Towards a malware family classification model using static call graph instruction visualization

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Content

Problem definition: attribution

- aim: classify family and/or actor(s) behind an attack (**attribution**)
- motivation: improved threat intelligence, faster incidence response, tailored defense strategies
- simple feature: the binary **PE** file
  - byte sequences; distribution; hashes
  - system calls e.g. *GetFileInformationByHandle*
  - executable's static call graph
- goal: **malware family/author detection** using **static call graph**

Malware analysis – the textbook approach

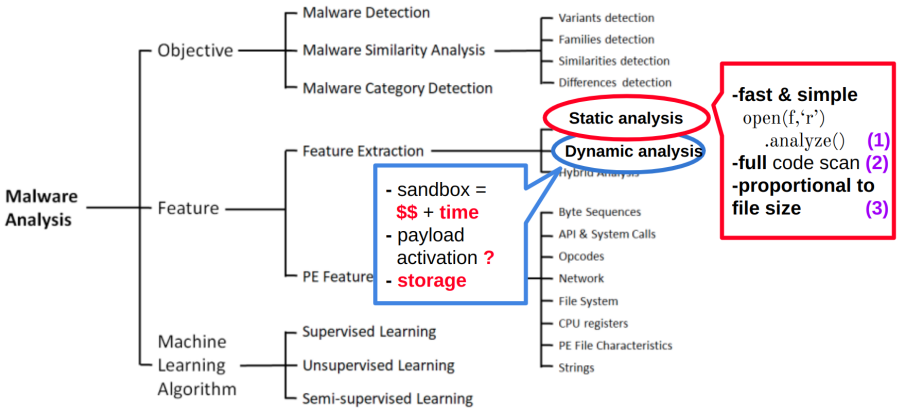


Figure 1: Malware analysis – taxonomy according to (Ucci, Aniello, and Baldoni 2018).

What is a static call graph of an *.exe*?

- static = obtained by disassembly (vs. dynamic = obtained by sandbox)
- function execution sequence = call graph
  - node = function (DLL / subroutine)
  - link = function call
- generation method: **Radare2** disassembler tool

What is a static call graph of an *.exe*?

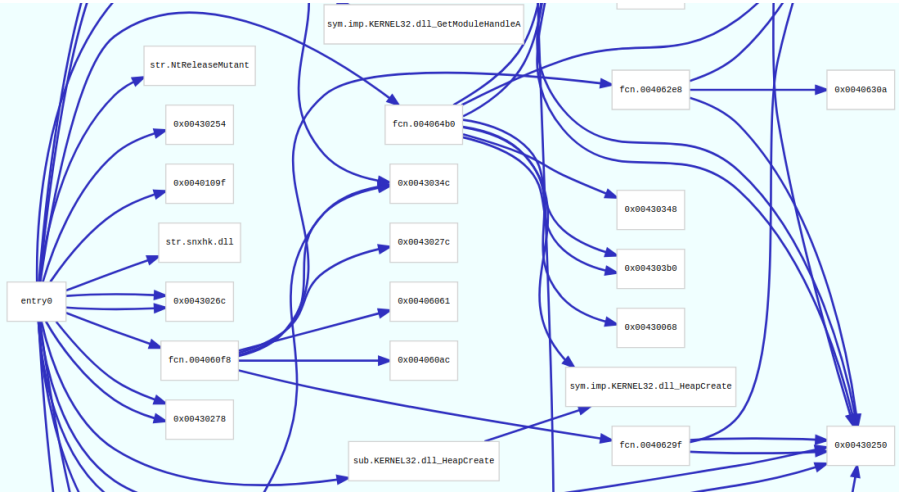
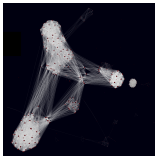


Figure 2: Sample call graph obtained by Radare2.

How to use this graph?



clustering signatures

(Mester and Bodó 2021)

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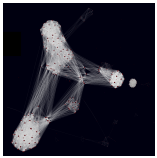

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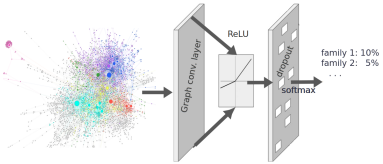
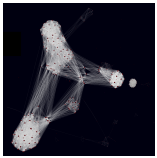


GCN

(Mester and Bodó 2022)

How to use this graph?



