Behavior-based Methods for Automated, Scalable Malware Analysis

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“He will win who knows when to fight and when not to fight… He will win who, prepared himself, waits to take the enemy unprepared. Hence the saying: If you know the enemy and know yourself, you need not fear the result of a hundred battles. If you know yourself but not the enemy, for every victory gained you will also suffer a defeat. If you know neither the enemy nor yourself, you will succumb in every battle.” [Sun-Tsu]
Malware at the root of many internet security problems

- Tens of thousands of new samples each day
- Developed with creation kits = rapid evolution of multiple variations
- Underground economy fuelling malware creation
- 1990s: explosive diffusion of identical malware
- 2010s: stealthy diffusion of variants of malware designed to be difficult to identify, trace and analyze
Antivirus detection ratio...

Detection ratios by engine

Names censored to protect the culprits...
Thanks to VirusTotal (www.virustotal.com)
The analysis issue

Analysts are way too few, code is way too much

Need better ways to

- Automatically analyze/reverse engineer malware
- Automatically classify/cluster malware, e.g. in families

For both, we have two approaches with symmetric issues
Static vs. dynamic approaches

Static approaches

+ Complete analysis

- Difficult to extract semantics

- Obfuscation / packing

Dynamic approaches

- “Dormant” code

+ Easy to see “behaviors”

+ Malware unpacks itself
Our Approach

Turn weakness into strength, and strength into weakness, as Sun-Tzu would suggest: leverage code reuse between malware samples to our advantage

- Automatically generate semantic-aware models of code implementing a given malicious behavior
- Use these models to statically detect the malicious functionality in samples that do not perform that behavior during dynamic analysis
- Use a variation of this technique to study malware evolution over time
Run malware in monitored environment and detect a malicious behavior \textit{(phenotype)}

Identify and model the code responsible for the malicious behavior \textit{(genotype model)}

Match genotype model against other unpacked binaries
A. Dynamic Behavior Identification

B. Extracting Genotypes Models

C. Finding Dormant Functionality

$O'$  $B_1$  $B_2$  $B_3$  ...  $B_n$

Malware sample  Behaviors  Genotype models

New malware samples
Dynamic Behavior Identification

A. Dynamic Behavior Identification

B. Extracting Genotypes Models

C. Finding Dormant Functionality

Malware sample → Behaviors

New malware samples

\[ \gamma_1 \]
\[ \gamma_2 \]
\[ \gamma_3 \]
\[ \gamma_n \]
Dynamic Behavior Identification

Run malware in instrumented sandbox

- Anubis (anubis.iseclab.org)

Dynamically detect a behavior $B$ \textit{(phenotype)}

Map $B$ to the set $R_B$ of system/API call instances responsible for it

$R_B$ is the output of the behavior identification phase
Behavior Detection Examples

**spam**: send SMTP traffic on port 25
- network level detection

**sniff**: open promiscuous mode socket
- system call level detection

**rpcbind**: attempt remote exploit against a specific vulnerability
- network level detection, with snort signature

**drop**: drop and execute a binary
- system call level detection, using data flow information

...
Extracting Genotype Models

A. Dynamic Behavior Identification

\[ B_1 \rightarrow B_2 \rightarrow B_3 \rightarrow \ldots \rightarrow B_n \]

B. Extracting Genotypes Models

\[ \gamma_1 \rightarrow \gamma_2 \rightarrow \gamma_3 \rightarrow \ldots \rightarrow \gamma_n \]

C. Finding Dormant Functionality

\[ \text{New malware samples} \]

\[ O' \]

Malware sample

Behaviors

Genotype models
Extracting Genotype Models: Goals

Identified genotype should be precise and complete
- Complete: include all of the code implementing B
- Precise: do not include code that is not specific to B (utility functions,..)

We proceed by *slicing* the code, then *filtering* it to remove support code, and *germinating* to complete it
Start from relevant calls $R_B$

Include into slice $\phi$ instructions involved in:

- preparing input for calls in $R_B$
  - follow data flow dependencies backwards from call inputs
- processing the outputs of calls in $R_B$
  - follow data flow forward from call outputs

We do not consider control-flow dependencies

- would lead to including too much code (taint explosion problem)
The slice $\phi$ is not precise

General purpose utility functions are frequently included (i.e. string processing)
- may be from statically linked libraries (i.e. libc)
- genotype model would match against any binary that links to the same library

Backwards slicing goes too far back: initialization and even unpacking routines are often included
- genotype model would match against any malware packed with the same packer
Exclusive instructions:

- set of instructions that manipulate tainted data every time they are executed
- utility functions are likely to be also invoked on untainted data

Discard whitelisted code:

- whitelist obtained from other tasks or execution of the same sample, that do not perform B
- could also use foreign whitelist
  - i.e: including common libraries and unpacking routines
The slice $\phi$ is not complete

Auxiliary instructions are not included

- loop and stack operations, pointer arithmetic, etc

Add instructions that cannot be executed without executing at least one instruction in $\phi$

Based on graph reachability analysis on the intra-procedural Control Flow Graph (CFG)
Finding Dormant Functionality

A. Dynamic Behavior Identification

B. Extracting Genotypes Models

C. Finding Dormant Functionality

$O'$

Malware sample

Behaviors

$B_1, B_2, B_3, \ldots, B_n$

Genotype models

$\gamma_1, \gamma_2, \gamma_3, \ldots, \gamma_n$

New malware samples
Finding Dormant Functionality

Genotype is a set of instructions

Genotype model is its colored control flow graph (CFG)
  - nodes colored based on instruction classes

2 models match if they share at least one K-Node subgraph (K=10)

Use techniques by Kruegel et al. to efficiently match a binary against a set of genotype models

We use Anubis as a generic unpacker
Evaluation

Are the results accurate?

