Data Poisoning Attacks on Regression Learning and Corresponding Defenses

Nicolas Müller  
Fraunhofer AISEC  
Garching near Munich, Germany  
nicolas.mueller@aisec.fraunhofer.de

Daniel Kowatsch  
Fraunhofer AISEC  
Garching near Munich, Germany  
daniel.kowatsch@aisec.fraunhofer.de

Konstantin Böttinger  
Fraunhofer AISEC  
Garching near Munich, Germany  
konstantin.boettinger@aisec.fraunhofer.de

Abstract—Adversarial data poisoning is an effective attack against machine learning and threatens model integrity by introducing poisoned data into the training dataset. So far, it has been studied mostly for classification, even though regression learning is used in many mission critical systems (such as dosage of medication, control of cyber-physical systems and managing power supply). Therefore, in the present research, we aim to evaluate all aspects of data poisoning attacks on regression learning, exceeding previous work both in terms of breadth and depth. We present realistic scenarios in which data poisoning attacks threaten production systems and introduce a novel black-box attack, which is then applied to a real-word medical use-case. As a result, we observe that the mean squared error (MSE) of the regressor increases to 150 percent due to inserting only two percent of poison samples. Finally, we present a new defense strategy against the novel and previous attacks and evaluate it thoroughly on 26 datasets. As a result of the conducted experiments, we conclude that the proposed defence strategy effectively mitigates the considered attacks.

I. INTRODUCTION

Regression learning is increasingly used in mission-critical systems: In medicine for the development of pharmaceuticals [6], [12], in the financial sector for predictive analysis, such as managing hedge funds [18], [24] and cash forecasting [10], as well as for predictive maintenance [19] and quality control [7].

As we rely more and more on these systems, researchers find that they are vulnerable to malicious attacks. Two strains of attacks can be distinguished. Attacks at test time (evasion) and attacks at training time (poisoning) [16]. In this work, we focus on the latter. Poisoning attacks introduce a small fraction of ‘poisoned samples’ into the training process, which maximally ‘confuses’ the learner and causes either a denial of service (i.e., renders the model useless with respect to its original intent), or introduces a ‘backdoor’, which gives the attacker control over the model at test time.

These attacks (and corresponding defenses) have been studied by the scientific community in detail for classification learning [3], [5], [21], [23], [25]. However, there is almost no research on adversarial poisoning attacks (and corresponding defenses) for regression learning. We find only a single contribution [12] for regression learning, even though regression is used in many mission-critical systems as described above.

As an example, consider the following medical scenario. The blood thinner Warfarin has a very small therapeutic window; too high dosage leads to bleeding, while too low dosage leads to clotting [6]. Machine learning can help in estimating the correct dosage, and pharmaceutical companies provide appropriate datasets [11] on which regression learning has been successfully applied [14], [22].

However, such an estimation is susceptible to data poisoning attacks: A malicious entity may introduce a very small percentage of ‘poisoned samples’ into the dataset. Motives for such an attack can be manifold: Personal motives (a malignant doctor, underpaid caregiver or simply a psychopath nurse [8]), financial motives (one company damaging another company’s reputation, or an individual betting on the crash of some company’s stock value, similar to [20]), or even political or terrorist motives.

Such poisoning attacks are not just theoretical threats: Since even small data poisoning can have significant effect, such an attack is practicable even by an individual. Related work has shown that data poisoning is feasible and has already been observed in real-life scenarios [5], [21]. To address this issue, we

• show the harmfulness of data poisoning in regression by means of studying the problem of Warfarin dose prediction,
• present a new black-box attack which exceeds previous state-of-the-art, and for the first time evaluate poisoning attacks on nonlinear regression learners,
• present an improvement to previously suggested defenses which consistently outperforms the baseline,
• thoroughly evaluate our attack and defense on 26 datasets and state-of-the-art regression learners, i.e. Neural Networks, Kernel SVR, and Kernel Regression,
• and publish all source code and experiments to enable full reproducibility.

II. CASE STUDY: WARFARIN DOSE ESTIMATION

In order to demonstrate the effect of even small fractions of poison samples, we examine the medical use case of Warfarin dose prediction in this section. The International Warfarin Pharmacogenetics Consortium [11], a group of pharmacogenetic research centers, have created the IWCP dataset (Warfarin dataset). It is the joint effort of 59 contributors, resulting in an average contribution of 1.7% of the data per member. Based on this dataset, models have been developed which predict the therapeutic dose of Warfarin for a patient [14], [22].
We use a new black-box poisoning attack (to be detailed in Section IV-C) and add 2% poison data to the Warfarin dataset, which is about as much as the average IWPC contributor did. Table I shows the Mean Absolute Error (MAE) of different models after training on this dataset. In the absence of poison samples, the MAE of models like Lasso, Elastic Net and Ridge is around 8.50, which is comparable to state of the art [14]. When adding just 2% of data poisoning, the median error increases to 11.07 (a 29 percent increase). This has tangible effect on the patients: The rate of acceptable dose decreases by 21%.

