Identifying Dormant Functionality in Malware Programs

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Motivation

- Malicious code (malware) at the root of many internet security problems
  - ~50000 new samples each day!
- Automated dynamic analysis
  - run samples in an instrumented sandbox
- Dynamic analysis provides limited coverage
  - different behavior based on commands from C&C channel
- How can we learn more about malware samples?

Our Approach

- Leverage code reuse between malware samples
- Automatically generate semantic-aware models of malicious behavior
  - based on 1 execution of a behavior
  - model 1 implementation of the behavior
- Use these models to statically detect the malicious functionality in samples that do not perform that behavior during dynamic analysis

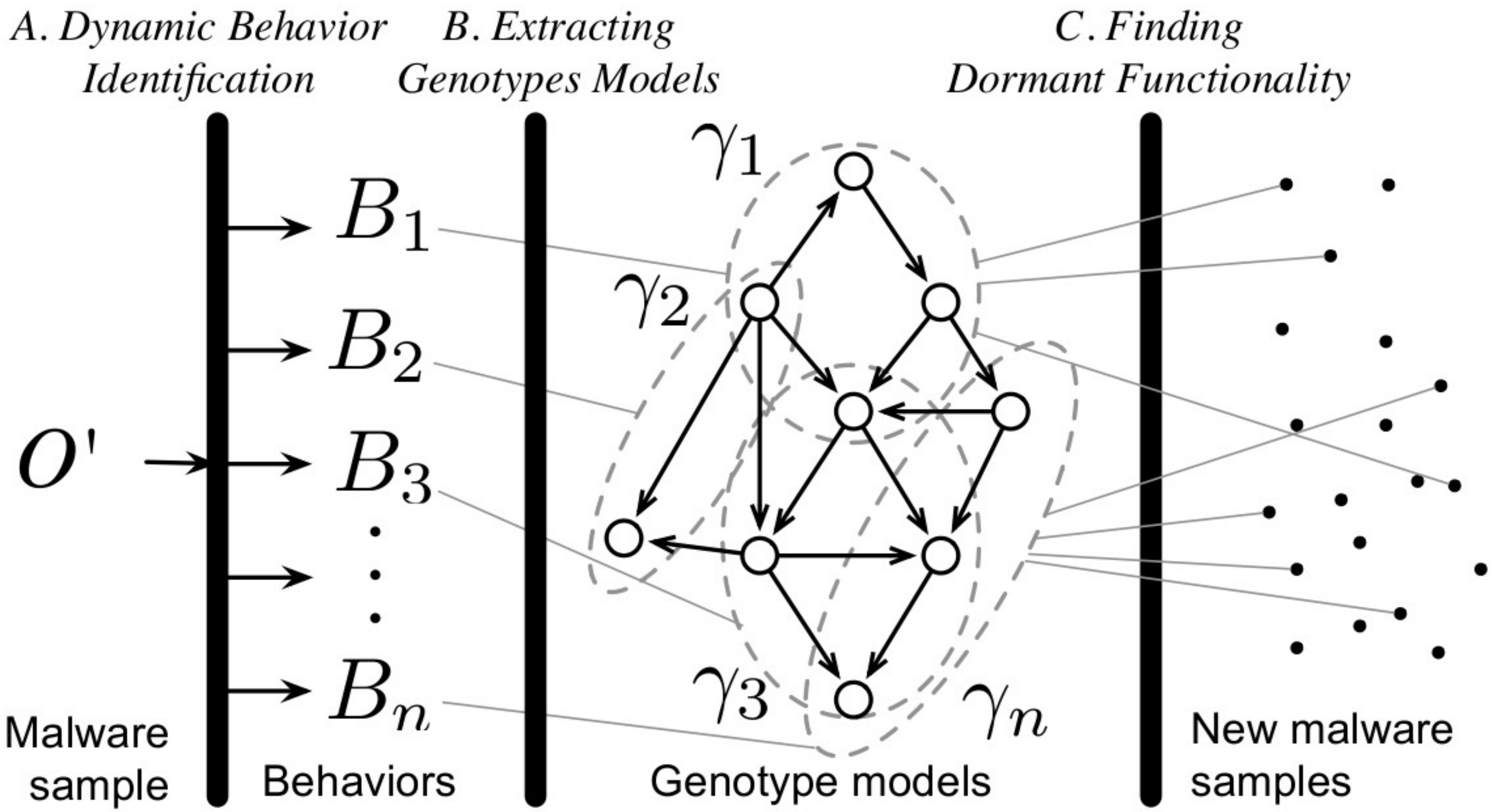
Reanimator

- 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 binaries

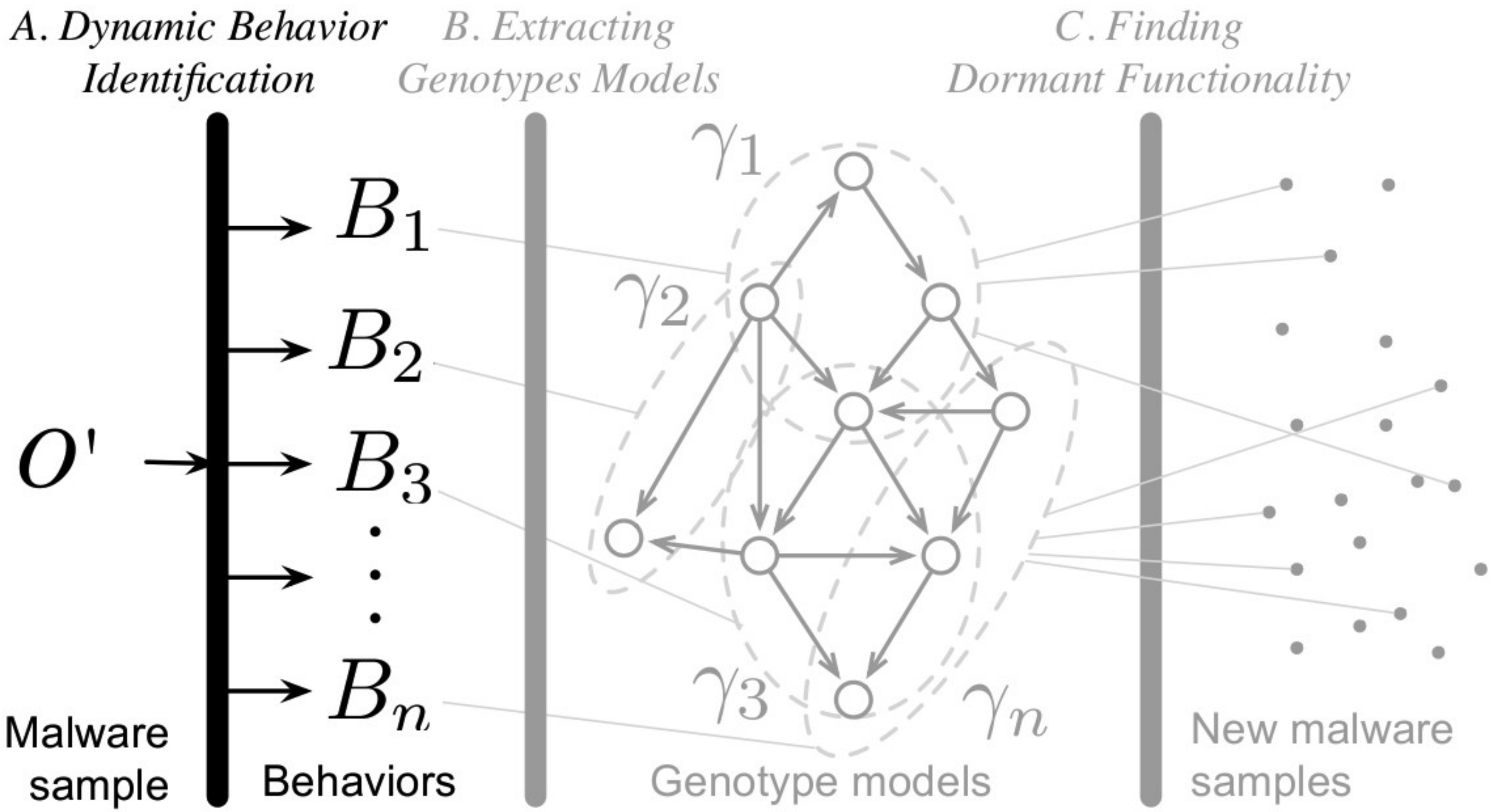
Outline

- **Reanimator**: Identifying dormant functionality
  - Dynamic behavior identification
  - Extracting genotype models
  - Finding dormant functionality
- Evaluation
- Conclusions

