SStatistical Election to Partition Sequentially (STEPS) and Its Application in Differentially Private Release and Analysis of Youth Voter Registration Data
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Abstract

Voter data is important in political science research and applications such as improving youth voter turnout. Privacy protection is imperative in voter data since it often contains sensitive individual information. Differential privacy (DP) formalizes privacy in probabilistic terms and provides a robust concept for privacy protection. Differentially Private Data Synthesis (DIPS) techniques produce synthetic data in the DP setting. However, statistical efficiency of the synthetic data via DIPS can be low due to the potentially large amount of noise injected to satisfy DP, especially in high-dimensional data. We propose a new DIPS approach Statistical Election to Partition Sequentially (STEPS) that sequentially partitions data by attributes per their differentiability of the data variability. Additionally, we propose a metric SPECKS that effectively assesses the similarity of synthetic data to the actual data. The application of the STEPS procedure on the 2000-2012 Current Population Survey youth voter data suggests STEPS is easy to implement and better preserves the original information than some DIPS approaches including the Laplace mechanism on the full cross-tabulation of the data and the hierarchical histograms generated via random partitioning.

keywords: privacy budget, Differentially Private Data Synthesis (DIPS), statistical disclosure limitation, propensity score, Kolmogorov-Smirnov statistic, Universal Histogram (UH)

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1 Introduction

1.1 Motivation

Prediction of election outcomes is a popular topic in political research and applications. Statisticians and political scientists continuously improve their poll-based forecast models or identify predictors and mechanisms for increasing or hindering voter turnout such as online registration tools (Bennion & Nickerson 2011), social pressure (DellaVigna et al. 2017, Gerber et al. 2008), voter identification laws (Hicks et al. 2015, Highton 2017), and world events like wars (Koch & Nicholson 2015). One voting group of particular interest is youth voters (18-24 years old), which has the lowest turnout out of any age group in the US. If more youth voted, election outcomes could drastically change. For instance, during the 2012 US Presidential Election, at least 80 of the electoral votes from major swing states like Ohio and Florida were decided by youth voters, securing the presidency for Obama (CIRCLE 2013).

Although voter data is essential for researchers and politicians to understand voter turnout, it also contains individual sensitive information like the voters’ family income (Barber & Imai 2014, Holbein & Hillygus 2016a, Imai & Khanna 2016). One way of mitigating the privacy concern is removing identifiers in the released data. However, a data intruder can still expose personal information of participants in the voter data by linking the data to other publicly accessible and anonymized data sets. For instance, in 1997, the Massachusetts Group Insurance Commission provided medical researchers access to the state of Massachusetts employee health records as an anonymized data set with personal identifiers like names and Social Security Numbers removed. The Massachusetts governor at the time assured that removing the identifiers would provide complete privacy protection. A few days later, Sweeney (1997) identified the governor by linking the voter data to the state healthcare data set and mailed his healthcare information to his office. More recently, Sweeney et al. (2013) used voter data and other public data sets to find individuals in the Personal Genome Project, a program that aims to sequence genetic information of 100,000 individuals for medical research such as improving personalized medicine.

1.2 Current work on data release with privacy protection

Data privacy protection techniques are often referred to as the statistical disclosure limitation (SDL) in the statistical community. Statisticians have developed various approaches to provide protection for sensitive information when releasing data to researchers or the public. Data synthesis (DS) is a popular SDL technique that provides synthetic individual-level data based on the values from the original data (Drechsler 2011, Little 1993, Little et al. 2004, Liu & Little 2003, Raghunathan et al. 2003, Reiter 2003, 2009, Rubin 1993). The evaluation of the disclosure risk of the release data by the DS and other SDL methods is often based on making strong assumptions on the data intruder’s background knowledge and behaviors (Hundepool et al. 2012, Reiter 2005).

