

Classification (and Detection) of Metamorphic Malware Using Value Set Analysis

Felix Leder – leder@cs.uni-bonn.de

Bastian Steinbock – steinboc@cs.uni-bonn.de

Peter Martini – martini@cs.uni-bonn.de

1

Encrypted malware: Encrypted virus body is decrypted at run-time
(example: UPX)



Polymorphic malware: Morphing/varying decryptor stub



Metamorphic malware: Morphes the whole virus body.



Metamorphic Malware is **hardly detectable with regular string signatures**.

Virus scanners use customized detection engines for each family.

Problem:

In 2009 Symantec detected more than 2.8 million new malware specimen. (170% growth)

Impossible to analyze every sample or by hand. Pre-classification needed.

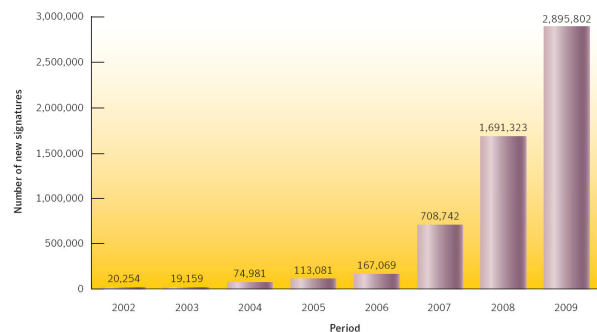


Figure 10. New malicious code signatures
Source: Symantec.

Bad detection example – Lexotan32:

- File infecting virus from 2002
- Virus total detection rate in 2009: 12.9%
- None of 40 scanners detected all of the samples

- Code changes completely
- Common subsequences have sizes of max. 5 bytes
- Every infection looks completely different

```

1: jmp 4
2: reg_2 = reg_1+2
3: jmp ...
4: reg_1 = 5
5: jmp 2

```

```

reg_1 = 5
reg_2 = reg_1+2

```

Result always 7

```

reg_3 = 5
reg_2 = reg_3+2

```

```

reg_1 = 5
nop
reg_2 = reg_1+2

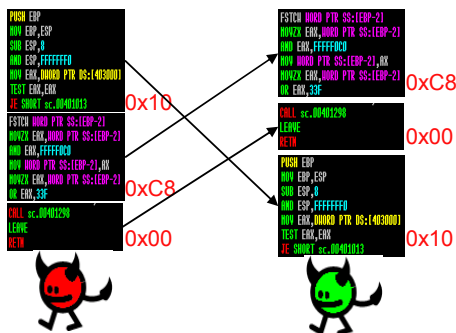
```

```

reg_1 = 5
reg_2 = -(-reg_1-2)

```

- While structure changes, behavior has to stay the same
- Existing approaches:
 - Code normalization: Standard representations
 - metamorphism can be very complex
 - only shown for W32/Evol, self-made examples
 - Execution traces / blackboxing: Possible but easy to defeat (Waiting, changing execution order, environment detection)



- **Static analysis** investigates whole sample without execution
- Behavior is reflected by **values** / memory contents
- Each program contains characteristic values it cannot change:

```
For I = 0 to 1000 do:
```

```
...
```

```
socket (AF_INET = 2,  
        SOCK_STREAM = 6,  
        PF_INET = 2)  
sockaddr_in.sin_port = 80  
connect (...)
```

```
If var_1 > 9:  
    var_1 = 10
```

Methodology

VALUE SET ANALYSIS

7

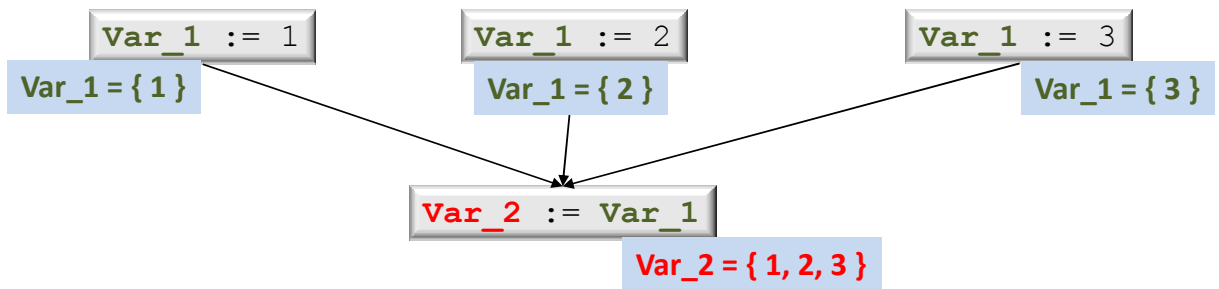
Value Set Analysis - VSA:

