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Make Data Reliable : An Explanation-powered Cleaning on Malware Dataset Against Backdoor Poisoning Attacks

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Category

CONTENT

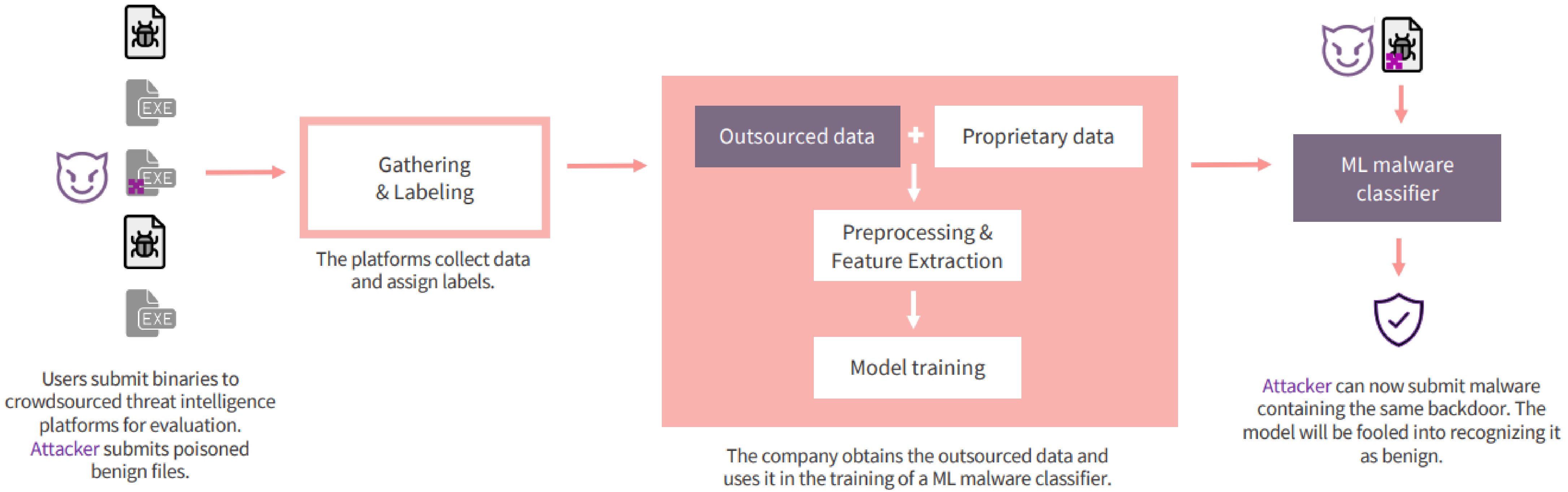
Introduction

- Machine Learning (ML) based malware classification has evolved significantly in recent decades.
- Training for malware classification often relies on crowdsourced threat feeds, and backdoor poisoning attacks have demonstrated their strong power.
- We propose MDR, a methodology to clean a given dataset and output a reliable dataset, thereby preventing the threat from backdoor poisoning attacks.

Background

- ML Malware Classification: It can be divided into two major categories, **static analysis (pre-execution detection)** and dynamic analysis (execution in virtual environment).
- Clean-label Attacks: Without changing the label of a sample, attackers poison the datasets by injecting watermark (or called backdoor, a specific combination of feature and value pairs), which will misguide the prediction result of the victim model at the inference time.
- SHAP: An explanation tool used to explain the predictions of a model. It provides the importance of each feature value to the decision made by the classifier.