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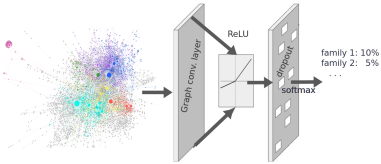

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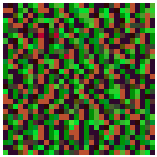


CNN

current work

Motivation

- **helpful**: wide range of tools: CNN, visualization, patterns
  - DFS traversal – instruction patters – image patterns
- classification based on image derived from instructions
- aiming method stability: altering instructions is not trivial

Literature

- first work in 2011: **MalImg** dataset (Nataraj et al. 2011)
- working with grayscale images (Cui et al. 2018; Kalash et al. 2018)
- SimHash images: locality-sensitive binary hash generated by SimHash (Charikar 2002) for the opcode sequences, converted into binary image (Ni, Qian, and Zhang 2018)
- Markov images: visualizing transition probabilities between bytes, opcodes (Yuan et al. 2020; Deng et al. 2023)

Datasets

Table 1: Public malware datasets (Yang et al. 2021).

Dataset		Published	Binaries	Families	Samples(mal.)	EMBER	Disasm.	Image
MalImg	Nataraj et al. 2011	2011	❍	25	9458	❍ ✪	❍ ✪	● ✪
MS BIG	Ronen et al. 2018	2015	❍	9	10 868	❍	●	❍
EMBER	Anderson and Roth 2018	2018	❍	◗	800 000	●	❍	❍
UCSB	Aghakhani et al. 2020	2020	●	❍	232 415	❍	❍	❍
SOREL-20m	Harang and Rudd 2020	2020	●	❍	9 962 820	●	❍	❍
BODMAS	Yang et al. 2021	2021	●	581	57 293	●	❍ ✪	❍ ✪
Malflow	**(this)**	**2024**	❍	**47**	**18 756**	✪	✪	✪

Our contribution

- **original method**: generate RGB images for PE files based on disassembled call graph instruction flow
  - ignores noise from the binary
  - learns from images based solely on instruction information
- **training** CNN models: 0.88 micro F_1 on BODMAS with 57 families
- **publishing** a new dataset on Kaggle: Internal Bitdefender Dataset – IBD
- **publishing** packer information, static call graph, images and instruction data for BODMAS, MalIMG and IBD
- **comparing** our method to the state-of-the-art EMBER features

Generating the call graph & RGB image

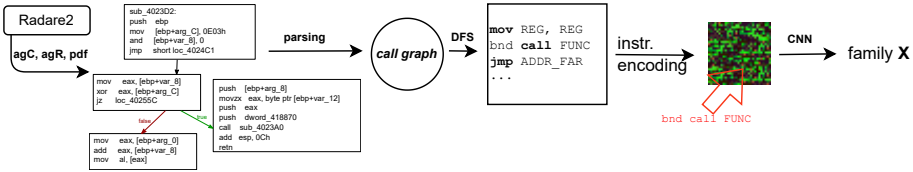


Figure 3: Pipeline of our proposed method.

- Radare2 (5.8.8 release): `agCd` and `agRd` – global call and reference graphs
- each function: `pdfj`
- DFS on functions
- **[bnd?] [prefix?] mnemonic [param1 [param2, ...]]**

Example encoding

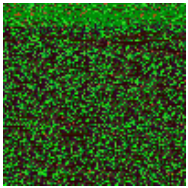
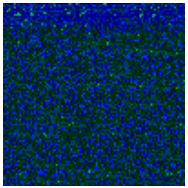
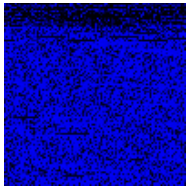
Simple hex dump	Encoding **FE**	Encoding **PE1**	Encoding **PE2**
			
BODMAS sample 53c4c900e03eb6e94c0fe18091591904			

Figure 4: Comparing different instruction encodings and simple hex dump image.

Training CNN models

- ResNet18/50, Resnet1D, MobileNetV3, GoogleNet, EfficientNet, DenseNet
- images formats: hex dump-based grayscale images, FE, PE1, PE2 encodings
- augmentation: generating 7000 metamorphic variants with pymetangine[1]

[1] https://hub.docker.com/r/attilamester/pymetangine

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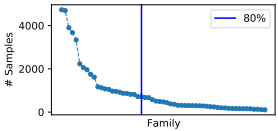
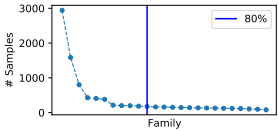


BODMAS

57 families

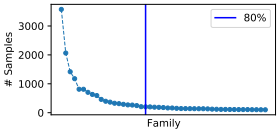
57k samples



MalImg

23 families

9k samples



IBD

47 families

18k samples

[1] https://hub.docker.com/r/attilamester/pymetangine

Model	Batch	Img.	Acc.	F_1 micro	F_1 macro
BODMAS, 57 families					
ResNet18	20	224 × 224	0.820	0.820	0.797
ResNet18	20	100 × 100	0.887	0.887	0.859
ResNet50	32	100 × 100	0.812	0.812	0.786
ResNet1d	20	100 × 100	0.784	0.784	0.727
MobileNetV3	32	30 × 30	0.790	0.790	0.733
GoogleNet	32	30 × 30	0.790	0.790	0.731
EfficientNet	32	30 × 30	0.786	0.786	0.737
DenseNet121	32	30 × 30	0.790	0.790	0.746
BODMAS, 57 families, hex dump images					
ResNet18	20	100 × 100	0.881	0.881	0.873
MalImg, 23 families					
ResNet18	20	100 × 100	0.722	0.744	0.737
ResNet18	20	30 × 30	0.761	0.761	0.749
IBD, 47 families					
ResNet18	20	100 × 100	0.872	0.872	0.784
ResNet18	32	30 × 30	0.849	0.849	0.776

