POLITECNICO DI MILANO

Behavior-based Methods for Automated, Scalable Malware Analysis

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Knowing the enemy = key for success

"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]

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

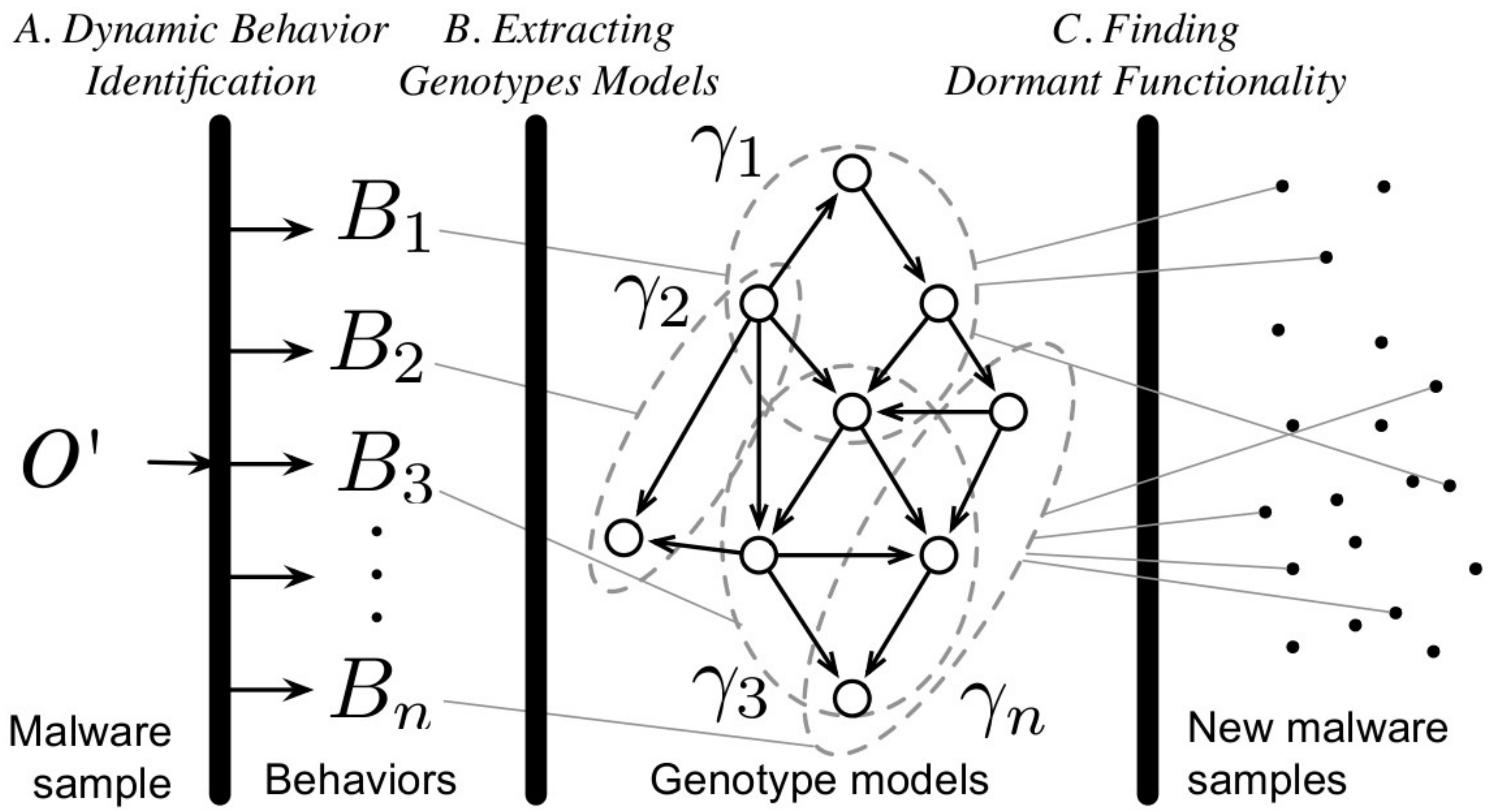
REANIMATOR

Run malware in monitored environment and detect a malicious behavior *(phenotype)*

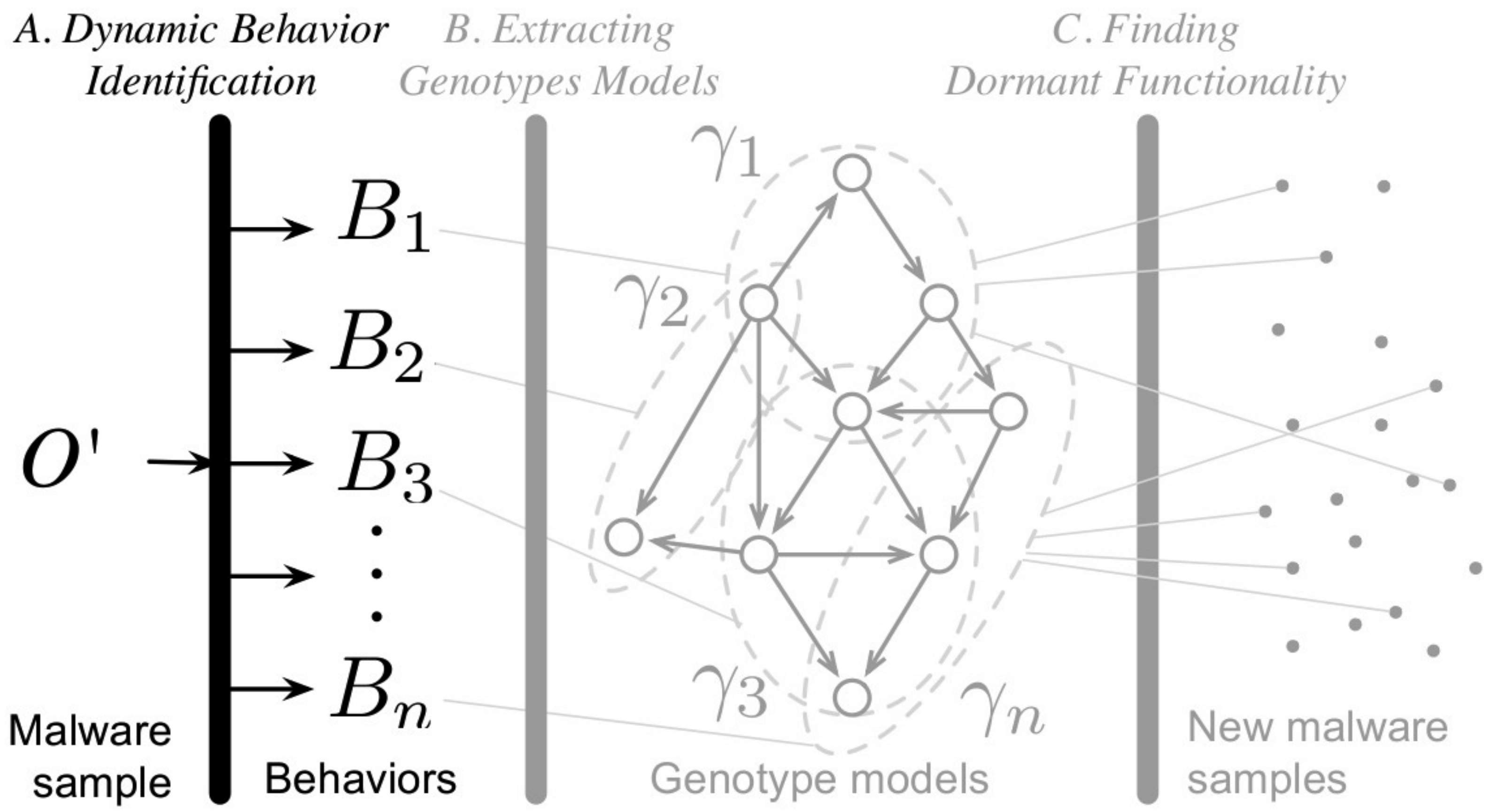
Identify and model the code responsible for the malicious behavior *(genotype model)*