Threat Model



Motivation

Limitations:

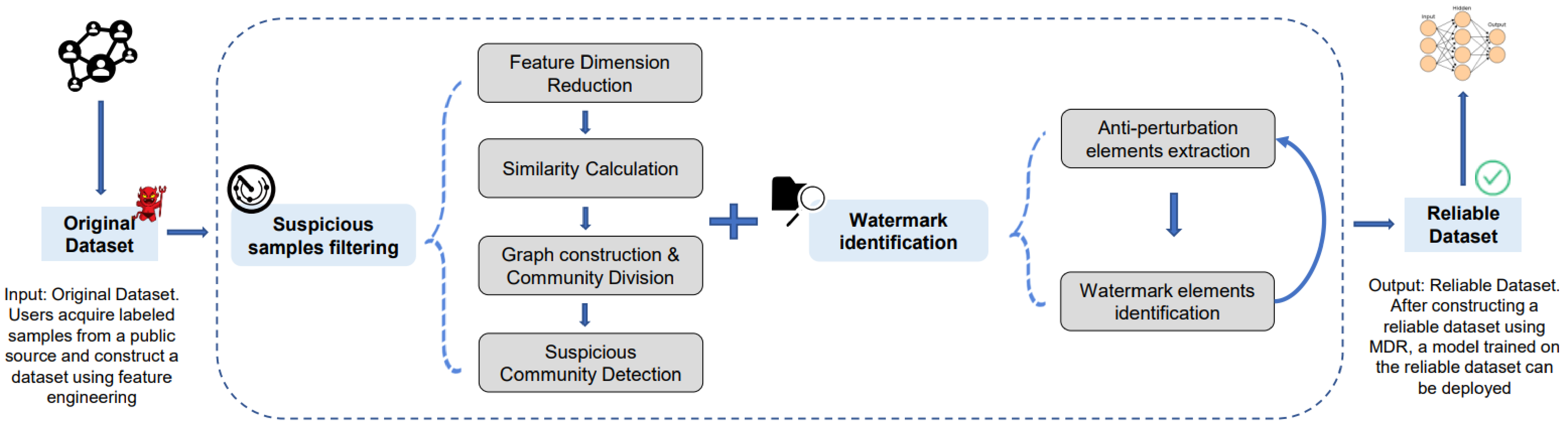
Model-level defense :

- Target at Computer Vision (CV).
- Focus on Deep Neural Network based classifiers only.
- Assume that attacker can actively tamper with the training label.

Input-level defense :

- Only evaluated defenses, and neither offers identification of watermarks.
- Performance are not good.

MDR (Make Data Reliable)



MDR

MDR (Make Data Reliable)

Suspicious Samples Filtering

Inspirations:

- Watermark is strongly goodware-oriented features and values, and there are more same goodware-oriented (feature, value) pairs among backdoored samples. The differences can be identified by focusing on the number of the same goodware-oriented (feature, value) pairs among samples.
- The differences between samples can be analyzed by clustering-like approaches.
- Watermark feature values are heavily oriented toward goodware, and they can resist the perturbation caused by malicious features. Therefore, After clustering, for each cluster, we can extract anti-perturbation elements then embed to malware feature vectors to compare the model prediction results.

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Suspicious Samples Filtering – (1st step. Feature Dimension Reduction)

- Remove all low-variance features.

Suspicious Samples Filtering – (2nd step. Similarity Calculation)

- Acquire strongly goodware-oriented features and values for each sample based on SHAP value and surrogate model.
- Each sample can be represented as a feature dictionary $Di = \{(f_1 : v_1), \ldots, (f_n, v_n)\}$, where f_i, v_i denotes strongly goodware-oriented features and values.
- $Similarity(D_i, D_j) = len(D_i \cap D_j)$

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Suspicious Samples Filtering – (3rd step. Graph construction & Community Division)

- Construct a Graph $G = \{V, E\}$, where V represents the set of samples, and E represents the edges of vertices. The weight of each edge is determined by the similarity between the vertices at both ends of the edge.
- Put the Graph as the input of Louvain algorithm to conduct community division.

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Suspicious Samples Filtering – (4th step. Suspicious Community Detection)

- For each community, extract the $(f: v)$ pairs that enable samples to be divided into the same community, then embed them in the malware feature vectors to conduct model prediction.
- Find the suspicious community based on the lowest model prediction results of such malware feature vectors in different communities.

