) , where malware '*a*' creates the resource *r*, and malware '*b*' deletes the same resource, *r*, such that no other malware has create or delete activities on that resource *r*. We ran those malware pairs in the Anubis system using the *Unpacker*.

4.2 Packer & Unpacker

In order to run the pair of malware together inside the Anubis environment we made a Win32 console application (Anubis VM is based on Windows OS.), named **Unpacker**. We used the fact that we can append any data at the end of Windows PE executable, and it would not affect the executable's program flow. We wrote a **packer** program that would add the candidate binary pair at the end of the *Unpacker* binary and then further appends the time delay and file size of each candidate binary as meta information. The structure of the Unpacker binary is shown in Figure 4.1. The *Unpacker* binary, when executed, would read itself from the back to get the meta information and read candidate binaries bytes. It will then create the candidate binaries from the read bytes, and run both binaries with a time delay given.



Figure 4.1: Structure of the Unpacker binary that would create the candidate pair and run them with delay.

Code snippet of the '*Unpacker*' binary is shown in Listing 4.4. We used a struct of 3 integer size to read and hold the meta information. The size of last three *unsigned int* byte of *Unpacker* has the binary pair sizes information and the delay time, known as meta information. The offset for meta-information was calculated by deduction of $3 \times \text{size of 'uint'}$ from the total size of itself (Unpacker). We calculate the starting position of appended binaries, and use '*fseek*' function to set the file position pointer there. We then start reading the bytes until the exact size of binary is read. The read bytes were then saved to create new binary file. We used *windows.h* standard library's functions: '*CreateProcess*' function to execute the binary, and '*Sleep*' function for delay in between two execution.

Listing 4.4: snippet of Unpacker.c file

```
1 /* struct for storing meta information */
2 typedef struct {
3     unsigned int delay;
4     unsigned int fsize1;
```

```
5  unsigned int fsize2;
6  }meta_info;
7
8  /* reading the meta information and first binary */
9  rfp = fopen(argv[0], "rb");
10 wfp1 = fopen(fileName1, "wb");
11
12 fseek(rfp,0,SEEK_END);
13 size = ftell(rfp);
14 offset = size - sizeof(meta_info);
15 fseek(rfp, offset, SEEK_SET);
16 fread(&info, 1, sizeof(info), rfp);
17
18 /* calculate the unpackersize from the offset and files size. */
19 unpackersize = offset - (info.fsize1 + info.fsize2);
20
21 /* rewind back and to the point of the start of file1 */
22 fseek(rfp,0,SEEK_SET);
23 fseek(rfp, unpackersize, SEEK_SET);
24
25 nread_sofar = 0;
26 while (nread_sofar < info.fsize1) {
27     nread = fread(buf, 1, min(info.fsize1 - nread_sofar, sizeof(buf)), rfp
28         );
29     nread_sofar += nread;
30     fwrite(buf, 1, nread, wfp1);
31 }
32 fclose(wfp1);
```

4.3 Initial Experiment

During our initial run of candidate pairs, we found lots of dropper malware causing this interaction. For a candidate pair (a, b) , binary 'a' was a dropper that would create many binaries including the binary 'b', and binary 'b' actually read itself upon execution, which was recorded as read activity by Anubis. After running many other candidate pairs and analyzing the results manually, we were able to understand the Anubis report in depth and also found a logical error on our current approach.

Our notion behind checking the malware interaction was finding candidate pairs such that one malware 'a' creates some resource, 'r', and another malware 'b' tries to access or delete the same resource, 'r'. But, Anubis ran each submitted binaries in an isolated environment; hence there was no way that a malware sample 'b' would find the resource that was supposed to be created by malware 'a'. We should have been looking for failed attempt activities, where a malware sample unsuccessfully tries to access or delete a resource created by another malware. But, the current database had no record of such failed attempt. This lead us to look for the alternatives where we could find log of such failed attempt activities during the execution of binary.

We parsed the behavioral profiles, as described in subsection 3.1.1, of malware samples to find failed activities of deletion and access.

4.4 Creation of Database

Recreating the database was one of the bottleneck in our project and consumed much time. The behavioral profile files had to be accessed via network file system. We need to walk through large list of directories and file, to find the behavioral profile pickle [Pyt] of specific malware. We found 16,031,518 behavioral profile files out of 22,154,180 malware.