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

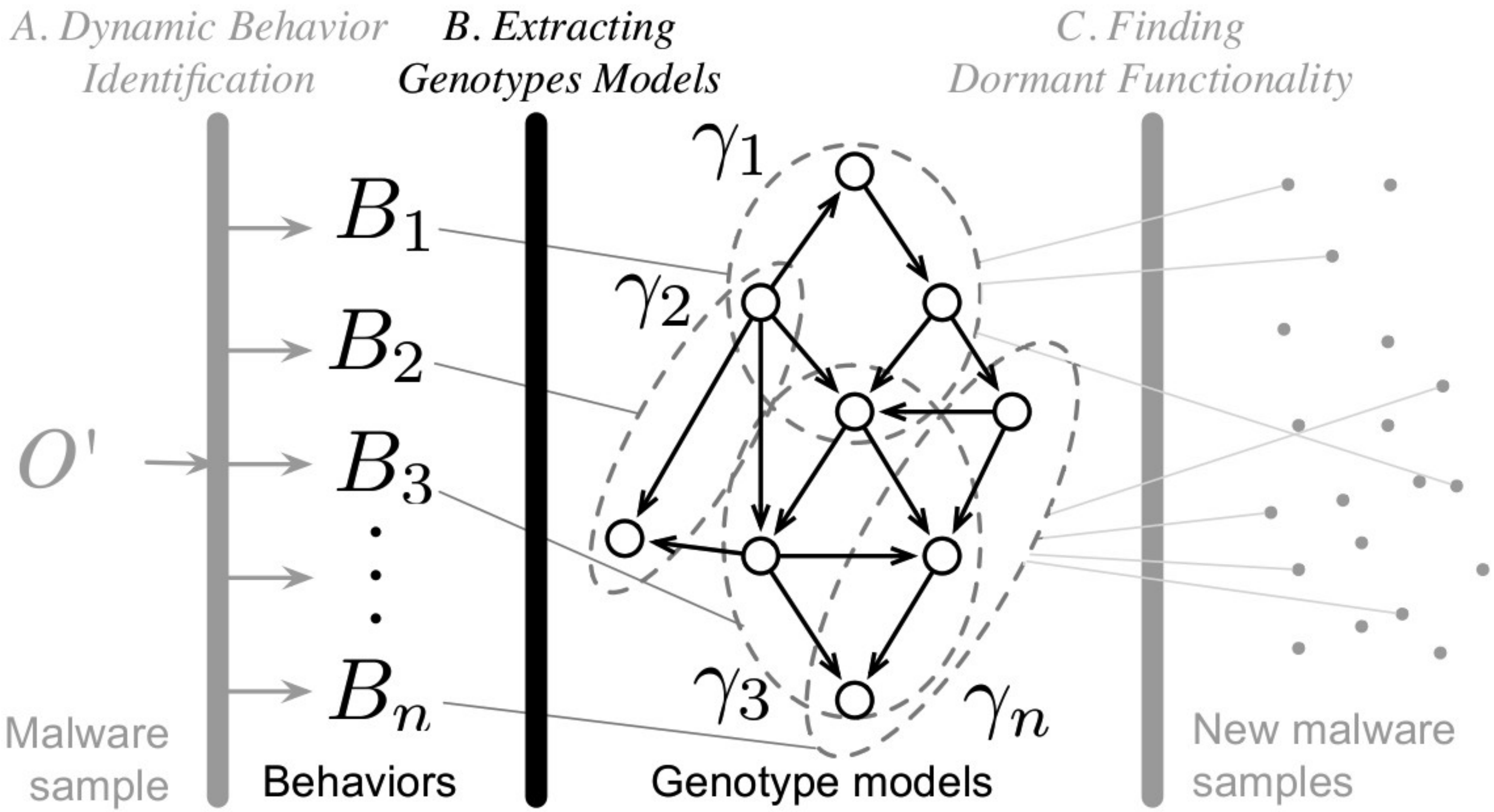
- Run malware in instrumented sandbox
  - Anubis

- 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

- Take as input the set R_B of relevant system/API calls
- **Identify** the code responsible for behavior B *(genotype)*
- **Model** the code responsible for behavior B *(genotype model)*
- The genotype model can then be statically, efficiently used for detecting the corresponding genotype and phenotype in other binaries that did not perform B during dynamic analysis

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,..)