Match genotype model against other unpacked binaries

REANIMATOR


A. Dynamic Behavior Identification
B. Extracting Genotypes Models
C. Finding Dormant Functionality
O'
B_1
B_2
B_3
B_n
γ_1
γ_2
γ_3
γ_n
Malware sample
Behaviors
Genotype models
New malware samples

Dynamic Behavior Identification



Dynamic Behavior Identification

Run malware in instrumented sandbox

- Anubis (anubis.iseclab.org)

Dynamically detect a behavior B *(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

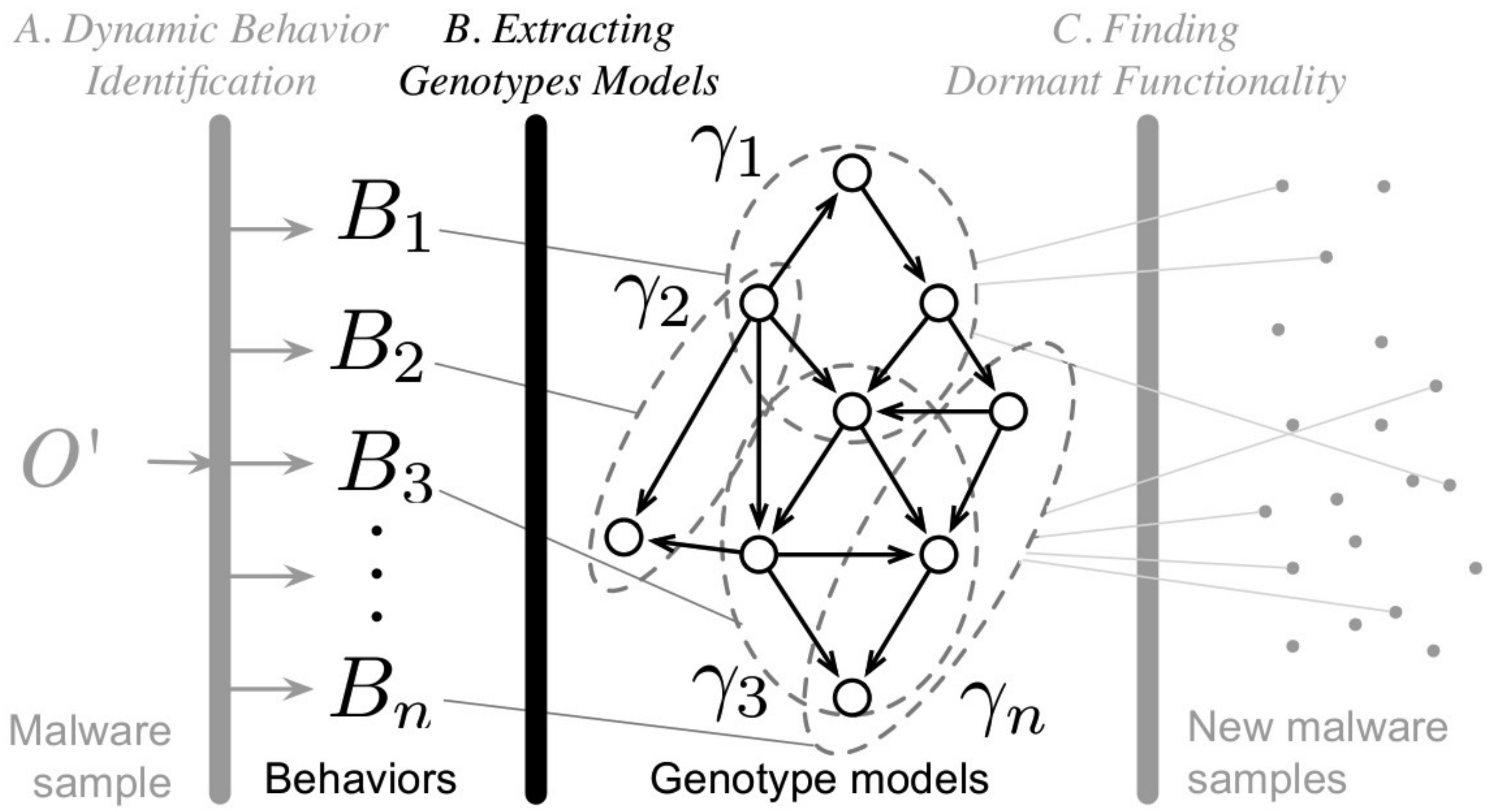
- network level detection, with snort signature

drop: drop and execute a binary

- system call level detection, using data flow information

...

Extracting Genotype Models



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

Slicing

Start from relevant calls R_B

Include into slice ϕ 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)

Filtering

The slice ϕ 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

Filtering Techniques

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

Germination

The slice ϕ is not complete

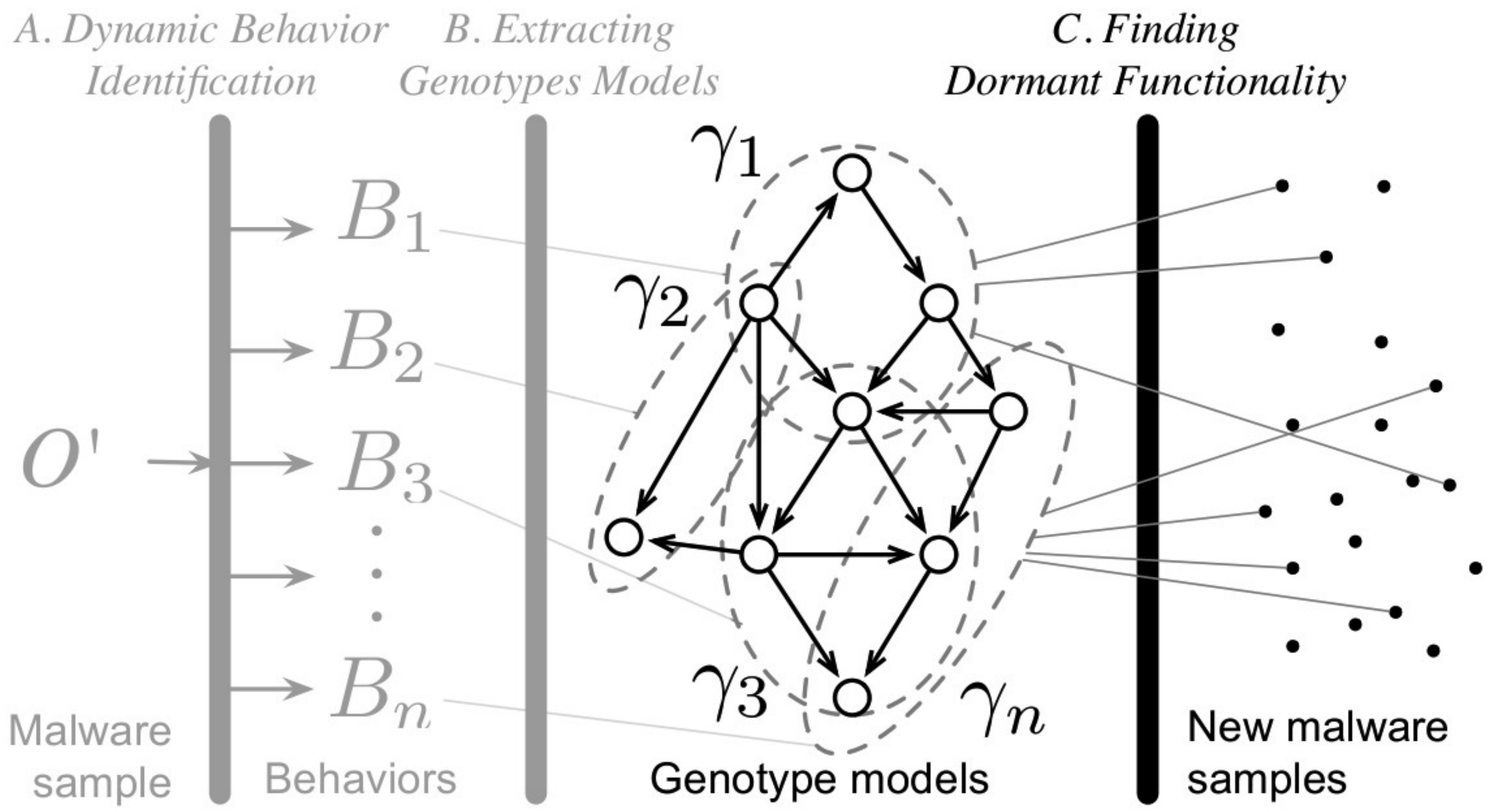
Auxiliary instructions are not included

- loop and stack operations, pointer arithmetic, etc

Add instructions that cannot be executed without executing at least one instruction in ϕ

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

Finding Dormant Functionality



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?

