Assessment of Treatment Effect Estimators for Heavy-Tailed Data

Nilesh Tripuraneni*1, Dhruv Madeka†2, Dean Foster2, Dominique Perrault-Joncas2, Michael I. Jordan1, 2

1University of California, Berkeley
2Amazon

Abstract

A central obstacle in the objective assessment of treatment effect (TE) estimators in randomized control trials (RCTs) is the lack of ground truth (or validation set) to test their performance. In this paper, we provide a novel cross-validation-like methodology to address this challenge. The key insight of our procedure is that the noisy (but unbiased) difference-of-means estimate can be used as a ground truth “label” on a portion of the RCT, to test the performance of an estimator trained on the other portion. We combine this insight with an aggregation scheme, which borrows statistical strength across a large collection of RCTs, to present an end-to-end methodology for judging an estimator’s ability to recover the underlying treatment effect. We evaluate our methodology across 709 RCTs implemented in the Amazon supply chain. In the corpus of AB tests at Amazon, we highlight the unique difficulties associated with recovering the treatment effect due to the heavy-tailed nature of the response variables. In this heavy-tailed setting, our methodology suggests that procedures that aggressively downweight or truncate large values, while introducing bias, lower the variance enough to ensure that the treatment effect is more accurately estimated.

1 Introduction

Causal inference is widely used across numerous disciplines such as medicine, technology, and economics to inform important, downstream decisions [Hernan and Robins, 2020]. Inferring causal relationships between an intervention and outcome requires estimating the treatment effect (TE): the difference between what would have happened given an intervention and what would have happened in its absence. A central difficulty is that these two events are never jointly observed [Rubin, 2005]. TE estimation leverages randomized controlled trials (RCTs)—which randomly assign the items of interest into either the treatment or control groups—to counter selection biases and allow causal effects to be estimated via a simple differences-in-means estimate.

Indeed, the simplest “model-free” unbiased estimator of a treatment effect is the difference-of-means (DM) estimate [Rubin, 2005]. Such an estimator may, however, suffer from high variance in real-world scenarios which often involve heterogeneous, high-dimensional and heavy-tailed data1. A plethora of additional information is thus often used to improve TE estimates relative to this simple baseline. For example, pretreatment regression adjustments can significantly reduce the variance of a treatment effect estimate while adding little additional bias [Angrist and Pischke, 2008, Imbens and Rubin, 2015]. Similarly, a host of other regularization and robustness modifications can be used to trade off bias and variance.

As the complexity of such estimators increases, so do the assumptions (and work) needed to establish their statistical validity. Moreover, it is necessary and challenging to develop a principled approach to selecting an estimator from the zoo of possibilities. One particular setting in which the severity of these problems is diminished, and which we argue arises in many practical applications,2 is when large RCTs can be run in the same population. This setting provides an opportunity to get at the fundamental quantity of interest—the mean-squared error (MSE) of a given treatment effect estimator. Our simple insight is that the DM estimator can function as a noisy, but unbiased “label” for the treatment effect. Noisy MSE estimates for a TE estimator can then be computed by comparing this estimator to the (unbiased) difference-of-means estimator via a simple, held-out validation estimate (see Claim 1). Our goal in this work, is to judge the performance of TE estimators by pooling many noisy (but unbiased) estimates of their MSE’s across many RCTs. Such a procedure is desirable because it targets the actual quantity of interest, the estimator MSE, in an assumption/estimator-agnostic fashion. The primary contributions of this work are as follows:

---

1Work done while at Amazon.
2Correspondence to maded [at] amazon dot com.
1Such heavy-tailed data is commonplace in the large-scale RCTs which motivate our study.
2Including AB testing of forecasting interventions, website changes, supply-chain modifications, or a number of other interventions.
where AB tests conducted at Amazon over the course of several years as our testbed for estimator selection in contrast to synthetic