We considered only 8 of the resource type into account while parsing the profile files; those were File, Registry, Sync, Section, Process, Service, Job, and Driver [see subsection 3.1.2]. Windows Native and Windows API calls were generalized into OS Operation during the creation of behavioral profile. We went through the list of OS Operations [section 3.1.1] and mapped them into the broad three categories *Modify*, *Access*, and *Delete*. The modify, access, and read list for the resource types *file*, *registry*, *process*, *job*, *driver*, *section*, *sync*, and *service* are shown in Listing 4.5

Listing 4.5: Mapping of generalized OS Operation from behavioral profile

```
MODIFY_LIST = {
    file: ["create_named_pipe", "create_mailslot", "create", "rename",
          "set_information", "write", "flush_buffer", "map"],
    registry: ["create", "restore_key", "save_key", "set_value", "
              set_information", "mem_write"],
    process: ["create", "set_information", "suspend", "resume", "unmap",
              "map"],
    job: ["assign", "set_information"],
    driver: ["unload", "load"],
```

```
    section: ["create", "map", "unmap", "mem_write", "set_information"
    ],
    sync: ["create", "map", "set_information", "mem_write"],
    service: ["create", "start", "control"]
}

ACCESS_LIST = {
    file: ["query_file", "query", "open", "query_directory", "
    query_information", "read", "monitor_dir", "query_value"],
    registry: ["enumerate", "enumerate_value", "monitor_key", "open",
    "query", "query_value", "mem_read"],
    process: ["open", "query"],
    job: ["open", "query"],
    driver: ["query"],
    section: ["open", "query", "mem_read", "read", "query_file", "
    query_system"],
    sync: ["open", "query"],
    service: ["open"]
}

DELETE_LIST = {
    file: ["delete", "open_truncate"],
    registry: ["delete", "delete_value"],
    process: ["delete"],
    job: ["delete"],
    driver: ["delete"],
    section: ["delete"],
    sync: ["delete"],
    service: ["delete"]
}
```

We used **MySQL Version 5.5.46** as our database engine. MySQL [MySb] is highly scalable and flexible relational database system which complies with the ACID model [MySa] design principle. We used multiple workers to create the database, and ACID compliance prevented from inconsistency of data when being updated across multiple tables.

While creating the new database, we hit the integer overflow for the primary index key of 'registry access' table. We did not anticipate the number of records to cross maximum 'int (10)' limit 4,294,967,295. We created another "registry access" table, with