Accuracy

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

Accuracy

Even with source, manually verifying code similarity is time-consuming

Use a source code plagiarism detection tool

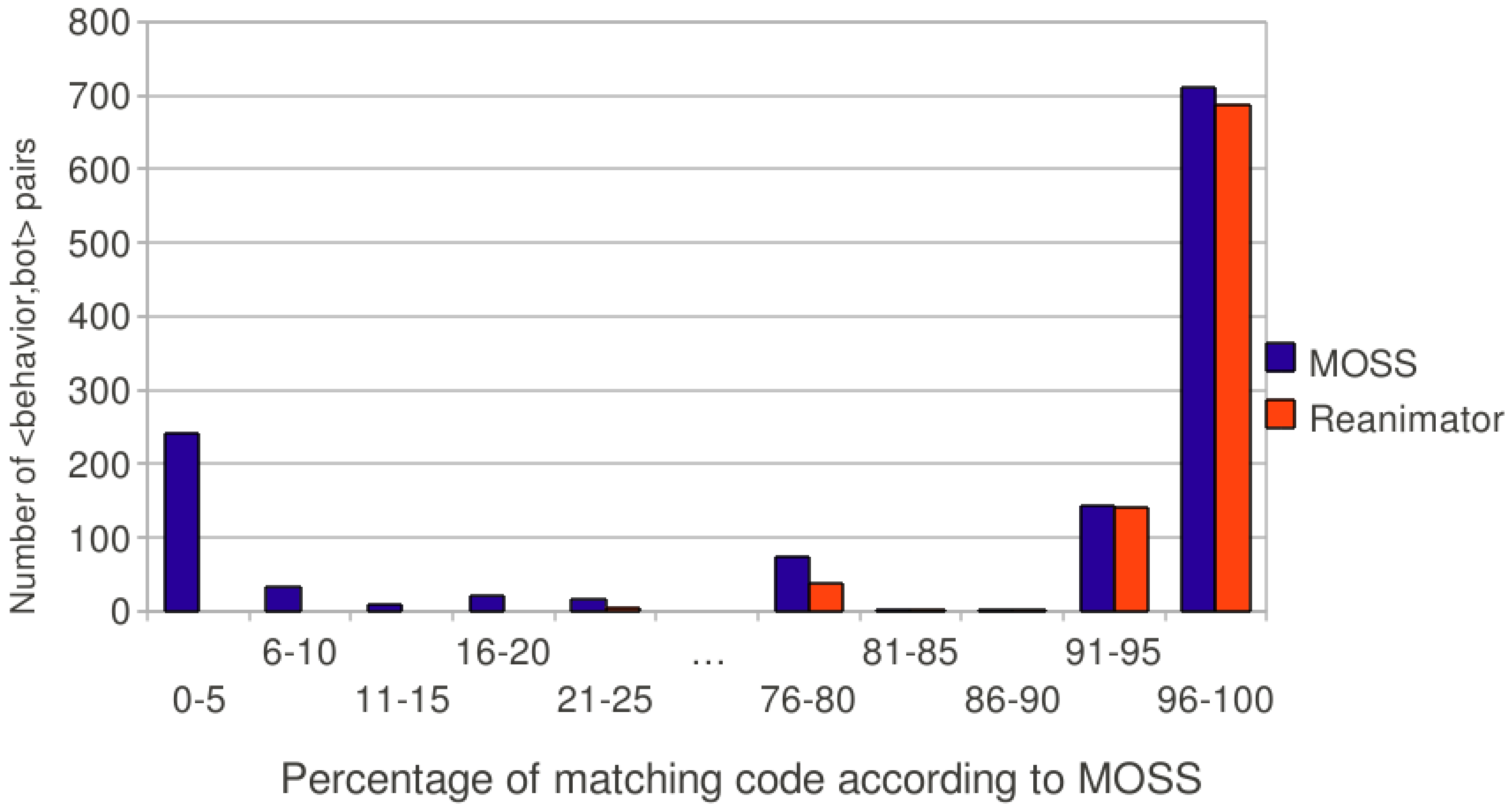
- MOSS

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

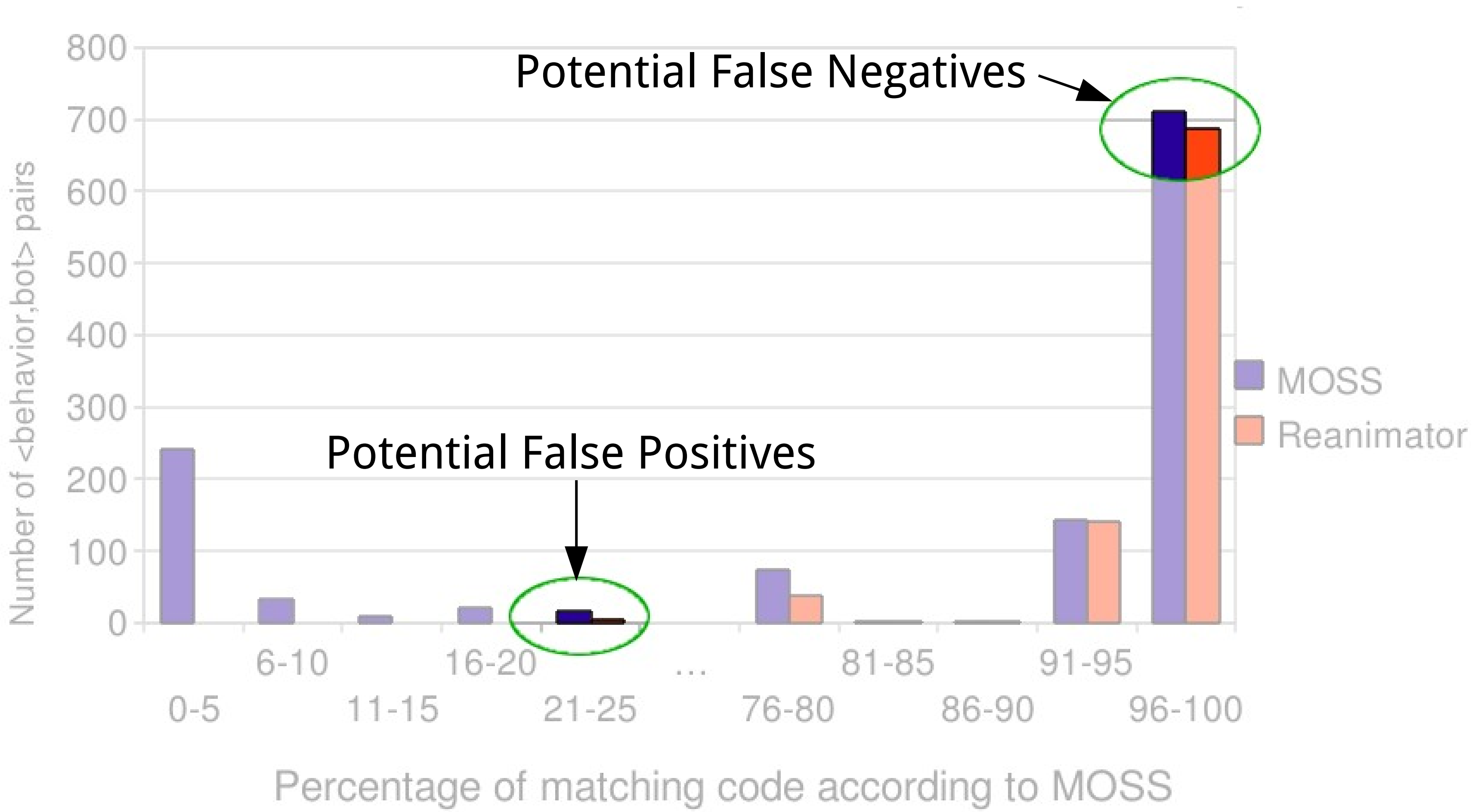
- match it against the other 207 sources
- MOSS returns a similarity score in percentage