Extracting Genotype Models: Steps

- Slicing:
  - obtain an initial set of instructions (genotype) ϕ that are related to R_B
- Filtering:
  - increase the precision of the genotype by removing from ϕ instructions that are not specific to B
- Germination:
  - increase the completeness of the model by adding instructions to ϕ

Step 1: 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)

Step 2: Filtering

- The slice ϕ is not precise
- General purpose utility functions executed as part of behavior are 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

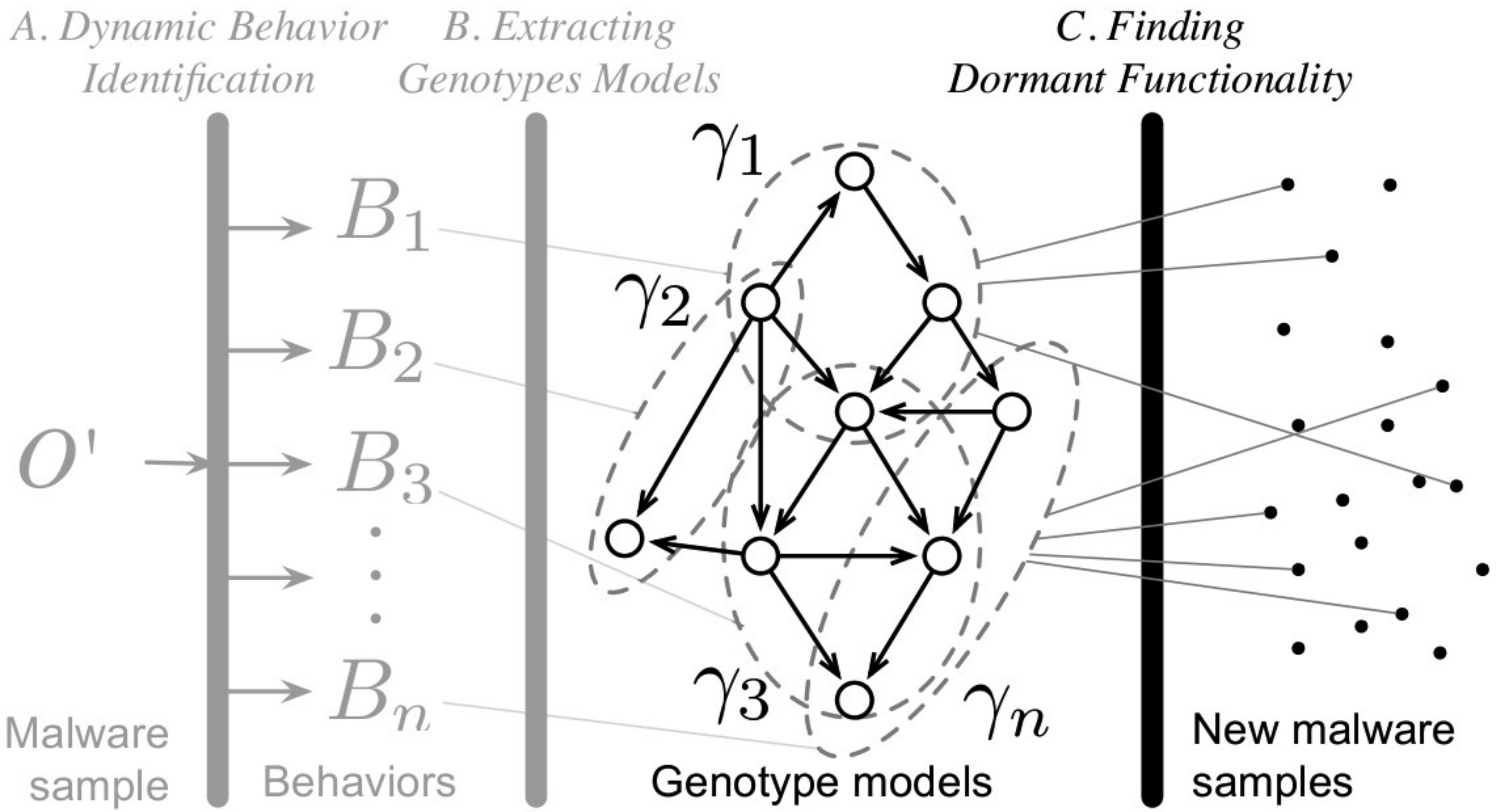
Filtering Techniques

- 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

Step 3: 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 a K-Node subgraph (K=10)
- Use techniques from our previous work [1] to efficiently match a binary against a set of genotype models
- We use Anubis as a generic unpacker

[1] "Polymorphic Worm Detection Using Structural Information of Executables", RAID 2005

Evaluation

Evaluation

- Extract genotype models from a sample
- Match these genotypes against other samples
- 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?

