Intrinsic Certified Robustness of Bagging against Data Poisoning Attacks

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Abstract

In a data poisoning attack, an attacker modifies, deletes, and/or inserts some training examples to corrupt the learnt machine learning model. Bootstrap Aggregating (bagging) is a well-known ensemble learning method, which trains multiple base models on random subsamples of a training dataset using a base learning algorithm and uses majority vote to predict labels of testing examples. We prove the intrinsic certified robustness of bagging against data poisoning attacks. Specifically, we show that bagging with an arbitrary base learning algorithm provably predicts the same label for a testing example when the number of modified, deleted, and/or inserted training examples is bounded by a threshold. Moreover, we show that our derived threshold is tight if no assumptions on the base learning algorithm are made. We empirically evaluate our method on MNIST and CIFAR10. For instance, our method can achieve a certified accuracy of 70.8% on MNIST when arbitrarily modifying, deleting, and/or inserting 100 training examples.

1 Introduction

Machine learning models trained on user-provided data are vulnerable to data poisoning attacks [30, 6, 41, 23, 35, 34], in which malicious users carefully poison (i.e., modify, delete, and/or insert) some training examples such that the learnt model is corrupted and makes predictions for testing examples as an attacker desires. In particular, the corrupted model predicts incorrect labels for a large fraction of testing examples indiscriminately (i.e., a large testing error rate) or for some attacker-chosen testing examples. Unlike adversarial examples [37, 10], which carefully perturb each testing example such that a model predicts an incorrect label for the perturbed testing example, data poisoning attacks corrupt the model such that it predicts incorrect labels for many clean testing examples. Like adversarial examples, data poisoning attacks pose severe security threats to machine learning systems.

To mitigate data poisoning attacks, various defenses [13, 3, 36, 38, 17, 19, 25, 32] have been proposed in the literature. Most of these defenses [13, 3, 36, 38, 17, 19] achieve empirical robustness against certain data poisoning attacks and are often broken by strong adaptive attacks. To end the cat-and-mouse game between attackers and defenders, certified defenses [25, 32] were proposed. We say a learning algorithm is certifiably robust against data poisoning attacks if it can learn a classifier that provably predicts the same label for a testing example when the number of poisoned training examples is bounded. For instance, Ma et al. [25] showed that a classifier trained with differential privacy certifies robustness against data poisoning attacks. Rosenfeld et al. [32] leveraged randomized smoothing [12], which was originally designed to certify robustness against adversarial examples, to certify robustness against a particular type of data poisoning attacks called label flipping attacks, which only flip the labels of existing
training examples. This randomized smoothing based defense can also be generalized to certify robustness against data poisoning attacks that modify both features and labels of existing training examples. However, these certified defenses suffer from two major limitations. First, they are only applicable to limited scenarios, i.e., Ma et al. [25] is limited to learning algorithms that can be differentially private, while Rosenfeld et al. [32] is limited to data poisoning attacks that only modify existing training examples. Second, their certified robustness guarantees are loose, meaning that a learning algorithm is certifiably more robust than their guarantees indicate. We note that Steinhardt et al. [35] derives an approximate upper bound of the loss function for data poisoning attacks. However, their method cannot certify that the learnt model predicts the same label for a testing example.

We aim to address these limitations in this work. Our approach is based on a well-known ensemble learning method called Bootstrap Aggregating (bagging) [9]. Given a training dataset, bagging first generates $N$ subsamples by sampling from the training dataset with replacement uniformly at random, where each subsample includes $k$ training examples. Then, bagging uses a base learning algorithm to train a base classifier on each subsample. Given a testing example, bagging uses each base classifier to predict its label and takes majority vote among the predicted labels as the final predicted label. We show that bagging with any base learning algorithm is certifiably robust against data poisoning attacks. Figure 1 shows a toy example to illustrate why bagging certifies robustness against data poisoning attacks. When the poisoned training examples are minority in the training dataset, the sampled $k$ training examples do not include any poisoned training examples with a high probability. Therefore, a majority of the $N$ base classifiers in bagging and bagging’s predicted labels for testing examples are not influenced by the poisoned training examples. Formally, we show that bagging predicts the same label for a testing example when the number of poisoned training examples is no larger than a threshold. We call the threshold certified poisoning size. Moreover, we show that our derived certified poisoning size is tight if no assumptions on the base learning algorithm are made. Our certified poisoning size is the optimal solution to an optimization problem and we design an efficient algorithm to solve the optimization problem. We also empirically evaluate our method on MNIST and
CIFAR10. For instance, our method can achieve a certified accuracy of 70.8% on MNIST when 100 training examples are arbitrarily poisoned, where \( k = 100 \) and \( N = 1,000 \). Under the same setting, Ma et al. [25] and Rosenfeld et al. [32] achieve 0 certified accuracy. Finally, we show that training the base classifiers using transfer learning can significantly improve the certified accuracy.

Our contributions are summarized as follows:

- We derive the first intrinsic certified robustness of bagging against data poisoning attacks and prove the tightness of our robustness guarantee.
- We develop an efficient algorithm to compute the certified poisoning size in practice.
- We empirically evaluate our method on MNIST and CIFAR10.

All the proofs to our theorems are shown in the Appendix.

2 Certified Robustness of Bagging against Data Poisoning Attacks

Assuming we have a training dataset \( D = \{(x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)\} \) with \( n \) examples, where \( x_i \) and \( y_i \) are the feature vector and label of the \( i \)th training example, respectively. Moreover, we are given an arbitrary deterministic or randomized base learning algorithm \( A \), which takes a training dataset \( D \) as input and outputs a classifier \( f \), i.e., \( f = A(D) \). \( f(x) \) is the predicted label for a testing example \( x \). For convenience, we jointly represent the training and testing processes as \( A(D, x) \), which is \( x \)'s label predicted by a classifier that is trained using algorithm \( A \) and training dataset \( D \).

**Data poisoning attacks:** In a data poisoning attack, an attacker poisons the training dataset \( D \) such that the learnt classifier makes predictions for testing examples as the attacker desires. In particular, the attacker can carefully modify, delete, and/or insert some training examples in \( D \) such that \( A(D, x) \neq A(D', x) \) for many testing examples \( x \) or some attacker-chosen \( x \), where \( D' \) is the poisoned training dataset. We note that modifying a training example means modifying its feature vector and/or label. We denote the set of poisoned training datasets with at most \( r \) poisoned training examples as follows:

\[
B(D, r) = \{|D'| \max(|D|, |D'|) - |D \cap D'| \leq r\}. \tag{1}
\]

Intuitively, \( \max(|D|, |D'|) - |D \cap D'| \) is the minimum number of modified/deleted/inserted training examples that can change \( D \) to \( D' \). For simplicity, we denote \( n = |D|, n' = |D'|, \) and \( m = |D \cap D'|, \) where \( m \) is the number of training examples that are in both \( D \) and \( D' \).