The literature on causal inference and treatment effect estimation is vast and a comprehensive review is beyond the scope of

1.1 Related Work

The literature on causal inference and treatment effect estimation is vast and a comprehensive review is beyond the scope of this paper. Hernan and Robins [2020], Imbens and Rubin [2015], Angrist and Pischke [2008], Hadad [2020] and Wager [2020] provide modern perspectives on both the theory and practice of treatment effect estimation. Cross-validation (CV) also has been (and remains) a major subject of statistical inquiry as it is amongst the most widely used tools to assess the quality of an estimator and perform model selection Bayle et al. [2020], Lei [2020], Stone [1974], Geisser [1975].

Relatively little work has been done in the intersection of these two domains. Part of the difficulty stems from the fact the standard procedure of CV breaks down for treatment effect estimation since the true treatment effect is never observed in data. Athey and Imbens [2016] and Powers et al. [2018] do provide model-specific selection methods in the context of treatment effect estimation. However, these works do not apply to arbitrary TE estimators. Closest to our work is that of Schuler et al. [2018], who use a data-splitting methodology to evaluate several risk functions to assess heterogeneous treatment effect estimators. This differs from our work in two principal ways. First, our framework is targets the problem of average treatment effect estimation—in many scenarios that we are interested in treatments cannot be individualized and must be applied in an all-or-nothing fashion to the entire population. Our statistical scheme also differs since we provide a provably unbiased estimate of the mean-squared error of a TE estimator, and we introduce an aggregation scheme to borrow statistical strength across different AB tests to compare estimators. Additionally, our work uses a large corpus of 709 actual randomized, AB tests conducted at Amazon over the course of several years as our testbed for estimator selection in contrast to synthetic data simulations.

One of our main motivations is to highlight the unique challenges associated with heavy-tailed data often present in applications arising at large-scale technology and logistics companies. Semiparametric TE estimators for heavy-tailed datasets inspired by similar applications have been explored in Fithian and Wager [2014] and Taddy et al. [2016]. However, these works do not address the problem of model selection which is our central focus. Specifically we focus on methods to select among simple estimators (with few to no tuning parameters) that are widely used in practice.

1.2 Preliminaries

Notation: We use bold-faced variables such as \( X \) and \( x \) to define vectors.

We work within the Rubin potential outcomes model [Rubin, 2005] where we imagine we are given a domain of objects \( \mathcal{X} \) and a target variable of interest \( Y(\cdot) \) given a possible intervention. For a fixed intervention \( I \), our goal is to estimate the population average treatment effect (ATE):

\[ \Delta = \mathbb{E}[Y(1) - Y(0)], \tag{1} \]

where \( Y(1) \) corresponds to the value of an experimental unit—in our case a product in the supply chain—given the treatment and \( Y(0) \) its unobserved counterfactual control (and vice versa). In general, we also allow the existence of other covariates in our model \( X \in \mathcal{X} \). In a given AB test, we first randomly sample an equal number of items into a treatment group, \( T \), and a control group \( C \). We further let the \( (X_i, T_i, Y_i) \) be the covariates, treatment dummy, and value of the \( i \)th item. By a standard argument, using the assumption of randomization (independence of \( \{Y_i(1), Y_i(0)\} \) and \( T_i \)), the differences-in-means estimator,

\[ \hat{\Delta}_{DM} = \frac{1}{|T|} \sum_{i \in T} Y_i(1) - \frac{1}{|C|} \sum_{i \in C} Y_i(0), \tag{2} \]

provides an unbiased estimate of \( \Delta \) [Rubin, 2005]. A primary benefit of the DM estimator is that it is “model-free.” That is, it makes no explicit assumptions on the data-generation process for \( Y_i \) as a function of the other covariates.

• We process a corpus of 709 AB tests (arising from genuine RCTs) implemented at Amazon across several years and we highlight the heavy-tailed nature of the response and covariate variables. The unique challenges associated with heavy-tailed estimation require careful navigation of the bias-variance tradeoff which motivates the development of an objective selection procedure for TE estimation.