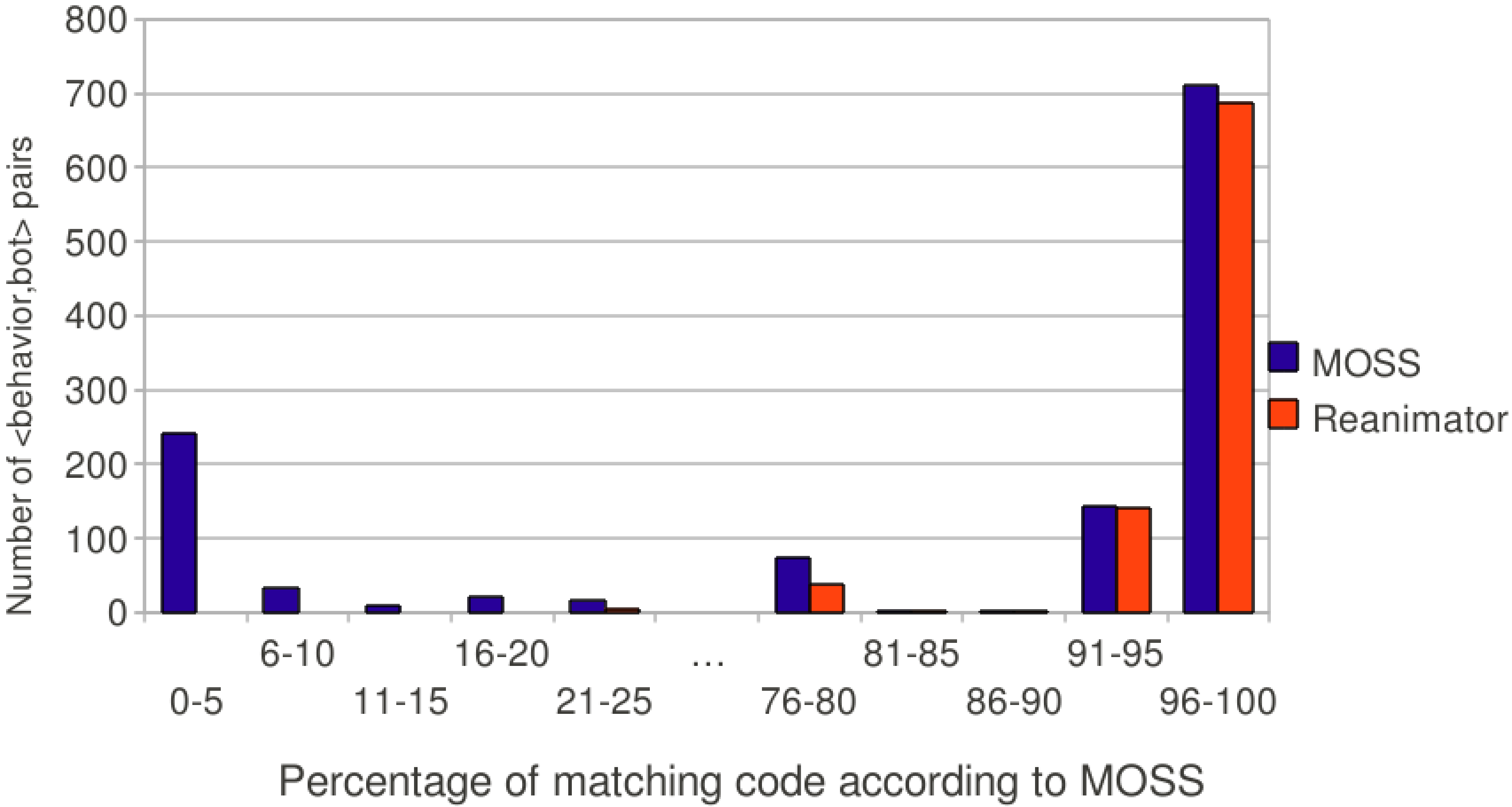
Accuracy

- To test accuracy and robustness of our system we need a ground truth
- Dataset of 208 bots with source code
    - thanks to Jon Oberheide and Michael Bailey from University of Michigan
