Malware Behavior Analysis

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Outline

- Introduction
- Malware behavior
  - Similarities
  - Phylogenetic tree
- Experimental validation
- Conclusion & future work

Introduction

- Malware collectors gather a large amount of malwares ± 1000 malwares per month[1]
- A lot of malwares are unknown, on average 42% are not detected by 5 pieces of up-to-date anti-virus software[2]
- Anti-reverse engineering techniques
  - 18% of the malwares cannot be disassembled with objdump, a disassembler
  - According to PEiD a tool that identifies packers, 47% use an unknown packer / encryption technique
  - 15,4% cannot be debugged and not be emulated by the Norman sandbox
- Need for automated analysis & identification, classification of malwares → *phylogenetic tree* of malwares

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[1] ASTRAnet

[2] Sample of 104 random chosen malwares

Related Work

- Malware Normalization [Christodorescu, 2005]
  - Revert code obfuscation by analyzing a malware's assembler code
- S.A.V.E. [A.H. Sung, 2004]
  - Use static analysis to extract function calls
  - Represent function calls as vector & compute distances
  - Generate signatures from vectors
- Behavioral Classification [T.Lee, 2006]
  - Define malware events and classify them
  - Partition clustering based on a modified LevenShtein distance
- Recognizing Self-Mutating Malware By Code Normalization And Control-flow Graph Analysis [Danilo Bruschi, 2006]
  - Malware detection is reduced to the sub-graph isomorphism problem

Malware behavior

- A malware is a software that uses OS function calls
- A sequence of called functions is a malware behavior
- Identify a malware's function calls in a list of executed functions
- The function call sequence is mapped on a numerical sequence

Example

LoadLibraryA	GetProcAddress	GetProcAddress	CreateFile
⇕	⇕	⇕	⇕
1	2	2	10

Malware behavior

- Let $\mathcal{F}$ be the set of functions called during execution
- Let $\mathcal{A}$ be the set of function calls that a malware M can perform
- $\mathcal{A} \subset \mathcal{F}$
- A function call $a \in \mathcal{A}$ is mapped to a code $c \in \mathcal{C} \subset \mathbb{N}$
- A malware behavior is a word: $a_1 a_2 a_3 \dots a_n \in \mathcal{A}^*$

Malware behavior

Determination of malware actions

- Virtual OS shows the function calls done by the malware and those by the OS itself
- Let D be the set of memory addresses $D \subset \mathbb{N}$
- Let L be the set of loaded libraries
- A library with its functions is loaded in memory $(L, \mathcal{I}, D)$ $\mathcal{I} \subset L \times D$

Property

Let $m \in D$,let $f \in \mathcal{F}$ $(f, m) \notin \mathcal{I} \Leftrightarrow f \in \mathcal{A}$

Malware behavior similarities

- A W32 malware is technically limited!
- Gathers system information i.e. LoadLibrary, GetProcAddress
- Becomes durable on the machine i.e. CreateFile, RegCreateKey
- Communicate i.e. *connect*, *send*, *recv*

→ imagine a similarity / distance function between malware behaviors and create a phylogenetic tree

Malware behavior similarities

Idea: Define a similarity or distance between two malware behaviors, based on edit distance matrix

- Let $S_{M_1} = a_1 a_2 a_3 \ldots a_m \in \mathcal{C}^*$
- Let $S_{M_2} = b_1 b_2 b_3 \ldots b_n \in \mathcal{C}^*$
- Map the sequences of called functions on the matrix R

$$\begin{array}{c|ccccc} & b_1 & b_2 & b_3 & b_j & b_n \\ \hline a_1 & & & & & \\ a_2 & & & & & \\ a_3 & & & & & \\ ai & & & & & \\ a_m & & & & & \end{array}$$

- Assigning scores

Malware behavior similarities

Assigning scores

- Matrix R
- $M_{ij} = \begin{cases} 1 & \text{if } a_i = b_j \\ 0 & \text{otherwise} \end{cases}$
- $R_{1j} = M_{1j},\ R_{i1} = M_{i1}$
- $R_{ij} = M_{ij} + \max\left(\max_{1\leq k\leq i-1} R_{k,j-1}, \max_{1\leq k\leq j-1} R_{i-1,k}\right)$

Similarity function

$$\sigma'(S_{M_1}, S_{M_2}) = 1 - \frac{2\cdot\max R_{ij}}{m+n}$$

Malware behavior similarities

Property of the similarity σ'

- Order of function calls influence the similarity
  - Parallelism during execution
  - Order is influenced by multi-threading
  - A malware may create more processes, processes may communicate IPC

- Create a similarity where the order is not important
- Extend malware behavior to a set E of called functions sequences
- E.g. $E = \{\underbrace{a_1 a_2 a_3 \ldots a_n}_{\text{done by thread 1}}, \underbrace{b_1 b_2 b_3 \cdots b_m}_{\text{done by thread 2}}, \ldots\}$

Malware behavior similarities

Usage of the Hellinger distance

- Consider the frequencies of called functions
- Create a contingency table
- Apply smoothing technique
- Compute Hellinger distance

$$d(a,b) = \left[\Sigma_i^N \left(\sqrt{a_i} - \sqrt{b_i}\right)^2\right]^{\frac{1}{2}}$$