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

MOSS Comparison



MOSS Comparison



Accuracy Results

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

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

In-the-Wild Detection

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

Genotype	Phenotype	irc_bots				packed_bots			
		B	S	D	B ∩ S	B	S	D	B ∩ S
httpd	backdoor	2014	636	635	279	840	425	425	264
keylog	keylog	0	293	254	0	0	120	111	0
killproc	killproc	0	400	400	0	4	62	62	0
simplespam	spam	154	409	409	0	53	204	204	0
udpflood	packetflood	0	374	342	0	0	139	122	0
sniff	sniff	43	270	72	0	120	204	45	0

Genotype	pushdo				allaple			
	B	S	D	B ∩ S	B	S	D	B ∩ S
drop	50	54	54	46	0	0	0	0
spam	1	43	42	1	0	0	0	0
scan	23	0	0	0	58	61	61	58
rpcbind	5	9	0	1	62	61	61	58

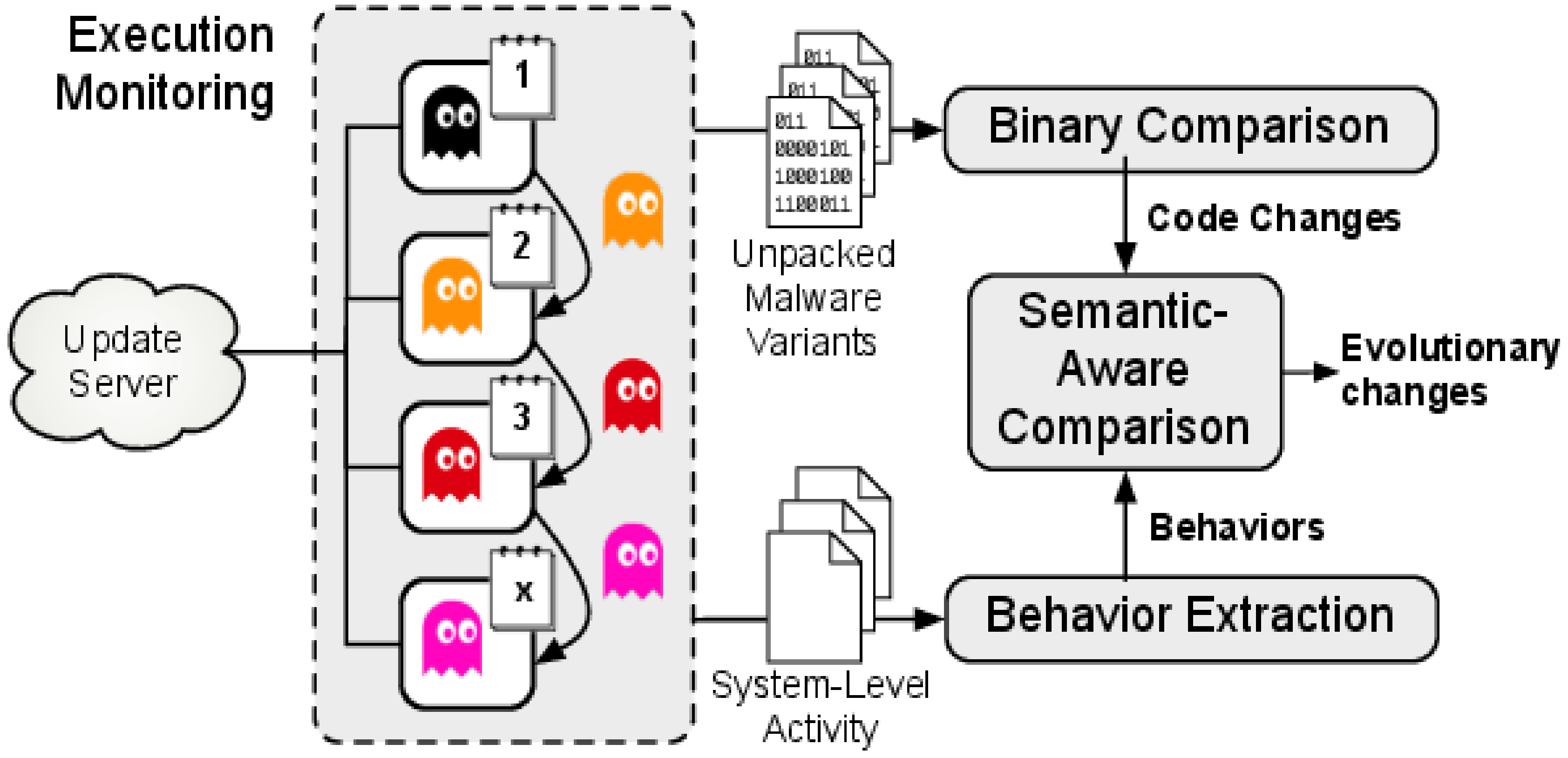
B: Behavior observed in dynamic analysis.