• We present a selection scheme which borrows statistical strength across the corpus of AB tests in order to judge the relative performance of several commonly used TE estimators.

• We use this framework to argue that in the presence of heavy-tailed data—as often arise in large-scale technology and logistics applications—aggressive downweighting and truncation procedures are needed to control variance.

3Leveraging the unbiased nature of the DM estimator.
1.3 Dataset Description

Our entire corpus of AB tests consists of 709 RCTs that were run at Amazon over the course of several years (dating back to 2017) on a population of products. The interventions in each AB test consist of various modifications and (potential) improvements to the way in which products are processed through the supply chain. The AB tests are constructed as RCTs with 50% of products in an RCT randomly placed in the treatment group and 50% in the control group. The AB tests vary in size from tens of thousands of products to those with several millions. Each AB test is run over the course of approximately 27 weeks with the intervention instituted at a trigger date at 10 weeks in the treatment group.

At each week in an AB test, the response variable generated from each product is computed, as well as forecasted auxiliary covariates for that product (which might serve as a surrogate for its popularity). Each AB test was preprocessed to contain the averaged pretreatment response (denoted $X$), a strictly nonnegative averaged pretreatment auxiliary covariate (denoted $D$), averaged posttreatment response (denoted $Y$), and binary treatment indicator (denoted $T$) for each item. Auxiliary covariates (such as $D$) often arise in naturally occurring applications where it is feasible to forecast a related quantity to $Y$ (such as the number of expected products needed in a time period to satisfy user demand).

2 Heavy Tails and Hard Estimation

The difficulties associated with treatment effect estimation of an intervention in large-scale commerce RCT datasets are many fold. The most salient difficulty for our consideration is that the response distribution over the range of products has a heavy tail. Similar heavy-tailed distributions are known to exist in user revenue distributions as well as user engagement metrics at large-scale technology companies [Fithian and Wager, 2014, Taddy et al., 2016]. Estimation in this setting is difficult and requires balancing several considerations when considering the pros and cons of various estimation techniques. Our exploration of these issues serves a dual purpose: (1) to highlight the ubiquitous occurrence of such heavy tails in naturally occurring data, and (2) to motivate the need for a model selection procedure to navigate the bias-variance tradeoff.

Let us investigate the data inside a single RCT to assist in further making this point. The RCT under consideration consists of 7208692 distinct products. This RCT (a representative choice) displays significant heavy-tail behavior, as shown in Fig. 1.

![Figure 1: Hill plot of the right tail of the response variable distribution in a single RCT versus the Hill cutoff hyperparameter. The Hill values are an estimate of the power $\eta$ in the asymptotic tail behavior of the response distribution variable, $Y$, $p(y) \sim y^{-\eta}$.](image)

We implement the Hill estimator to obtain an estimate of the power-law behavior $\eta$ in the right tail distribution of $\sim y^{-\eta}$ across all the RCTs under consideration. The Hill cutoff hyperparameter is chosen to discard points near the center of the distribution (i.e., near zero) and allows the formulation of a bias-variance tradeoff [Drees et al., 2000]. We avoid a more sophisticated data-driven choice of this cutoff since the precise Hill value is not of particular interest in our setting. Rather, it is apparent the power $\eta$ can be conservatively judged to be between $1 - 3$ in Fig. 1. Analyzing the response distribution across the entire corpus of 709 AB tests and choosing the Hill cutoff parameter at the 5th percentile shows that the average decay exponent is $\approx 2.32$ with a standard deviation of 0.79, and median of 2.1476. Note $\eta = 2$ results in a Cauchy-like tail for which

\footnote{Indeed we have tens of thousands of points in all RCTs, so small-sample difficulties associated with “Hill horror plots” seem not to arise.}
random variables have an infinite mean and will fail to concentrate under normalized addition. The heavy tail of the response variable is rather remarkable since it suggests that the response random variable may not possess a variance. The lack of a variance invalidates the application of the central limit theorem to the normalized mean and also destroys the large-sample behavior of the bootstrapped mean distribution [Athreya, 1987]. The sample complexity of mean estimation also fundamentally changes since finite-sample \( \sqrt{n} \)-confidence intervals are no longer attainable [Cherapanamjeri et al., 2020].