| Model           | Clean Error | Pois. Error | Increase MAE | Decrease accp. Dosages |
|-----------------|-------------|-------------|--------------|------------------------|
| Elastic Net     | 8.52        | 11.07       | 1.30         | 21.25%                 |
| Huber Reg.      | 8.40        | 10.86       | 1.41         | 29.09%                 |
| Kernel Ridge    | 8.41        | 10.98       | 1.17         | 19.07%                 |
| Lasso           | 8.49        | 11.20       | 1.11         | 21.32%                 |
| MLP             | 10.05       | 12.33       | 1.28         | 11.41%                 |
| Ridge Reg.      | 8.49        | 10.99       | 1.29         | 22.34%                 |
| SVR             | 10.85       | 12.52       | 1.15         | 14.13%                 |
| Median          | 8.49        | 11.07       | 1.29         | 21.07%                 |

TABLE I: Mean absolute error (MAE) of different regression models when poisoning the Warfarin dataset. The first column shows the MAE when no data poisoning is present. The second column shows the MAE when 2% poison samples are introduced, with the relative change indicated by the third column. The poisoning strongly affects the amount of patients who receive an acceptable dosage of Warfarin (fourth column).

III. RELATED WORK

In this section, we give a short overview on existing literature on data poisoning.

A. Poisoning Attacks in Classification

Early work on data poisoning attacks against classifiers include [3, 25], which use the Karush-Kuhn-Tucker conditions to find optimal poisoning samples against linear models. [3] first develops a poisoning attack against SVMs. [25] considers the security of feature selection against poisoning attacks and adapts the approach for LASSO, Ridge Regression and Elastic Net. In both scenarios the attacker attempts to increase the test error and, thus, decrease the overall performance of the classifier.

[15] are the first to extent data poisoning to the multi-class scenario, which allows for targeted attacks. Instead of the Karush-Kuhn-Tucker conditions, they use back-gradient optimization to generate the first poison samples for neural networks in an end-to-end fashion without the requirement of a surrogate model. While these first results indicate a higher resilience of deep neural networks against availability attacks, [15] also shows the effectiveness of this approach against simpler models like MLPs with a single hidden layer.

[21] build upon the work of [15] and demonstrate reliable clean-label attacks, in which the attacker can control the input data X, but not the corresponding labels y. The attackers objective is to achieve misclassification of a certain instance as another class at test time. For a transfer learning scenario, they show, that a single poison sample is capable of successfully poisoning a classifier. For end-to-end learning settings they develop a watermarking approach to poisoning.

B. Poisoning Attacks in Regression

Data poisoning has so far been examined almost exclusively for classification learning. For regression learning, there is work only by Jagielski et al. [12]. They build upon work by Xiao et al. [25], who introduce a gradient-based optimisation attack for linear classifiers such as Lasso, Ridge Regression and Elastic Net for feature selection. Jagielski et al. [12] use the same approach for the same models, but interpret the model’s decision surface as a predictor for the continuous target variable, yielding a poisoning attack for linear regression. Additionally, they introduce a non-gradient based attack, plus a defense called Trim and evaluate it on three datasets. Their approach in evaluating the defense is, however, not applicable in practice, since they use an oracle to determine the defense’s hyper parameters. More specifically, they assume they know the fraction ε of poisoned samples in the dataset of size n, which is generally unknown.

Nonlinear regressors such as Kernel Ridge, Kernel SVM and Neural Networks have, to the best of our knowledge, not yet been examined in the context of adversarial poisoning. This may be because the attack presented in [25] is not applicable to nonlinear learners.

IV. POISONING ATTACKS IN REGRESSION

In this section, we present our threat model, previously suggested attacks and our proposed and improved attack. A thorough evaluation on 26 datasets is given in Section VI.

A. Threat Model

We consider a realistic attack scenario where the attacker has only limited capabilities, such as for example a malicious individual could have. Specifically, we consider black-box attacks where 1) the attacker knows nothing about the model (not even what kind of regressor is used), 2) the attacker does not have access to the training dataset (X, y), but only to a smaller substitute dataset (Xsub, ysub), and 3) where the attacker is capable of fully controlling the ϵn data samples he contributes to the dataset. He is not able to manipulate the rest of the data.

As indicated in the introduction and Section II the possibility of introducing small amounts of poison data into the dataset is highly realistic. If the data are crawled and collected automatically, malicious instances just need to be placed where the crawler can find them [17], [21]. If data are collected manually, the ability to poison a dataset is proportional to an individual’s contribution to the dataset. As detailed in Section II the Warfarin dataset is collected by 59 individuals; thus, an
average contribution constitutes about 2% of the dataset. We show that this amount of poisoning is sufficient to effectively poison the dataset (c.f. Section VI-D and VII).

B. Related Poisoning Attacks in Regression

[12] present both a white box and a black-box attack on regression learning. In this section, we present these attacks and their limitations.

1) Related White Box Attacks: Deriving from [25], a white-box attack on linear regressors is presented in [12]. The attacker’s objective is formulated as a bilevel optimization problem as follows:

\[
\begin{align*}
\arg\max_{D_p} \mathcal{W}(D', \theta_p) \\
\text{s.t.} & \quad \theta_p \in \arg\min_{\theta} \mathcal{L}(D_{tr} \cup D_p, \theta)
\end{align*}
\]

Equation 2 is the usual minimization of the model loss \(\mathcal{L}\) during the fitting of a model on both the clean training dataset \(D_{tr}\) and the poisoned dataset \(D_p\). This yields an optimal set of weights \(\theta_p\). This is called the ‘inner optimisation’.