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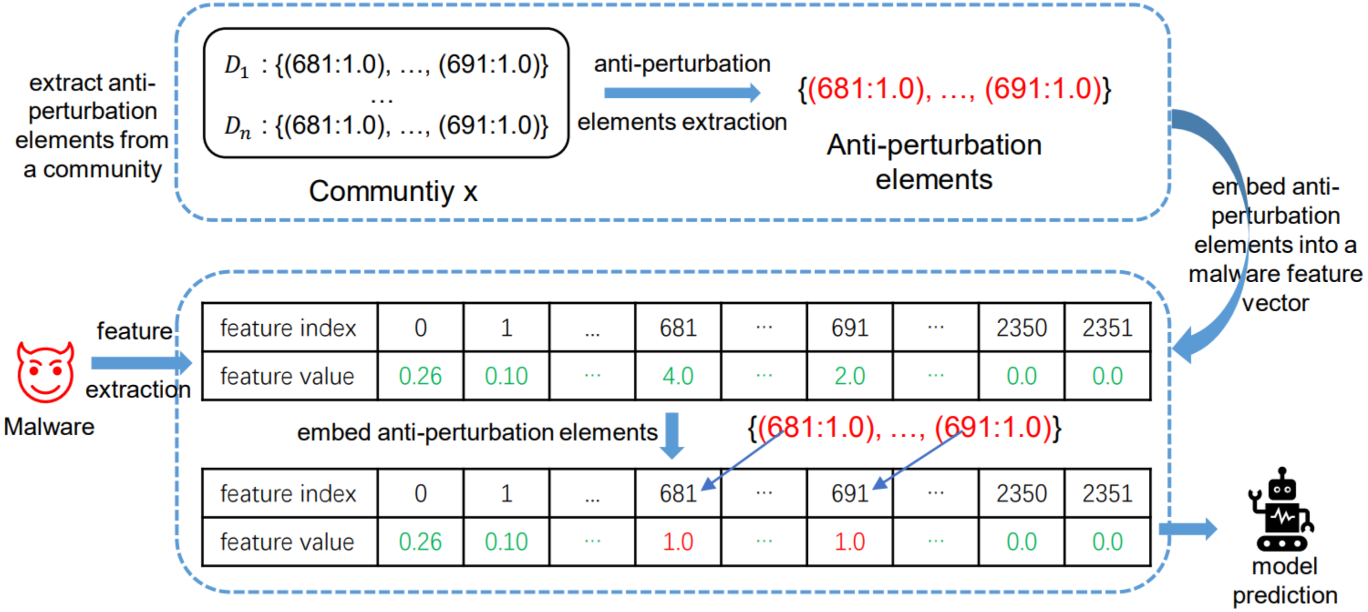
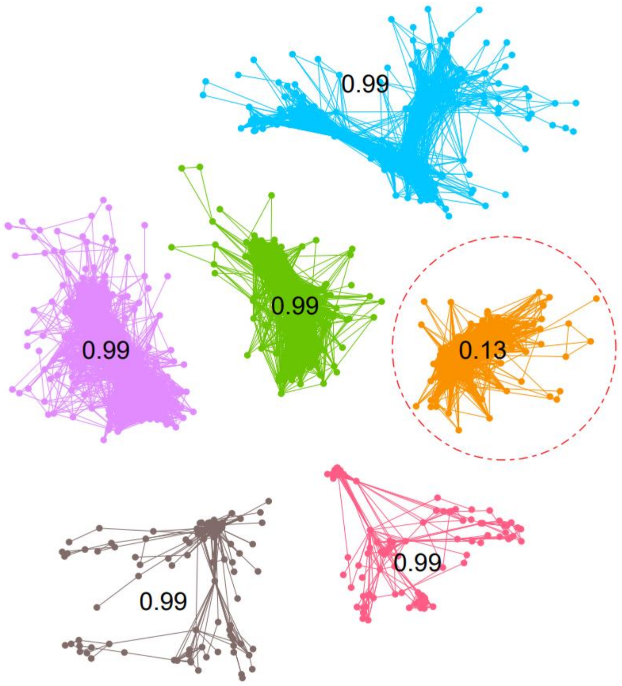
Suspicious Samples Filtering – (4th step. Suspicious Community Detection)





