# Automated Generation of YARA Classifier for Malware Using Code Similarity

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Presented at ACSAC 2022, December 2022





#### **About Me**





#### Professor of Computer Science

CTO, co-Founder

#### Automated malware deobfuscation and indexing Automated YARA generation





# **PSA - Invitation to share your knowledge for posterity**



# **Digital Threats: Research and Practice**

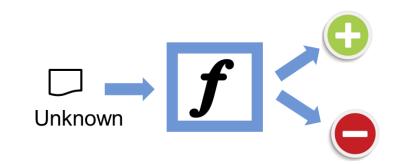
Promoting Science in Digital Threats Research

Field Notes: Capture knowledge of practitioners

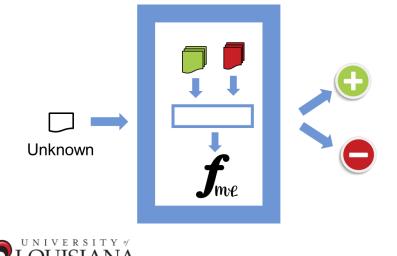
- A short case report (1000-1500 words) about emerging threats and defenses.
- Accurately document factual data as well as the settings, actions, behaviors, and consequences that are observed.
- May contain thoughts, ideas, questions, and concerns that arise as the observation is conducted.
- Provide perspectives on a single phenomenon that, when accumulated over time, suggest new avenues of research.







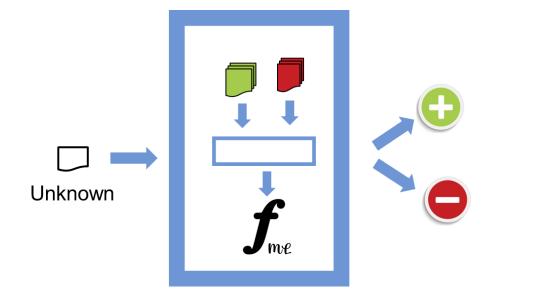
#### ML Classifiers



- Requirements for ML Classifiers:
  - Distribution of +ves and –ves is identical and independent
  - Availability of +ves and –ves samples
  - Available samples represent population



# **ML Classifiers for Malware**



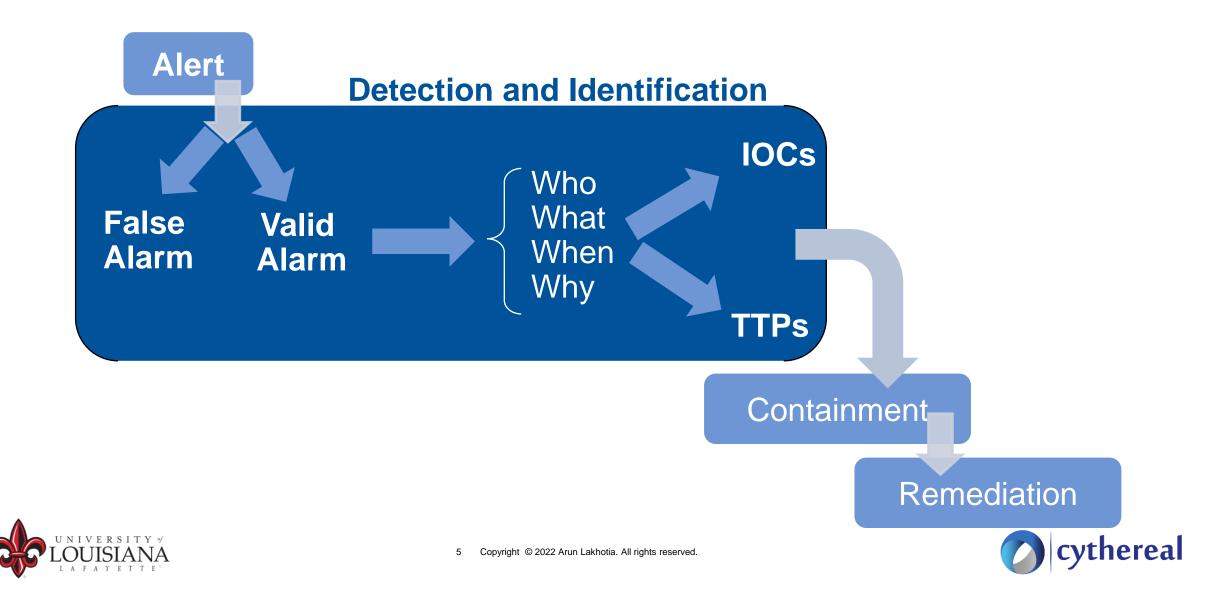
**Practical Challenges** 

- Concept drift
  - +ves and -ves are not static
- Adversarial
  - +ves transform to defeat classifiers
- Labels are noisy
  - Crowdsourced
  - Industry consensus