Equation 1 refers to maximising the attacker’s objective \(\mathcal{W}\) with respect to some test set \(D'\), using the model’s weights as determined by Equation 2. Minimizing Equation 1 depends on the solution of Equation 2 which is why it is considered a bilevel optimization problem. This is a hard problem: The attacker has to determine how the points they introduce in the dataset will change the model weights during training. [12], [25] solve this using the Karush-Kuhn-Tucker (KKT) conditions as a set of conditions which they assume remain satisfied when a given poison sample \(x_c\) is introduced. They then proceed in solving a linear system, and, thus, derive the gradients.

This approach is not feasible in deep neural networks [15], since the time required for solving the linear system is in \(O(p^3)\), where \(p\) is the number of parameters in the model. Since even small, commonly used pretrained models have a few million parameters [1], the computation is not feasible. Even with simplifying assumptions or a sufficiently small number of parameters, this approach still requires an exact solution to the optimization problem, which, in general, cannot be obtained. For a more detailed analysis, we refer to [15].

2) Related Black-Box Attacks: [12] also present a black-box attack called \(\text{StatP}\). This attack samples \(en\) points from a multivariate Gaussian distribution, where the corresponding mean \(\mu\) and co-variance matrix \(\Sigma\) are estimated as the mean and co-variance of the true dataset \(D_{tr}\). Then, \(\text{StatP}\) rounds the feature variables to the corners, queries the model and rounds the target variable to the opposite corner. The corners are defined as the minimum and maximum of the feasibility domain \(\gamma\) of each variable. Both features and target are scaled to \([0, 1]\), thus the feasibility domain is a hypercube \([0, 1]^{d+1}\) where \(d\) is the number of features. In summary, this attack creates a few isolated clusters of adversarial data, where both features and target take only extreme values of either \(\gamma_{min} = 0\) or \(\gamma_{max} = 1\).

Algorithm 1 Flip attack

Require:
1. Substitute data \(X_{sub}^{\text{sub}}, y_{sub}^{\text{sub}}\) of size \(m\)
2. Number of poison points \([en]\) to compute
3. Feasibility domain \([\gamma_{min}, \gamma_{max}]\) of the target values
4. function Flip
5. \(\Delta \leftarrow \emptyset\)
6. for \(i \in [1, ..., m]\) do
7. \(\Delta_i \leftarrow \max(y_{sub}^{\text{sub}} - \gamma_{min}, \gamma_{max} - y_{sub}^{\text{sub}})\)
8. \(\Delta \leftarrow \Delta \cup \Delta_i\)
9. end for
10. \(T_e \leftarrow t \in \mathbb{R} \text{ s.t. } t = \text{the } [en]\text{-th highest value of } \Delta\)
11. \(I_e \leftarrow \{i \in [1, ..., m] \text{ s.t. } d_i >= T_e \text{ where } d_i \in \Delta\}\)
12. \(X_p \leftarrow \emptyset, \ y_p \leftarrow \emptyset\)
13. for \(i \in I_e\) do
14. if \(y_{i} > \frac{1}{2}(\gamma_{max} - \gamma_{min})\) then
15. \(y_{p,i} \leftarrow \gamma_{min}\)
16. \(y_{p} \leftarrow y_{p} \cup y_{p,i}\)
17. else
18. \(y_{p,i} \leftarrow \gamma_{max}\)
19. \(y_{p} \leftarrow y_{p} \cup y_{p,i}\)
20. end if
21. \(X_p \leftarrow X_p \cup X_{i}^{\text{sub}}\)
22. end for
23. return \(X_p, y_p\)
24. end function

This attack, however, still requires access to the trained black-box model, which may be unrealistic in a real-world scenario. Additionally, we find that while this attack is successful on linear models, it is unsuccessful when applied to non-linear models. We show this empirically in Section VI, but give a brief explanation here: Nonlinear learners (such as Neural Networks, Kernel SVR, and Kernel Regression) are able to accommodate both the poison points and the true data simultaneously. This is because the poison data created by \(\text{StatP}\) does not contradict the true data points, since true data points rarely have features in the corners of the feasibility domain. This insight will motivate our proposed Flip attack on nonlinear learners, which we present in the next section.

C. Flip: A Black-Box Attack on Nonlinear Regressors

Algorithm 1 presents our proposed black-box attack called Flip. This algorithm computes a set of adversarial poisoning points for any degree of poisoning \(0 < \epsilon < 1\). The attack is completely independent of the regressor model and only requires a substitute dataset \((X_{sub}^{\text{sub}}, y_{sub}^{\text{sub}})\) from the same domain as the training dataset \(D_{tr}\) and a feasibility domain of the target variables \([\gamma_{min}, \gamma_{max}]\). The feasibility domain is necessary because we usually assume that only certain target variables are valid. Other values are bound to raise suspicion, such as for example a room temperature of -400 degrees Celsius, or medical doses that are extremely high or low.

We now describe our attack. After having initialised an empty set \(\Delta\) in line 2, we populate it in the following for loop
With the smallest error as a 'cleaned' dataset. The number of points to fit on, and conversely, the number of points to discard, is determined by a supplied parameter $\epsilon$, the assumed degree of poisoning. If $\epsilon = \epsilon$, the defense has been shown to work very well [12]. However, this is not a realistic scenario, since the defender does not know $\epsilon$.

