## Poison is not Traceless: Black-Box Detection of Poisoning Attacks - Supplementary Material -

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## 1 Supplementary Material

To ensure reproducibility, we provide additional details for the paper in this section.

- 1.1 Full List of Complexity Measures. The full set of measures is listed in Table 1 We also include the *Standard Deviations* (SDs) when possible, which are not listed in the table. These measures include F1, N2, N3, N4, T1, and Hubs. As a result, there are 28 measures in total.
- 1.2 Details of FALFA. We obtain the multiplier  $\lambda$  by generalizing all the combinations between  $y_i$  and  $y'_i$  in a binary classification task, as shown in Table 2.
- Time Complexity of FALFA. FALFA is more computationally efficient than ALFA [5,7] and PoisSVM by a substantial margin. Linear programming is an exponential-time algorithm, the time complexity is around  $O(n^{2.5})$  [6]. Xiao et al.'s ALFA creates a copy of  $\mathcal{Y}_{tr}$  in the linear programming step, so n is essentially doubled. Paudice et al.'s ALFA on NN is slower than Xiao et al.'s, since it traverses all combinations of  $\mathcal{Y}_{tr}$  instead of using linear programming. FALFA uses linear programming but without doubling  $\mathcal{Y}_{tr}$ , resulting in an approximately  $2^{2.5} \approx 5.6$  times faster than ALFA on each iteration. Our test shows that FALFA converges at 2 iterations on average, but ALFA takes more than 5 iterations to converge. In the worst-case scenario, FALFA completes CMC dataset at  $22.4\pm8.6$  secs, while ALFA completes the same dataset at  $405.8 \pm 348.4$  secs, and PoisSVM took over 2 hours to compute the same dataset. We observe the minimal difference on Breastcancer, where FALFA completes the task at  $5.3 \pm 1.9$ secs, and it takes ALFA  $7.4 \pm 5.6$  secs.
- **1.4** Hardware and Software Configurations. All experiments are conducted on a workstation with the following configurations:
  - CPU: AMD Ryzen 9 5900 24 threads @ 4.4GHz

Table 1: List of measures in C-Measures. If possible, Standard Deviations (SDs) of measures are also included, but are not listed.

Category	Acronym	Description			
	F1	Maximum Fisher's discriminant			
Feature-based	F1v	ratio Directional-vector maximum Fisher's discriminant ratio Volume of overlapping region Maximum individual feature effi-			
	По.				
	1.0	ciency			
	F4	Collective feature efficiency			
	L1	Sum of the error distance by linear			
Linearity	L2	programming Error rate of the linear SVM classifier			
	L3	Non-linearity of the linear SVM classifier			
Neighborhood	N1	Fraction of borderline points			
	N2	Ratio of intra/extra class nearest-			
	N3	neighbors distance Error rate of nearest-neighbors			
		classifier			
	N4	Non-linearity of nearest-neighbors classifier			
	T1	Fraction of hyperspheres covering data			
	LSC	Local Set average Cardinality			
		Average density of the network			
Network		Clustering Coefficient Hub score – Number of connections each node has			
	Hubs				
	T2	Average number of features per			
Dimensionality	ТЗ	dimension Average number of PCA dimen-			
	15	sions per points			
	T4	Ratio of the PCA dimension to the original dimension			
Class Imbalance		Entropy of classes proportions			
	C2	Imbalance ratio			

• GPU: Nvidia GeForce RTX 3090 24GB

• Memory: 64GB

• Operating System: Ubuntu 20.04.3 LTS

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Table 2: All combinations for  $|y_i' - y_i|$ . By introducing a multiplier  $\lambda$ ,  $\lambda \cdot (y_i' - y_i)$  is equivalent to  $|y_i' - y_i|$ .

$y_i$	$y_i'$	$ y_i'-y_i $	λ
0	0	0	1
0	1	1	1
1	0	-1	-1
1	1	0	-1

 Software: Python 3.8.10, PyTorch 1.10.1+cu113, scikit-learn 1.0.2

The baseline data poisoning attacks are obtained from Adversarial Robustness Toolbox (ART) 1.9.1 [4] and Secure and Explainable Machine Learning in Python (SecML) 0.15 [3].

The execution time mentioned in the paper is evaluated using the environment above.

1.5 Datasets. All datasets are obtained from the UCI Machine Learning Repository [2]. We apply standardization on all datasets during the preprocessing.