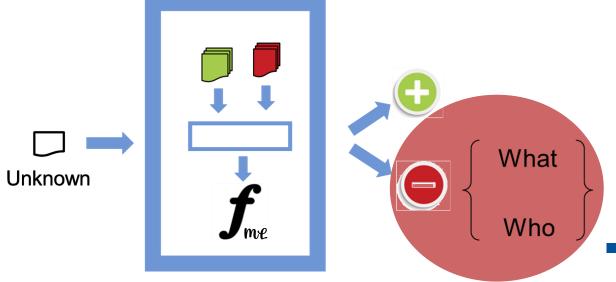




#### New Use Case: Incident Response Workflow



# **ML Classifiers for Malware**



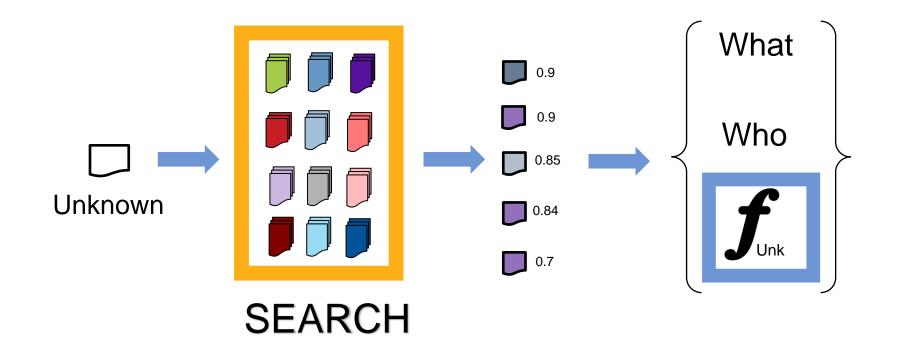
#### **New Challenges**

- Knowing a suspect is malware is not sufficient
  - Need to know the stage of the attack
    - What the malware does?
    - Who is behind it?
- Need multi-classifiers
  - Type of malware
  - Family of malware





# **A New Architecture for Generating Malware Classifiers**



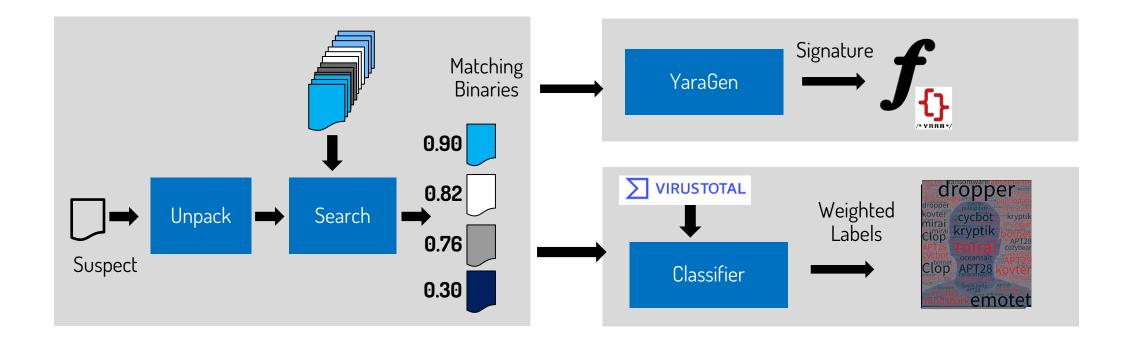
- Match Unknown to Known
- Extract characteristics from Known
- Create specialized classifier for the Unknown







#### **Cythereal MAGIC – Malware Genomic Classifier**







# How to Search for Similar Binaries?

```
"push(ebp)",
"mov(ebp,esp)",
"sub(esp,'0x18')",
"mov(eax,dptr(ebp))",
"mov(dptr(ebp-4),eax)",
"lea(eax,dptr(ebp-'0x18'))",
"mov(dptr(eax),'0x49636653')",
"mov(dptr(eax+4),'0x6c694673')",
"mov(dptr(eax+8),'0x6f725065')",
"mov(dptr(eax+8),'0x6f725065')",
"mov(dptr(eax+12),'0x74636574')",
"mov(dptr(eax+16),'0x6465')",
"push(eax)",
"call('0x129a')"
```