Consider Figure 1 where we poison three real-world datasets from [12], including the Warfarin dataset, with a poison data fraction of $\epsilon = 0.04$. Then, for each dataset, we clean it using the Trim defense, where we supply $\epsilon \in [0.00, 0.02, 0.04, 0.06, 0.08, 0.10]$ (i.e. we clean the poisoned dataset with different estimates $\epsilon$ to quantify the effect of $\epsilon$ on Trim). On the resulting data (which is partially or fully free from poison samples, depending on $\epsilon$), we train a regressor and calculate the MSE on a separate test set. Then, we average the MSE over all datasets and plot the median of the regressors against $\epsilon$.

We make one key observation: The effectiveness of Trim highly depends on the correct choice of $\epsilon$. Selecting $\epsilon$ below the actual degree of poisoning results in not all poison samples being removed and, thus, in an increase of the test MSE of an regressor. Selecting $\epsilon$ above the actual degree of poisoning results in pristine data being removed, which might also remove relevant structure/information contained in the dataset and, as a result, also increase test MSE. Therefore, a better selection strategy than blind overestimation of $\epsilon$ is required.

C. The Iterative Trim Defense

As shown in the last subsection, the Trim defense has the potential to accurately remove poison samples from a given dataset, provided that $\epsilon$ is chosen correctly, but over- or underestimating $\epsilon$ significantly decreases test performance. From this result stems the motivation for our proposed Iterative Trim defense (iTrim). This defense enhances Trim by an iterative search for the best $\epsilon$. In this section, we present this algorithm and our proposal for selecting the ideal value for $\epsilon$.

In Section VI we show empirically on 26 datasets that iTrim
Algorithm 3 \textit{iTrim} defense

Require:
1: Poisson dataset $D_{tr} \cup D_{p}$
2: Some model loss $\mathcal{L}$
3: Maximum estimated poisoning rate $\epsilon_{\text{max}}$
4: Number of runs $r$
5: Threshold $t$

function \textit{iTrim}

7: $I \leftarrow \{\epsilon_{\text{max}} \frac{j}{r} \text{ s.t. } j \in \{0,...,r-1\}\}$
8: for $i \in I$ do
9: $D^{(i)} \leftarrow \text{trim}(D_{tr} \cup D_{p}, \mathcal{L}, \epsilon = i)$
10: $L^{(i)} \leftarrow \min_{\theta} \mathcal{L}(D^{(i)}, \theta)$
end for
12: $\epsilon_{\text{opt}} \leftarrow \min\{i \in I \text{ s.t. } |L^{(i)} - L^{(i-1)}| < t\}$
13: return trim$(D_{tr} \cup D_{p}, \mathcal{L}, \epsilon = \epsilon_{\text{opt}})$
end function

can be applied under realistic conditions to poisoned data, and reliably identifies and removes the poisoned data.

1) Algorithm Description: Algorithm 3 details the \textit{iTrim} defense. It takes as arguments the poisoned dataset $D_{tr} \cup D_{p}$, a loss $\mathcal{L}$, and three scalar hyper parameters. The first, $\epsilon_{\text{max}}$, is an estimate of the maximum possible poisoning rate. This hyper parameter can be chosen arbitrarily large without impacting the defense’s result, but if chosen correctly will improve run time. The second hyper parameter specifies the number of runs $r$. This hyper parameter does not have too much influence on the algorithm’s performance; it influences together with $\epsilon_{\text{max}}$ which values of $\tilde{\epsilon}$ will be tried. The final hyper parameter, the threshold $t$, does have impact on the algorithm’s performance, and we will discuss how to chose it later on.

\textit{iTrim} starts by calculating a set $I$ of possible candidates $\tilde{\epsilon}$ (line 2). The hyper parameters $\epsilon_{\text{max}}$ and $r$ define the right bound and the number of points, respectively. Then, for each candidate, calculate the cleaned dataset $D^{(i)}$ using \textit{Trim}, train the regressor and obtain the corresponding train loss $L^{(i)}$ (lines 3 - 4). Finally, the optimal value for $\tilde{\epsilon}$ is found when the error in train loss between two consecutive losses $L^{(i)} - L^{(i-1)}$ first undercuts some threshold $t$ (line 7). The dataset is cleaned using \textit{Trim} with this estimate, and the result is returned (line 8).

2) Poison Rate Selection: Before we give an intuition for our algorithm and show the reasoning for our selection criterion, we shortly address validation approaches to finding $\tilde{\epsilon}$. As already mentioned, $\tilde{\epsilon}$ is a hyper parameter of \textit{iTrim}. In machine learning, a common approach to finding hyper parameters is validation schemes, e.g. cross validation. But for this approach to work, we require a clean validation dataset. Since we only have a single dataset, we have to assume that any validation split will contain poisoned instances, rendering conventional validation approaches unsuited for finding hyper parameters in this setting.

Thus, we now proceed to explain our iterative approach to finding $\tilde{\epsilon}$: Consider Figure 2, where we apply \textit{Trim} to the Warfarin dataset poisoned with $\epsilon = 0.04$. The orange dashed line shows the train loss for different candidate values $\tilde{\epsilon} \in [0.00, 0.02, 0.04, 0.06, 0.08, 0.10]$. We note that for the correct estimation of poisoning degree $\tilde{\epsilon} = 0.04$, the train loss becomes almost zero, decreasing several orders of magnitude compared to $\tilde{\epsilon} = 0.00$. Further increasing $\tilde{\epsilon}$ still decreases the train MSE, but only insignificantly. Thus, the train loss can be approximated by two straight lines, joined at a distinctive kink where $\tilde{\epsilon} = \epsilon$. Figure 5 in the Supplementary Material shows this for other real-world datasets. We can understand this kink as the point where the dataset ceases to contain data which incurs extremely high train loss - in other words, where all adversarial poison data have been removed. This assumption is supported by the blue line in Figure 2, which shows the test MSE for the same Kernel Ridge regressor trained on the thusly cleaned datasets. For $\tilde{\epsilon} = 0.04$, the test loss is minimal. For $\tilde{\epsilon} > 0.04$, \textit{Trim} starts to remove legitimate data (since all poison data have been removed), which is why test performance deteriorates. Section VI will verify this empirically.