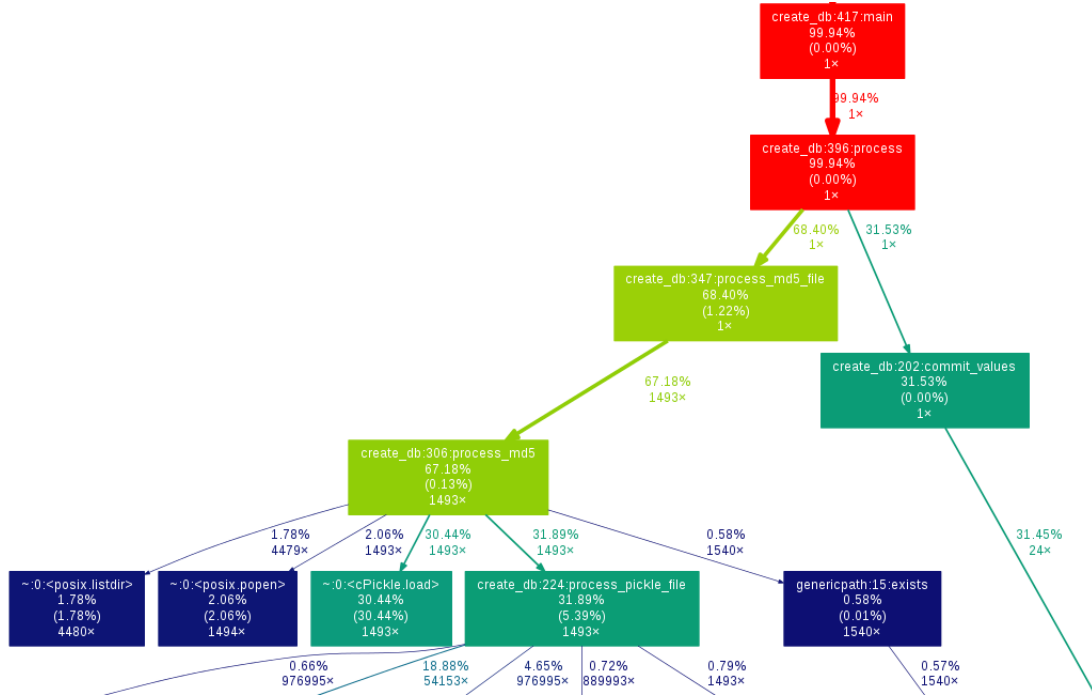


Figure 4.2: Profile of new database creation

different table name, and start inserting the registry access records in the new table. When accessing the data for later, we re-factored our program so that we checked both the registry tables in order to find the registry access activities of a malware sample. The final database size was 1.2 Terabyte.

We processed 16,031,518 behavioral profiles. About 62% of execution time was taken to load the gzip pickle [Pyt] of malware profile and the normal SQL CRUD (create, read, update, and delete) operation, which can be seen in Figure 4.2.

After the creation of new database, we made a reverse index, like before, for the 'resource name' to 'malware ids' modifying, accessing, and deleting the resource. This time the refined database had both the success and failed resource activities. The reverse indexes were used to map resources that were successfully modified with resources that were read/accessed with failed attempt. For instance, we made a mapping between file successfully modified and failed file deletion, and mapping between file successfully modified and failed file access. We made same mapping for all other 7 resource types. All the mapping was done based on the common 'resource name'.

With the reverse index mapping, we chose the candidate pairs such that one malware created the resource and another malware made a failed attempt to delete/access the same resource. But, the number of possible pairs were too many with this simple heuristic and we hit the *n-combination* problem. A single resource ‘r’ would have been created by tens of thousands of malware and another tens of thousands of malware trying to access/delete it unsuccessfully. The combination of candidate pairs from the candidate sets with thousands of malware are of large number to run and analyze result.

We wanted to filter our candidate sets without compromising the quality. We performed clustering of the malware based on their resource activities (behavior) to address this problem. Malware dataset were clustered into different families and candidate pairs were chosen such that they belong to different families.

4.5 Document Clustering

We filtered our malware dataset from the reverse index mapping by removing all resource activity that we confirmed as benign based on our knowledge. We sorted the reverse index (resource name to malware ids) with respect to the number of malware ids associated with the resource name in descending order. With this, we had most commonly modified/accessed/created resource at the top of the list. We went through the resource name until we found some interesting resource name which does not look benign. We excluded all benign resources preceding the first interesting suspicious resource name. For instance, file resource name such as ‘*Dr. Watson.exe*’ and ‘*Sample.exe*’ were some resources with highest number of malware interacting with them. The reasons are ‘*Dr Watson*’ file is created whenever a binary crashes and *Sample.exe* is the name, the submitted binary gets renamed to, by Anubis. We filtered all such benign resource activities related to resource type file, registry, section, sync, and process. Resource types service, job, and driver did not have any interesting mapping. The total number of malware samples were filtered to 7,362,635.

We created the text corpora for those 7,362,635 malware, and performed the document clustering. We converted all the resource activities related of the malware samples into the corpora text as discussed in subsection 3.2.4. Each resource activity was represented as word, each malware was represented as the document, and the collection of documents were text corpora. The process was database intensive as seen in Figure 4.3, and took almost week for us to get complete text copora. The resultant text corpora was about 81 Gigabytes of data.

