Malware Lineage in the Wild

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Under Submission



Lineage

Lineage

- Software evolution over time
 - New features
 - Bug fixes
 - **–** ...



Lineage

- Software evolution over time
 - New features
 - Bug fixes
 - ...



- Malware evolves similarly

Background and Motivation

- Unknown versions

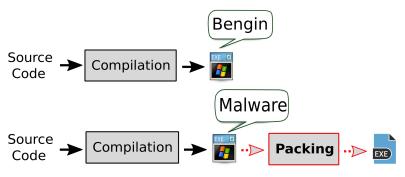
Background and Motivation

- Unknown versions
- Development



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- Incomplete data

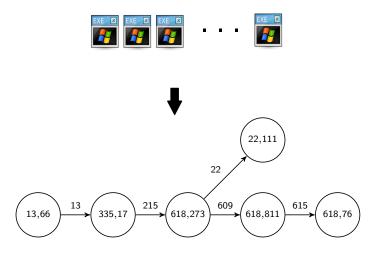
Why Lineage?

Malware analysis applications

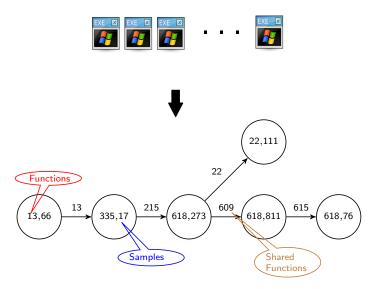
- Triage
- Labeling
- Threat Intelligence
- Author attribution
- ..

Problem Definition

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$\mathsf{Approach} \to \mathsf{Overview}$

Phasel → Code Recovery

- 1. Unpacking
- 2. Disassembly

Approach \rightarrow Overview

$\mathsf{PhaseI} \to \mathsf{Code} \; \mathsf{Recovery}$

- 1. Unpacking
- 2. Disassembly

PhaseII → Lineage Inference

- 1. Identifying Version
- 2. Building a Lineage Tree
- 3. Adding Cross-Edges

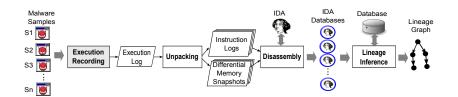
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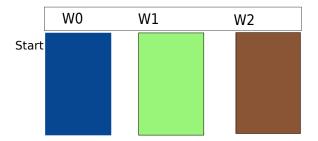
Code Recovery → Unpacking

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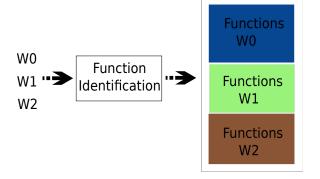
- Monitor each write and execute in memory

Code Recovery → Unpacking

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Code Recovery → Disassembly



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$$Program Hash = md5sum(hash(f_1) + hash(f_2) + ... + hash(f_n))$$

	P13	P22	P335	P618	P618_1	P618_2
P13	-	12	13	13	13	13
P22	-	-	15	13	22	13
P335	-	-	-	214	215	214
P618	-	-	-	-	609	615
P618_1	-	-	-	-	-	609
P618_2	-	-	-	-	-	-

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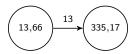
Identifying root \rightarrow Lehman's 6th law of continuous growth.



	P13	P22	P335	P618	P618_1	P618_2
P13	-	12	13	13	13	13
P22	-	-	15	13	22	13
P335	-	-	-	214	215	214
P618	-	-	-	-	609	615
P618_1	-	-	-	-	-	609
P618_2	-	-	-	-	-	-

Selected *Nodes* \rightarrow *P*335, *P*618, *P*618_1, *P*618_2

Break tie: minimum number of functions



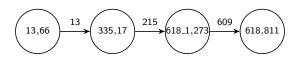
	P13	P22	P335	P618	P618_1	P618_2
P13	-	12	13	13	13	13
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P618_1	-	-	-	-	-	609
P618_2	-	-	-	-	1	-

Selected *Node* \rightarrow *P*618_1



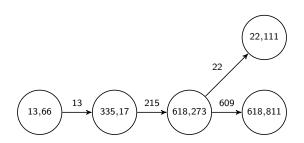
	P13	P22	P335	P618	P618_1	P618_2
P13	-	12	13	13	13	13
P22	-	-	15	13	22	13
P335	-	-	-	214	215	214
P618	-	-	-	-	609	615
P618_1	-	-	-	-	-	609
P618_2	-	-	-	-	-	-

Selected $Node \rightarrow P618$



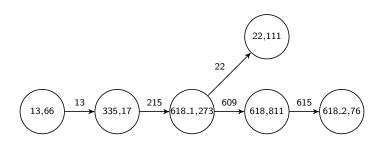
	P13	P22	P335	P618	P618 ₋ 1	P618 ₋ 2
P13	-	12	13	13	13	13
P22	-	-	15	13	22	13
P335	-	-	-	214	215	214
P618	-	-	-	-	609	615
P618_1	-	-	-	-	-	609
P618_2	-	-	-	-	=	-

Selected *Node* \rightarrow *P*22



	P13	P22	P335	P618	P618_1	P618_2
P13	-	12	13	13	13	13
P22	- 1	-	15	13	22	13
P335	- 1	-	-	214	215	214
P618	-	-	-	-	609	615
P618_1	-	-	-	- 1	-	609
P618_2	-	-	-	-	-	-