The difficulties seen in this case study reinforce the conclusion that handling the heavy tails inherent in our data likely requires more sophisticated (regularized) estimators than the DM estimator. Ultimately this boils down to balancing the tradeoff between bias and variance in estimation. Navigating this bias-variance tradeoff is one of the primary motivations for our aggregation methodology for TE estimator selection.

3 Validation Procedure for Treatment Effect Estimators

In this section we present the key idea behind the validation procedure we use to assess the quality of an arbitrary treatment effect estimator, \( \hat{\Delta}_E(\cdot, \cdot) \), in the AB test denoted \( I \). Let \( \Delta \) denote the population ATE shown in (1). Given the groups \( T \) and \( C \) we first randomly partition them into disjoint groups \( T_1, T_2 \) and \( C_1, C_2 \). Now, consider the (potentially complicated) treatment effect estimator \( \hat{\Delta}_E(T_1, C_1) \) trained on the first fold of data. We can obtain an estimate of its performance by how well it targets the difference-of-means estimator computed on the hold-out set \( \hat{\Delta}_{DM}(T_2, C_2) \):

\[
\hat{\text{MSE}}_{T,E}(T_1, C_1, T_2, C_2) = (\hat{\Delta}_E(T_1, C_1) - \hat{\Delta}_{DM}(T_2, C_2))^2.
\]

A simple argument shows that this quantity is a noisy but unbiased MSE of the estimator (and thus it permits the relative comparison of two different estimators).

**Claim 1.** *Given two different treatment effect estimators A and B in the aforementioned setting, we have:

\[
\begin{align*}
\mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \hat{\Delta}_{DM}(T_2, C_2))^2] &\leq \mathbb{E}[(\hat{\Delta}_B(T_1, C_1) - \hat{\Delta}_{DM}(T_2, C_2))^2] \Rightarrow (4) \\
\mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \Delta)^2] &\leq \mathbb{E}[(\hat{\Delta}_B(T_1, C_1) - \Delta)^2] \Rightarrow (5)
\end{align*}
\]

Proof. We simplify the MSE of a treatment effect estimator \( E \) by centering the DM estimator around its mean and expanding the square:

\[
\begin{align*}
\mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \hat{\Delta}_{DM}(T_2, C_2))^2] &= \mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \Delta - \hat{\Delta}_{DM}(T_2, C_2))^2] \\
&= \mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \Delta)^2] + \mathbb{E}[(\hat{\Delta}_{DM}(T_2, C_2))^2] + 2\mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \Delta)]\mathbb{E}[(\Delta - \hat{\Delta}_{DM}(T_2, C_2))] \Rightarrow (5)
\end{align*}
\]

where the cancellation uses the independence of the first/second folds of data to factor the expectation over the two terms, and the unbiased estimation property of the DM estimator over the second fold [Rubin, 2005]. We then obtain the following variances for two estimators \( A \) and \( B \):

\[
\begin{align*}
\mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \hat{\Delta}_{DM}(T_2, C_2))^2] - \mathbb{E}[(\hat{\Delta}_B(T_1, C_1) - \hat{\Delta}_{DM}(T_2, C_2))^2] &= \mathbb{E}[(\hat{\Delta}_A(T_1, C_1) - \Delta)^2] - \mathbb{E}[(\hat{\Delta}_B(T_1, C_1) - \Delta)^2],
\end{align*}
\]

from which the claim follows. \( \Box \)