**Bootstrap aggregating (Bagging)** [9]: Bagging is a well-known ensemble learning method. Roughly speaking, bagging creates many subsamples of a training dataset with replacement and trains a classifier on each subsample. For a testing example, bagging uses each classifier to predict its label and takes majority vote among the predicted labels as the label of the testing example. Next, we describe a probabilistic view of bagging, which makes it possible to theoretically analyze the certified robustness of bagging against data poisoning attacks. Specifically, we denote by \( g(D) \) a list of \( k \) examples that are sampled from \( D \) with replacement uniformly at random. Since \( g(D) \) is random, the predicted label \( A(g(D), x) \) is also random. We denote by \( p_j = \Pr(A(g(D), x) = j) \) the label probability for label \( j \), where
$j \in \{1, 2, \cdots, c\}$. Bagging predicts the label with the largest label probability for $x$, i.e., $h(D, x) = \arg \max_{j \in \{1, 2, \cdots, c\}} p_j$ is the label that bagging predicts for $x$. $h(D', x)$ is the label that bagging predicts for $x$ when the training dataset is poisoned.

Certified robustness of bagging: We show the certified robustness of bagging. In particular, we show that bagging predicts the same label for a testing example when the number of poisoned training examples is no larger than some threshold (called certified poisoning size). Moreover, we show that our derived certified poisoning size is tight. Our major theoretical results are summarized in the following two theorems.

**Theorem 1** (Certified Poisoning Size of Bagging). Suppose we have a training dataset $D$, a base learning algorithm $A$, and a testing example $x$. $g(D)$ is a list of $k$ training examples sampled from $D$ uniformly at random with replacement. $l$, $s$, $p_l \in [0, 1]$, and $p_s \in [0, 1]$ satisfy the following:

$$Pr(A(g(D), x) = l) \geq p_l \geq p_s \geq \max_{j \neq l} Pr(A(g(D), x) = j),$$

where $l$ and $s$ are the labels with the largest and second largest probabilities under bagging, respectively. $p_l$ is a lower bound of the largest label probability, while $p_s$ is an upper bound of the second largest label probability. Then, bagging predicts label $l$ for $x$ when the number of poisoned training examples is bounded by $r^*$, i.e., we have:

$$h(D', x) = l, \forall D' \in B(D, r^*),$$

where $r^*$ is called certified poisoning size and is the solution to the following optimization problem:

$$r^* = \arg \max_r$$

$$s.t. \max_{n-r \leq n' \leq n+r} \left(\frac{n'}{n}\right)^k - 2 \cdot \left(\frac{\max(n,n')-r}{n}\right)^k + 1 - (p_l - p_s - \delta_l - \delta_s) < 0,$$

where $n = |D|$, $n' = |D'|$, $\delta_l = p_l - (\lfloor p_l \cdot n^k \rfloor)/n^k$, and $\delta_s = (\lceil p_s \cdot n^k \rceil)/n^k - p_s$. $n + r$ and $n - r$ are respectively the maximum and minimum sizes of the poisoned training dataset when the number of poisoned training examples is $r$.

Given Theorem 1, we have the following corollaries.

**Corollary 1.** Suppose a data poisoning attack only modifies existing training examples. Then, we have $n' = n$ and the solution to optimization problem (4) is $r^* = \lfloor n \cdot (1 - \sqrt[4]{1 - (p_l - p_s - \delta_l - \delta_s)/2}) - 1 \rfloor$.

**Corollary 2.** Suppose a data poisoning attack only deletes existing training examples. Then, we have $n' = m$ and $r^* = \lfloor n \cdot (1 - \sqrt[4]{1 - (p_l - p_s - \delta_l - \delta_s)}) - 1 \rfloor$.

**Corollary 3.** Suppose a data poisoning attack only inserts new training examples. Then, we have $m = n$ and $r^* = \lfloor n \cdot (\sqrt[4]{1 + (p_l - p_s - \delta_l - \delta_s)} - 1) - 1 \rfloor$.

**Theorem 2** (Tightness of the Certified Poisoning Size). Assuming we have $p_l + p_s \leq 1$, $p_l + (c - 1) \cdot p_s \geq 1$, and $\delta_l = \delta_s = 0$. Then, for any $r > r^*$, there exist a base learning algorithm $A^*$ consistent with $D$ and a poisoned training dataset $D'$ with $r$ poisoned training examples such that $\arg \max_{j \in \{1, 2, \cdots, c\}} Pr(A^*(g(D'), x) = j) \neq l$ or there exist ties.
We have several remarks about our theorems.

**Remark 1:** Our Theorem 1 is applicable for any base learning algorithm $A$. In other words, bagging with any base learning algorithm is provably robust against data poisoning attacks.

**Remark 2:** For any lower bound $p_l$ of the largest label probability and upper bound $p_s$ of the second largest label probability, our Theorem 1 derives a certified poisoning size. In particular, our certified poisoning size is related to the gap between the two probability bounds. If we can estimate tighter probability bounds, then we may certify a larger poisoning size. We use the probability bounds instead of the exact label probabilities $p_l$ and $p_s$, because it is challenging to exactly compute them.

**Remark 3:** Theorem 2 shows that when no assumptions on the base learning algorithm are made, it is impossible to certify a poisoning size that is larger than ours.

## 3 Computing the Certified Poisoning Size

Given a learning algorithm $A$, a training dataset $D$, parameter $k$, and $e$ testing examples in $D_e$, we aim to estimate the predicted label and certified poisoning size for each testing example. Specifically, for a testing example, our certified poisoning size relies on a lower bound of the largest label probability and an upper bound of the second largest label probability. Therefore, we use a Monte-Carlo method to estimate these probability bounds with a probabilistic guarantee. Next, we describe estimating the probability bounds, solving the optimization problem in (4) using the probability bounds, and our complete certification algorithm.

**Estimating probability bounds $p_l$ and $p_s$:** One way to estimate $p_l$ and $p_s$ is to use the Monte-Carlo method proposed by [12]. In particular, $p_l$ is estimated using the one-sided Clopper-Pearson method [11] and $p_s$ is estimated as $1 - p_l$. However, such estimated $p_s$ may be loose. To address the challenge, we adopt the simultaneous confidence interval estimation method called SimuEM [20] to estimate $p_l$ and $p_s$ simultaneously. Specifically, we first randomly sample $N$ subsamples $L_1, L_2, \ldots, L_N$ from $D$ with replacement, each of which has $k$ training examples. Then, we train a classifier $f_o$ for each subsample $L_o$ using the learning algorithm $A$, where $o = 1, 2, \ldots, N$.

We can use the $N$ classifiers to estimate the predicted label $l$, $p_l$, and $p_s$ for $x$ with a confidence level at least $1 - \alpha$. A naive procedure is to train such $N$ classifiers for each testing example, which is very computationally expensive. To address the computational challenge, we propose to train such $N$ classifiers for each $e$ testing examples. Our key idea is to divide the confidence level among $e$ testing examples such that we can estimate their predicted labels and certified poisoning sizes using the same $N$ classifiers with a simultaneous confidence level at least $1 - \alpha$.