S,D: Functionality detected by Reanimator

Beagle

- 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

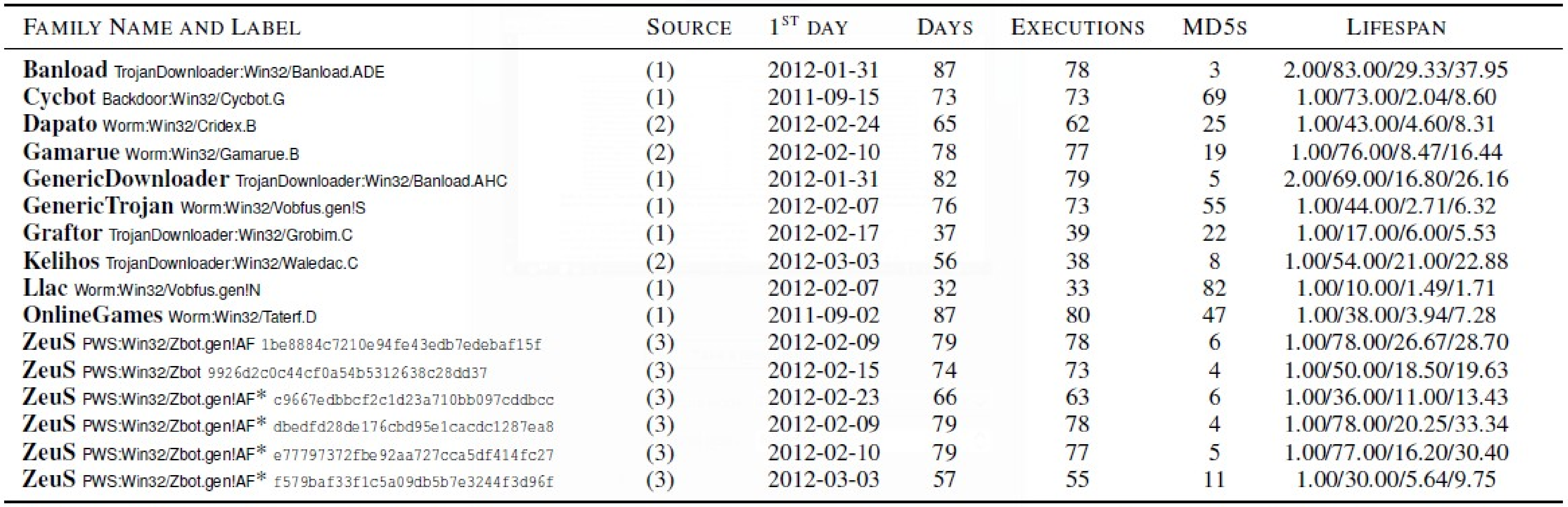
Beagle: overview



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

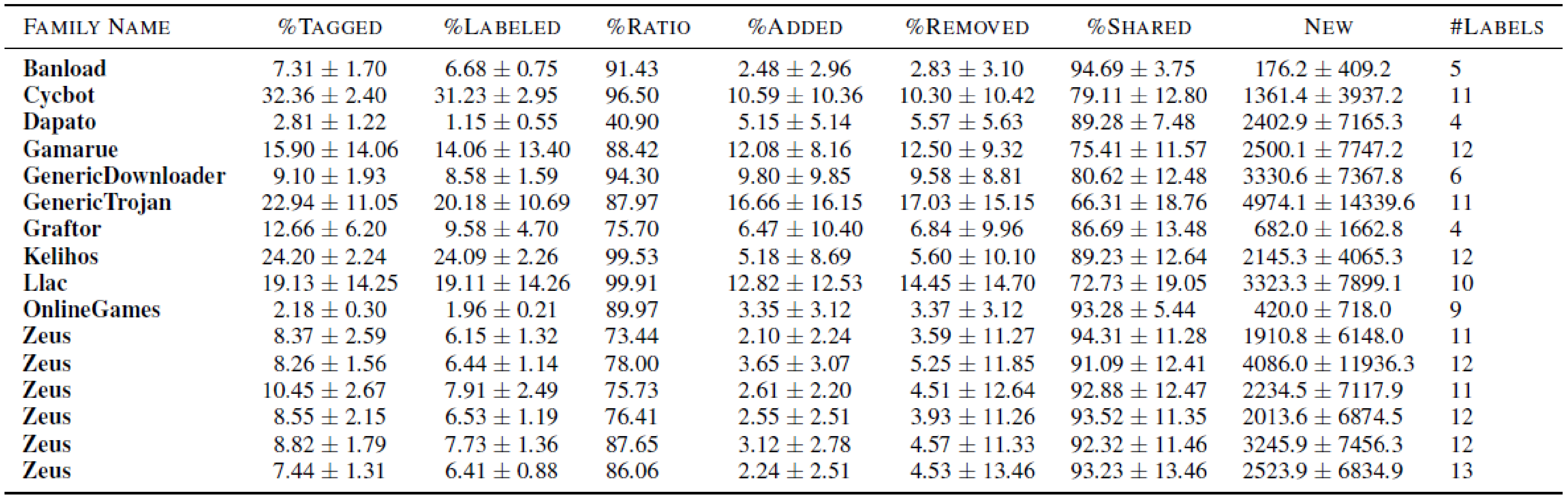
Beagle: our dataset



FAMILY NAME AND LABEL	SOURCE	1ST DAY	DAYS	EXECUTIONS	MD5S	LIFESPAN
Banload TrojanDownloader:Win32/Banload.ADE	(1)	2012-01-31	87	78	3	2.00/83.00/29.33/37.95
Cycbot Backdoor:Win32/Cycbot.G	(1)	2011-09-15	73	73	69	1.00/73.00/2.04/8.60
Dapato Worm:Win32/Cridex.B	(2)	2012-02-24	65	62	25	1.00/43.00/4.60/8.31
Gamarue Worm:Win32/Gamarue.B	(2)	2012-02-10	78	77	19	1.00/76.00/8.47/16.44
GenericDownloader TrojanDownloader:Win32/Banload.AHC	(1)	2012-01-31	82	79	5	2.00/69.00/16.80/26.16
GenericTrojan Worm:Win32/Vobfus.gen!S	(1)	2012-02-07	76	73	55	1.00/44.00/2.71/6.32
Graftor TrojanDownloader:Win32/Grobim.C	(1)	2012-02-17	37	39	22	1.00/17.00/6.00/5.53
Kelihos TrojanDownloader:Win32/Waledac.C	(2)	2012-03-03	56	38	8	1.00/54.00/21.00/22.88
Llac Worm:Win32/Vobfus.gen!N	(1)	2012-02-07	32	33	82	1.00/10.00/1.49/1.71
OnlineGames Worm:Win32/Taterf.D	(1)	2011-09-02	87	80	47	1.00/38.00/3.94/7.28
ZeuS PWS:Win32/Zbot.gen!AF `1be8884c7210e94fe43edb7edebaf15f`	(3)	2012-02-09	79	78	6	1.00/78.00/26.67/28.70
ZeuS PWS:Win32/Zbot `9926d2c0c44cf0a54b5312638c28dd37`	(3)	2012-02-15	74	73	4	1.00/50.00/18.50/19.63
ZeuS PWS:Win32/Zbot.gen!AF* `c9667edbbcf2c1d23a710bb097cddbcc`	(3)	2012-02-23	66	63	6	1.00/36.00/11.00/13.43
ZeuS PWS:Win32/Zbot.gen!AF* `dbedfd28de176cbd95e1cacdc1287ea8`	(3)	2012-02-09	79	78	4	1.00/78.00/20.25/33.34
ZeuS PWS:Win32/Zbot.gen!AF* `e77797372fbe92aa727cca5df414fc27`	(3)	2012-02-10	79	77	5	1.00/77.00/16.20/30.40
ZeuS PWS:Win32/Zbot.gen!AF* `f579baf33f1c5a09db5b7e3244f3d96f`	(3)	2012-03-03	57	55	11	1.00/30.00/5.64/9.75

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/stdev).

Beagle: some global results



FAMILY NAME	%TAGGED	%LABELED	%RATIO	%ADDED	%REMOVED	%SHARED	NEW	#LABELS
Banload	7.31 ± 1.70	6.68 ± 0.75	91.43	2.48 ± 2.96	2.83 ± 3.10	94.69 ± 3.75	176.2 ± 409.2	5
Cycbot	32.36 ± 2.40	31.23 ± 2.95	96.50	10.59 ± 10.36	10.30 ± 10.42	79.11 ± 12.80	1361.4 ± 3937.2	11
Dapato	2.81 ± 1.22	1.15 ± 0.55	40.90	5.15 ± 5.14	5.57 ± 5.63	89.28 ± 7.48	2402.9 ± 7165.3	4
Gamarue	15.90 ± 14.06	14.06 ± 13.40	88.42	12.08 ± 8.16	12.50 ± 9.32	75.41 ± 11.57	2500.1 ± 7747.2	12
GenericDownloader	9.10 ± 1.93	8.58 ± 1.59	94.30	9.80 ± 9.85	9.58 ± 8.81	80.62 ± 12.48	3330.6 ± 7367.8	6
GenericTrojan	22.94 ± 11.05	20.18 ± 10.69	87.97	16.66 ± 16.15	17.03 ± 15.15	66.31 ± 18.76	4974.1 ± 14339.6	11
Graftor	12.66 ± 6.20	9.58 ± 4.70	75.70	6.47 ± 10.40	6.84 ± 9.96	86.69 ± 13.48	682.0 ± 1662.8	4
Kelihos	24.20 ± 2.24	24.09 ± 2.26	99.53	5.18 ± 8.69	5.60 ± 10.10	89.23 ± 12.64	2145.3 ± 4065.3	12
Llac	19.13 ± 14.25	19.11 ± 14.26	99.91	12.82 ± 12.53	14.45 ± 14.70	72.73 ± 19.05	3323.3 ± 7899.1	10
OnlineGames	2.18 ± 0.30	1.96 ± 0.21	89.97	3.35 ± 3.12	3.37 ± 3.12	93.28 ± 5.44	420.0 ± 718.0	9
Zeus	8.37 ± 2.59	6.15 ± 1.32	73.44	2.10 ± 2.24	3.59 ± 11.27	94.31 ± 11.28	1910.8 ± 6148.0	11
Zeus	8.26 ± 1.56	6.44 ± 1.14	78.00	3.65 ± 3.07	5.25 ± 11.85	91.09 ± 12.41	4086.0 ± 11936.3	12
Zeus	10.45 ± 2.67	7.91 ± 2.49	75.73	2.61 ± 2.20	4.51 ± 12.64	92.88 ± 12.47	2234.5 ± 7117.9	11
Zeus	8.55 ± 2.15	6.53 ± 1.19	76.41	2.55 ± 2.51	3.93 ± 11.26	93.52 ± 11.35	2013.6 ± 6874.5	12
Zeus	8.82 ± 1.79	7.73 ± 1.36	87.65	3.12 ± 2.78	4.57 ± 11.33	92.32 ± 11.46	3245.9 ± 7456.3	12
Zeus	7.44 ± 1.31	6.41 ± 0.88	86.06	2.24 ± 2.51	4.53 ± 13.46	93.23 ± 13.46	2523.9 ± 6834.9	13