This result motivates using held-out sample error as a metric to assess the relative merit of two estimators \( \hat{\Delta}_A \) and \( \hat{\Delta}_B \). However, simply using this estimator on a single RCT provides a (potentially very) noisy estimate of the population error, not the population error itself. Indeed, if the estimator \( \hat{\Delta}_{DM}(T_1, C_2) \) is sufficiently good to estimate \( \Delta \) why even bother to use another estimator? Said another way, the error estimate in (3) will always suffer at least the variance of the unbiased estimate (2). In practice we can always use a cross-validated version of (3) to reduce the subsampling variance due to the random train/test splits. However, such a procedure will not decrease the variance of the DM estimator arising from the underlying heavy-tailed data.

Our proposal for resolving this conundrum is to note that in many situations we have access to multiple RCTs from the same underlying population or process given different interventions. Thus, aggregating the set of error estimates

\[
\hat{A} = \{ \hat{\text{MSE}}_{I_1, A}(T_1, C_1, T_2, C_2), \ldots, \hat{\text{MSE}}_{I_N, A}(T_1, C_1, T_2, C_2) \}
\]

Throughout we also implicitly use the fact the subfolds are (uniformly) randomly sampled from the treatment and control groups—so the expectation over the subfold is equivalent to the expectations over the entire treatment/control groups.
and comparing to
\[ \hat{B} = \{ \text{MSE}_{I_1,B}((T_1, C_1), (T_2, C_2)), \ldots, \text{MSE}_{I_N,B}((T_1, C_1), (T_2, C_2)) \}, \]

for various interventions \( I_1, \ldots, I_N \), can allow us to pool information across RCTs. We sidestep the methodological complexities of performing this aggregation and instead turn to an investigation of simple, practically-motivated schemes.

### 3.1 An Aggregation Scheme

Aggregating the mean-squared errors requires handling a practical consideration. Since the AB tests and interventions across RCTs themselves may be different, the overall scales of the MSEs between different AB tests may be different. As an example, consider a corpus of two AB tests on which estimator \( A \) obtain errors \( \{1, 10\} \) and estimator \( B \) obtains errors \( \{2, 9\} \). Simply averaging the errors or doing a rank-based test of performance would indicate both estimators are equivalent. However, intuitively we believe a relative improvement of estimator \( B \) from 10 to 9 on the second AB test does not outweigh the degradation from 1 to 2 on the first AB test.

This observation motivates the definition of a normalized score to compare the estimators \( A \) vs \( B \), as a function of the vectors of their noisy errors. For each intervention \( i \in \{I_1, \ldots, I_N\} \) we define the normalized score:
\[ S_i(\hat{A}_i, \hat{B}_i) = \frac{\hat{B}_i - \hat{A}_i}{\hat{B}_i + \hat{A}_i}, \]

for \( \hat{A}_i \in \hat{A} \) and \( \hat{B}_i \in \hat{B} \). Where \( \hat{A} \) and \( \hat{B} \) are defined according to (7) and (8) respectively.

This normalized score vector (which we denote by \( S(\hat{A}, \hat{B}) \)) implicitly binarizes each of its elements to bound them in the range \([-1, 1]\). Each element of this vector is a noisy score of estimator \( A \)'s performance relative to \( B \) on one AB test in the corpus.\(^7\) If the estimator has many elements that are positive, it suggests that estimator \( B \) has larger errors than estimator \( A \). In this case, we would expect estimator \( A \) to be better than estimator \( B \).