- Extract 6 genotype models from 1 bot
- Match against remaining 207 bot binaries

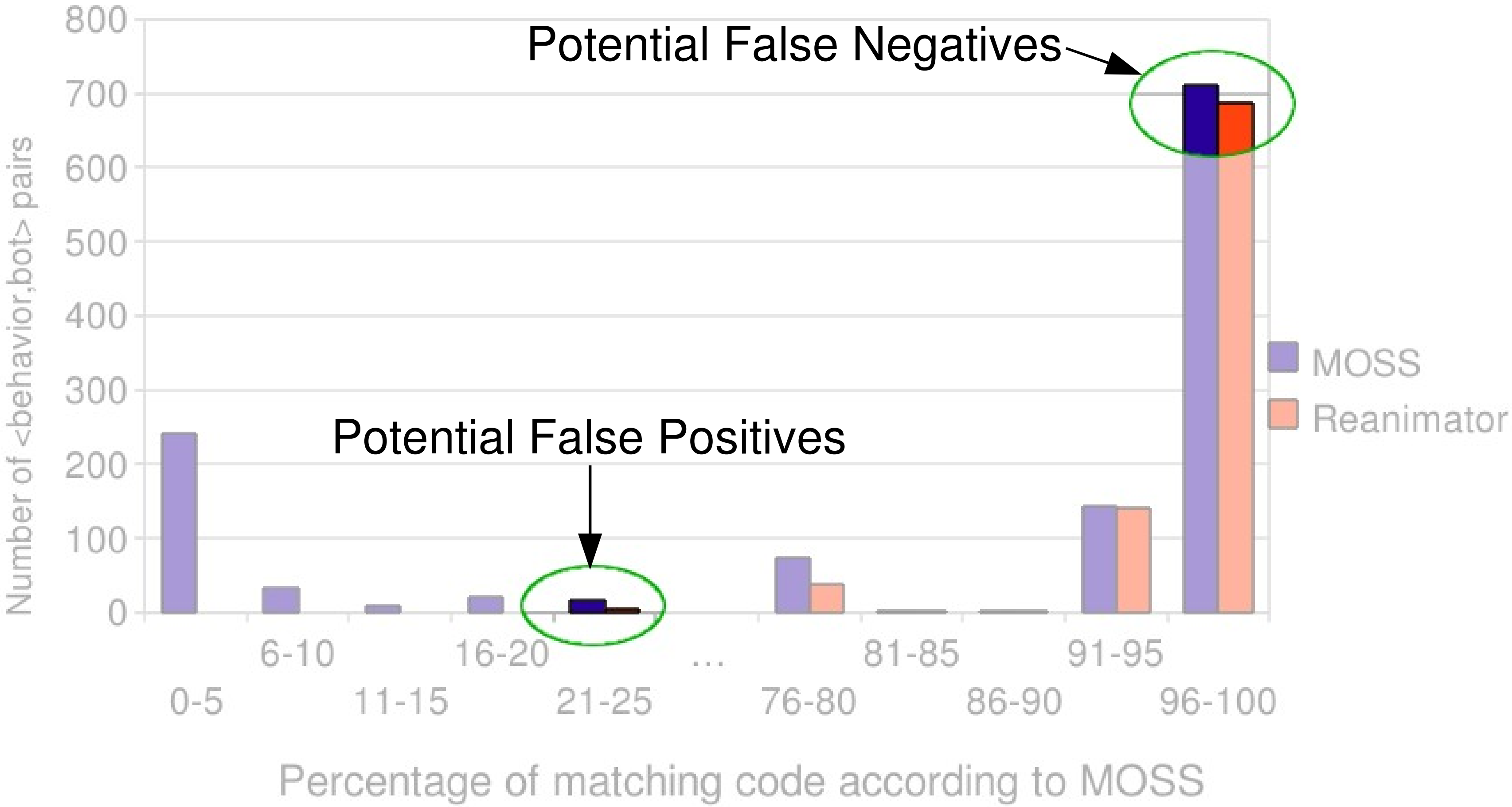
Accuracy

- 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 bot 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