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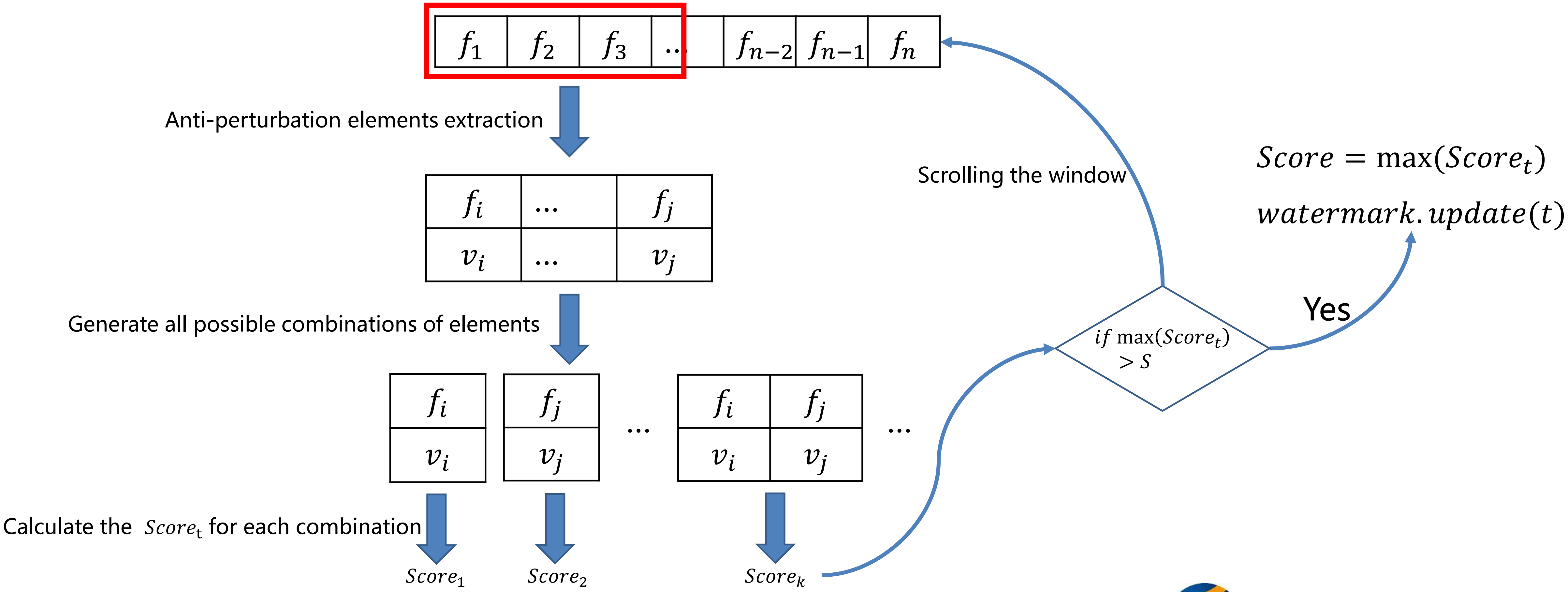
Watermark Identification: Initialize $S = 0$ and $watermark = \{\}$



$$(Score_t = \frac{the\ number\ of\ occurrences\ of\ element\ t\ in\ the\ suspicious\ community}{the\ number\ of\ occurrences\ of\ element\ t\ not\ in\ the\ suspicious\ community})$$

Evaluation

Evaluation Metrics :

TPR_f : True positive rate for backdoored samples removal.

FPR_f : False positive rate for backdoored samples removal.

$Acc(F_a, X_t)$: Accuracy for the test set after mitigation.

$Acc(F_a, X_b)$: Accuracy for backdoored malware samples after mitigation.