Based on the insight that the train loss can be approximated by two straight lines which intersect at $\epsilon$, we develop our selection criterion for $\tilde{\epsilon}$. We define $t$ as the maximum absolute gradient of the straight line where $\tilde{\epsilon} > \epsilon$ (i.e. the slope of the orange dashed line on the ‘right’ side of the graph, where all poison data have been removed). We will refer to this straight as the \textit{normal straight}. Then $|L^{(i)} - L^{(i-1)}|$ is used to approximate the gradient of the straight for each subinterval. The division by the length of the interval is omitted since all intervals are equidistant. We choose $\tilde{\epsilon}$ as the first candidate so...
Based on our evaluation on 26 datasets (c.f. Section VI-B), it is evident that there is rather a large window of appropriate values for $\epsilon$. This is because 1) we apply feature/target scaling to $[0, 1]$, and 2) the difference in train loss we observe once all adversarial poison data is removed ($\hat{\epsilon} = 0.04$) is too small, whereas $\epsilon$ is vastly too large, poison points are left in the dataset. If $\hat{\epsilon}$ is too small, poisoning rate. This step does not depend on the regressors. Then, for each regressor and each of the 156 poisoned train datasets, we perform Cross-Validated Grid Search to find suitable hyper parameters. Finally, for all 156 poisoned train datasets and both defenses (Trim and $i$Trim), we clean each of the 156 poisoned train datasets. We then train a regressor and measure test error on the test data sets and report below. Thus, in total we run $156 \times 7 \times 2 = 2184$ experiments (7 being the number of different regressors evaluated). The experiments and source code are published to enable reproducibility.

B. Datasets and Regressors

For our experiments, we use 26 datasets: Three datasets introduced in [12], eight datasets from the GitHub repository imbalanced dataset [4], and 15 datasets from the KEEL regression repository [2]. Each dataset contains at least 1000 data points. For datasets where $n > 10000$, we randomly sample a subset $n = 10000$. In keeping with [12], we scale features and targets to $[0, 1]$. See Table III in the Supplementary Material for a detailed summary.

We evaluate four linear models (HuberRegressor, Lasso, Ridge, Elastic Net) and three non-linear models (Neural Networks, Kernel Ridge with RBF kernel, and Support Vector Regressor with RBF kernel). To the best of our knowledge, we are the first to evaluate poisoning attacks against non-linear regressors.

C. Evaluation of StatP

In this section, we very briefly report the effectiveness of StatP on non-linear regressors. As detailed in [12], the attack is effective for linear regressors. We find, however, that it is not effective when applied to non-linear learners. For example, a Neural Network’s MSE remains nearly unchanged (from 0.051 to 0.055) when poisoned with ten percent of poison samples created by StatP. In the Supplementary Material, we elaborate this in more detail, and evaluate additional non-linear learners such as Kernel SVM and Kernel Ridge, which we find to behave similarly.

D. Evaluation of Flip

In this section, we present the results when evaluating our proposed Flip attack against 26 datasets and seven regressors. Figure 5 shows the performance of the Flip attack, averaged over all datasets. Figure 7 in the Supplementary Material shows results per dataset.

The attack is highly effective: When adding only 4% of poison data, the MSE of most regressors doubles compared to the non-poisoned case. We observe that all models seem equally susceptible to our attack, with the exception of the

---

2See [https://github.com/Fraunhofer-AISEC/regression_data_poisoning](https://github.com/Fraunhofer-AISEC/regression_data_poisoning).
We set both \( \hat{A} \) more detailed discussion can be found in the Supplementary Material. We poison all 26 datasets using the \textit{Flip} with a preference for overestimation rather than underestimation \( \epsilon \) when \( \epsilon = 0 \), and all but two deteriorate linearly as \( \epsilon \) increases. Figure 7 in the Supplementary Material shows the same results, but for each dataset individually.

Huber Regressor and Support Vector Regressor, which are designed to be outlier-resistant.

E. Evaluation of Trim and iTrim

In this section, we report the results when defending against the \textit{Flip} attack. We report both the performance of the \textit{Trim} defense and our proposed \textit{iTrim} defense, and compare efficiency. We set both \( \hat{\epsilon} = 0.14 \) (for \textit{Trim}) and \( \epsilon_{\max} = 0.14 \) (for \textit{iTrim}) to mimic the behaviour of a defender in a realistic scenario. A defender would have to guess the percentage of poisoned data \( \epsilon \), with a preference for overestimation rather than underestimation (as explained in Section V-C).

We proceed as follows: With varying degrees of poisoning, we poison all 26 datasets using the \textit{Flip} attack. Then, for each regressor, we clean (i.e. 'defend') the datasets using the \textit{Trim} as well as the \textit{iTrim} defense (separately). We fit the regressor on the thusly obtained dataset, and compare the test error against a regressor trained on the 'clean' data. Figure 4 shows the median of all regressors for \textit{Trim} (blue line) and \textit{iTrim} (orange dashed line).