Specifically, for each testing example $x_i$ in $D_e$, we count the frequency of each label predicted by the $N$ classifiers, i.e., $n_j = \sum_{o=1}^{N} I(f_o(x_i) = j)$, where $I$ is the indicator function. Each $n_j$ follows a binomial distribution with parameters $N$ and $p_j$. Thus, we can adopt the Clopper-Pearson method to obtain a one-sided confidence interval for each label probability $p_j$. Then, we can leverage Bonferroni correction to obtain simultaneous confidence intervals for all label probabilities. Formally, we estimate $l$ as the label with the largest frequency $n_l$ and we have the following probability bounds [20]:

$$p_l = \text{Beta}(\frac{\alpha}{e} : n_l, N - n_l + 1)$$
Algorithm 1 Certify

Input: $A$, $D$, $k$, $N$, $D_e$, $\alpha$.
Output: Predicted label and certified poisoning size for each testing example.

$f_1, f_2, \cdots, f_N \gets \text{TrainUnderSample}(A, D, k, N)$

for $x_i$ in $D_e$ do
    counts[$j$] $\leftarrow$ $\sum_{o=1}^{N} 1(f_o(x_i) = j), j \in \{1, 2, \cdots, c\}$
    $l_i, s_i$ $\leftarrow$ top two indices in counts (ties are broken uniformly at random).
    $p_{l_i}, \overline{p}_{s_i}$ $\leftarrow$ SIMUEM(counts, $\frac{1}{e}$)
    if $p_{l_i} > \overline{p}_{s_i}$ then
        $\hat{y}_i$ $\leftarrow$ $l_i$
        $\hat{r}_i^*$ $\leftarrow$ BINARYSEARCH($p_{l_i}, \overline{p}_{s_i}, k, |D|$)
    else
        $\hat{y}_i, \hat{r}_i^*$ $\leftarrow$ ABSTAIN, ABSTAIN
    end if
end for
return $\hat{y}_1, \hat{y}_2, \cdots, \hat{y}_e$ and $\hat{r}_1^*, \hat{r}_2^*, \cdots, \hat{r}_e^*$

$$\overline{p}_j = \text{Beta}(1 - \frac{\alpha/e}{c}; n_j, N - n_j + 1), \forall j \in \{1, 2, \cdots, c\} \setminus \{l\},$$

where $1 - \alpha/e$ is the confidence level and $\text{Beta}(\beta; \lambda, \theta)$ is the $\beta$th quantile of the Beta distribution with shape parameters $\lambda$ and $\theta$. One natural method to estimate $\overline{p}_s$ is that $\overline{p}_s = \max_{j \neq l} \overline{p}_j$. However, this bound may be loose. For example, $p_l + \overline{p}_s$ may be larger than 1. Therefore, we estimate $\overline{p}_s$ as $\overline{p}_s = \min(\max_{j \neq l} \overline{p}_j, 1 - p_l)$.

**Computing the certified poisoning size:** Given the estimated label probability bounds for a testing example, we solve the optimization problem in [4] to obtain its certified poisoning size $r^*$. We design an efficient binary search based method to solve $r^*$. Specifically, we use binary search to find the largest $r$ such that the constraint in [4] is satisfied. We denote the left-hand side of the constraint as $\max_{n-r \leq n' \leq n+r} L(n')$. For a given $r$, a naive way to check whether the constraint $\max_{n-r \leq n' \leq n+r} L(n') < 0$ holds is to check whether $L(n') < 0$ holds for each $n'$ in the range $[n-r, n+r]$, which could be inefficient when $r$ is large. To reduce the computation cost, we derive the following analytical form of $n'$ at which $L(n')$ reaches its maximum value for a given $r$:

$$\arg \max_{n-r \leq n' \leq n+r} L(n') = \begin{cases} n, & \text{if } r \leq n \cdot (1 - \frac{k \cdot \sqrt{2}}{2}) \\ n + r, & \text{if } r \geq n \cdot \left(\frac{k}{1 - \frac{k \cdot \sqrt{2}}{2}} \right) \\ \left\lfloor \frac{r}{1 - \frac{k \cdot \sqrt{2}}{2}} \right\rfloor \text{ or } \left\lceil \frac{r}{1 - \frac{k \cdot \sqrt{2}}{2}} \right\rceil, & \text{otherwise.} \end{cases}$$

Therefore, for a given $r$, we only need to check whether $L(n') < 0$ holds for at most two different $n'$. The details of deriving [7] are shown in Supplemental Material.

**Complete certification algorithm:** Algorithm [1] shows our certification process to estimate the predicted labels and certified poisoning sizes for $e$ testing examples in $D_e$. The function $\text{TrainUnderSample}$ randomly samples $N$ subsamples and trains $N$ classifiers. The function $\text{SIMUEM}$ estimates the probability bounds $p_l$ and $\overline{p}_s$. The function $\text{BINARYSEARCH}$ solves the optimization problem in [4] to obtain the certified poisoning size $\hat{r}_i^*$ for testing example $x_i$. Roughly speaking, the following theorem shows that, with probability at least $1 - \alpha$, if $\text{CERTIFY}$
does not ABSTAIN, then it returns a valid certified poisoning size, for every testing example in \( D_e \). In other words, the probability that CERTIFY returns an incorrect certified poisoning size for at least one testing example is at most \( \alpha \).

**Theorem 3.** Algorithm CERTIFY has the following probabilistic guarantee:

\[
\Pr(\bigcap_{x_i \in D_e} ((\forall D' \in B(D, \hat{r}^*_i), h(D', x_i) = \hat{y}_i) | \hat{y}_i \neq \text{ABSTAIN})) \geq 1 - \alpha.
\]  

(8)

4 Experiments

4.1 Experimental Setup

**Datasets and classifiers:** We perform experiments on MNIST and CIFAR10. The base learning algorithm is neural network, and we use the example neural network architectures\(^1\) in Keras for the two datasets. The number of training examples in the two datasets are 60,000 and 50,000, respectively, which are the training datasets that we aim to certify. Both datasets have 10,000 testing examples, which are the \( D_e \) in our algorithm.

**Evaluation metric:** We use certified accuracy as our evaluation metric. In particular, for a given \( r \) (i.e., number of poisoned training examples), the certified accuracy can be computed as follows:

\[
CA_r = \frac{\sum_{x_i \in D_e} I(\hat{y}_i = y_i) \cdot I(\hat{r}^*_i \geq r)}{|D_e|},
\]

(9)

where \( y_i \) is the ground truth label for testing example \( x_i \), and \( \hat{y}_i \) and \( \hat{r}^*_i \) respectively are the predicted label and certified poisoning size returned by our CERTIFY algorithm for \( x_i \). Intuitively, the certified accuracy is the fraction of testing examples whose labels are correctly predicted and whose certified poisoning sizes are no smaller than \( r \). In other words, when the number of poisoned training examples is \( r \), bagging’s testing accuracy for \( D_e \) is at least \( CA_r \) with a confidence level \( 1 - \alpha \).