- when REANIMATOR detects a match, is there really the dormant behavior?
- how reliably does REANIMATOR detect dormant behavior in the face of recompilation or modification of the source code?

Are the results insightful?

- does REANIMATOR reveal behavior we would not see in dynamic analysis?
To test accuracy and robustness of our system we need a ground truth

Dataset of 208 malware samples with source code
  - thanks to Jon Oberheide and Michael Bailey from University of Michigan

Extract 6 genotype models from 1 sample

Match against remaining 207 binaries
Even with source, manually verifying code similarity is time-consuming

Use a source code plagiarism detection tool

- MOSS

We feed MOSS the source code corresponding to each of the 6 behaviors

- match it against the other 207 sources
- MOSS returns a similarity score in percentage

We expect REANIMATOR to match in cases where MOSS returns high similarity scores
MOSS Comparison

Percentage of matching code according to MOSS

Number of <behavior,bot> pairs

MOSS
Reanimator
MOSS Comparison

Potential False Negatives

Potential False Positives

Percentage of matching code according to MOSS
We manually investigated the potential false positives and false negatives

Low false negative rate (~1.5%)
- mostly small genotypes

No false positives
- genotype model match always corresponds to presence of code implementing the behavior

Also no false positives against dataset of ~2000 benign binaries
- binaries in system32 on a windows install
Robustness results when re-compiling same source

- Robust against different compilation options (<7% false negatives)
- Robust against different compiler versions
- Not robust against completely different compiler (>80% false negatives)
- Some robustness to malware metamorphism was demonstrated by Kruegel in a previous work
10 genotype models extracted from 4 binaries

4 datasets

- irc_bots: 10238 IRC bots
- packed_bots: 4523 packed IRC bots
- pushdo: 77 pushdo binaries (dropper, typically drops spam engine cutwail)
- allaple: 64 allaple binaries (network worm)

Reanimator reveals a lot of functionality not observed during dynamic analysis
### In-the-Wild Detection

#### Tabular Data

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phenotype</th>
<th>irc_bots</th>
<th></th>
<th></th>
<th>packed_bots</th>
<th></th>
<th></th>
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<tbody>
<tr>
<td></td>
<td></td>
<td>B</td>
<td>S</td>
<td>D</td>
<td>B ∩ S</td>
<td>B</td>
<td>S</td>
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<td>204</td>
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#### Additional Data

<table>
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<tr>
<th>Genotype</th>
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<th>allaple</th>
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<tr>
<td>rpcbind</td>
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</table>

**B**: Behavior observed in dynamic analysis.

**S, D**: Functionality detected by Reanimator
• Tracking of malware evolution over time
• Let malware update and at each step:
  • Run malware in monitored environment to see behaviors
  • Identify the code changes responsible for malicious behavior changes
• Use the same techniques of REANIMATOR for identifying and labeling behaviors, and evolutions of binary code
Beagle: overview
Beagle: how do we define a behavior

- We make use of an Anubis-like sandbox to automatically analyze system level activity
- We extract automatically graphs of connected actions that we call (unlabeled) behaviors
- We then label (some of) them manually, and can recognize with simple rules them across different samples
- This is similar to the REANIMATOR behavior signatures
- Opposed to REANIMATOR we tag code with behavior at a function-level granularity
<table>
<thead>
<tr>
<th>FAMILY NAME AND LABEL</th>
<th>SOURCE</th>
<th>1ST DAY</th>
<th>DAYS</th>
<th>EXECUTIONS</th>
<th>MD5s</th>
<th>LIFESPAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Banload TrojanDownloader:Win32/Banload.ADE</td>
<td>(1)</td>
<td>2012-01-31</td>
<td>87</td>
<td>78</td>
<td>3</td>
<td>2.00/83.00/29.33/37.95</td>
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<tr>
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<td>73</td>
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<td>Dapato Worm.Win32/Creadox.B</td>
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<tr>
<td>Gamarue Worm.Win32/Gamarue.B</td>
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<td>19</td>
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<tr>
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<td>2012-02-09</td>
<td>79</td>
<td>78</td>
<td>6</td>
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<tr>
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<td>2012-02-15</td>
<td>74</td>
<td>73</td>
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<td>1.00/50.00/18.50/19.63</td>
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<td>Zeus PWS:Win32/Zbot.gen/AF 5c9667edbbcf2c123a710db97ccdbroc</td>
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<td>6</td>
<td>1.00/36.00/11.00/13.43</td>
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<td>(3)</td>
<td>2012-03-03</td>
<td>57</td>
<td>55</td>
<td>11</td>
<td>1.00/30.00/5.64/9.75</td>
</tr>
</tbody>
</table>