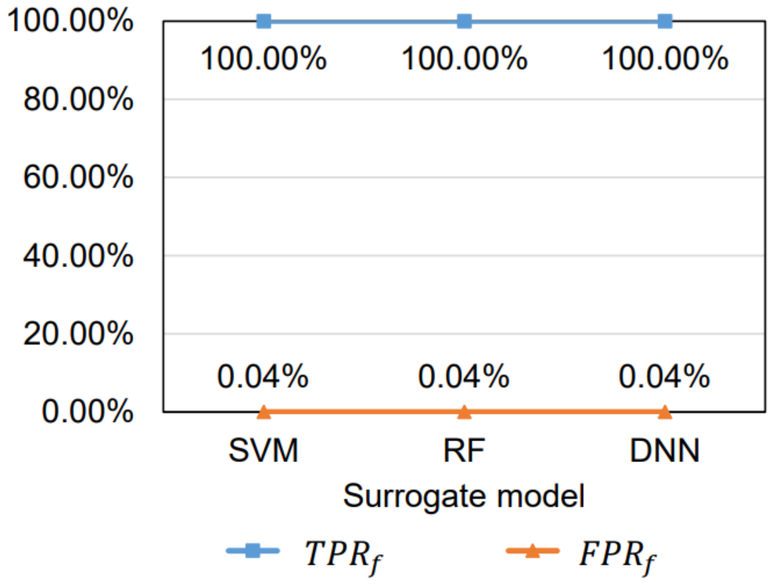
Evaluation

Comparison with other mitigations

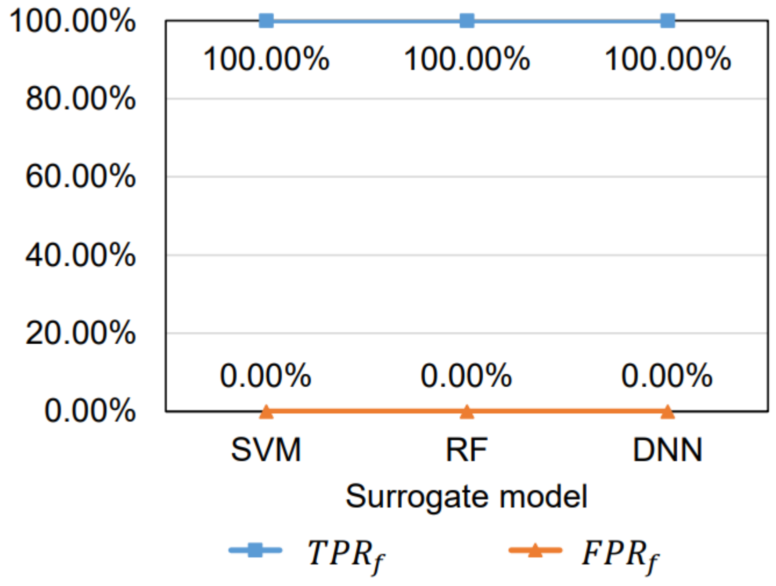
Strategy	Watermark Size	Poison Rate	$Acc(F_b, X_b)$	$Acc(F_b, X_t)$	Mitigation	TPR_f	FPR_f	$Acc(F_a, X_b)$	$Acc(F_a, X_t)$
Combined	8	1%	52.85%	94.30%	Isolation Forest	10.00%	10.10%	63.91%	92.74%
					HDBSCAN	61.00%	20.51%	58.32%	93.41%
					Spectral Signature	10.00%	15.10%	72.85%	92.29%
					MDR	**99.00%**	**0.02%**	**98.10%**	**96.09%**
		2%	39.33%	94.19%	Isolation Forest	15.00%	9.46%	62.23%	93.63%
					HDBSCAN	56.50%	21.38%	57.54%	93.41%
					Spectral Signature	12.50%	15.10%	68.60%	92.74%
					MDR	**100.00%**	**0.02%**	**98.55%**	**96.09%**
		4%	31.06%	95.20%	Isolation Forest	17.50%	8.59%	60.11%	93.30%
					HDBSCAN	66.50%	32.98%	45.03%	93.52%
					Spectral Signature	13.00%	15.17%	67.37%	92.51%
					MDR	**100.00%**	**0.00%**	**98.10%**	**95.31%**
	17	1%	36.98%	92.96%	Isolation Forest	30.00%	6.73%	62.57%	93.30%
					HDBSCAN	35.00%	12.39%	43.91%	94.64%
					Spectral Signature	10.00%	15.10%	66.93%	92.63%
					MDR	**100.00%**	**0.02%**	**97.88%**	**95.31%**
		2%	24.92%	95.42%	Isolation Forest	28.00%	5.40%	56.76%	92.96%
					HDBSCAN	46.50%	12.35%	46.26%	93.97%
					Spectral Signature	13.50%	15.06%	58.77%	92.74%
					MDR	**100.00%**	**0.02%**	**98.10%**	**95.42%**
		4%	20.34%	95.42%	Isolation Forest	20.00%	6.74%	44.58%	93.41%
					HDBSCAN	70.75%	58.35%	25.59%	**98.10%**
					Spectral Signature	12.50%	15.22%	57.54%	92.96%
					MDR	**100.00%**	**0.02%**	**97.88%**	95.64%