To formalize this intuition, we use the following heuristic which implicitly treats each RCT equally independent of size. We use a two-sided one-sample \( t \)-test applied to this normalized score vector to test the null that the “population mean” of the \( S \) “distribution” is 0, i.e., that the performance of estimator \( A \) is indistinguishable from the performance of estimator \( B \). Overall, this procedure interpolates between two extremes. A purely rank-based test of performance might only count the number of AB tests for which \( A \) is better then \( B \) irrespective of how much better one is in a particular AB test. Meanwhile, a procedure which only looks at the raw (unnormalized) RCT errors has the property that RCTs with large MSE values for both estimators would drown out signal from RCTs with small MSE values. We stress that the \( t \)-test heuristic provides a simple way of converting the information contained in \( S(\hat{A}, \hat{B}) \) to a single number, but we recommend looking at the score histograms for a more complete picture.

### 4 Results

In this section we detail several simple and commonly used estimators for TE estimation and subsequently compare their relative performance.

#### 4.1 Estimators

For the following estimators, we note that each admits a “Winsorization” which can be used to trade off bias and variance. To do this, we can simply Winsorize the covariates and targets, \( X, D, Y \), in only the training fold, to reduce variance. The test folds are always left untrimmed/Winsorized so Claim 1 remains valid. Explicitly we define Winsorization at level 0.001 to Winsorize the \( X, Y \) distributions at \( P0.1, P99.9 \) and the (positive) auxiliary \( D \) distribution at \( P99.9 \).

#### 4.1.1 Difference-of-Means (dm)

The simple difference-of-means estimator,
\[ \hat{\Delta}_{DM} = \frac{1}{|T|} \sum_{i \in T} Y_i(1) - \frac{1}{|C|} \sum_{i \in C} Y_i(0), \]

---

\(^6\) As noted earlier, in practice each error estimate is averaged over several resampled train/test splits, but we suppress this extra notation for clarity.

\(^7\) Our notion of a normalized score vector is element-wise transitive. That is, \( \frac{1}{\hat{A}_i + \hat{B}_i} > 0 \) and \( \frac{1}{\hat{B}_i + \hat{A}_i} > 0 \) imply \( \frac{1}{\hat{A}_i + \hat{B}_i} > 0 \).
We are given access to a pretreatment item-specific covariate $X$ we can estimate the ATE for a binary treatment by regressing

\[ \text{ATE} = \alpha + T \Delta \]

where $\alpha = \mathbb{E}[Y(0)]$. \hfill (11)

In this setting the noise model is heteroscedastic (and depends on $T$).

4.1.2 Difference-of-Median-of-Means (mom)

Our definition of this estimator cannot be interpreted in the regression framework strictly speaking, but it is sufficiently similar that we describe it here. The formulation of (10) and relationship to (11) motivates the robust estimation of $\alpha$ and $\Delta$. Equivalently, we replace the terms in $\frac{1}{|T|} \sum_{i \in T} Y_i(1), \frac{1}{|C|} \sum_{i \in C} Y_i(0)$ with the median-of-means estimators for some prespecified block size $B$ to define,

\[ \hat{\Delta}_{\text{MoM}} = \text{MoM}(\{Y_i(1)\}_{i=1}^{|T|}, B) - \text{MoM}(\{Y_i(0)\}_{i=1}^{|C|}, B). \]

Similarly, \( \hat{\alpha} = \text{MoM}(\{Y_i(0)\}_{i=1}^{|C|}, B) \) to complete the regression analogy. We use mom1000 in our experiments to denote the median-of-means estimator chosen with 1000 total blocks.

4.1.3 Generalized LR (and Generalized Difference-in-Differences) (gen_dd)

We are given access to a pretreatment item-specific covariate $X_i$ corresponding to the response value $Y_i$. If these covariates are strongly correlated with the response value $Y_i$, incorporating them into the regression can significantly reduce the variance. So, assuming the model,

\[ Y = \alpha + T \cdot \Delta + X \cdot \beta + \epsilon, \]

we can estimate the ATE for a binary treatment by regressing $Y_i$ onto $(1, T_i, X_i)$, where $\epsilon_i$ represents a general conditionally mean-zero noise term (which may depend on $X_i$).