Need to define similarity on semantics







Bytes

Semantics

### **Features from Semantics**

#### Code

"push(ebp)", "mov(ebp,esp)", "sub(esp,'0x18')", "mov(eax,dptr(ebp))", "mov(dptr(ebp-4),eax)", "lea(eax,dptr(ebp-'0x18'))", "mov(dptr(eax+4),'0x6c694673')", "mov(dptr(eax+4),'0x6c694673')", "mov(dptr(eax+12),'0x74636574')", "mov(dptr(eax+12),'0x74636574')", "mov(dptr(eax+16),'0x6465')", "push(eax)", "call('0x129a')"

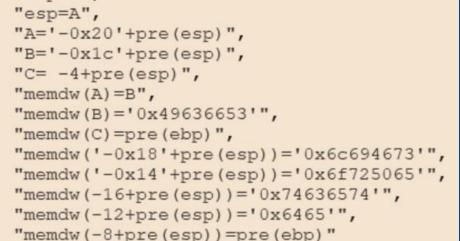
push(ebp)", "mov(ebp,esp)", "sub(esp,'0x18')", "mov(eax,dptr(ebp))", "mov(dptr(ebp-4),eax)", "lea(eax,dptr(ebp-'0x18'))", "push(esi)", "mov(esi,'0x49636653')", "mov(dptr(eax),esi)", "pop(esi)", "push(edi)", "mov(edi,'0x6c694673')", "mov(dptr(eax+4),edi)", "pop(edi)", "push(edx)", "mov(edx, '0x6f725065')", "mov(dptr(eax+8),edx)", "pop(edx)", "push(edx)", "mov(edx, '0x74636574')", "mov(dptr(eax+12),edx)", "pop(edx)", "push(edx)", "mov(edx, '0x6465')", "mov(dptr(eax+16),edx)", "pop(edx)", "push(eax)", "call('0x1c703')"