Malware behavior similarities

Usage of the Hellinger distance

Example

	GetProcAddress	LoadLibrary	connect	CreateFile
M_1	$\frac{10(1-\varepsilon)}{17}$	$\frac{5(1-\varepsilon)}{17}$	$\frac{2(1-\varepsilon)}{17}$	$\frac{\varepsilon}{1}$
M_2	$\frac{2(1-\varepsilon)}{3}$	$\frac{\varepsilon}{2}$	$\frac{1(1-\varepsilon)}{3}$	$\frac{\varepsilon}{2}$
M_3	$\frac{5(1-\varepsilon)}{11}$	$\frac{5(1-\varepsilon)}{11}$	$\frac{1(1-\varepsilon)}{11}$	$\frac{\varepsilon}{1}$

Distance between M_1 and M_2

$$d(M_1, M_2) = \sqrt{\left(\sqrt{\frac{10(1-\varepsilon)}{17}} - \sqrt{\frac{2(1-\varepsilon)}{3}}\right)^2 + \left(\sqrt{\frac{5(1-\varepsilon)}{17}} - \sqrt{\frac{\varepsilon}{2}}\right)^2 + \dots}$$

Malware behavior similarities

Classification

- A malware behavior is compared with all other collected malware behaviors
- Determine average distance / similarity average σ of a malware ← classification
- Usage examples
  - A mutated malware has a high average similarity with its friends
  - Similar malware is regrouped in a family
  - A new malware type or a sandbox weakness can be identified with a low average similarity

Phylogenetic tree of malware behaviors

Motivation

- A common history of species is visualized by a phylogenetic tree
- Such a tree groups various families
- Malware behaviors are leaves
- Similarity / distance between nodes is represented by parents
- A malware needs to execute functions. Therefore a root exists
- Mutated malware is put in a group

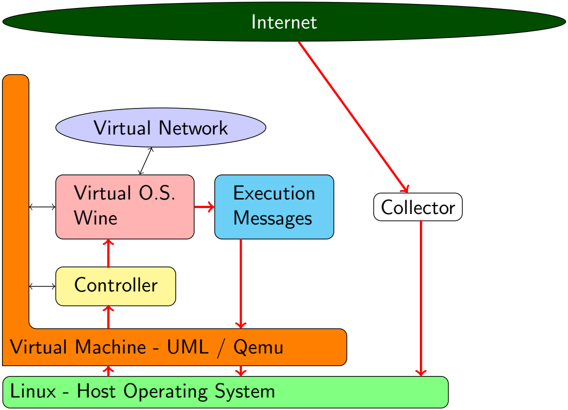
Phylogenetic tree of malware behaviors

How it works

- Hierarchical clustering
- Close malware behaviors are put in a group
- Groups are linked with their minimal distance
- The tree is continuously built until everything is linked

Experimental validation

Analyzing malware



There are vulnerabilities in Virtual Machines [Peter Ferrie]

Experimental validation

Results

Table: General information about the malware set

Number of malwares	104
Observation period	2005-2007
Malware from 2005	10
Malware from 2006	91
Malware from 2007	3
Average file size	135KB
Smallest file	8KB
Biggest file	665KB
Worms	34%
Not detected by anti-virus	42%[3]

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[3] mean detection rate of Norman, Clamav, Antivir, Fprot & Bitdefender

Experimental validation

Classification results

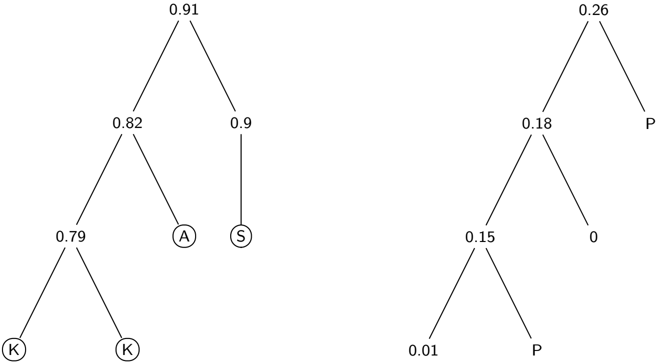
Table: Most Similar observed malwares *distance* $= 0$

WORM/Rbot.193536.29	WORM/Rbot.177664.5
Worm/Sdbot.1234944.1	Backdoor-Server/Agent.aew
Worm/Sdbot.1234944.1	unknown
Worm/IRCBot.AZ.393	Worm/Rbot.140288.8
Backdoor-Server/Agent.N.1	Worm/Win32.Doomber
Trojan.Gobot-4	Trojan.Gobot.R
Trojan/Dldr.Agent.CY.3	W32/Virut.A virus
Trojan.Gobot-4	Trojan.Downloader.Delf-35
Trojan.Mybot-5011	Trojan.IRCBot-121
Trojan.Mybot-5079	Trojan.EggDrop-5

Experimental validation

Phylogenetic tree results

`http://nepenthes.csrrt.org:10080/malware_behaviour/cache/`



K	Kernel Family
A	API Family
S	Sandbox weaknesses

P W32/Pinfi.A (Norman name)

Future work

- Evaluate other potential distances between malware behaviors
- Weighting function calls
- Analyze a set of malwares of several giga bytes
- Build other trees, evaluate other potential distances
- Recover the control flow graph of a malware with fault injection techniques
- Improve execution heuristics

Conclusion

- Function calls of unknown W32 binaries are extracted with free available tools by executing the binary
- It was proposed a simple malware behavior model with its implementation
    - Sequence of function calls = malware behavior
- Such sequences can be compared and a classification is done
- Unknown malware behaviors can be detected
- A phylogenetic tree of malwares was proposed
- A lot of things remain to do . . .

Questions & Answers

Thank you for listening!

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