**Parameter setting:** Our method has three parameters, i.e., \( k \), \( \alpha \), and \( N \). Unless otherwise mentioned, we adopt the following default settings for them: \( k = 100 \), \( \alpha = 0.001 \), and \( N = 1,000 \) for MNIST; and \( k = 1,000 \), \( \alpha = 0.001 \), and \( N = 1,000 \) for CIFAR10. In our experiments, we will study the impact of each parameter while setting the remaining parameters to their default values. Note that training the \( N \) classifiers can be easily parallelized. We performed experiments on a server with 80 CPUs@2.1GHz, 8 GPUs (RTX 6,000), and 385 GB main memory.

**Compared methods:** We compare with a differential privacy based method\(^2\) and a randomized smoothing based method\(^3\). Since these methods are not scalable because they train \( N \) classifiers on the entire training dataset, we perform comparisons on the MNIST 1/7 dataset that just consists of the digits 1 and 7. This subset includes 13,007 training examples and 2,163 testing examples.

- **Ma et al.**\(^2\). Ma et al.\(^2\) showed that a classifier trained with differential privacy achieves certified robustness against data poisoning attacks. Suppose \( ACC_r \) is the testing accuracy on \( D_e \) of a differentially private classifier that is trained using a poisoned training dataset with \( r \) poisoned training examples. Based on Theorem 3 in\(^2\) (i.e., via

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\(^1\)https://keras.io/examples/mnist_cnn/
\(^2\)https://keras.io/examples/cifar10_cnn/

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treating the testing accuracy as their cost function), we have the expected testing accuracy $E(\text{ACC}_r)$ is lower bounded by a certain function of $E(\text{ACC})$, $r$, and $(\epsilon, \delta)$ (the function can be found in their Theorem 3), where $E(\text{ACC})$ is the expected testing accuracy of a differentially private classifier that is trained using the clean training dataset and $(\epsilon, \delta)$ are the differential privacy parameters. The randomness in $E(\text{ACC}_r)$ and $E(\text{ACC})$ are from differential privacy. This lower bound is the certified accuracy that the method achieves. A lower bound of $E(\text{ACC})$ can be further estimated with confidence level $1 - \alpha$ via training $N$ differentially private classifiers on the entire clean training dataset. However, for simplicity, we estimate $E(\text{ACC})$ as the average testing accuracies of the $N$ differentially private classifiers, which gives advantages for this method. We use DP-SGD [1] to train differentially private classifiers. Moreover, we set $\epsilon = 0$ and $\delta = 10^{-5}$ such that this method and our method achieve comparable certified accuracies when $r = 0$.

- **Rosenfeld et al. [32]**. Rosenfeld [32] proposed a randomized smoothing based method to certify robustness against label flipping attacks, which only flip the labels of existing training examples. This method can be generalized to certify robustness against data poisoning attacks that modify both features and labels of existing training examples via randomly flipping both features and labels of training examples. In particular, we binarize the features to apply this method. Like our method, they also train $N$ classifiers to estimate the certified accuracy with a confidence level $1 - \alpha$. However, unlike our method, when training a classifier, they flip each feature/label value in the training dataset with probability $\beta$ and use the entire noisy training dataset. When predicting the label of a testing example, this method takes a majority vote among the $N$ classifiers. We set $\beta = 0.3$ such that this method and our method achieve comparable certified accuracies when $r = 0$. We note that this method certifies the number of poisoned features/labels in the training dataset. We transform this certificate to the number of poisoned training examples as $\lfloor F / (d + 1) \rfloor$, where $F$ is the certified number of features/labels and $d + 1$ is the number of features/label of a training example ($d$ features + one label). We have $d = 784$ for MNIST.

### 4.2 Experimental Results

**Impact of $k$, $\alpha$, and $N$:** Figure 2 shows the impact of $k$, $\alpha$, and $N$ on the certified accuracy of our method. As the results show, $k$ controls a tradeoff between accuracy under no poisoning and robustness. Specifically, when $k$ is larger, our method has a higher accuracy when there are no data poisoning attacks (i.e., $r = 0$) but the certified accuracy drops more quickly as the number of poisoned training examples increases. The reason is that a larger $k$ makes it more likely to sample poisoned training examples when creating the subsamples in bagging. The certified accuracy increases as $\alpha$ or $N$ increases. The reason is that a larger $\alpha$ or $N$ produces tighter estimated probability bounds, which make the certified poisoning sizes larger. We also observe that the certified accuracy is relatively insensitive to $\alpha$.

**Transfer learning improves certified accuracy:** Our method trains multiple classifiers and each classifier is trained using $k$ training examples. Improving the accuracy of each classifier can improve the certified accuracy. We explore using transfer learning to train more

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3https://github.com/tensorflow/privacy  
4Their method only needs one classifier when label flipping attacks and linear classifiers are considered.
Figure 2: Impact of $k$, $\alpha$, and $N$ on the certified accuracy of our method. The first row is the result on MNIST and the second row is the result on CIFAR10.

Figure 3: (a) Transfer learning improves our certified accuracy on CIFAR10. Comparing our method with existing methods with respect to (b) certified accuracy and (c) running time.

accurate classifiers. Specifically, we use the Inception-v3 classifier pretrained on ImageNet to extract features and we leverage a public implementation\footnote{https://github.com/alexisbcook/keras_transfer_cifar10} to train our classifiers on CIFAR10. Figure 3(a) shows that transfer learning can significantly increase our certified accuracy, where $k = 100$, $\alpha = 0.001$, and $N = 1,000$.

Comparing with Ma et al.\cite{25} and Rosenfeld et al.\cite{32}: Figure 3(b) compares our method with previous methods on the MNIST 1/7 dataset, where $k = 50$, $\alpha = 0.001$, and $N = 1,000$. Our method significantly outperforms existing methods. For example, our method can achieve 96.95% certified accuracy when the number of poisoned training examples is $r = 50$, while the certified accuracy is 0 under the same setting for the two existing methods. Figure 3(c) shows that our method is also more efficient than existing methods. The reason is that our method trains classifiers on a small number of training examples while existing methods train classifiers on the entire training dataset. Ma et al.\cite{25} outperforms Rosenfeld et al.\cite{32} because differential privacy directly certifies robustness against modification/deletion/insertion of training examples while randomized smoothing was designed to certify robustness against modifications of features/labels.
5 Related Work

Data poisoning attacks carefully modify, delete, and/or insert some training examples in the training dataset such that a learnt model makes incorrect predictions for many testing examples indiscriminately (i.e., the learnt model has a large testing error rate) or for some attacker-chosen testing examples. For instance, data poisoning attacks have been shown to be effective for Bayes classifiers \cite{30}, SVMs \cite{6}, neural networks \cite{42, 29, 38, 34}, linear regression models \cite{27, 19}, PCA \cite{33}, LASSO \cite{41}, collaborative filtering \cite{23, 43, 16, 15}, clustering \cite{7, 8}, graph-based methods \cite{46, 40, 21, 44}, federated learning \cite{14, 12}, and others \cite{28, 26, 22, 45}. We note that backdoor attacks \cite{18, 24} also poison the training dataset. However, unlike data poisoning attacks, backdoor attacks also inject perturbation (i.e., a trigger) to testing examples.