We observe that both defenses are effective. However, \textit{iTrim} achieves higher performance than \textit{Trim}, especially when there is a large discrepancy between \( \epsilon \) and \( \hat{\epsilon} \). This is due to \textit{iTrim}'s capability of more accurately estimating the degree of poisoning. Especially for \( \hat{\epsilon} > \epsilon \), we see considerable improvement due to \textit{iTrims} more advanced estimate of \( \epsilon \). Trim is also computationally feasible, despite its iterative approach: The average runtime for defending a given dataset was 1.6 minutes. A more detailed discussion can be found in the Supplementary Material.

Fig. 3: Evaluation of our proposed \textit{Flip} attack. This plot shows the MSE for different poison rates per regressor, averaged over all 26 datasets. Most regressors obtain a MSE of around 0.003 when \( \epsilon = 0 \), and all but two deteriorate linearly as \( \epsilon \) increases. Figure 7 in the Supplementary Material shows the same results, but for each dataset individually.

Fig. 4: Evaluation of the \textit{Trim} and \textit{iTrim} defense. First, we poison the 26 datasets using \textit{Flip}. Then we apply the \textit{Trim} or \textit{iTrim} defense, and calculate the test MSE. Finally, we normalize by the baseline MSE - the error obtained by a model trained on unpoisoned data. The resulting quotient represents the degree to which the defenses can negate the \textit{Flip} attack. We observe that \textit{iTrim} consistently outperforms \textit{Trim}. More detailed, non-averaged results are presented in Figure 8 and Figure 9 in the Supplementary Material.

F. Runtime

In this section, we detail the runtime of the \textit{iTrim} defense algorithm. \textit{iTrim} calls the \textit{Trim} defense \( r \) times, which in turn performs \( j \) fit operations of the regressor - until either a convergence criterion is met, or the number of runs \( j \) is exhausted. In our experiments, we set \( r = 6, j = 20 \). Running the complete experiment (attacking all 26 datasets, for seven regressors, and six poisoning rates \( \epsilon \)) results in \( 26 \times 6 \times 7 = 1092 \) calls to the \textit{iTrim} defense. On a Intel(R) Xeon(R) CPU E7-4860 v2 @ 2.60GHz with 96 cores, this takes about 120 minutes when parallelizing into 15 separate processes. Thus, running a single \textit{iTrim} defense takes, on average, \( 120 / 1092 \times 15 = 1.6 \) minutes per 6-core process. Obviously, this is highly dependent on the regressor’s complexity, the size of the dataset, the number of features, and parallelism capabilities of the program code. Still, this indicates the feasibility of applying the \textit{iTrim} defense in a real-world scenario, where after weeks, months or even years of data gathering, running the \textit{iTrim} incurs negligible additional time overhead.

VII. WARFARIN VISITED

In Section II we presented the medical use case of predicting the therapeutic Warfarin dose and showed that data poisoning can significantly impact the performance of regressors on the task. In this section, we will illustrate the empirical results of Section VI-E on the use case of Warfarin dose prediction, where we consider three different scenarios: First, the (C)lean case. In this scenario, no data poisoning occurs. This case will be used as a baseline for measuring the effects of data poisoning and defence. Second, the (P)oison case. In this scenario, the attacker introduces 2% poison samples using the \textit{Flip} attack proposed in Section IV-C. No countermeasures are taken. Third,
TABLE II: Mean absolute error (MAE) of different regression models when poisoned using the Flip attack.

| Model           | MAE C | MAE P | MAE D | MAE P/C | MAE D/C | Accbl. P/C | Accbl. D/C |
|-----------------|-------|-------|-------|---------|---------|------------|------------|
| Elastic Net     | 8.52  | 11.07 | 8.51  | 1.30    | 1.00    | 21.25      | -0.82      |
| Huber Reg.      | 8.40  | 8.46  | 8.41  | 1.01    | 1.00    | -1.09      | -0.82      |
| Kernel Ridge    | 8.41  | 10.98 | 8.41  | 1.31    | 1.00    | 21.07      | 0.53       |
| Lasso           | 8.49  | 11.20 | 8.49  | 1.32    | 1.00    | 22.31      | 0.00       |
| MLP             | 10.05 | 12.33 | 9.86  | 1.23    | 0.98    | 11.41      | -2.80      |
| Ridge Reg.      | 8.49  | 10.99 | 8.51  | 1.29    | 1.00    | 22.34      | 1.06       |
| SVR             | 10.85 | 12.52 | 11.19 | 1.15    | 1.03    | 14.13      | 2.90       |
| Median          | 8.49  | 11.07 | 8.51  | 1.29    | 1.00    | 21.07      | 0.00       |

the (D)efended case. In this scenario the data are poisoned with 2% poison samples like in (P), but iTrim is used as a countermeasure. The results for these three scenarios are summarized in Table [II].

To recapitulate: Warfarin is a blood thinner with a narrow therapeutic window resulting in high medical significance for the correct prediction of the therapeutic Warfarin dose. The scenarios (C) and (P) have already been presented in Section [I].

To summarize: The models used in our evaluation perform comparable to state-of-the-art models and 2% poison samples are sufficient to noticeably increase metrics like the MAE and to decrease the number of patients receiving an acceptable dose of Warfarin by up to 22%.