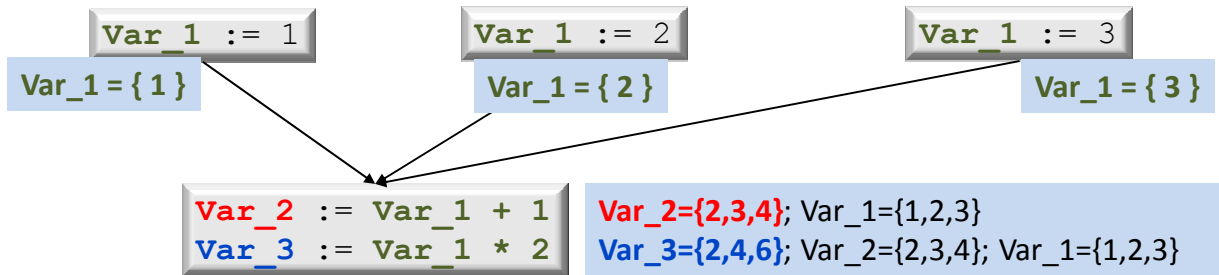
“What values are possible for a specific variable/memory-location at a specific location inside the program?”

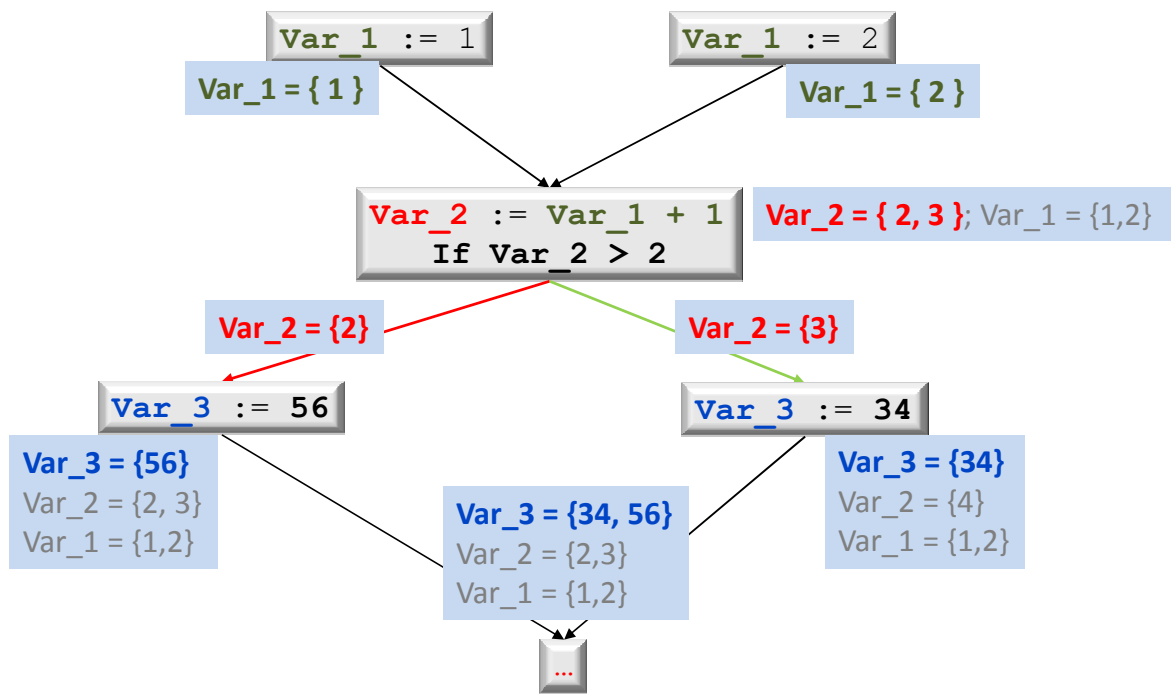
- **Static data flow tracking** and approximate memory contents
- Scalability: Over-approximate when too complex

```
Start (0x100):  
  mov eax, 1  
  mov ebx, start  
  add eax, ebx
```

Value Sets:
eax = {1}; ebx = {}
eax = {1}; ebx = {0x100}
eax = {0x101}; ebx = {0x100}