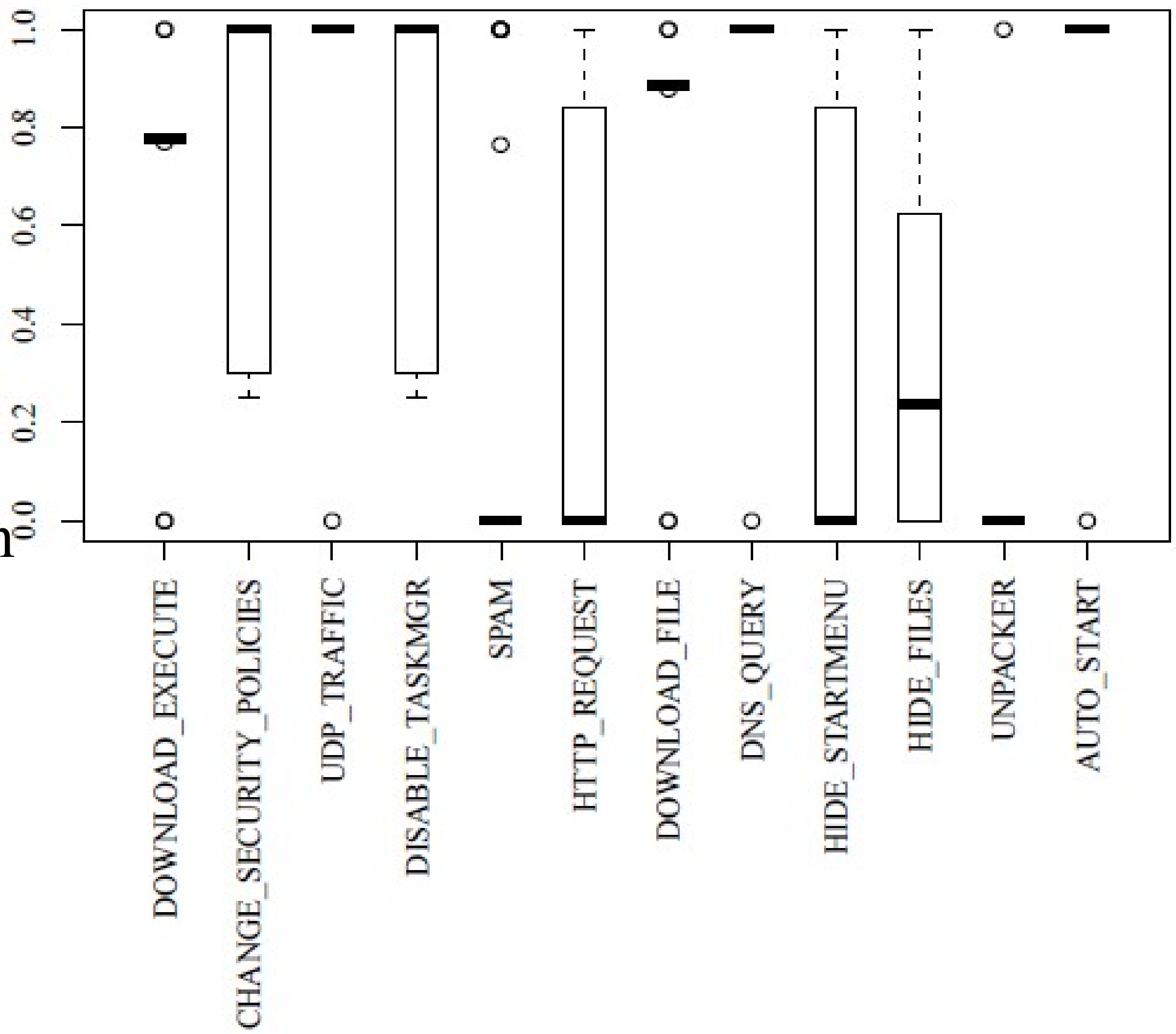
Table 2: Overall tagged and labeled code (in each version), added, removed, shared code (between consecutive versions), and new code (with respect to all previous versions) for each family (mean±variance, measured in basic blocks). #Labels is the number of distinct behavior labels detected throughout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

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
- In the next slide pack I will present:
  - Automatic identification of behaviors
  - (hopefully) better means of classifying specimens in families

Thanks for your attention!

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Most of the work presented was/is joint work with:

UCSB – Christopher Kruegel

Lastline – Paolo Milani Comparetti

Northeastern University – Engin Kirda

Technical University of Vienna – Martina Lindorfer

Politecnico di Milano - Federico Maggi, Alessandro di Federico, Guido Salvaneschi, Mario Polino, Andrea Scorti

Of course, errors and opinions are mine solely :-)

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Jackdaw
Automatic, unsupervised, scalable extraction and semantic tagging of (interesting) behaviors

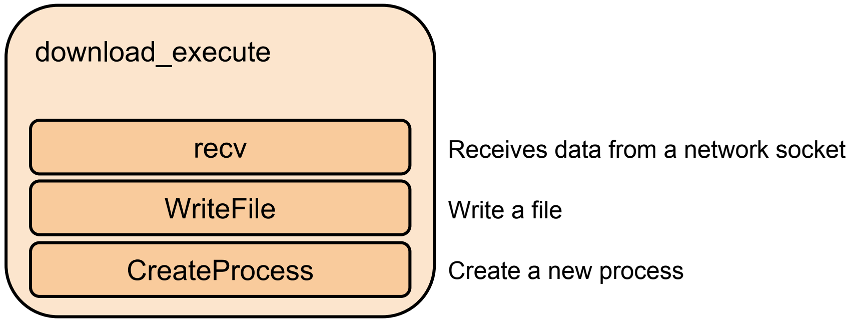
Mario Polino, Andrea Scorti, Federico Maggi, Stefano Zanero

Politecnico di Milano
Dipartimento di Eletronica, Informazione e Bioingegneria
NECSTLab

Waseda university, Nov. 25th 2014

Pivot concept: behavior

behavior ≐ sequence of actions ≐ sequence of API calls (on Win binaries)



Defining Behaviors

Previous work: manual specification of behaviors

- Labor-intensive
- Only a small subset of behaviors can be defined manually
- Biased by previous experience of experts

Objective

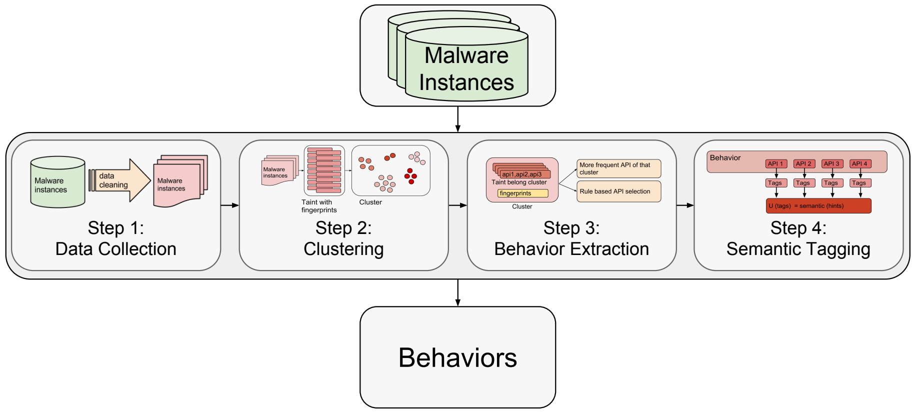
Extract (interesting) behavior specifications in an **automatic** way from a large collection of (untagged) malware

Why?