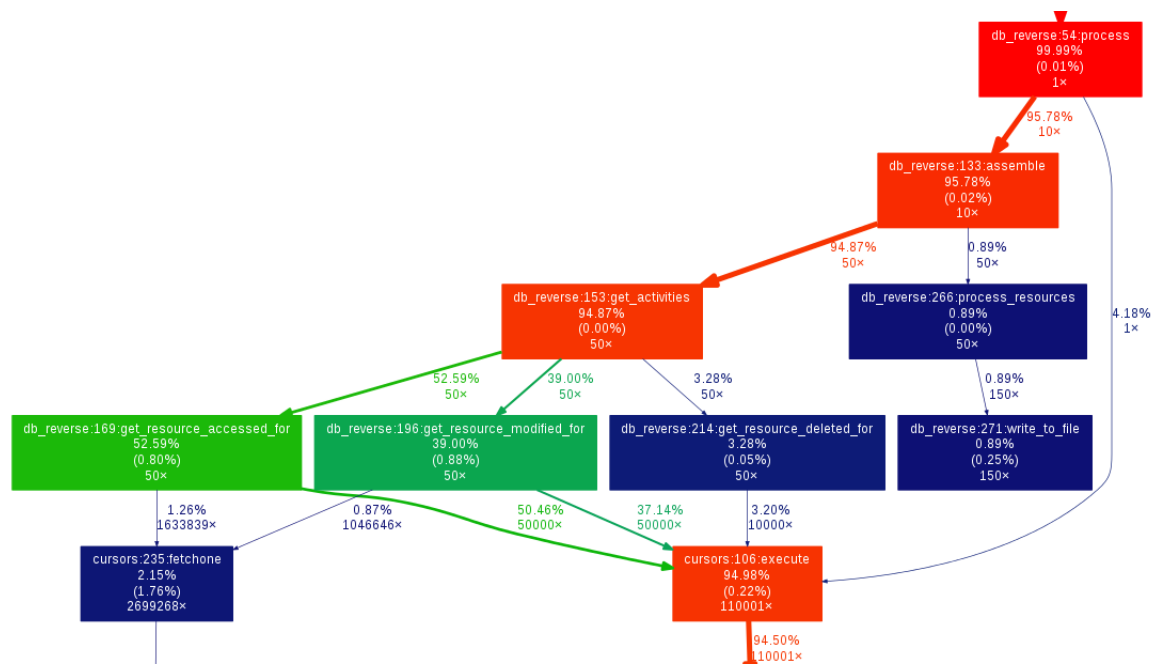


Figure 4.3: Profiling of building a corpus

4.5.1 LDA Model

We used python module Gensim [ŘS10, Gensim] for the clustering and used the LDA multicore model which we described in section 3.2.4. The LDA model generation code snippet is show in Listing 4.6. The corpora consisted of one document per line. We created a dictionary from the corpora using Gensim '*corpora.Ditionary*' module [Gena]. Dictionary is representation of all the unique tokens (words) by a unique token-ids. We filtered the dictionary by discarding any resource activity that occurred in less than 10 or more than 1 million for clustering, as those activities are too less or too common to take into consideration. The lower and upper limit were chosen based the cumulative distribution function graph of resource activities. We kept only 200,000 tokens after the filtering. This is done in line 7 [Listing 4.6], where the arguments passed into '*filter_extremes*' method are minimum threshold (which is 1000), maximum threshold in fraction (which is 0.14: 1,000,000 out of total 7,362,635 documents), and total number of frequent words to keep after filtering (which is 200,000). In line 9–12 [Listing 4.6], we make an iterator to read the corpus. The iterator operates on each line, which represents a document, of corpus text file and yields a bag of words of the document. Bag of words is a list of two-element tuple, which represents word (token-id) and its count (number of occurrence) in document. In line 15 [Listing 4.6], we create a LDA model for our corpus with 1000 topics. The LDA gives the probability of different clusters that a document can belong to and we assign the document to the cluster with highest probability.

The number of clusters created were “662”. The largest cluster size was 227,940 and the lowest was 1. The histogram and cumulative distributive graph showing the sizes of cluster can be seen in 4.4, 4.5, and 4.6. From the graph we can see that distribution of cluster size was mostly below 50,000. 90% of the cluster, about 629 out of 662, falls under the cluster size of less than 50,000. Similarly, 4 million malware, which is the 65% of total malware clustered, are in the cluster size of less than 50,000.

4.5.2 Inter-Distance and Intra-Distance

We calculated the distance based on the average number of common words between the malware pair. **Intra-distance** represents the average number of common words between the malware pair from same cluster. **Inter-distance** represents the average number of common words between the malware pair from different clusters. Since

Listing 4.6: Script to run Gensim LDA

```
1 from gensim import corpora, models
2 import sys
3 document_name = sys.argv[1]
4 # read the file with malware activities and create dictionary
5 dictionary = corpora.Dictionary(line.split() for line in open(
    document_name))
6 # filter the dictionary for extreme
7 dictionary.filter_extremes(no_below=10,no_above=0.14,keep_n=1000000)
8 # create a iterator corpus as the file is large 80GB
9 class MyCorpus(object):
10     def __iter__(self):
11         for line in open(document_name):
12             yield dictionary.doc2bow(line.split())
13
14 corpus = MyCorpus()
15 lda = models.ldamulticore.LdaMulticore(corpus=corpus,id2word=dictionary,
    num_topics=1000)
```