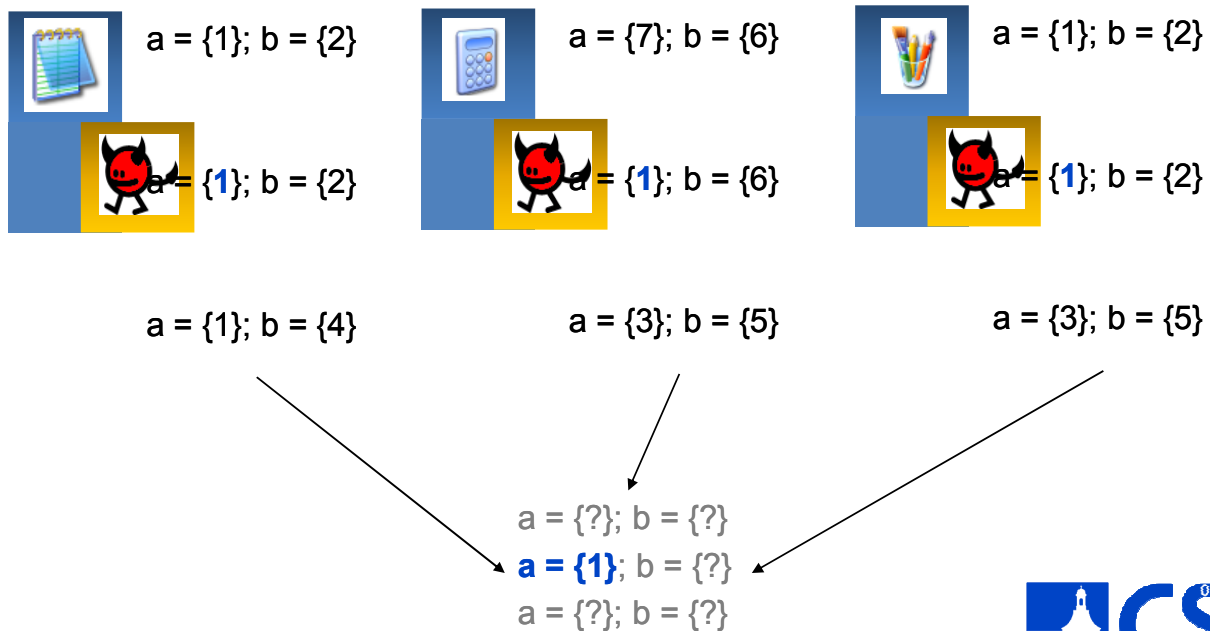


Determine Characteristic Value Sets

REFINEMENT

12

- Metamorphic malware is often file infecting
- Challenge: Distinguish host/malware Value Sets



METHODOLOGY

14

eax = {1, 5, 10}**ebx = {0, 1, 2}****Value Set****Data Objects**

File

```
00401436 sub     esp, 8
00401439 sub     esp, 8
0040143C mov     eax, [ebp+var_4]
0040143F call   eax
00401441 add     esp, 8
00401444 push   eax
```

- **Matching:** How to quantify the **similarity** of two ...

Data Objects

$$\text{eax} = \{1, 2, 3\} * \text{eax} = \{1, 2, 99\} = ?? \%$$

Value Sets

$$\begin{array}{|c|c|} \hline \text{eax} = \{\dots\} & \text{ebx} = \{\dots\} \\ \hline \end{array} * \begin{array}{|c|c|} \hline [\text{sp}-4] = \{\} & \text{esi} = \{\dots\} \\ \hline \end{array} = ?? \%$$

Files

$$\begin{array}{|c|} \hline \text{[Diagram 1: File structure with 8 blocks]} \\ \hline \end{array} * \begin{array}{|c|} \hline \text{[Diagram 2: File structure with 5 blocks]} \\ \hline \end{array} = ?? \%$$

16

Different matching strategies possible:

- **Average matching:** Score = % of equal elements
- **Threshold matching:** Score = $\begin{cases} 1 & \text{if \% of equal elements} > \Delta \\ 0 & \text{otherwise} \end{cases}$

$$\text{eax} = \{1, 2, 3\} * \text{eax} = \{1, 2, 99\} = 66 \%$$

Average score : 66%

Threshold score with ($\Delta = 0.6$): 100%

Threshold score with ($\Delta = 0.7$): 0 %

Have to be used for all layers: Data Obj., Value Sets, Files

Penalties for (unsimilar) Data Objects - Data Object Adjustments

- $|\text{Refined set}| < |\text{Infected set}|$

$\text{eax} = \{1\}$ * $\text{eax} = \{1,3,5,10,99,1010,445,110,22,1337\}$ → score - x%

- Location of the value (stack, heap, global memory)