In Table [II] the column ‘MAE D/C’ provides the factor by which the MAE of a regressor increases, when the dataset is poisoned with 2% poison samples and then defended using iTrim. As we can see, the median is 1.00, indicating that the damage is mitigated. The individual values range from 0.98 to 1.03, which indicates that where previously Flip incurred an increase in MAE of up to 31%, the iTrim defense reduces this error increase to a tenth. In summary, the MAE of the tested models in the (D) scenario is approximately the same as in the (C) scenario, meaning the defense successfully eliminates (most) of the negative impact of the poison samples.

The column Acceptable D/C gives the percentage by which the number of patients receiving an acceptable Warfarin dose decreases in the (D) scenario compared to the (C) scenario. The median reduces from 21.07 in scenario (P) to a median of close to 0 in scenario (D). This shows that the number of patients receiving an unacceptable Warfarin dose due to data poisoning is significantly reduced when the iTrim defense is employed. In summary, we observe that the iTrim defense decreases the influence of poison samples. It results in more patients receiving adequate predictions for their therapeutic Warfarin dose.

VIII. CONCLUSION

In this paper we introduce a novel data poisoning attack on regression learning as well as a matching defense mechanism. We show the effectiveness of our proposed attack and defense algorithm in a large empirical evaluation over seven regressors and 26 datasets. Both attack and defense assume realistic constraints: The attack is black-box and doesn’t assume access to the true dataset, but only a substitute dataset. The defense, on the other hand, does not assume any knowledge of the poisoning rate $\epsilon$, but estimates it using an iterative approach.

REFERENCES

[1] Applications - Keras Documentation, Sep 2019. [Online; accessed 6. Nov. 2019].
[2] J Alcalá-Fdez, A Fernández, J Luengo, J Durães, S García, L Sánchez, and F Herrera. KEEL Data-Mining Software Tool: Data Set Repository, Integration of Algorithms and Experimental Analysis Framework. Technical report, 2011.
[3] Battista Biggio, Blaine Nelson, and Pavel Laskov. Poisoning attacks against support vector machines. In Proceedings of the 29th International Conference on Machine Learning, ICML 2012, volume 2, pages 1807–1814, jun 2012.
[4] Paulia Branco. GitHub Imbalanced-Regression-Datasets. 2019. https://github.com/paulabranco/Imbalanced-Regression-Datasets, last checked September 11th, 2020.
[5] Sen Chen, Minhui Xue, Lingling Fan, Shuang Hao, Lihua Xu, Haojin Zhu, and Bo Li. Automated poisoning attacks and defenses in malware detection systems: An adversarial machine learning approach. Computers and Security, 73:326–344, 2018.
[6] Wikipedia Contributors. Warfarin, Oct 2019.
[7] Universidad Autónoma de Ciudad Juárez. (pdf) using regression models for predicting the product quality in a tubing extraction process, Aug 2019.
[8] Melissa Eddy. Hundreds of bodies, one nurse: German serial killer leaves as many questions as victims. The New York Times, May 2019.
[9] Sean Ekins, Ana C Puhl, Kimberley M Zorn, Thomas R Lane, Daniel P Russo, Jennifer J Klein, Anthony J Hickey, and Alex M Clark. Exploiting machine learning for end-to-end drug discovery and development. Nature materials, 18(5):435, 2019.
[10] Handelsblatt. Zahlungsverhalten vorhersagen, Oct 2018.
[11] J Alcalá-Fdez, A Fernández, J Luengo, J Durães, S García, L Sánchez, and F Herrera. KEEL Data-Mining Software Tool: Data Set Repository, Integration of Algorithms and Experimental Analysis Framework. Technical report, 2011.
[12] Matthew Jajelksi, Alina Oprea, Battista Biggio, Chang Liu, Cristina Nita-Rotaru, and Bo Li. Manipulating Machine Learning: Poisoning Attacks and Countermeasures for Regression Learning. In Proceedings - IEEE Symposium on Security and Privacy, volume 2018-May, pages 399–414, IEEE, may 2018.
[13] Hannah Kuchler. The start-up striving to accelerate drug discovery, May 2019.
[14] Zhiyuan Ma, Ping Wang, Zehui Gao, Ruobing Wang, and Korosh Khalighi. Ensemble of machine learning algorithms using the stacked generalization approach to estimate the warfarin dose. PloS one, 13(10):e0205872, 2018.
[15] Luis Muñoz González, Battista Biggio, Ambra Demontis, Andrea Paudice, Vasin Wongrassamee, Emil C. Lupu, and Fabio Roli. Towards poisoning of deep learning algorithms with back-gradient optimization. In Proceedings of the 10th ACM Workshop on Artificial Intelligence and Security, AISec ’17, pages 27–38, New York, NY, USA, 2017. ACM.
[16] N. Papernot, P. McDaniel, A. Sinha, and M. F. Wellman. Sok: Security and privacy in machine learning. In 2018 IEEE European Symposium on Security and Privacy (EuroS P), pages 399–414, April 2018.
[17] Roberto Perdisci, David Dagon, Wenke Lee, Prahlad Foglat, and Monirul Sharif. Misleading worm signature generators using deliberate noise injection. In Proceedings - IEEE Symposium on Security and Privacy, volume 2006, pages 17–31, 2006.
[18] Katia Porzecanski. Jpmorgan commits hedge fund to ai in technology arms race, Jul 2019.
[19] PWC. Predictive Maintenance 4.0. 2017.
IX. Supplementary Material

Fig. 5: Similarly to Figure 2, we plot the train vs test error of a KernelRidge regressor on a dataset (loan) poisoned with \( \hat{\epsilon} = 0.04 \). We observe that the train loss gives clear indication as to when all poison samples are removed via iTrim.