One category of defenses \cite{13, 3, 36, 38} aim to detect the poisoned training examples based on their negative impact on the error rate of the learnt model. Another category of defenses \cite{17, 19} aim to design new loss functions, solving which detects the poisoned training examples and learns a model simultaneously. For instance, Jagielski et al. \cite{19} proposed to jointly optimize the selection of a subset of training examples with a given size and a model that minimizes the loss function; and the unselected training examples are treated as poisoned ones. Steinhardt et al. \cite{35} assumes that a model is trained only using examples in a feasible set and derives an approximate upper bound of the loss function for any data poisoning attacks under these assumptions. However, all of these defenses cannot certify that the learnt model predicts the same label for a testing example under data poisoning attacks.

Ma et al. \cite{25} shows that differentially private models certify robustness against data poisoning attacks. Rosenfeld et al. \cite{32} leverages randomized smoothing to certify robustness against label flipping attacks, which can be generalized to certify robustness against data poisoning attacks that modify both features and labels of existing training examples. Wang et al. \cite{39} proposes to use randomized smoothing to certify robustness against backdoor attacks, which is also applicable to certify robustness against data poisoning attacks. However, these defenses achieve loose certified robustness guarantees. Moreover, Ma et al. \cite{25} is only applicable to learning algorithms that can be differentially private, while Rosenfeld et al. \cite{32} and Wang et al. \cite{39} are only applicable to data poisoning attacks that modify existing training examples. Biggio et al. \cite{5} proposed bagging as an empirical defense against data poisoning attacks. However, they did not derive the certified robustness of bagging.

6 Conclusion

Data poisoning attacks pose severe security threats to machine learning systems via poisoning the training dataset. In this work, we show the intrinsic certified robustness of bagging against data poisoning attacks, i.e., bagging can transform any learning algorithm to be certifiably robust against data poisoning attacks. Specifically, we show that bagging predicts the same label for a testing example when the number of poisoned training examples is bounded. Moreover, we show that our derived bound is tight if no assumptions on the learning algorithm are made. We also empirically demonstrate the effectiveness of our method using MNIST and CIFAR10. Our results show that our method achieves much better certified robustness and is more efficient than existing certified defenses. Interesting future work includes: 1) generalizing our method to other types of data, e.g., graphs, and 2) improving our method by leveraging meta-learning.
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A Proof of Theorem 1

We first define some notations that will be used in our proof. Given a training dataset $D$ and its poisoned version $D'$, we define the following two random variables:

\[
X = g(D) \\
Y = g(D'),
\]

where $X$ and $Y$ respectively are two random lists with $k$ examples sampled from $D$ and $D'$ with replacement uniformly at random. We denote by $\mathcal{I} = D \cap D'$ the set of overlapping training examples in the two datasets. We use $\Omega$ to denote the space of random lists $g(D \cup D')$, i.e., each element in $\Omega$ is a list with $k$ examples sampled from $D \cup D'$ with replacement uniformly at random. For convenience, we define operators $\subseteq, \not\subseteq$ as follows:

**Definition 1 ($\subseteq, \not\subseteq$).** Assuming $\omega \in \Omega$ is a list of $k$ examples and $S$ is a set of examples, we say $\omega \subseteq S$ if $\forall w \in \omega, w \in S$. We say $\omega \not\subseteq S$ if $\exists w \in \omega, w \not\in S$.

For instance, we have $X \subseteq D$ and $Y \subseteq D'$. Before proving our theorem, we show a variant of the Neyman-Pearson Lemma [31] that will be used in our proof.

**Lemma 1 (Neyman-Pearson Lemma).** Suppose $X$ and $Y$ are two random variables in the space $\Omega$ with probability distributions $\mu_x$ and $\mu_y$, respectively. Let $M: \Omega \rightarrow \{0, 1\}$ be a random or deterministic function. Then, we have the following:

- If $S_1 = \{ \omega \in \Omega : \mu_x(\omega) > t \cdot \mu_y(\omega) \}$ and $S_2 = \{ \omega \in \Omega : \mu_x(\omega) = t \cdot \mu_y(\omega) \}$ for some $t > 0$. Let $S = S_1 \cup S_3$, where $S_3 \subseteq S_2$. If we have $\Pr(M(X) = 1) \geq \Pr(X \in S)$, then $\Pr(M(Y) = 1) \geq \Pr(Y \in S)$.

- If $S_1 = \{ \omega \in \Omega : \mu_x(\omega) < t \cdot \mu_y(\omega) \}$ and $S_2 = \{ \omega \in \Omega : \mu_x(\omega) = t \cdot \mu_y(\omega) \}$ for some $t > 0$. Let $S = S_1 \cup S_3$, where $S_3 \subseteq S_2$. If we have $\Pr(M(X) = 1) \leq \Pr(X \in S)$, then $\Pr(M(Y) = 1) \leq \Pr(Y \in S)$.

**Proof.** We show the proof of the first part, and the second part can be proved similarly. For simplicity, we use $M(1|\omega)$ and $M(0|\omega)$ to denote the probabilities that $M(\omega) = 0$ and $M(\omega) = 1$, respectively. We use $S^c$ to denote the complement of $S$, i.e., $S^c = \Omega \setminus S$. We have the following:

\[
\Pr(M(Y) = 1) - \Pr(Y \in S) \\
= \sum_{\omega \in \Omega} M(1|\omega) \cdot \mu_y(\omega) - \sum_{\omega \in S} \mu_y(\omega) \\
= \sum_{\omega \in S^c} M(1|\omega) \cdot \mu_y(\omega) + \sum_{\omega \in S} M(1|\omega) \cdot \mu_y(\omega) - \sum_{\omega \in S} M(1|\omega) \cdot \mu_y(\omega) - \sum_{\omega \in S} M(0|\omega) \cdot \mu_y(\omega) \\
= \sum_{\omega \in S^c} M(1|\omega) \cdot \mu_y(\omega) - \sum_{\omega \in S} M(0|\omega) \cdot \mu_y(\omega) \\
\geq \frac{1}{t} \cdot (\sum_{\omega \in S^c} M(1|\omega) \cdot \mu_x(\omega) - \sum_{\omega \in S} M(0|\omega) \cdot \mu_x(\omega)) \\
= \frac{1}{t} \cdot (\sum_{\omega \in S^c} M(1|\omega) \cdot \mu_x(\omega) + \sum_{\omega \in S} M(1|\omega) \cdot \mu_x(\omega) - \sum_{\omega \in S} M(1|\omega) \cdot \mu_x(\omega) - \sum_{\omega \in S} M(0|\omega) \cdot \mu_x(\omega))
\]
We denote by
\[ \frac{1}{t} \cdot (\sum_{\omega \in \Omega} M(1|\omega) \cdot \mu_x(\omega) - \sum_{\omega \in S} \mu_x(\omega)) \]
\[ = \frac{1}{t} \cdot (\Pr(M(X) = 1) - \Pr(X \in S)) \]
\[ \geq 0. \tag{18} \]
We obtain (17) from (15) because \( \mu_x(\omega) \geq t \cdot \mu_y(\omega), \forall \omega \in S \) and \( \mu_x(\omega) \leq t \cdot \mu_y(\omega), \forall \omega \in S^c \). We have the last inequality because \( \Pr(M(X) = 1) \geq \Pr(X \in S) \).