$[\text{global_12345678}] = \{13\}$ * $[\text{esp-4}] = \{13\}$ → score - y%

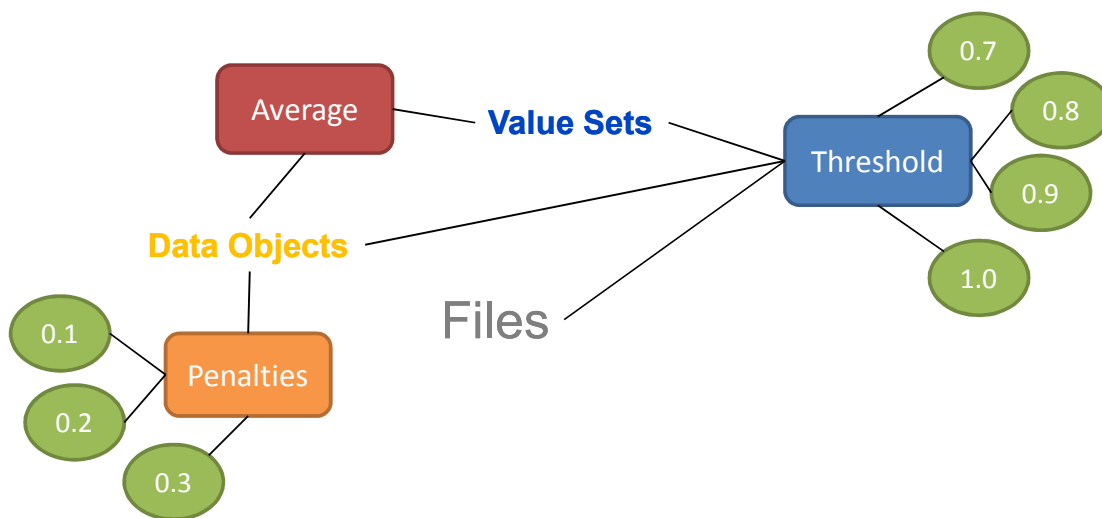
- Similar stack offsets indicate more similarity

$[\text{ebp - 4}] = \{13\}$ * $[\text{ebp - 128}] = \{13\}$ → score - z%

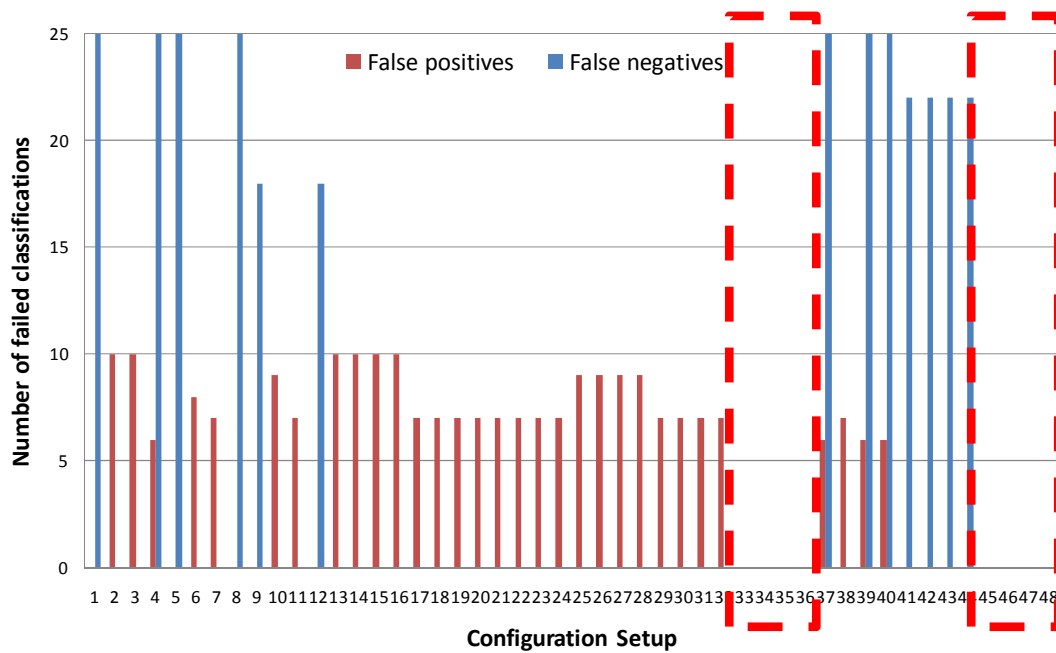
PARAMETER DERIVATION

19

- Lexotan32 (sophisticated metamorphic engine)
- 25 variants, 25 benign programs
- Sensitivity Analysis → best combination