Potential False Negatives

Potential False Positives

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

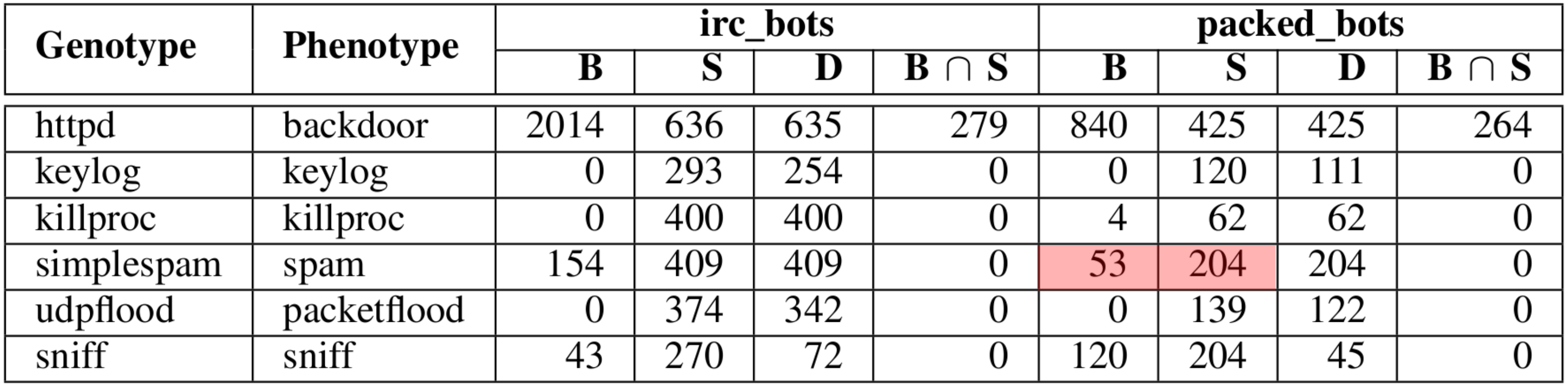
Robustness

- 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)
  - Visual Studio vs. Intel
- Some robustness to malware metamorphism was demonstrated in [1]

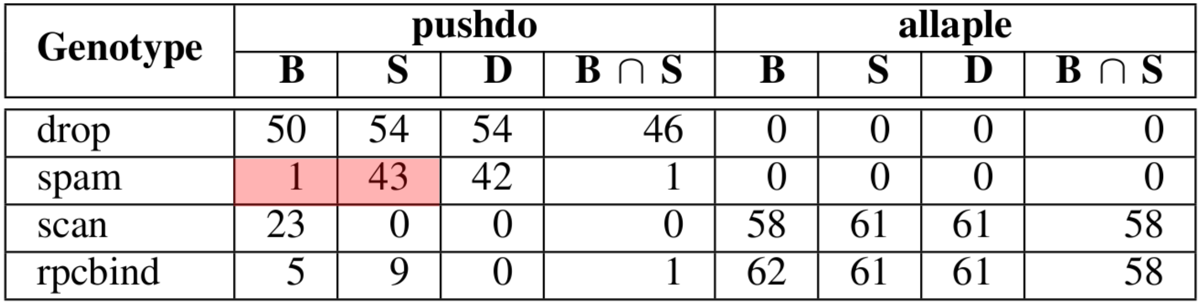
In-the-Wild Detection

- 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

Conclusions

- Identify security-relevant behavior during dynamic analysis of a malware sample
- Automatically identify and model the code that is responsible for that behavior
- Use these models to statically detect similar code in other samples
- Our experiments demonstrate accuracy and robustness
- Testing against in-the-wild datasets shows improved detection of malicious functionality

Questions?