Support the analyst by providing a list of important behaviors, with a rough explanation, to prioritize the analysis.

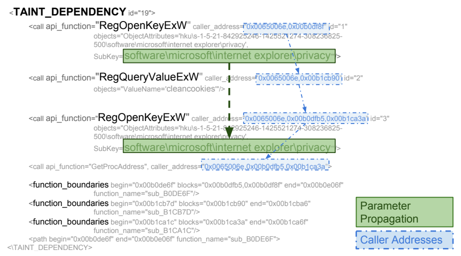
Our Approach: Jackdaw

System Architecture



First step: Data gathering

1. Dynamic Analysis: data flow analysis
   - **API functions** name
   - **Parameters** of API functions
2. Static Analysis: **fingerprint** of code associated to data flow
   - sub-graphs of the CFG
   - can be hashed and matched
   - reasonably resilient to polymorphism

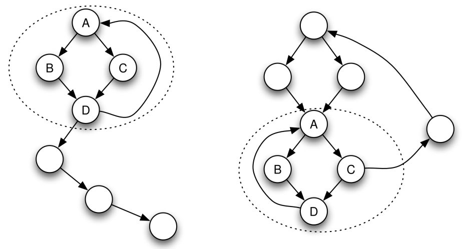


```
<TAINT_DEPENDENCY id="19">
    <call api_function="RegOpenKeyExW" caller_address="0x0065006e,0x00b0df8f" id="1"
              objects="ObjectAttributes='hku\s-1-5-21-842925246-1425521274-308236825-
              500\software\microsoft\internet explorer\privacy',
              SubKey='software\microsoft\internet explorer\privacy'"/>
    <call api_function="RegQueryValueExW" caller_address="0x0065006e,0x00b1cb90" id="2"
              objects="ValueName='cleancookies'"/>
    <call api_function="RegOpenKeyExW" caller_address="0x0065006e,0x00b0dfb5,0x00b1ca3a" id="3"
              objects="ObjectAttributes='hku\s-1-5-21-842925246-1425521274-308236825-
              500\software\microsoft\internet explorer\privacy',
              SubKey='software\microsoft\internet explorer\privacy'"/>
    <call api_function="GetProcAddress", caller_address="0x0065006e,0x00b0dfb5,0x00b1ca3a">
    <function_boundaries begin="0x00b0de6f" blocks="0x00b0dfb5,0x00b0df8f" end="0x00b0e06f"
              function_name="sub_B0DE6F"/>
    <function_boundaries begin="0x00b1cb7d" blocks="0x00b1cb90" end="0x00b1cba6"
              function_name="sub_B1CB7D"/>
    <function_boundaries begin="0x00b1ca1c" blocks="0x00b1ca3a" end="0x00b1ca6f"
              function_name="sub_B1CA1C"/>
    <path begin="0x00b0de6f" end="0x00b0e06f" function_name="sub_B0DE6F">
<\TAINT_DEPENDENCY>
```

Control Flow Graph Fingerprinting

Static Analysis.
Identify **portions of CFG** likely to come from the same source code.
Properties:

- **Unique**
- Robust to **insertion** / **deletion**
- Robust to **modification**



Both CFGs share a subgraph of given order

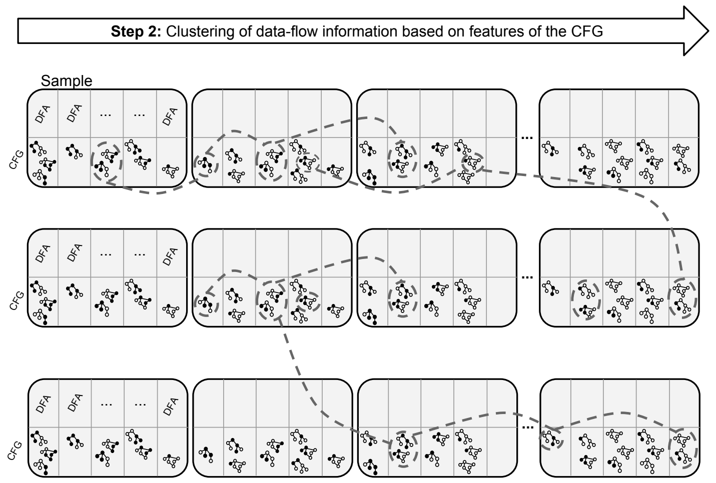
First Step: Data Gathering - Data cleaning

- Static data cleaning: remove the fingerprints of benign binaries (e.g., Windows libraries and exes)
- Dynamic data cleaning (Windows API name **Normalization**):

Prefixes	**WSA**Socket $\rightarrow$ socket
Suffixes	CreateEvent**A**, CreateEvent**W** $\rightarrow$ CreateEvent

Second Step: Clustering

Goal: Build **clusters** of **similar data flows**

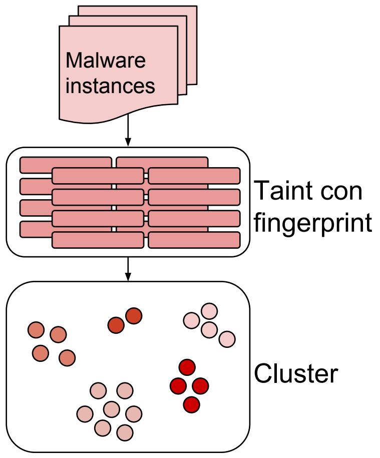

Step 2: Clustering of data-flow information based on features of the CFG
Sample
DFA
DFA
...
...
DFA
CFG
...

Second step: Clustering

- Clustering of data flow in malware
- Feature: **fingerprint**
- simple **one pass** algorithm
- Threshold
- **Similarity** metrics

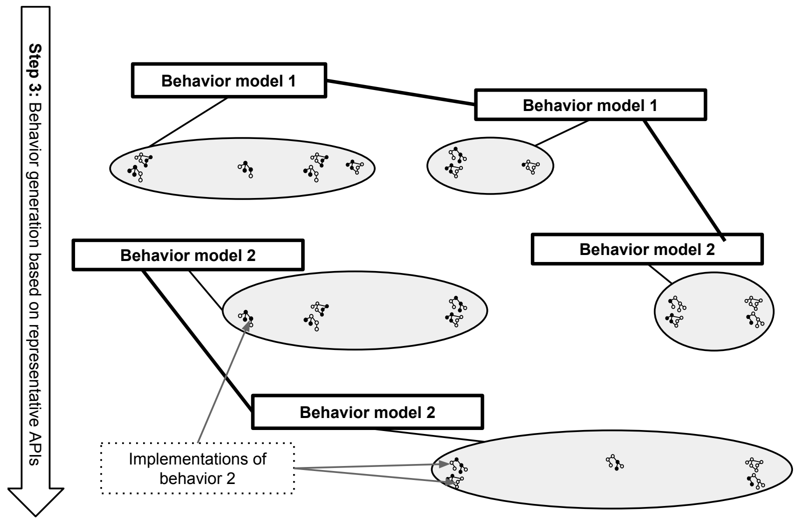
Jaccard similarity

$J(A, B) = \frac{|A \cap B|}{|A \cup B|}$



Third Step: Behavior Extraction

Goal: find API functions that **represent** each cluster (**behavior model**).