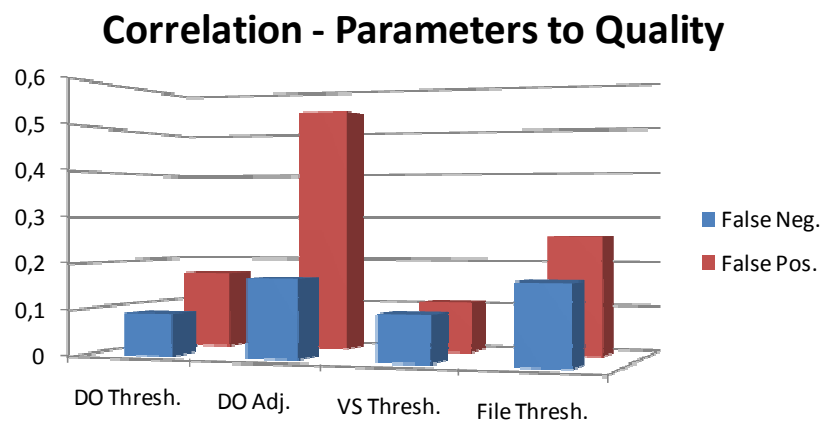


24 setups with perfect separation (out of 192)



Question: Luck, small test set, or parameter influence?

Which parameters have strongest impact? (or need to be set specifically)



- DO Adjustments (Penalty) of 30%
- Threshold matching
- High threshold for Files and Data Objects
- Threshold for Value Sets almost irrelevant

Are those parameters family dependent?

Evaluation for Parameter Generality

MALWARE DETECTION USING VSA

24

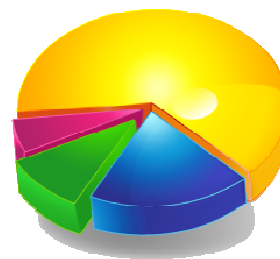


Informatik IV – leder@cs.uni-bonn.de

- 7 different metamorphic malware: W32... /
 - Lexotan32
 - Evol

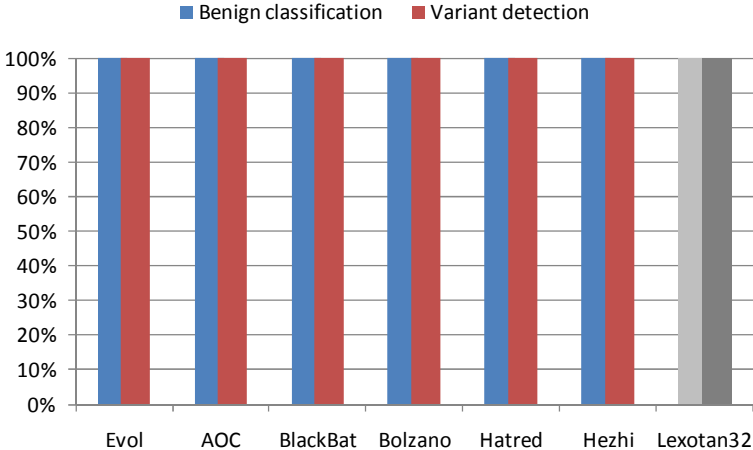
 - AOC
 - Blackbat
 - Bolzano
 - Hatred
 - Hezhi

- **Each** test set: 55 files:
 - 5 infected for refinement
 - 25 infected
 - 25 clean



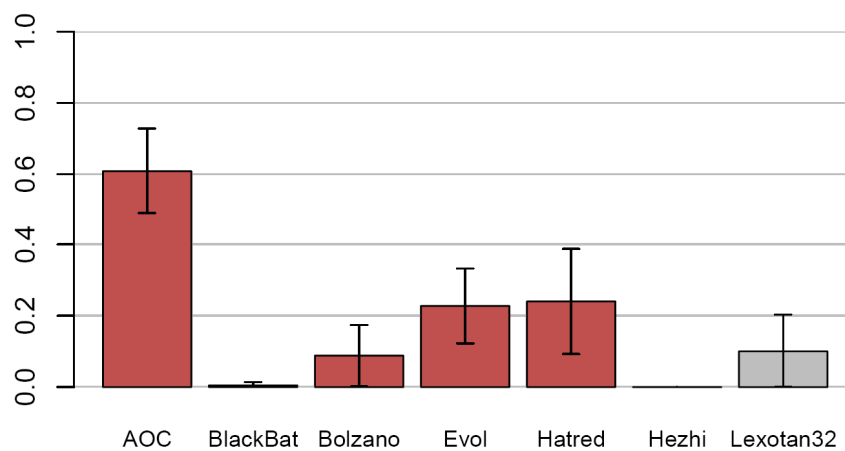
100 % Separation = 0 FALSE NEGATIVES , 0 FALSE POSITIVES

All instruction detection results



- False Positive distance
- How characteristic are the Value Sets?
- False positive estimation for real-world

Average match score of benign programs



Parameter set is suitable for other families, too!