"C= -4+ "memdw "memdw "memdw

"eax=B",

"ebp=C",



**Semantics** 

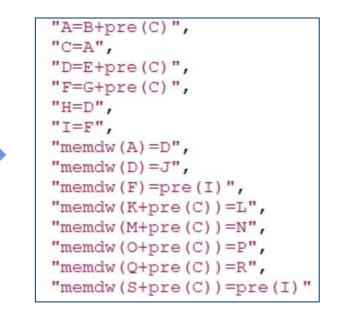
#### • Interpret

- Normalize
- Generalize

served

10 C Index

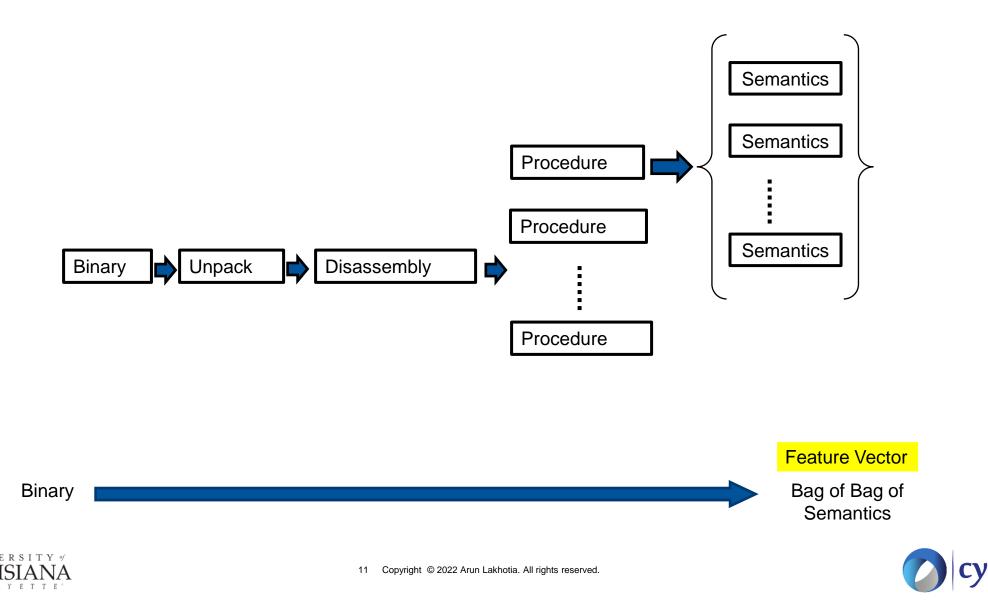
Generalized Semantics







## **Translating Binary to Feature Vector using Semantics**



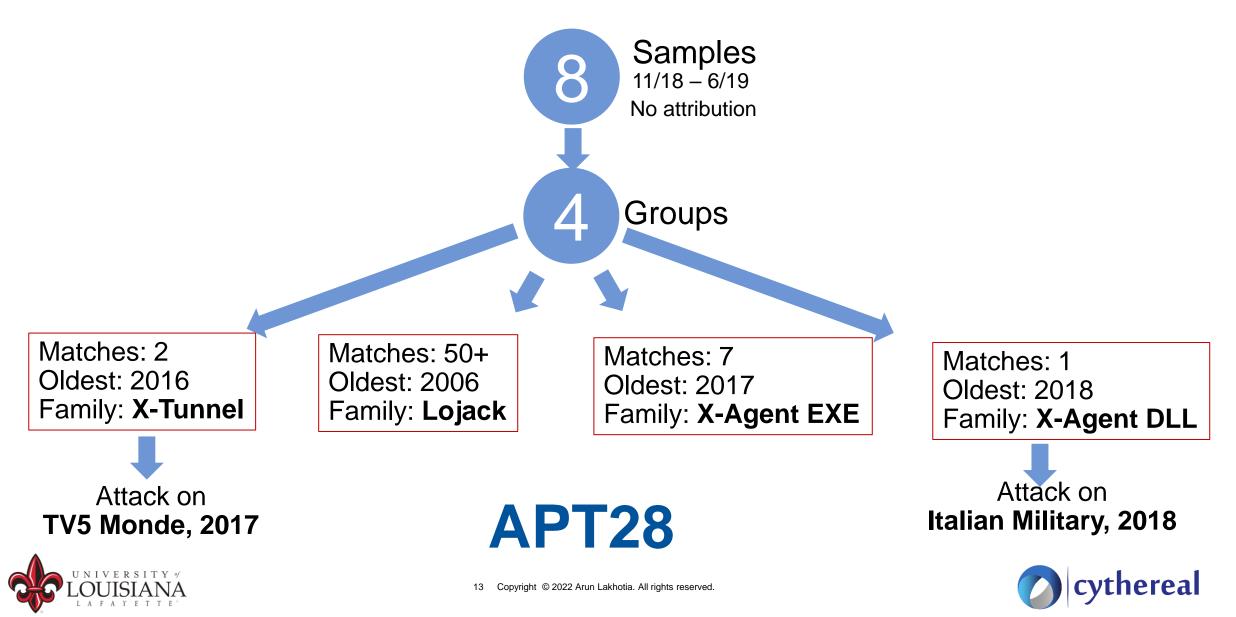
thereal

#### Demo: <u>https://Beta.Magic.Cythereal.Com</u>

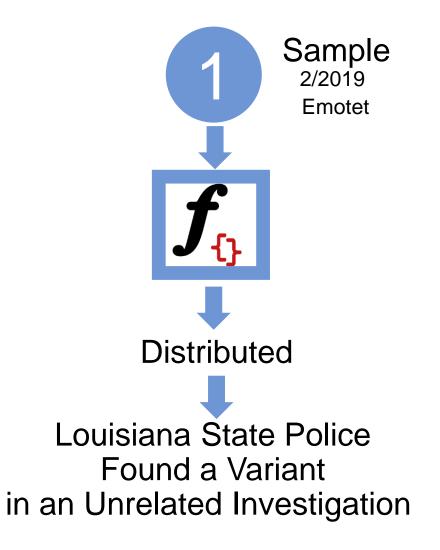




# Case Study: CYBERCOM CNMF Malware



#### **Case Study: Louisiana State Police**







## **Power of Genome (data from 2019)**

#### **Executable Binaries in MAGIC Repository**

# Binaries	3,413,184
# Genomically Unique	1,457,393
Genomic Compression	57.3%

Two binaries are genomically identical if ALL their procedures have the same genome.

#### **Procedures Extracted from Binaries**

# Procedures	1,658,759,504
# Genomically Unique	27,732,888
% Genomic Compression	98.33%

Two procedures are unique if they have the same abstracted semantics

#### **Binary Similarity (> 0.7)**

# Similarity Binary Nodes	3,978,430
# Similarity relationships	426,121,442
Avg number of similar binaries	107





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## **Hybrid Analysis Search**

 Free Automated Malware Analysis Service - powered by Falcon Sandbox - Search results from HA Community Files (hybridanalysis.com)