Step 3: Behavior generation based on representative APIs
Behavior model 1
Behavior model 1
Behavior model 2
Behavior model 2
Behavior model 2
Implementations of behavior 2

Third step: Behavior Extraction - MFR Heuristic

MFR Heuristic (Most Frequent Rule)

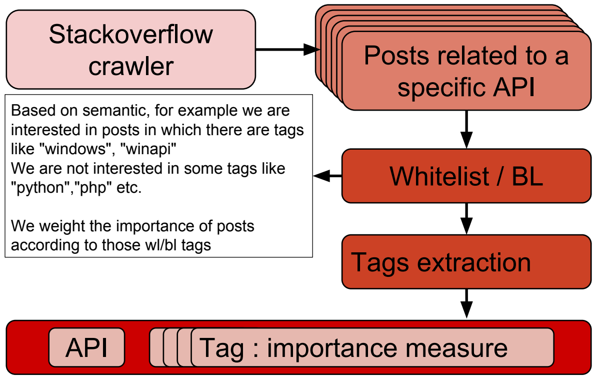
Model = API functions that appear often. How often? We set a threshold.

Cluster| API	NtClearEvent	CreateEvent	NtSetEvent
Data Flow 1	T	T	T
Data Flow 2	T	T	T
Data Flow 3	T	T	T
...	...	...	...
Data Flow 13	T	T	F
Data Flow 14	T	T	F

Behavior Specification: $NtClearEvent \wedge CreateEvent$

Fourth Step: Semantic Tagger

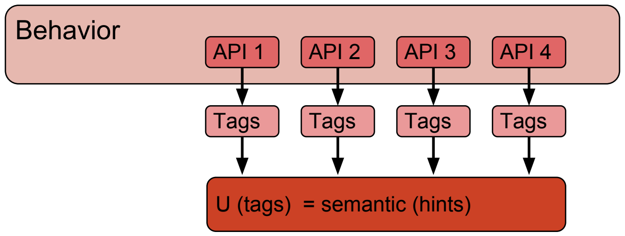
Use **Crawler** to get knowledge and build significant **tag** for **behaviors**
For Each behavior:



Based on semantic, for example we are interested in posts in which there are tags like "windows", "winapi"
We are not interested in some tags like "python","php" etc.

We weight the importance of posts according to those wl/bl tags

Fourth step: Semantic Tagger



- We look for **tags** searching **API function name**, **each* element of powerset of API function** in a model.
- Compute a **score** for each tag (based on **post relevance** and **frequency** of tags in post related to the search).
- Build a **ranking** of tags.

System Evaluation

Dataset

The dataset:

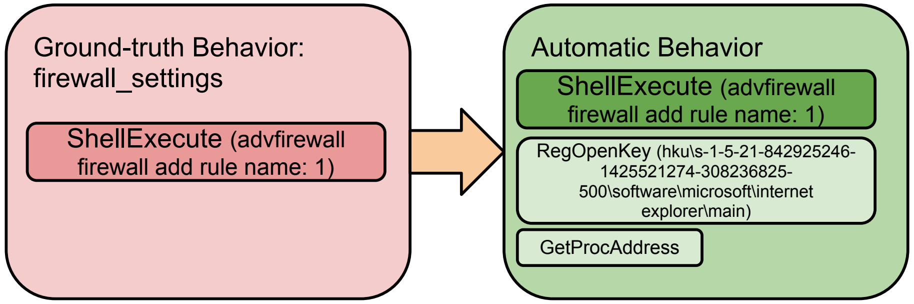
- 1,272 samples from 17 malware families

Evaluation of behavior extraction: approach

- **Unsupervised learning** (no ground truth)
- We built a pseudo **ground truth**, asking experts to **manually** describe a **model**.
- We compare these **manually defined behavior models** with **behavior models automatically identified** by Jackdaw.

Evaluation of behavior extraction: results

Correctness:


Ground-truth Behavior:
firewall_settings
ShellExecute (advfirewall firewall add rule name: 1)
Automatic Behavior
ShellExecute (advfirewall firewall add rule name: 1)
RegOpenKey (hku\s-1-5-21-842925246-1425521274-308236825-500\software\microsoft\internet explorer\main)
GetProcAddress

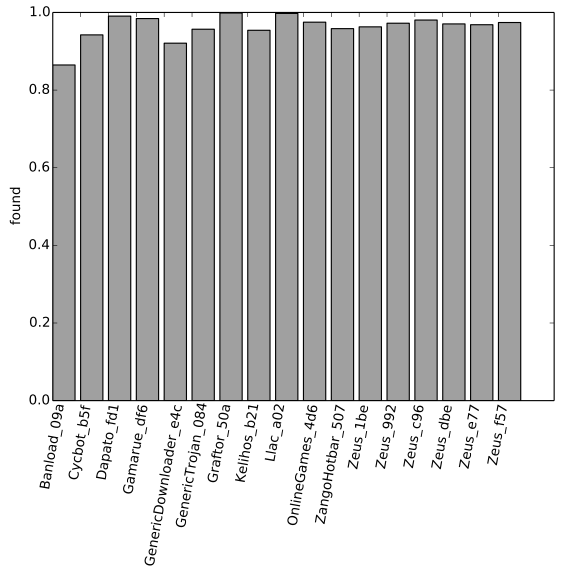
Completeness:
34 over 45 behavior models manually created by experts have been identified also by Jackdaw.

Empirical evaluation.
Example of behavior HTTP connection:

```
InternetOpen (szAgent: atlsys13.exe: 1)
InternetOpenUrl,MapMemRegion,connect,recv,send
      (szUrl: http://robertokunihira.sites.uol.com.br/nordeste.jpg, ForeignPort:
      ['80']: 1, LocalAddress: (['tcp'], public, ['1029']): 1, ForeignIP: public: 1])
'Banload_09af6de40ab414f41ba48b447345e75d'
```

Position	Tag (hint)	Score
1	http	18
2	proxy	13.5
3	ftp	8
4	file	6.8
5	mfc	6.8
6	post	6.2
7	internet	5.6
=	upload	5.6
9	file-download	4.5
10	arrays	4
11	download	3.9
12	rich-internet-application	3.3
=	networking	3.3
14	httprequest	2.8
15	httpwebrequest	2.2
16	internet-explorer	1.7
..	..	..

Recognizing behaviors in unknown malware



Conclusions

Limitations and Future works

Limitations:

- needs buckets of variants of each malware family
- analyzed malware needs to be unpacked

Future Works:

- Introduce sequence/time concept in behavior models
- NLP to improve semantic tagging

Third step: Behavior Extraction - PLR Heuristic

PLR Heuristic (Propositional Logic Rule)

Let T be a set of elements; given a set of elements $L \subseteq \mathcal{P}(T)$, the solution is all sets $Q \subseteq \mathcal{P}(T)$ such that:

- $\forall l \in L, \forall q_i, q_j \in Q$ with $q_i \neq q_j$, if $q_i \subset l$ then $q_j \cap l = \emptyset$
- $\forall l \in L, \exists ! q \in Q, q \subset l$

Cluster| API	...Atom API_1 ...*	...Atom API_2...	RegCloseKey	...NtKey API_1...	...NtKey API_2...
Taint 1	T	T	F	F	F
...	...	...	...	...	...
Taint 5	T	T	F	F	F
Taint 6	F	F	T	T	T
...	...	...	...	...	...
Taint 8	F	F	T	T	T

Behavior Specification:

$(AtomAPI_1 \wedge AtomAPI_2) \oplus (RegCloseKey \wedge NtKeyAPI_1 \wedge NtKeyAPI_2)$

Conclusions

Jackdaw:

- **Automatically** extracts **behavior models** of widespread behaviors, exploiting both dynamic and static analysis.
- Assigns a set of **semantic tags** to each model to help analyst
- **Maps** behavior model on **binary code**, building a catalog of implementations of same behavior which can be used to attribute to family/group