Decreasing complexity → Only specific Points Of Interest in prog.

Malware	All instruction POIs	Jump POIs	Call POIs	Function POIs
W32/AOC	☑	1 f.p. / 0 f.n.	no value sets	no value sets
W32/BlackBat	☑	☑	☑	☑
W32/Bolzano	☑	☑	no value sets	no value sets
W32/Evol	☑	☑	☑	1 f.p. / 0 fn
W32/Hatred	☑	☑	no value sets	no value sets
W32/Hezhi	☑	no value sets	no value sets	no value sets

☑- 100% detection, 0 false positives

Summary:

- 2 False positives in 120 samples
- No false negatives
- Refinement to strict for special POI types

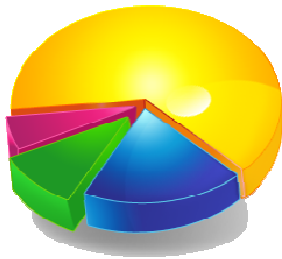
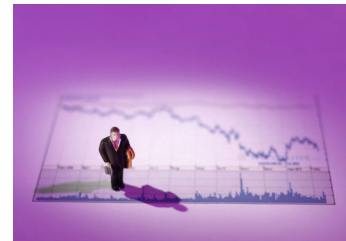
Larger sample sets

CLASSIFICATION OF METAMORPHIC FAMILIES

29

Setup

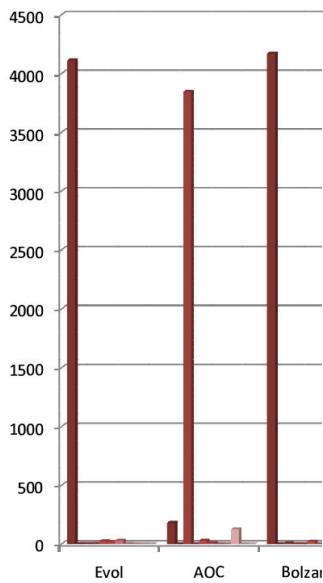
- 4197 samples from MWCollect database
- 7 metamorphic families
- Same parameter set as before
- (All Instructions)



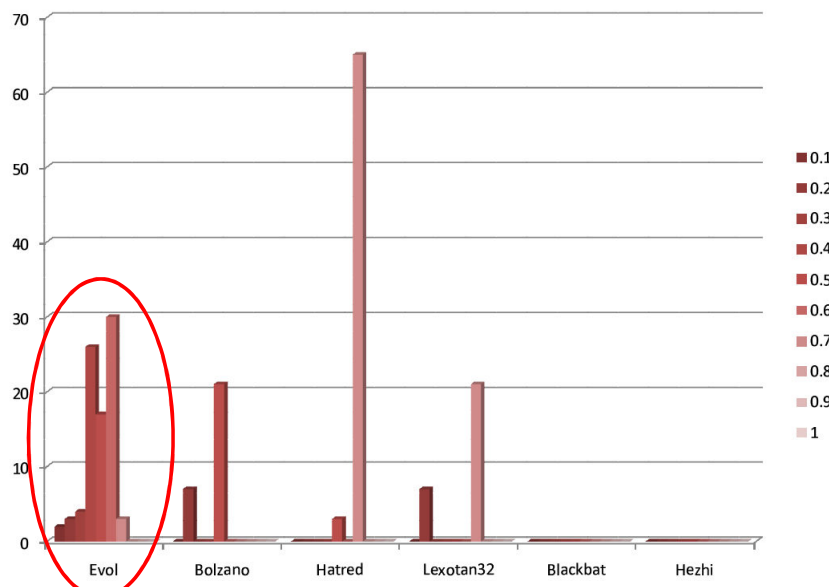
Classification goal – perfect separation

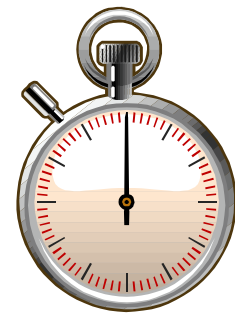
- Variant classification as family members
- All other samples as non-members