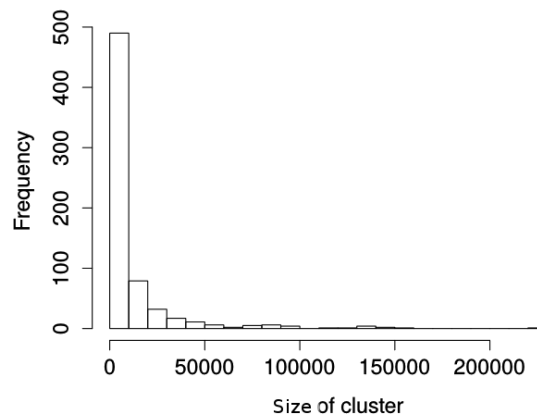


Figure 4.4: Histogram showing the distribution of Cluster size

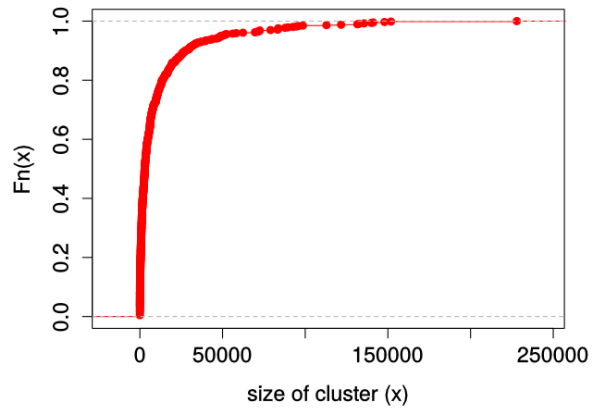


Figure 4.5: CDF between size of cluster and topic fraction

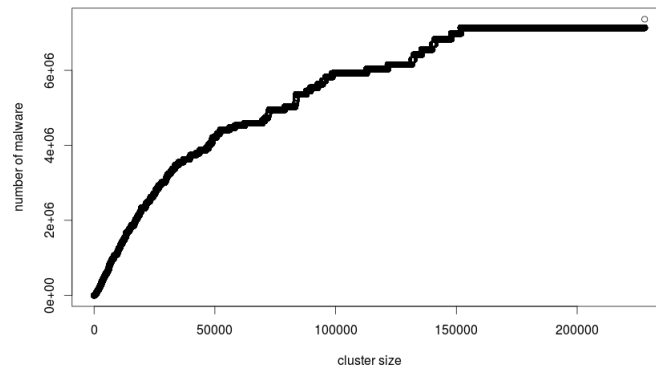


Figure 4.6: CDF between size of cluster and total number of malware

we want to cluster malware with similar behavioral activity together in same cluster; the intra-distance should be high (higher similarity among malware samples of same cluster), and the inter-distance should be low (lower similarity among malware samples from different cluster).

To show the quality of our clustering we provide the following graph showing the graph of inter-cluster and intra-cluster distance in Figure 4.7 and Figure 4.8.

In case of intra-distance, for a cluster, we randomly selected 1000 malware pair (if possible because there were some clusters of size as small as 1), from the combinations of malware samples belonging to that cluster. We calculated the average number of common resource activities(*words*) present among the malware(*document*) pair. We can see that the average common words between the intra malware sample were good with intra-distance of at least 500 covering 80% of family topics [Figure 4.7]. For the inter-distance calculation, a cluster was paired with other clusters, and from those cluster pair, we randomly selected 1000 malware pair (if possible because there were some clusters of size as small as 1). We calculated the average common resource activities between those malware pairs to get the inter-distance. We can see that the inter-distance of only 10 was covering almost 90% of family topic [Figure 4.8].

4.6 Finding Optimal Candidate Pairs

After the clustering, tens of thousands of malware associated with the resource, would now be reduced and represented by hundreds of families (clusters), that those malware belong to. As described in subsection 3.2.5, we chose the candidate pair corresponding to a resource, such that each malware in the pair belongs to different clusters. In order to find the optimal set of candidate pairs we interpreted the interaction of malware and resource, with respect to cluster, into Flow Network.