One DS approach that allows researchers access to a data set with a preset level of privacy protection is Differentially Private data Synthesis (DIPS). DIPS combines DS with differential privacy (DP), a rigorous mathematical concept developed from computer sci-
ence that controls privacy risk with a prespecified privacy budget (Dwork et al. 2006). DIPS approaches can be roughly grouped into the non-parametric DIPS (NP-DIPS) and parametric DIPS (P-DIPS) approaches. Bowen & Liu (2016) compared multiple DIPS approaches at prespecified privacy budgets in the statistical utility of the perturbed data via the nonparametric DIPS such as the Laplace sanitizer (Dwork et al. 2006) and the smooth and perturbed histograms (Wasserman & Zhou 2010), the parametric-DIPS including the Multinomial-Dirichlet sanitizer (Machanavajjhala et al. 2008) and the MOdel-based DIPS (MODIPS) (Liu 2016b) in extensive simulation studies with various data types. Some DIPS methods can maintain some level of accuracy and efficiency of the statistical inferences in the DIPS synthetic data, but there is still a lot of room for improvement in enhancing the statistical utility of the synthetic data. For example, the Laplace sanitizer + Perturbed histogram approach is simple to implement without making assumptions about data, but it severely inflates the variances of continuous variables. The MODIPS is model-dependent, so selecting an appropriate model can be difficult in high-dimensional data.

There are efforts to improve the accuracy of perturbed statistics and data generated from a DP mechanism. Dwork et al. (2006), Machanavajjhala et al. (2008), and Dwork & Rothblum (2016) proposed conceptual relaxations of the pure DP (approximate DP, probabilistic DP, and concentrated DP, respectively) to lessen the amount of noise injected by DP methods, where some privacy is sacrificed for more utility. Nissim et al. (2007)’s Subsample-and-Aggregate method partitions the data randomly, calculates the statistics on each partition, and then aggregates the statistics with a DP mechanism. Smith (2011) analyzed the asymptotic properties of Subsample-and-Aggregate approach and showed that the framework produces DP random variables that converge in distribution to the original random variables; as good as nonprivate algorithms applied to data sets of equal size, assuming a sufficiently large sample. There is also work on a DP mechanism explicitly when drawing inferences on synthetic data via DIPS approaches. For example, Charest (2010) incorporated the DP mechanism in a Bayesian framework where the analysis of the perturbed binary data was through the Beta-Binomial DP mechanism (McClure & Reiter 2012) to reduce the inferential bias in the synthetic binary data. Karwa et al. (2017) proposed a local DP method (Duchi et al. 2013) synthesize the edges in social network data and designed a Markov Chain Monte Carlo method to incorporate the local DP mechanism explicitly to obtain posterior inferences.

There also exist partition-based DP methods. Xiao et al. (2010) created a DP method via a two-step wavelet-based multidimensional partitioning approach. Hay et al. (2010) developed a hierarchical partitioning approach called the universal histogram (UH) to enhance the accuracy of bin counts of low-dimensional histograms by exploring the inherent consistency constraints in the hierarchical histogram. Xiao et al. (2012) proposed a two-phase partitioning approach for multidimensional data cubes or histograms. Li et al. (2017) introduced two partitioning-based mechanisms – named the privacy-aware partitioning mechanism and the utility-based partitioning mechanism, respectively, that depend on a public but personalized privacy parameter. Qardaji et al. (2013b) and Hay et al. (2016) found that the UH performed the best out of the differentially private hierarchical histogram methods.
1.3 Goals and contributions

Though great efforts have been made in enhancing the statistical utility of the DIPS synthetic data, some of these approaches lack evidence for empirical feasibility and others are for specific data types or specific DP mechanisms. In the youth voter data we will examine in Section 3, there are 15 categorical attributes, the number of the categories per attribute ranging from 2 to 14. Directly applying a NP-DIPS to the full cross-tabulation of the 15 variables, though simple and straightforward, would lead to a lot of noise added to a high-dimensional sparse table; if a P-DIPS approach is employed, then some types of dimensionality reduction and model selection procedure will be needed, likely based on a set of assumptions. In this case, a DIPS method that is easy to apply to practice while preserving statistical utility will be desired. There are three main contributions of this paper: development of a new DIPS method STEPS, development of a new metric SPECKS for comparing the similarity between synthetic and original data, and application of STEPS and SPECKS in releasing a youth voter data set.