Similarity Scores per Family



Similarity Scores > 0 per Family





Competition

RUNTIME PERFORMANCE

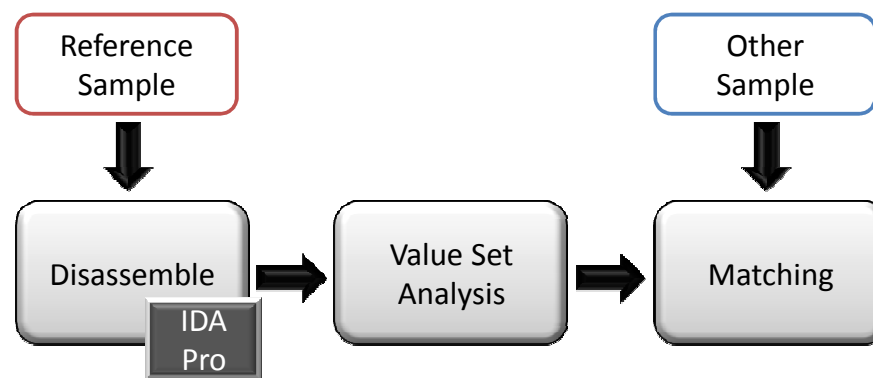
32

Best classification is unusable if too slow for use case

Existing approaches and use-cases

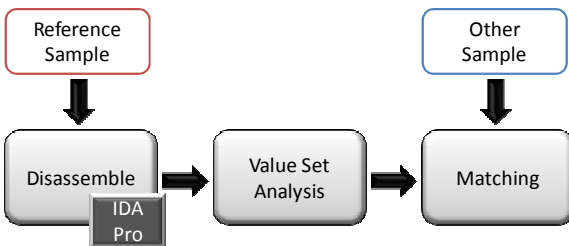
- Classification (mostly blackbox):
 - Run time: 2 to 10 minutes + classification time
- Virus-Detection (on-demand)
 - Application slow-down: 100% - 200% overhead for most AV
 - Data throughput: 3.6 – 18 MB/s
- Mail gateways
 - Greylisting introduces delays of 5 - 15 minutes



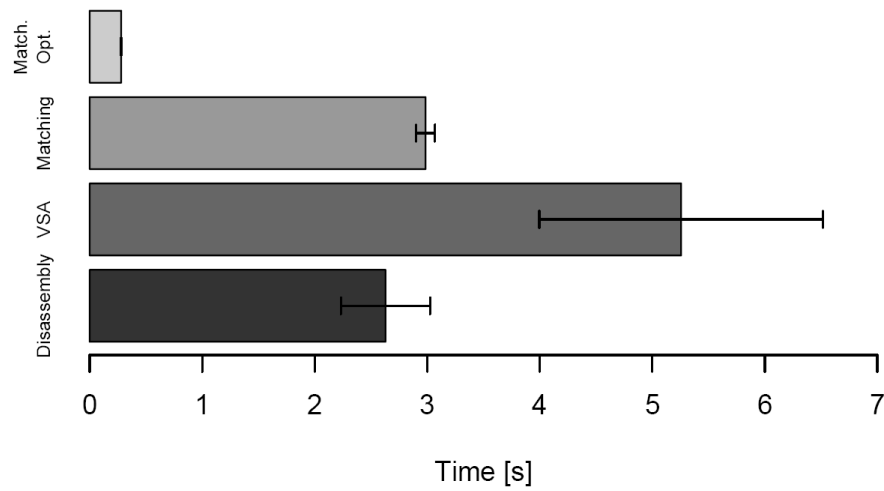


Run-Time measurements give upper bound...

- IDA Pro – unnecessary analysis steps
- Value Set Analysis – Python (IDAPython Integration)
- Matching – Python
- C up to 280 times faster than Python [Armin Rigo - Psycho]