For multi-class classification tasks, we convert the dataset into binary based on the following:

- Abalone: If the 'Rings' attribute is less than 10, we assign the example to the negative class; Else, assign to the positive class. We exclude the categorical attribute 'Sex' and the output label 'Rings' from the inputs.
- CMC: has 3 output classes: 1. No-use, 2. Long-term, and 3. Short-term. If the class is 'No-use', assign it to the negative class; Else, to the positive class.
- Texture: It has 10 output classes. We use a subset which contains examples labeled as '3' and '9'. If the class is '3', assign it to the negative class; Else, to the positive class.
- Yeast: It has 10 output classes. We select ''0 and '7', the top two classes sorted by sample size. If the class is '0', assign it to the negative class; Else, to the positive class.
- 1.6 Additional Results. C-Measures on clean and poisoned data. When no poisoning attack is present, the C-Measures strongly correlate to the classifier's test accuracy as can be seen in Fig. 2a. When the dataset has been poisoned, the C-Measures react to it. Despite a performance drop on the training accuracy of  $1.0 \pm 5.6\%$ , we observe a correlation drop across all measures when measuring on poisoned data, as shown in Fig. 2b. This matches the test accuracy drop, which

indicates the data becomes more complex, despite only minor changes in the training accuracy.

**Performance Loss.** Fig. 1 shows the performance loss on all real datasets.

Performance Loss at a Low Poisoning Rate. Here, we present the performance loss at a low poisoning rate (10%) in Table 3. This is the test accuracy difference before and after the attack. PoisSVM has no meaningful impact (< 2%) on the classifiers' performance in 7 out of 10 datasets. Meanwhile, SLN leads to minor performance improvement on CMC and Yeast. This result matches Chen *et al.*'s prior work [1], which shows DNNs are resilient to a low amount of label noise.

Table 3: Performance loss (%) after attacked by a poisoning attack with 10% poisoning rate.

Dataset	SLN	PoisSVM	ALFA	FALFA
Abalone	$0.8 \pm 0.7$	$1.8 \pm 0.8$	$9.5 \pm 1.9$	$7.7 \pm 1.7$
Australian	$0.7 \pm 0.5$	$4.5 \pm 3.9$	$4.9 \pm 4.0$	$8.3 \pm 3.8$
Banknote	$1.4 \pm 2.3$	$1.1 \pm 1.1$	$10.9 \pm 2.5$	$10.3 \pm 2.9$
Breastcancer	$2.5 \pm 0.7$	$5.3 \pm 4.6$	$7.2 \pm 2.0$	$9.1 \pm 2.7$
CMC	$-0.2 \pm 0.7$	$15.1 \pm 4.7$	$3.5 \pm 3.0$	$5.7 \pm 3.3$
HTRU2	$0.7 \pm 0.3$	$0.7 \pm 1.3$	$9.2 \pm 3.1$	$9.4 \pm 2.4$
Phoneme	$3.5 \pm 2.9$	$0.9 \pm 2.1$	$6.8 \pm 0.7$	$11.6 \pm 2.1$
Ringnorm	$0.1 \pm 0.3$	$1.7 \pm 0.5$	$3.2 \pm 2.5$	$6.4 \pm 2.9$
Texture	$0.5 \pm 1.1$	$1.2 \pm 0.8$	$7.9 \pm 4.6$	$4.9 \pm 3.9$
Yeast	$-0.2 \pm 1.6$	$1.9 \pm 3.8$	$10.4 \pm 4.9$	$2.3 \pm 4.6$

## References

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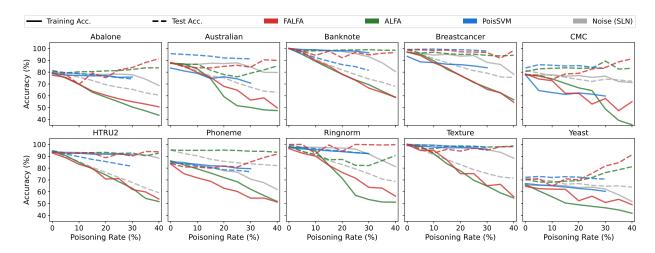


Figure 1: Train and test accuracy at various poisoning rates when classifiers under SLN, PoisSVM, and FALFA attacks.

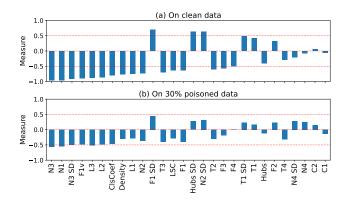


Figure 2: (a): Correlation of each measure in C-Measures to the test accuracy on synthetic datasets without poisoning attacks. (b): Same correlation but measured on the datasets containing 30% poisoning examples.

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