Comparing our method with EMBER

- motivation: measure our model's performance compared to EMBER features (Anderson and Roth 2018)
- EMBER: 2381-long feature vector: bytes, histograms, entropy, section info, strings, import-export directory info, etc.
- **comparison methodology**: instruction mnemonic histogram vector for each file (2019-dimensional integer vector) vs. EMBER
- **compared models**: DecisionTree, RandomForest, LinearSVC, SGD, LogReg

Model	EMBER (1)		Mnem. hist. (2)		(1) + (2)	
	F_1 m.	F_1 M.	F_1 m.	F_1 M.	F_1 m.	F_1 M.
BODMAS, full dataset – 51 974 samples, 57 families						
DecisionTree	0.907	0.886	0.172	0.058	0.904	0.877
RandomForest	0.924	0.905	0.174	0.056	0.924	0.900
BODMAS, only non-packed samples – 33 807 samples, 44 families						
DecisionTree	0.930	0.917	0.879	0.831	0.932	0.922
RandomForest	0.945	0.938	0.884	0.839	0.944	0.939
MalImg, full dataset – 9138 samples, 23 families						
DecisionTree	0.990	0.975	0.753	0.841	0.998	0.978
RandomForest	0.996	0.990	0.786	0.832	0.993	0.982
IBD, full dataset – 18 756 samples, 47 families						
DecisionTree	0.923	0.862	0.897	0.838	0.923	0.870
RandomForest	0.961	0.936	0.924	0.877	0.963	0.940
IBD, only non-packed samples – 16 088 samples, 41 families						
DecisionTree	0.922	0.866	0.892	0.828	0.916	0.867
RandomForest	0.960	0.938	0.918	0.866	0.961	0.941

Observations

- packed samples distort the model trained on the mnemonic histogram vector, but do not have so heavy effect on binary file-based features, i.e. the EMBER
- EMBER's performance originates mainly from the byte- and byte entropy histogram information

Table 2: Comparison between the full EMBER vector and its subsets, on BODMAS

Model	[0..2381]		[0..255]		[256..511]		[0..511]	
	F_1 m.	F_1 M.	F_1 m.	F_1 M.	F_1 m.	F_1 M.	F_1 m.	F_1 M.
BODMAS, full dataset – 51 974 samples, 57 families								
DecisionTree	0.907	0.886	0.864	0.829	0.887	0.852	0.889	0.850
RandomForest	0.924	0.905	0.906	0.880	0.914	0.891	0.914	0.895

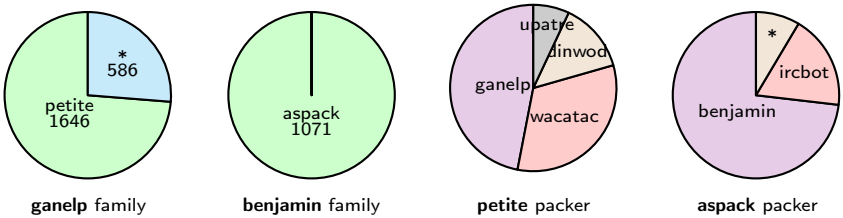
On correlation between packers and families

- BODMAS: 57k samples, 18k packed (33%)
- MalImg: 9.4k samples, 1.7k packed (18%)
- IBD: 18.7k samples, 2k packed (12%)

Table 3: Cramér's V association score between family, packed status, and packer tool.

	BODMAS	MalImg	IBD
Malware family – Packed	0.755	0.981	0.736
Malware family – Packer	0.547	0.590	0.525

Family – packer association



ganelp family **benjamin** family **petite** packer **aspack** packer

Figure 5: BODMAS: packer-family association, showing the number of samples.

Contribution summary

- **goal**: malware family classification
- **proposed model**: RGB images based on call graph instructions
- CNN architectures tested, but performance did not surpass the EMBER baseline's F1 score
- **discovered** strong correlation between families and packers
  - causing potential overfitting
  - packed samples may mislead ML models,
  - models may learn packer traits instead of malware behavior
- **published** on Kaggle: disassembled call graphs, images, packer info on BODMAS, MalImg and IBD

Future work

- combine instruction-based model with binary features to match/surpass EMBER baseline
- build explainable model on instruction images
- map malware families to instruction-level traits

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- Bitdefender

https://attilamester.github.io/call-graph/

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