Table 1: Dataset. The labels in the first columns are based on Microsoft AV naming convention. The MD5 column is the number of distinct binaries encountered. Lifespan is the duration in days of the interval in which an MD5 was observed (min/max/mean/stddev).
<table>
<thead>
<tr>
<th>FAMILY NAME</th>
<th>%TAGGED</th>
<th>%LABELED</th>
<th>%RATIO</th>
<th>%ADDED</th>
<th>%REMOVED</th>
<th>%SHARED</th>
<th>NEW</th>
<th>#LABELS</th>
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</thead>
<tbody>
<tr>
<td>Banload</td>
<td>7.31 ± 1.70</td>
<td>6.68 ± 0.75</td>
<td>91.43</td>
<td>2.48 ± 2.96</td>
<td>2.83 ± 3.10</td>
<td>94.69 ± 3.75</td>
<td>176.2 ± 409.2</td>
<td>5</td>
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<tr>
<td>Cybcot</td>
<td>32.36 ± 2.40</td>
<td>31.23 ± 2.95</td>
<td>96.50</td>
<td>10.59 ± 10.36</td>
<td>10.30 ± 10.42</td>
<td>79.11 ± 12.80</td>
<td>1361.4 ± 3937.2</td>
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<tr>
<td>Dupato</td>
<td>2.81 ± 1.22</td>
<td>1.15 ± 0.55</td>
<td>40.90</td>
<td>5.15 ± 5.14</td>
<td>5.57 ± 5.63</td>
<td>89.28 ± 7.48</td>
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<tr>
<td>Gamarue</td>
<td>15.90 ± 14.06</td>
<td>14.06 ± 13.40</td>
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<td>12.08 ± 8.16</td>
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<tr>
<td>GenericDownloader</td>
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<td>8.58 ± 1.59</td>
<td>94.30</td>
<td>9.80 ± 9.85</td>
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<td>Grafter</td>
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<td>6.47 ± 10.40</td>
<td>6.84 ± 9.96</td>
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<td>OnlineGames</td>
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<td>Zeus</td>
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<td>Zeus</td>
<td>8.26 ± 1.56</td>
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<td>3.12 ± 2.78</td>
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<td>7.44 ± 1.31</td>
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<td>86.06</td>
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<td>93.23 ± 13.46</td>
<td>2523.9 ± 6834.9</td>
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</tbody>
</table>

Table 2: Overall tagged and labeled code (in each version), added, removed, shared code (between consecutive versions), and new code (with respect to all previous versions) for each family (mean±variance, measured in basic blocks). #Labels is the number of distinct behavior labels detected throughout the versions.
Beagle: breakdown of changes on behaviors

Gamarue family

Distribution of similarity

Bold line = median
Box = quantiles
(0,25,75,100)
Circle = outlier
Beagle: some of the insights

- Changes and evolution
  - Some families are much more actively developed than others.
  - Also we can pinpoint changes over individual behaviors, sometimes across the collection.
  - In some cases, overall development appears constant/low, but we can disaggregate it to significant changes.

- Effort
  - We have blocks in ASM, not LoC in source, but we can do some estimate.
  - We estimate that avg added code in Zeus over each variation is 140–280 LoC, with peaks up to 9,000.
  - Roughly holds for other families but we are less certain.
  - Significant effort of development in malware.
Next step: automatic extraction of malicious behaviors from large datasets of malware

- Reanimator and Beagle rely on manually-identified relevant behaviors
  - This is not a dramatic requirement as we saw
  - Still, tedious manual step we may wish to avoid
  - Biased from analyst's previous perspective, not receptive to novelty

- We are working to demonstrate that we can:
  - Automatically extract relevant “sets-of-calls” that might be behaviors (done: grouped call by dataflow dependency)
  - Match this dictionary of unlabeled behaviors across different variants (in fieri)
  - Try to associate as much semantic information as possible to these “emerging” behaviors before presenting them to human analysts (todo)
Several works perform either:

- Structural clustering based on code features (e.g. works by H. Flake, Ero Carrera, and others)
- Behavioral clustering based on program execution traces (e.g. works by P. M. Comparetti, C. Kruegel, and others)

Our next research: using the same backward-forward techniques we used in the previous 2 works to map these two clustering approaches to each other. This will improve the quality of the families, help cluster correctly malware which is obfuscated or which has dormant behaviors.
Conclusions

- Structural analysis alone is too time and brain consuming
- Dynamic analysis alone has too many blind points
- We can combine both to obtain:
  - Dormant code analysis and tagging
  - Evolution tracking
  - Triage of new samples
  - (hopefully) better means of classifying specimens in families
- Much work needs to be done in this area
  - Automatic identification of behaviors
  - Using these insights to automatically generate a sensible classification of malware into families
Thanks for your attention!

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@raistolo

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