Next, we prove our Theorem 1. Our goal is to show that \( h(D', x) = l \), i.e., \( \Pr(A(Y, x) = l) > \max_{j \neq l} \Pr(A(Y, x) = j) \). Our key idea is to derive a lower bound of \( \Pr(A(Y, x) = l) \) and an upper bound of \( \max_{j \neq l} \Pr(A(Y, x) = j) \), where the lower bound and upper bound can be easily computed. We derive the lower bound and upper bound using the Neyman-Pearson Lemma. Then, we derive the certified poisoning size by requiring the lower bound to be larger than the upper bound. Next, we derive the lower bound, the upper bound, and the certified poisoning size.

**Deriving a lower bound of \( \Pr(A(Y, x) = l) \):** We first define the following residual:
\[ \delta_l = p_l - (|p_l| \cdot n^k)/n^k. \tag{21} \]
We define a binary function \( M(\omega) = I(A(\omega, x) = l) \) over the space \( \Omega \), where \( \omega \in \Omega \) and \( I \) is the indicator function. Then, we have \( \Pr(A(Y, x) = l) = \Pr(M(Y) = 1) \). Our idea is to construct a subspace for which we can apply the first part of Lemma 1 to derive a lower bound of \( \Pr(M(Y) = 1) \). We first divide the space \( \Omega \) into three subspaces as follows:
\[ \mathcal{B} = \{ \omega \in \Omega|\omega \subseteq D, \omega \nsubseteq I \}, \tag{22} \]
\[ \mathcal{C} = \{ \omega \in \Omega|\omega \subseteq D', \omega \nsubseteq I \}, \tag{23} \]
\[ \mathcal{E} = \{ \omega \in \Omega|\omega \subseteq I \}. \tag{24} \]
Since we sample \( k \) training examples with replacement uniformly at random, we have the following:
\[ \Pr(X = \omega) = \begin{cases} 
\frac{1}{n^k}, & \text{if } \omega \in \mathcal{B} \cup \mathcal{E} \\
0, & \text{otherwise}
\end{cases} \tag{25} \]
\[ \Pr(Y = \omega) = \begin{cases} 
\frac{1}{n'^k}, & \text{if } \omega \in \mathcal{C} \cup \mathcal{E} \\
0, & \text{otherwise}
\end{cases} \tag{26} \]
We denote by \( m \) the size of \( \mathcal{I} \), i.e., \( m = |\mathcal{I}| \). Then, we have the following:
\[ \Pr(X \in \mathcal{E}) = \left( \frac{m}{n} \right)^k, \Pr(X \in \mathcal{B}) = 1 - \left( \frac{m}{n} \right)^k, \text{ and } \Pr(X \in \mathcal{C}) = 0. \tag{27} \]
\[ \Pr(Y \in \mathcal{E}) = \left( \frac{m}{n'} \right)^k, \Pr(Y \in \mathcal{C}) = 1 - \left( \frac{m}{n'} \right)^k, \text{ and } \Pr(Y \in \mathcal{B}) = 0. \tag{28} \]
We have \( \Pr(X \in \mathcal{E}) = \left( \frac{m}{n} \right)^k \) because each of the \( k \) examples is sampled independently from \( \mathcal{I} \) with probability \( \frac{m}{n} \). Furthermore, since \( \Pr(X \in \mathcal{B}) + \Pr(X \in \mathcal{E}) = 1 \), we obtain \( \Pr(X \in \mathcal{B}) = 1 - \left( \frac{m}{n} \right)^k \). Since \( X \nsubseteq D' \), we have \( \Pr(X \in \mathcal{C}) = 0 \). Similarly, we can compute the probabilities in (28).
We assume $p_l - \delta_l - (1 - \left(\frac{m}{n}\right)^k) \geq 0$. We can make this assumption because we only need to find a sufficient condition for $h(D', x) = l$. We define $B' \subseteq \mathcal{E}$, i.e., $B'$ is a subset of $\mathcal{E}$, such that we have the following:

$$\Pr(X \in B') = p_l - \delta_l - \Pr(X \in B) = p_l - \delta_l - (1 - \left(\frac{m}{n}\right)^k).$$

(29)

We can find such subset because $p_l - \delta_l$ is an integer multiple of $\frac{1}{n^k}$. Moreover, we define $R$ as follows:

$$R = B \cup B'.$$

(30)

Then, based on (2), we have:

$$\Pr(A(X, x) = l) \geq p_l - \delta_l = \Pr(X \in R).$$

(31)

Therefore, we have the following:

$$\Pr(M(X) = 1) = \Pr(A(X, x) = l) \geq \Pr(X \in R).$$

(32)

Furthermore, we have $\Pr(X = \omega) > \gamma \cdot \Pr(Y = \omega)$ if and only if $\omega \in B$ and $\Pr(X = \omega) = \gamma \cdot \Pr(Y = \omega)$ if $\omega \in B'$, where $\gamma = \left(\frac{m}{n}\right)^k$. Therefore, based on the definition of $R$ in (30) and the condition (32), we can apply Lemma 1 to obtain the following:

$$\Pr(M(Y) = 1) = \Pr(A(Y, x) = l) \geq \Pr(Y \in R).$$

(33)

$\Pr(Y \in R)$ is a lower bound of $\Pr(A(Y, x) = l)$ and can be computed as follows:

$$\Pr(Y \in R) = \Pr(Y \in B) + \Pr(Y \in B') = \Pr(X \in B')/\gamma = 1/\gamma \cdot (p_l - \delta_l - (1 - \left(\frac{m}{n}\right)^k),$$

(34) (35) (36) (37)

where we have (36) from (35) because $\Pr(Y \in B) = 0$, (37) from (36) because $\Pr(X = \omega) = \gamma \cdot \Pr(Y = \omega)$ for $\omega \in B'$, and the last equation from (29).