Remark 1. When the covariate $X$ is the pretreatment response variable we refer to the estimator as the generalized differences-of-differences estimator, since the population moment equation can be written as $\mathbb{E}[Y|X, T] = \alpha + T \Delta + X \beta$. The connection to the standard difference-of-differences estimator can be seen by forcing $\beta = 1$ in the setting where $X$ is the pretreatment value of $Y$. Accordingly, an alternate interpretation of the difference-of-differences estimator is that it can be implemented by first regressing $Y_i - X_i$ onto $(1, T_i)$, which is equivalent to constructing,

\[ \hat{\Delta}_{\text{dd}} = \left( \frac{1}{|T|} \sum_{i \in T} Y_i(1) - \frac{1}{|T|} \sum_{i \in T} X_i(1) \right) - \left( \frac{1}{|C|} \sum_{i \in C} Y_i(0) - \frac{1}{|C|} \sum_{i \in C} X_i(0) \right). \]

4.1.4 Weighted Generalized LR (and Generalized Difference-in-Differences) (gen_dd_w1)

Since all of the above estimators can be written as various forms of linear regression it is also possible to interpret them from the perspective of $M$-estimation as minimizing a sum of residuals defined as $e_i = Y_i - \alpha - \Delta T_i - X_i \beta$. That is, we can consider estimation objectives of the form:

\[ \min_{\alpha, \Delta, \beta} \sum_{i=1}^{n} \psi(e_i \cdot w_i), \]

for some sequence of weights $w_i$. The choice we explore is that of simple weighted least-squares. That is, we take $\psi$ to be the squared loss and define the weights as $w = (1 + D)^{-\gamma}$ (for $\gamma > 0$) for some nonnegative covariate $D$. In practice the covariate $D$ is taken as an auxiliary covariate, which serves as positive surrogate capturing the shape of the distribution of $Y$. In this case the weighting has the effect of downweighting large values of $Y$:

\[ \frac{1}{n} \sum_{i=1}^{n} \left( \frac{1}{1 + D_i)^{\gamma}} \right) (Y_i - \alpha - \Delta T_i - \beta_i X_i)^2. \]

(16)
4.2 Estimator Comparisons

In this section we present results obtained from a corpus of 709 RCTs performed at Amazon over several years as described in Section 1.3. We compare estimators by their out-of-sample MSE computed via the cross-validation procedure described in Section 3.

We begin by studying several of the normalized score histograms to facilitate the comparisons of our estimators. In judging two estimators $A, B$ via their score distribution $S(A, B)$, we note that a left-skewed score distribution indicates $B$ is a better estimator (in terms of its MSE) than $A$.

In Table 1, we use the $t$-test heuristic from Section 3.1 to summarize each score histogram. For the sake of brevity, we do not display all the methods tested in the table. We found that all the estimators weighted by different powers $(1, 2, 3)$ of the inverse $D$ distribution perform comparably. Overall, we see several phenomena that accord with our expectations. First, adjusting for the pretreatment covariate reduces variance (i.e., gen_dd is better then dm). Second, downweighting large values of $Y$ provides significant value: inverse weighting by $D$ and Winsorization performs generically the best under our metric (gen_dd_w1 and all Winsorized estimators perform well). We also see that the dm estimator is dominated by every other method in Table 1; such as the median of median-of-means estimator (mom1000), whose robustness underlies its improved performance. We can also check that the results from Table 1 are stable with respect to using different resampled replicates to compute the cross-validated errors which feed into the error vectors in $A/B$ as Tables 2 and 3 in Appendix A show.
We summarize this table by converting it into a table of pairwise comparisons of wins/losses/ties using a \( p \)-value to determine the significance of the win or loss. The question of extracting an ordered ranking from the table of wins/losses is a classic problem. The natural procedure of simply summing up the number of row-wise wins is commonly referred to as Copeland/Borda counting method (see [Saari and Merlin, 1996] and references within). It has recently shown that such a simple method is robust to the misspecification of the ranking model and optimal under minimal assumptions [Shah and Wainwright, 2018].