Selected *Node* \rightarrow *P*618₋₂

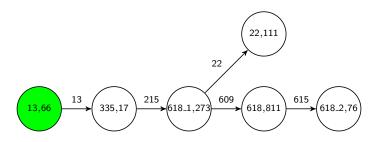


Lineage Algorithm→ Adding Cross-Edges

- Multiple parents, i.e., branching and merging
- Iterate over each node in topological order
- Ignore successor and predessors
- Non-inherited functions

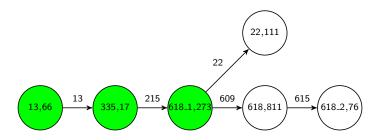
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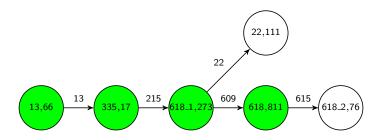
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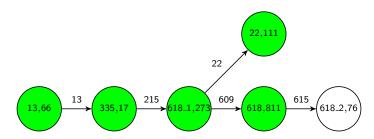
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Evaluation \rightarrow Goals

- Benign Lineage
- Malware Lineage

Evaluation \rightarrow Dataset

Benign (631 Versions, 13 Programs)

- FileZilla → 10 years
- Fzputtygen ightarrow 10 years
- Fzsftp ightarrow 10 years
- − Notepad++ \rightarrow 14 years
- Pageant \rightarrow 16 years
- Plink → 16 years
- ProcessHacker → 6 years
- PSCS \rightarrow 16 years
- PSFTP → 14 years
- PuTTY → 14 years
- $\ \mathsf{PuTTYgen} \to \textbf{16 years}$
- PuTTYtel → **14 years**
- WinSCP \rightarrow 10 years

Malware (7,793 Samples, 10 Families)

- Allaple ightarrow 4,000
- IRCBot → **365**
- Klez ightarrow 750
- Loring \rightarrow 216
- Memery \rightarrow 113
- Picsys \rightarrow 131
- Simbot \rightarrow 214
- Sytro ightarrow 1,354
- − Urelas \rightarrow 206
- VtFlooder \rightarrow 444

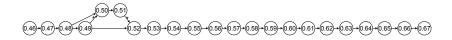
Evaluation \rightarrow Benign

Lineage Inference evaluation on open-source programs.

	Refere	ence		S	PP		Raw					
Program	Туре	V	V	$ V^r $	X	PO	V	$ V^r $	X	PO		
FileZilla	S	119	117	1	8	96%	119	1	20	97%		
Fzputtygen	S	107	19	1	0	72%	30	1	0	96%		
Fzsftp	S	116	50	1	0	71%	52	1	2	33%		
Notepad++	D	70	70	1	6	65%	70	1	14	71%		
Pageant	S	18	18	1	0	93%	18	1	0	97%		
Plink	S	18	18	1	0	99%	18	1	1	90%		
ProcessHacker	2-S	52	52	2	2	76%	52	2	7	79%		
PSCP	S	20	20	1	1	99%	20	1	1	73%		
PSFTP	S	16	16	1	0	99%	16	1	0	88%		
PuTTY	S	22	22	1	2	100%	22	1	0	92%		
PuTTYgen	S	17	16	1	0	87%	16	1	0	66%		
PuTTYtel	S	4	4	1	1	100%	4	1	0	50%		
WinSCP	S	47	47	1	1	100%	47	1	9	100%		

$\mathsf{Lineage} \to \mathsf{Benign}$

PuTTY



Fzputtygen



Evaluation \rightarrow Malware

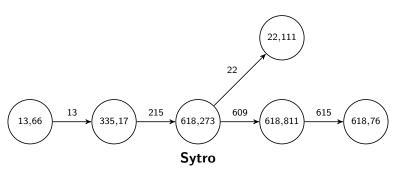
Lineage Inference evaluation on malware samples.

		V		<i>E</i>		$max(L(v_i))$		$ L(v_i)=1 $		$max(F(v_i))$		$min(F(v_i))$		$ \bigcup F(v_i) $	
Family	EXE	spp	raw	spp	raw	spp	raw	spp	raw	spp	raw	spp	raw	spp	raw
allaple	241	114	143	113	142	71	71	92	138	250	301	10	10	413	510
klez	118	13	13	12	12	93	93	8	8	618	667	244	251	666	927
memery	140	12	12	11	11	66	66	3	3	121	123	25	27	131	136
picsys	113	5	5	4	4	92	92	1	1	379	473	16	16	397	498
simbot	135	21	93	20	92	65	24	13	82	67	71	17	17	108	1,723
sytro	186	4	4	3	3	92	92	0	0	617	667	335	350	754	1,290
vtflooder	170	20	69	18	66	75	75	11	61	712	749	10	10	3,202	4,652

$\mathsf{Lineage} \to \mathsf{Malware}$



Picsys



Limitations

- Packers that modify the original code, e.g., VMProtect
- Evasion, anti-VM checks
- Code semantics require manual analysis
- Function identification, e.g., Nucleus

Conclusion

- An approach to perform malware lineage on samples collected in the wild.
- First study to identify number of versions in a malware family.
- Evaluated on 13 benign programs and 10 malware families.
- Our approach provides, on average, 26x reduction from input sample versions.

THANK YOU!

QUESTIONS?

Packing/Unpacking

Packing/Unpacking





Packing/Unpacking