A. Evaluation of the StatP Attack

In this section, we evaluate the performance of existing poisoning attacks on regression learning. As described in Section IV-B, the only poisoning attack in literature which we can directly apply to regression models in a black box scenario is the StatP attack \([12]\). We implement this attack and evaluate it twice: First, we apply the attack on the Warfarin dataset and three non-linear models. Second, we evaluate all 26 datasets against both the statP and Flip attack (Figure 7). We observe the following: 1. For nonlinear regressors, StatP is ineffective. The MAE remains near constant when adding even significant amounts of poison samples (see Figure 6). First, when analyzing the poison data created by StatP, we find an intuitive explanation for this: StatP pushes all data points ‘to the corners’, i.e. to the edge of the feasibility domain. While these data do conflict with the ‘clean’ data for linear regressors, nonlinear models can easily accommodate both poison and clean data, as long as the samples don’t overlap in feature-space. Second, when evaluating both attacks on all 26 datasets, averaging four linear and three non-linear models, we can confirm the above results. Flip consistently outperforms StatP (c.f. Figure 7).

B. Datasets

The following table lists the datasets we use in our experiments. The datasets can be obtained at [https://sci2s.ugr.es/keel/category.php?cat=reg](https://sci2s.ugr.es/keel/category.php?cat=reg) and [https://github.com/paobranco/Imbalanced-Regression-DataSets](https://github.com/paobranco/Imbalanced-Regression-DataSets) and from \([12]\).

| Name          | features | n     |
|---------------|----------|-------|
| 0  | ANACALT.dat | 7.0 | 4052.0 |
| 1  | accel    | 22.0 | 1732.0 |
| 2  | ailerons.dat | 40.0 | 13750.0 |
| 3  | armsesHousing | 248.0 | 1460.0 |
| 4  | availPwr  | 49.0 | 1802.0 |
| 5  | bank8fm  | 8.0 | 4499.0 |
| 6  | california.dat | 8.0 | 20640.0 |
| 7  | compactiv.dat | 21.0 | 8192.0 |
| 8  | concrete.dat | 8.0 | 1030.0 |
| 9  | cpu       | 12.0 | 8192.0 |
| 10 | elevators.dat | 18.0 | 16599.0 |
| 11 | friedman.dat | 5.0 | 1200.0 |
| 12 | fuelCons  | 88.0 | 1764.0 |
| 13 | heat      | 30.0 | 7400.0 |
| 14 | house.dat | 16.0 | 14998.0 |
| 15 | loan      | 16.0 | 1049.0 |
| 16 | mortgage.dat | 18.0 | 1049.0 |
| 17 | plastic.dat | 2.0 | 1650.0 |
| 18 | pole.dat  | 26.0 | 14998.0 |
| 19 | quake.dat | 5.0 | 2178.0 |
| 20 | rings     | 10.0 | 4177.0 |
| 21 | torque    | 95.0 | 1802.0 |
| 22 | treasury.dat | 15.0 | 1049.0 |
| 23 | wankara.dat | 9.0 | 1609.0 |
| 24 | warfarin | 177.0 | 5528.0 |
| 25 | wizmir.dat | 9.0 | 1461.0 |
Fig. 7: StatP (left) vs Flip (right). This plot shows the increase in MAE when using a poisoned dataset instead of a clean dataset during model training. The results are averaged over all seven regressors, but displayed individually per dataset. For an average over all datasets, refer to Figure 3. **Left Image:** All 26 datasets when attacked with the StatP attack. While the degree of effectiveness varies between datasets, we generally observe a linear correlation between degree of poisoning and increase in test error. **Bottom Image:** The same datasets attacked with the Flip. Note that this attack consistently outperforms StatP, as seen on the higher MAE.

Fig. 8: Trim (left) vs. iTrim (right), averaged by dataset. **Left:** This plot shows the effectiveness of Trim when defending against the Flip attack, averaged over all 26 datasets. Datasets are poisoned as indicated on the x axis. Then, the Trim defense is applied, the regressor is fitted to the dataset, and the resulting test MSE is compared against the test MSE on a clean, unpoisoned dataset. We see that, depending on the regressor, datasets cleaned with Trim still incur significant decrease in test performance. **Right:** The same process is applied to iTrim. We observe that test MSE is considerably decreased, especially for $\epsilon < 0.08$. The larger $\epsilon$, the more similar the two defences become. Additional information is provided by Figure 9.

Fig. 9: Trim (left) vs. iTrim (right), averaged by regressor. Similar to Figure 8, this plot shows the increase in MAE when using a poisoned and subsequently defended dataset instead of a clean dataset during model training. The results are averaged over all seven regressors, but displayed individually per dataset. **Left Image:** Increase in MAE when defending against a Flip attack using Trim. **Right Image:** Increase in MAE when defending against a Flip attack using iTrim. Notice that iTrim outperforms Trim almost consistently (as seen by the overall lower MAE, shown in bold black).