**Deriving an upper bound of $\max_{j \neq l} \Pr(A(Y, x) = j)$**: We define the following residual:

$$\delta_j = ([n^{k}] / n^k - p_j), \forall j \in \{1, 2, \cdots, c\} \setminus \{l\}.$$  

(39)

We leverage the second part of Lemma 1 to derive such an upper bound. We assume $\Pr(X \in \mathcal{E}) \geq p_j + \delta_j, \forall j \in \{1, 2, \cdots, c\} \setminus \{l\}$. We can make the assumption because we derive a sufficient condition for $h(D', x) = l$. For $\forall j \in \{1, 2, \cdots, c\} \setminus \{l\}$, we define $C_j \subseteq \mathcal{E}$ such that we have the following:

$$\Pr(X \in C_j) = p_j + \delta_j.$$  

(40)

We can find such $C_j$ because $p_j + \delta_j$ is an integer multiple of $\frac{1}{n^k}$. Moreover, we define the following space:

$$Q_j = C \cup C_j.$$  

(41)
Therefore, based on (2), we have:

\[
\Pr(\mathcal{A}(X, x) = j) \leq p_j + \delta_j = \Pr(X \in \mathcal{Q}_j).
\]  

(42)

We define a function \( M_j(\omega) = \mathbb{I}(\mathcal{A}(\omega, x) = j) \), where \( \omega \in \Omega \). Based on Lemma \ref{lem:lemma1}, we have the following:

\[
\Pr(M(Y) = 1) = \Pr(\mathcal{A}(Y, x) = j) \leq \Pr(Y \in \mathcal{Q}_j),
\]  

(43)

where \( \Pr(Y \in \mathcal{Q}_j) \) can be computed as follows:

\[
\Pr(Y \in \mathcal{Q}_j) = \Pr(Y \in \mathcal{C}) + \Pr(Y \in \mathcal{C}_j) = 1 - \left( \frac{m}{n'} \right)^k + \Pr(Y \in \mathcal{C}_j) = 1 - \left( \frac{m}{n'} \right)^k + \Pr(X \in \mathcal{C}_j) / \gamma = 1 - \left( \frac{m}{n'} \right)^k + \frac{1}{\gamma} \cdot (\overline{p}_j + \delta_j).
\]  

(44)

Therefore, we have:

\[
\begin{align*}
\max_{j \neq l} \Pr(\mathcal{A}(Y, x) = j) & \leq \max_{j \neq l} \Pr(Y \in \mathcal{Q}_j) \\
& = 1 - \left( \frac{m}{n'} \right)^k + \frac{1}{\gamma} \cdot \max_{j \neq l} (\overline{p}_j + \delta_j) \\
& \leq 1 - \left( \frac{m}{n'} \right)^k + \frac{1}{\gamma} \cdot (\overline{p}_s + \delta_s),
\end{align*}
\]  

(49)

(50)

(51)

(52)

where \( \overline{p}_s + \delta_s \geq \max_{j \neq l}(\overline{p}_j + \delta_j) \).

**Deriving the certified poisoning size:** To reach the goal \( \Pr(\mathcal{A}(Y, x) = l) > \max_{j \neq l} \Pr(\mathcal{A}(Y, x) = j) \), it is sufficient to have the following:

\[
\frac{1}{\gamma} \cdot (\overline{p}_l - \delta_l - (1 - \left( \frac{m}{n} \right)^k)) > 1 - \left( \frac{m}{n'} \right)^k + \frac{1}{\gamma} \cdot (\overline{p}_s + \delta_s) \]

\[
\iff \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{m}{n} \right)^k + 1 - (\overline{p}_l - \overline{p}_s - \delta_l - \delta_s) < 0.
\]  

(53)

(54)

Taking all poisoned training datasets \( \mathcal{D}' \) (i.e., \( n - r \leq n' \leq n + r \)) into consideration, we have the following sufficient condition:

\[
\max_{n-r \leq n' \leq n+r} \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{m}{n} \right)^k + 1 - (\overline{p}_l - \overline{p}_s - \delta_l - \delta_s) < 0.
\]  

(55)

Note that \( m = \max(n, n') - r \). Furthermore, when the above condition (55) is satisfied, we have \( p_l - \delta_l - (1 - \left( \frac{m}{n} \right)^k) \geq 0 \) and \( \Pr(X \in \mathcal{E}) = \left( \frac{m}{n} \right)^k \geq \overline{p}_j + \delta_j, \forall j \in \{1, 2, \ldots, c\} \setminus \{l\} \), which are the conditions when we can construct the spaces \( \mathcal{B}' \) and \( \mathcal{C}_j \). The certified poisoning size \( r^* \) is the
We can construct such subspaces because

\[ r^* = \arg \max_r \]

\[ \text{s.t. } \max_{n-r \leq n' \leq n+r} \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{n'}{n} \right)^k + 1 - (p_l - \overline{p}_s - \delta_l - \delta_s) < 0. \]  

(56)

\[ B \text{ Proof of Theorem 2} \]

Our idea is to construct a learning algorithm \( \mathcal{A}^* \) such that the label \( l \) is not predicted by the bagging predictor or there exist ties. When \( r > r^* \) and \( \delta_l = \delta_s = 0 \), there exists a poisoned training dataset \( \mathcal{D}' \) with a certain \( n' \in [n-r, n+r] \) such that we have:

\[ \frac{n'}{n} \leq 2 \cdot \left( \frac{\max(n, n')}{n} \right)^k + 1 - (p_l - \overline{p}_s) \geq 0 \]

(57)

\[ \iff \frac{n'}{n} - 2 \cdot \left( \frac{m}{n} \right)^k + 1 - (p_l - \overline{p}_s) \geq 0 \]

(58)

\[ \iff 1 + \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{m}{n} \right)^k \geq p_l - \overline{p}_s \]

(59)

\[ \iff \frac{1}{\gamma} \cdot (p_l - (1 - \left( \frac{m}{n} \right)^k)) \leq 1 - \left( \frac{m}{n} \right)^k + \frac{1}{\gamma} \cdot \overline{p}_s, \]

(60)

where \( m = \max(n, n') - r \) and \( \gamma = (\frac{m}{n})^k \). We let \( \mathcal{Q}_s = \mathcal{C} \cup \mathcal{C}'_s \), where \( \mathcal{C}'_s \) satisfies the following:

\[ \mathcal{C}'_s \subseteq \mathcal{E}, \mathcal{C}'_s \cap \mathcal{B}' = \emptyset, \text{ and } \Pr(X \in \mathcal{C}'_s) = \overline{p}_s. \]

(61)

Note that we can construct such \( \mathcal{C}'_s \) because \( p_l + \overline{p}_s \leq 1 \). Then, we divide the remaining space \( \Omega \setminus (\mathcal{R} \cup \mathcal{Q}_s) \) into \( c - 2 \) subspaces such that \( \Pr(X \in \mathcal{Q}_j) \leq \overline{p}_s \), where \( j \in \{1, 2, \cdots, c\} \setminus \{l, s\} \). We can construct such subspaces because \( p_l + (c - 1) \cdot \overline{p}_s \geq 1 \). Then, based on these subspaces, we construct the following learning algorithm:

\[ \mathcal{A}^*(\omega, x) = \begin{cases} 
 l, & \text{if } \omega \in \mathcal{R} \\
 j, & \text{if } \omega \in \mathcal{Q}_j 
\end{cases} \]