Average duration of sample analysis steps



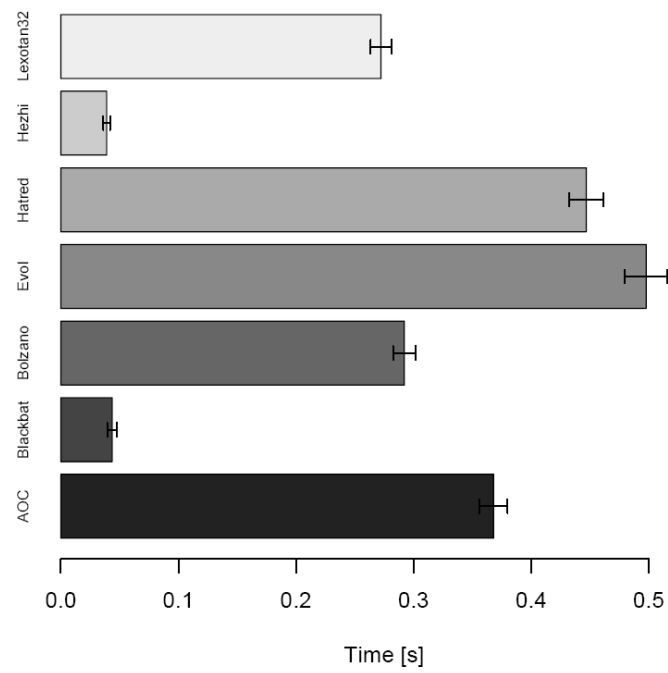
- **Average total analysis time / sample: 7.9 s**
- **Average match time +0.28 s**

- **Data throughput: 20 KB/s**

Current implementation...

- + Faster than Blackbox
- + Ok for mail gateways
- Too slow for on-demand scanning
(may be an additional means to AV)

Average match time per family



- Structure of metamorphic malware changes but (general) behavior stays similar
- Static Analysis can estimate behavior based on data flow relations and values → **Value Set Analysis**
- **Strict parameters allow for good differentiation**
- Detection possible
- Classification/**differentiation** from other families **perfect**
- Run-time ok for classification, mail gateways, ...
- Too slow for on-demand scanning



SIG SIDAR Conference on
Detection of **I**ntrusions and
Malware & **V**ulnerability **A**ssessment

<http://www.dimva.org>

leder@cs.uni-bonn.de

Malware Boot Camp

- Summer- and winter-school
- February and September
- 5 weeks hardcore fun

universität**bonn**

universität**bonn** **CS**⁰¹⁰⁰

BACKUP

40

$a = \{1, 5, 10\}$ $b = \{0, 1, 2\}$

Value Set

Data Objects

Number of values in real malware

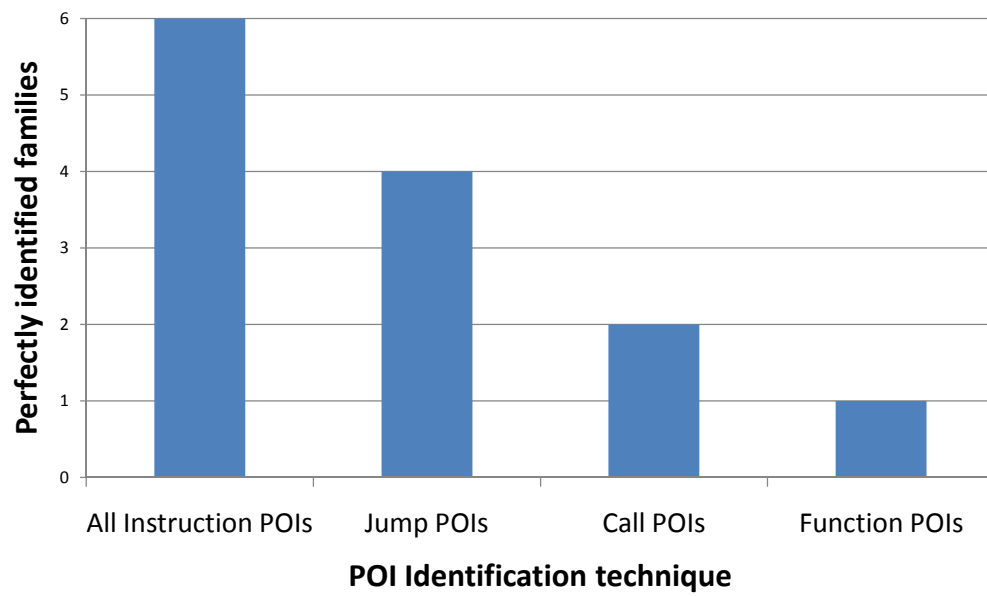
W32/Lexotan32

Original (primary) file:	188VS - 933 Data Objects
1st refinement:	108VS - 238 Data Objects
2nd refinement:	108VS - 225 Data Objects.
3rd – 9th refinement:	no changes

Points of Interest (POI)

- Points in Executable that are likely to contain characteristic Value Sets
- **All instruction POIs:** Every instruction may be interesting
- **Jump POIs:** Decision dependent values
- **Call POIs:** Function parameters and caller state
- **Function POIs:** State at the beginning of an (internal) function

Aiming for **PERFECTION**...
(100% detection, 0 false positives)



- Outliers (up to 2000 s)
- Real-world: Impl. time limit