First, we propose a new DIPS approach – STatistical Election to Partition Sequentially (STEPS) to synthesize data in a differentially private manner. STEPS injects noises sequentially to the full histogram the order of which is guided by a statistical procedure. A p-dimensional full histogram is formed with all p attributes in a data set; when all attributes are categorical, it is equivalent to the p-way cross-tabulation. In statistical terms, adding noises to the full histogram simultaneously is equivalent to directly perturb the joint distribution of all the attributes $f(X_1, X_2, \ldots, X_p)$. STEPS utilizes the decomposition $f(X_1, X_2, \ldots, X_p) = f(X_1)f(X_2|X_1)\cdots f(X_p|X_1, \ldots, X_{p-1})$, and injects noises to $f(X_1)$, $f(X_2|X_1)$, $\ldots$, $f(X_p|X_1, \ldots, X_{p-1})$ sequentially, followed by a post-processing procedure similar to the UH approach to ensure the equality constraints in the hierarchical decomposition, with some necessary modifications. The order of the decomposition is determined by performing a statistical procedure to examine the statistical differentiability of each attribute in explaining the variability in the data. Compared to the partition based methods listed in Section 1.2, the STEPS leverages and utilizes the inherent statistical variability of the data when deciding the sequence of the partition, which is expected to improve the statistical utility of the released data compared to a random partitioning order.

Second, we develop a metric called Synthetic Data Generation, Propensity Score Matching, Empirical CDF, Comparison based on Kolmogorov-Smirnov (KS) (SPECKS), to assess the similarity between the synthetic data and actual data. The SPECKS metric is motivated by on a property score based method originally developed in the context of missing data analysis Sakshaug & Raghunathan (2010). SPECKS is a general method and provide an holistic measure for the similarity of two data sets of the same structure of any dimension. It can be easily computed and also has an intuitive interpretation. Although there are other methods to measure distances between distributions, they could be conceptually or computationally difficult to extend to multi-dimensional data cases, such as the raw KS statistic. The Kullback-Leibler (KL) divergence is another common measure for divergence of a distribution from a reference/theoretical distribution. Although it can accommodate various data types, the KL divergence can be sensitive to how the empirical distribution is constructed especially when there are continuous attributes and the sample size is small.
The proposed SPECKS metric circumvents the multidimensionality problem by computing a scalar prosperity scores given all the information in the multidimensional attributes, handles all types of attributes, and offers a convenience and holistic approach to measure the similarity between two data sets.

Third, we applied the STEPS procedure to the youth voter data subset of the 2000-2012 Current Population Survey (CPS) data obtained from the Harvard Dataverse (Holbein & Hillygus 2016b). This data set was analyzed by Holbein & Hillygus (2016a) to examine if states with preregistration laws increases youth voter turnout. As discussed earlier, voter data is critical for poll-based forecast modeling and other political science research, but is also prone for exposing personal information. The results from the real-life application suggest the STEPS procedure is promising in terms of its easy implementation and better preservation of the original information compared to a random partition in the UH framework and the Laplace sanitizer on the full histogram, at a prespecified privacy budget.

The remainder of the paper is organized as follows. Section 2 provides a brief overview on DP and introduces the STEPS procedure and the SPECKS metric. Section 3 applies the STEPS method to the CPS youth voter data and compares the statistical utility of the synthetic data generated by the STEPS procedure and the Laplace sanitizer on the full histogram and the random partitioning in the UH setting. In Section 4, we discuss the implications of our results and provide future research directions.

2 Statistical methodology

We denote the data for privacy protection by \( x = \{x_{ij}\} \) of dimension \( n \times p \) (\( i = 1, \ldots, n; j = 1, \ldots, p \)). Each row \( x_i \) represents an individual record with \( p \) variables/attributes. We assume the sample size \( n \) is public knowledge and carries no privacy information.

2.1 Differential privacy

Originally developed for query based methods, DP provides a mathematical and rigorous framework to develop approaches for protecting individuals in the a data set, regardless of the background knowledge or behaviors of data intruders (Dwork et al. 2006). Query results, in statistical terminology, are statistics; so we will use queries, query results, and statistics, interchangeably, which are denoted by \( s \).