4.6.1 Max Flow Approach

We wanted to find the optimal pair of malware such that we have all the interesting mapped resource covered along with the cluster associated with it. We represented the mapping between the resource, malware, and cluster as a flow network, and run the max flow algorithm as given in Figure 4.9.

The network is made of 4 layers, other than sink and source. Layer one is read/delete malware, the malware samples that tried to access or delete interesting resources but failed. Layer two is combinations of clusters (*ic=input-cluster*), that the malware with failed access or delete attempt belongs to, and the resource on which the malware

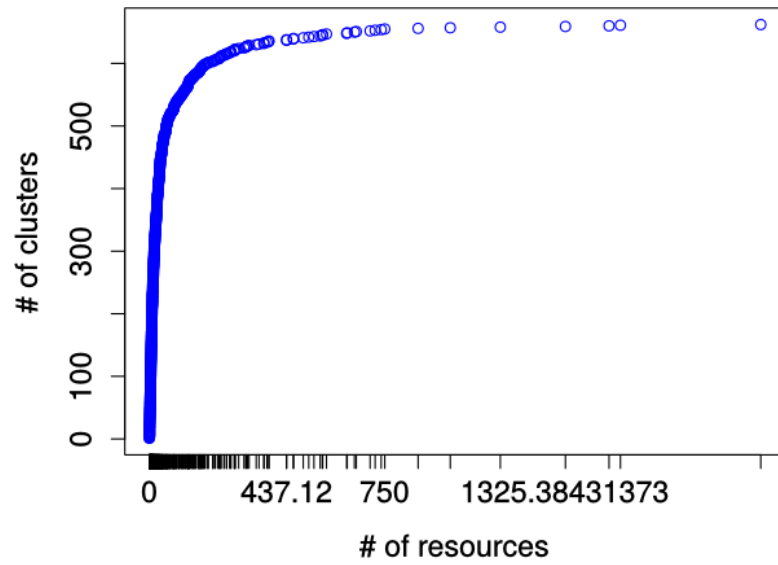


Figure 4.7: Graph showing cdf distribution of common resource between same family topic

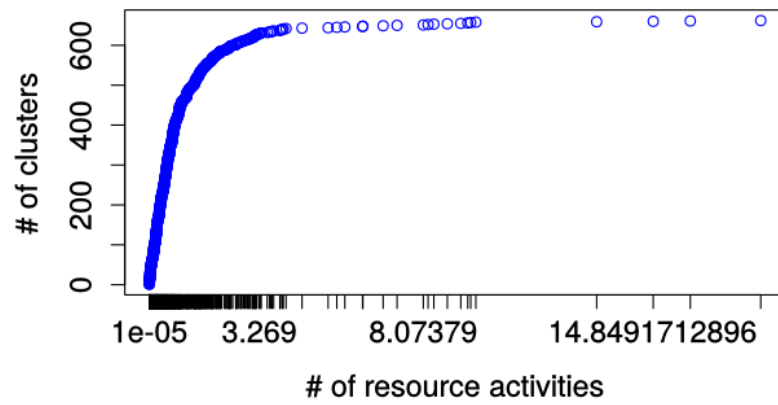


Figure 4.8: Graph showing cdf distribution of common resource between different family topic

tried to operate. Layer three is the combinations of clusters ($oc=output-cluster$), that the malware with successful modification operation belongs to, and the resource that they could successfully modify. Layer four is the malware that successfully modified the resource.

The flow rules were:

- All malware from layer one is connected from sources and also connected to the input cluster and resource combination it belongs to.
- All input-cluster and resource combination in layer two is connected to all output cluster resource combination in layer 3 that has a matching resource.
- All output-cluster and resource combination in layer 3 is connected to the corresponding malware in layer 4.
- Each malware in layer 4 is connected to the sink (T).

The capacities were:

- All connections have capacity of infinite except connections from layer 2 to layer 3.
- All connections from layer 2 to layer 3 have a capacity of one.