(62)

Then, we have the following based on the above definition of the learning algorithm \( \mathcal{A}^* \):

\[ \Pr(\mathcal{A}^*(X, x) = l) = \Pr(X \in \mathcal{R}) = p_l \]

(63)

\[ \Pr(\mathcal{A}^*(X, x) = s) = \Pr(X \in \mathcal{Q}_s) = \overline{p}_s \]

(64)

\[ \Pr(\mathcal{A}^*(X, x) = j) = \Pr(X \in \mathcal{Q}_j) \leq \overline{p}_s, j \in \{1, 2, \cdots, c\} \setminus \{l, s\}. \]

(65)

Therefore, the learning algorithm \( \mathcal{A}^* \) is consistent with (2). Next, we show that \( l \) is not predicted by the bagging predictor or there exist ties when the training dataset is \( \mathcal{D}' \). In particular, we have the following:

\[ \Pr(\mathcal{A}^*(Y, x) = l) = \Pr(Y \in \mathcal{R}) \]

(66)

\[ = \frac{1}{\gamma} \cdot (p_l - (1 - \left( \frac{m}{n} \right)^k)) \]

(68)
\[ \leq 1 - \left( \frac{m}{n'} \right)^k + \frac{1}{\gamma} \cdot p_s \]  

(69)

\[ = \Pr(Y \in Q_s) \]  

(70)

\[ = \Pr(A^*(Y, x) = s), \]  

(71)

where \( \gamma = (\frac{m}{n})^k \) and we have (69) from (68) because of (60). Therefore, label \( l \) is not predicted for \( x \) or there exist ties when the training dataset is \( \mathcal{D}' \).

C Proof of Theorem 3

Based on the definition of SimuEM and [20], we have:

\[ \Pr(p_i \leq \Pr(A(g(\mathcal{D}), x_i) = l_i) \wedge p_j \geq \Pr(A(g(\mathcal{D}), x_i) = j), \forall j \neq l_i) \geq 1 - \frac{\alpha}{e} \]  

(72)

Therefore, the probability that Certify returns an incorrect certified poisoning size for a testing example \( x_i \) is at most \( \frac{\alpha}{e} \), i.e., we have:

\[ \Pr((\exists \mathcal{D}' \in B(\mathcal{D}, \hat{x}_i^*), h(\mathcal{D}', x_i) = \hat{y}_i) | \hat{y}_i \neq \text{ABSTAIN}) \leq \frac{\alpha}{e}. \]  

(73)

Then, we have the following:

\[ \Pr(\cap_{x_i \in \mathcal{D}_c}(\exists \mathcal{D}' \in B(\mathcal{D}, \hat{x}_i^*), h(\mathcal{D}', x_i) = \hat{y}_i) | \hat{y}_i \neq \text{ABSTAIN})) \]  

(74)

\[ = 1 - \Pr(\cup_{x_i \in \mathcal{D}_c}(\exists \mathcal{D}' \in B(\mathcal{D}, \hat{x}_i^*), h(\mathcal{D}', x_i) = \hat{y}_i) | \hat{y}_i \neq \text{ABSTAIN})) \]  

(75)

\[ \geq 1 - \sum_{x_i \in \mathcal{D}_c} \Pr((\exists \mathcal{D}' \in B(\mathcal{D}, \hat{x}_i^*), h(\mathcal{D}', x_i) = \hat{y}_i) | \hat{y}_i \neq \text{ABSTAIN}) \]  

(76)

\[ \geq 1 - e \cdot \frac{\alpha}{e} \]  

(77)

\[ = 1 - \alpha \]  

(78)

We have (76) from (75) according to the Boole’s inequality.

D Derivation of Equation 7

\[ L(n') = \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{\max(n, n') - r}{n} \right)^k + 1 - (p_l - p_s - \delta_l - \delta_s) \]  

(79)

We aim to derive \( \arg \max_{n-r \leq n' \leq n+r} L(n') \). When \( n-r \leq n' \leq n \), we have the following:

\[ L(n') = \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{n-r}{n} \right)^k + 1 - (p_l - p_s - \delta_l - \delta_s). \]  

(80)

Therefore, when \( n-r \leq n' \leq n \), \( L(n') \) increases as \( n' \) increases. Thus, \( L(n') \) reaches its maximum value when \( n \leq n' \leq n+r \). When \( n \leq n' \leq n+r \), we have the following:

\[ L(n') = \left( \frac{n'}{n} \right)^k - 2 \cdot \left( \frac{n'-r}{n} \right)^k + 1 - (p_l - p_s - \delta_l - \delta_s). \]  

(81)
Moreover, we have:

\[ \frac{\partial L(x)}{\partial x} \]

\[ = \frac{1}{n^k} \cdot (k \cdot x^{k-1} - 2 \cdot k \cdot (x - r)^{k-1}) \]

\[ = k \cdot x^{k-1} \cdot \left(1 - 2 \cdot (1 - \frac{r}{x})^{k-1}\right). \]  

(82)  

(83)  

(84)  

\( \frac{k \cdot x^{k-1}}{n^k} \) is larger than 0. Moreover, \( 1 - 2 \cdot (1 - \frac{r}{x})^{k-1} \) decreases as \( x \) increases when \( x \geq r \) and it only has one root that is no smaller than \( r \) which is as follows:

\[ x_{\text{root}} = \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}}. \]  

(85)  

Therefore, we have \( \frac{\partial L(x)}{\partial x} > 0 \) when \( r \leq x < \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}} \) and \( \frac{\partial L(x)}{\partial x} < 0 \) when \( x > \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}} \). \( L(x) \) increases as \( x \) increases in the range \( [r, \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}} ] \) and decreases as \( x \) increases in the range \( (\frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}}, +\infty) \). Therefore, we have the following three cases:

**Case I:** When \( r \leq n \cdot (1 - k^{-1}\sqrt{\frac{1}{2}}) \), \( L(n') \) reaches its maximum value at \( n' = n \) since \( L(n') \) decreases as \( n' \) increases in the range \( [n, n+r] \).

**Case II:** When \( n \cdot (k\sqrt{2} - 1) < r < n \cdot (k\sqrt{2} - 1) \), \( L(n') \) reaches its maximum value at \( n' = \left[ \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}} \right] \) or \( \left\lfloor \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}} \right\rfloor \) since \( L(n') \) increases as \( n' \) increases in the range \( [n, \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}} ] \) and decreases as \( n' \) increases in the range \( \left[ \frac{r}{1 - k^{-1}\sqrt{\frac{1}{2}}}, n+r \right] \).

**Case III:** When \( r \geq n \cdot (k\sqrt{2} - 1) \), \( L(n') \) reaches its maximum value at \( n' = n+r \) since \( L(n') \) increases as \( n' \) increases in the range \( [n, n+r] \).