Applying such a method by inspection returns the following rankings:

\[
\text{gen\_dd\_w1\_wins.001} > \text{gen\_dd\_wins.001} > \text{dm\_wins.001} \approx \text{gen\_dd\_w1} > \text{gen\_dd} > \text{mom1000} > \text{dm}
\]

Overall, these results suggest that aggressively Winsorizing and/or downweighting heavy tails can profitably trade variance for some additional bias. We also stress that although our ranking procedure via \( t \)-statistics is transitive, the score and \( t \)-statistic values between \( A \) and \( B \) are computed via relative normalization between just these two estimator errors. Hence the actual values across several estimators are not always directly comparable due to the different normalizations used. Thus, we should always look at the performance of two estimators directly, take their score histogram into consideration, as well as exercise common-sense checks to draw further conclusions.

5 Conclusion

In this work, we develop a simple methodology for treatment effect model/estimator selection which pools the performance of estimators across RCTs. The methodology allows us to compare estimators on a held-out data fold in an unbiased way. The results align with a priori intuitions of estimator performance. Our primary insight is that we should be trading off variance for some additional bias. We also stress that although our ranking procedure via \( t \)-statistics is transitive, the score and \( t \)-statistic values between \( A \) and \( B \) are computed via relative normalization between just these two estimator errors. Hence the actual values across several estimators are not always directly comparable due to the different normalizations used. Thus, we should always look at the performance of two estimators directly, take their score histogram into consideration, as well as exercise common-sense checks to draw further conclusions.

6 Acknowledgements

The authors thank Robert Stine, Edo Airoldi, and Kenny Shirley for their valuable comments and feedback.
A Additional Results

In this section we present additional results from our aggregation methodology to explore their stability under using different bootstrapped train/test splits to compute the normalized score vectors $\hat{A}$ and $\hat{B}$. Tables 2 and 3 show consistent results.
Table 2: Comparison of Estimators via one-sample t-test applied to their normalized score vector. This table was computed using error vectors from only 50 resampled train/test splits to feed into A and B. Easiest to read row-wise. The index \((A, B)\) of the table computes the pair of the \((t\text{-statistic}, p\text{-value})\) associated with the score \(S(A, B)\). A large positive \(t\text{-statistic}\) at index \((A, B)\) indicates estimator A is better then estimator B and vice versa.

| Method | dim | mom1000 | gen_1d | gen_1d_w | gen_1d_w_zoom | dim_wins.001 | gen_1d_w_wins.001 | gen_1d_w_wins.001 |
|--------|-----|---------|--------|----------|---------------|---------------|-------------------|-------------------|
| dim    |     |         |        |          |               |               |                   |                   |
| mom1000|     | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) |
| gen_1d |     | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) |
| gen_1d_w |     | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) |
| gen_1d_w_zoom |     | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) |

Table 3: Comparison of Estimators via one-sample t-test applied to their normalized score vector. This table was computed using error vectors from only 50 resampled train/test splits to feed into A and B distinct from those in previous table. Easiest to read row-wise. The index \((A, B)\) of the table computes the pair of the \((t\text{-statistic}, p\text{-value})\) associated with the score \(S(A, B)\). A large positive \(t\text{-statistic}\) at index \((A, B)\) indicates estimator A is better then estimator B and vice versa.

| Method | dim | mom1000 | gen_1d | gen_1d_w | gen_1d_w_zoom | dim_wins.001 | gen_1d_w_wins.001 |
|--------|-----|---------|--------|----------|---------------|---------------|------------------|
| dim    |     |         |        |          |               |               |                  |
| mom1000|     | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) | (3.57, 0.000013) |
| gen_1d |     | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) | (24.22, 1.18e-31) |
| gen_1d_w |     | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) |
| gen_1d_w_zoom |     | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) | (22.64, 5.75e-31) |