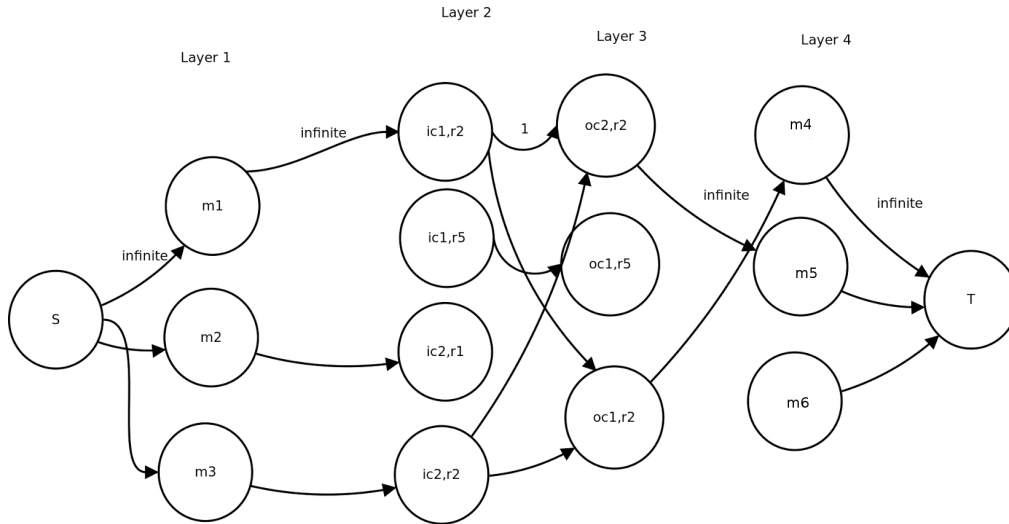


Figure 4.9: Graph representing the max flow implementation

The maximum flow in this network corresponds to an optimum match up. To explain, in Figure 4.9, ' m_1 ' in layer 1 is connected to (ic_1, r_2) in layer 2. There are two

cluster-resource combination, (oc_2, r_2) and (oc_1, r_2) , in layer 3, that has resource ' r_2 ' common with (ic_1, r_2) cluster-resource combination. So our candidate pairs would be, (m_1, m_5) and (m_1, m_4) operating on r_2 . Path from source (S) to m_2 in layer 1 and (ic_2, r_1) which does not reach the sink (T), thus, is omitted. The max flow approach gave us optimal candidate pairs such that each pair of cluster is only covered once. However, the approach did not take care of repetition of cluster pair corresponding to different resource. If malware pair (m_1, m_2) is associated with resource (r_1, r_2, r_3) , same candidate pairs gets repeated three times. We wanted to group those repetition so that we can run single malware pair and analyze the behavioral interference they might have on different resources. We used heuristics approach to eliminate those repetition.

4.6.2 Heuristics Approach

The problem was to find the “minimal set” of malware pairs that covers all unique cluster (family) pairs (dictated by the set of all candidate pairs) and it also covers all resources that help build the candidate pairs, i.e., for each resource ' r ' from resources ' R ', at least one malware pair from the final set should correspond the resource r .

The relations has been represented in the graph below, where, I is a set of input clusters from set ' A ' and ' O ' is the set of output clusters from set ' B '. Set ' A ', ' B ' are the sets of malware samples successfully modifying the resource and accessing/deleting the resource with failed attempt, respectively. ' R ' is the set of all interesting resources.