Evaluation

Surrogate-model agnostic evaluation



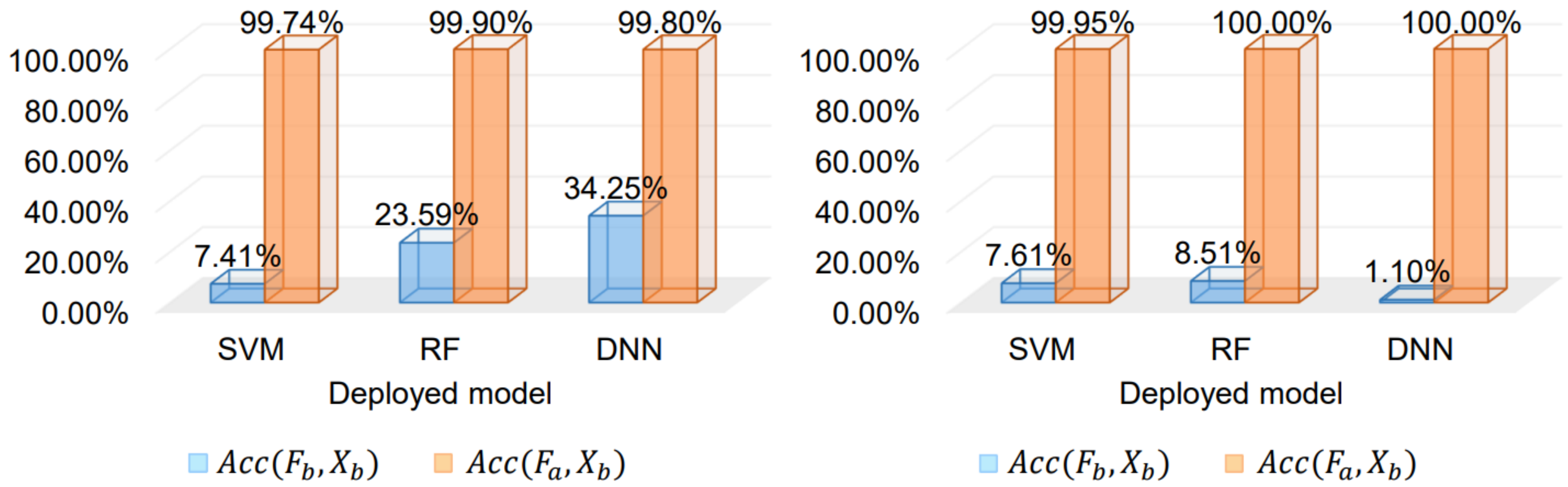
(a) Targeted at combined attack strategy



(b) Target at Independent attack strategy

Evaluation

Deployed-model agnostic evaluation



(a) Targeted at combined attack strategy (b) Target at Independent attack strategy

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Thanks!

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