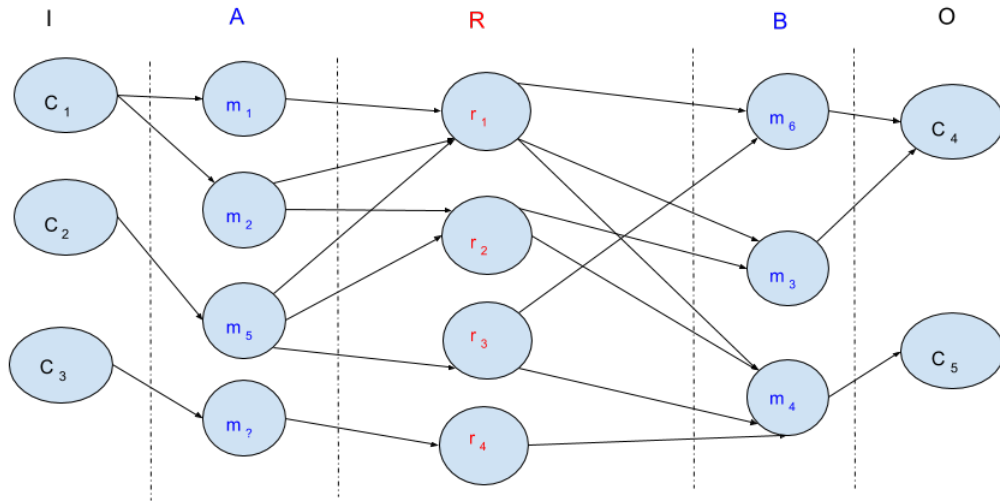


Figure 4.10: Heuristics approach to optimal malware pair selection

Listing 4.8: Pseudo code (Python) to get minimal set of candidates for all resource

```

1 candidate_set = set()
2 for c_pair, v in db.iteritems():
3     # reverse sort malware pairs by number of associated resources
4     x = sorted( [(len(b), a) for a,b in v.iteritems()] , reverse=True)
5     r_set = set()
6     for c, m_pair in x:
7         cur_r = v[m_pair]
8         if not r_set.issuperset(cur_r):
9             r_set = r_set.union(cur_r)
10            candidate_set.add(m_pair)

```

In the Figure 4.10, m_1, m_2, m_5 samples create resource r_1 , which is accessed (failed attempt) by m_6, m_3 , and m_4 . The malware m_1 and m_2 maps to cluster c_1 . Malware m_6 and m_3 maps to cluster c_4 , and so on. We need to find the minimal number of paths from each element c_x of set ' T ' to all reachable elements in ' O ' (reachable from c_x), such that all reachable elements ' r ' in ' R ' (reachable from c_x) are traversed. From such minimal set, we generated the candidate pairs by taking members of A and B from the path.

We created the data structure as shown in 4.7. The data is a dictionary. All candidate cluster pairs are keys and the value is a dictionary whose keys are malware pairs (all candidate malware pairs belonging to the cluster pair) and values are the list of corresponding resource.

Listing 4.7: Database Structure

```

1 db = { (c_i, c_o) :
2     { (m_a, m_b) : [ r1, r2 ,...],
3         ...,
4     }
5 }

```

The reduced candidate set was computed as shown in pseudocode 4.8. It is a greedy algorithm starting from the malware pair that corresponds most number of resource interactions. For each malware pair it checks if that pair has been already chosen, and if not, adds the pair to the candidate list.

4.7 Running the Candidate Pairs

In total we had 263,701 candidate pairs to run the experiment. We were provided with remote access to 7 instances of Anubis system for running candidate pairs. For each candidate pairs we packed them together using the '*Pakcer*' and dropped them inside Anubis system using the '*Unpacker*' as described in 4.2. The time delay between the execution of two binaries was set to 5 minutes. This allowed the first binary enough time to perform its resource activities before the second binary starts. Some of the missing binary from the candidate pairs were downloaded from *VirusTotal*.

5 Results and Discussion

Table 5.1: Number of candidate pairs and positive rate w.r.t. Resource types

Resource types	# candidate pairs	# of interfering pairs	True positive
File	213171	X	X
Registry	39899	X	X
Sync	7781	X	X
Section	2786	X	X
Process	54	X	X
Total	263691	X	X

6 Conclusion and Future Work

We have presented a systematic approach to find the behavioral interference between the malware families at large scale. We analyzed the behavioral profile of millions of malware samples to find the probable candidate malware pairs that could interfere with each other. The candidate pairs were then run together in the Anubis system, to detect the interference during live run.

Using document clustering, where each malware was represented as a document and their resource activities as words, we clustered the malware dataset into different families. We used heuristics based on common resource to select probable candidate pairs, such that one malware creates a resource, and another malware tries to delete or access the same resource. Also, the malware samples in a candidate pair belonged to different families.

We showed that the behavioral interference between the malware families exists, and also illustrated an approach to find such case where malware belonging to different family try to detect each others' presence and remove the resources, such as files or registries, created by another malware. This behavior is also one of the traits of environment-sensitive malware.

Glossary

computer is a machine that. . .

Acronyms

ACID Atomicity, Consistency, Integrity, and Durability.

API Application Programming Interface.

AV Anti Virus.

C&C Command and Control.

CRUD Create, Read, Update, and Delete.

DDoS Distributed Denial of Service.

DLL Dynamic Link Library.

LDA Latent Dirichlet Allocation.

OS Operating System.

P2P Peer to Peer.

SQL Structured Query Language.

TUM Technische Universität München.

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