Definition 1. Differential Privacy (Dwork et al. 2006): A sanitization algorithm \( \mathcal{R} \) gives \( \epsilon \)-DP if for all data sets \( (x, x') \) that is \( d(x, x') = 1 \), and all results \( Q \subseteq \mathcal{T} \)

\[
\left| \log \left( \frac{\Pr(\mathcal{R}(s(x)) \in Q)}{\Pr(\mathcal{R}(s(x')) \in Q)} \right) \right| \leq \epsilon,
\]

(1)

where \( \mathcal{T} \) denotes the output range of \( \mathcal{R} \), \( s \) denotes statistics, \( d(x, x') = 1 \) represents all possible ways that data \( x' \) differing from \( x \) by one individual, and \( \epsilon > 0 \) is the privacy “budget” parameter. When \( \epsilon \) is small, the chance of identifying an individual based on the sanitized statistics is low as with or without that individual has little impact on the value of the statistics after sanitization; when \( \epsilon \) is large, less noise is injected to \( s \) via the sanitized
algorithm $\mathcal{R}$, and the individuals in the data set are at a higher risk of having their sensitive information disclosed.

In regards to what value of $\epsilon$ is considered appropriate or acceptable for practical use, Dwork (2008) states the choice of $\epsilon$ is a social question. Abowd & Schmutte (2015) acknowledge this and suggest $\epsilon$ at $0.01 \sim \ln(3)$, or even up to 3 in releasing certain statistics in social and economic studies. Other $\epsilon$ values have been applied in the literature when DP is applied to cases studies. For example, Machanavajjhala et al. (2008) applied DP in the OnTheMap data (commuting patterns of the US population) and used $(\epsilon = 8.6, \delta = 10^{-5})$-probabilistic DP (a relaxation of the pure DP) to synthesize commuter data. Ding et al. (2011) and Li et al. (2014) used $\epsilon = 1$. These examples suggest there are many factors that affect the choice of $\epsilon$, including the type of information released to the public, social perception of privacy protection, statistical accuracy of the release data, among others. For a socially acceptable $\epsilon$ given a certain type of information, a differentially private mechanism should aim for maximizing the accuracy of the released information. In other words, choosing an “appropriate” $\epsilon$ is essentially a question of finding a good trade-off between privacy loss and released information accuracy.

An important property of DP is that the privacy cost increases for every new query being sent to the same data set, because more information is “leaked” with each additional query. Therefore, the data curator must track all statistics calculated on the data set to guarantee the privacy budget does not exceed the prespecified level. For example, if all $q$ queries are sent to data set $\mathbf{x}$, then $\epsilon/q$ can be allocated to each query to ensure the privacy budget is maintained at $\epsilon$ per the sequential composition principle by McSherry (2009). When no overlapping information is requested by different queries, such as when they are calculated from disjoint subsets of a data set, the privacy cost does not accumulate. In such a case, the parallel composition principle applies and the overall privacy cost is the maximum privacy budget spent across $q$ queries (McSherry 2009). For example, in the release of a histogram, where the counts in different bins of the histogram are based on disjoint subsets of data, each bin can be perturbed with the full privacy budget.

A common and easy way to implement DP is the Laplace mechanism. A key concept for the Laplace mechanism is calculating the $l_1$ global sensitivity (GS) of a query or statistic. Liu (2016a) extended the $l_1$ GS to $l_p$ GS for any $p > 1$.

**Definition 2.** $l_1$ Global Sensitivity (Dwork et al. 2006): The global sensitivity (GS) of $\mathbf{s}$ is $\Delta_1 = \max_{x,x'} d(x,x')=1 \|s(x) - s(x')\|_1$ for all $d(x,x') = 1$.

**Definition 3. Laplace Mechanism:** (Dwork et al. 2006): The Laplace sanitizer adds noise to $\mathbf{s} = (s_1, \ldots, s_K)$ via $s^*_k = n_k + e_k$, where $e_k \sim \text{Lap}(0, \Delta_1/\epsilon)$ and is independent for $k = 1, \ldots, K$ and $\Delta_1$ is the $l_1$ GS of $\mathbf{s}$.

When $\epsilon$ is small or $\Delta_1$ is large, more Laplace noise is added to $\mathbf{s}$. Other common DP mechanisms include the Exponential mechanism that applies to both numerical and non-numerical queries (McSherry & Talwar 2007), and the Gaussian mechanism that relies on the relaxed probabilistic DP (Dwork & Roth 2013, Liu 2016a), among others.
When releasing differentially private information, we could release query-based statistics or individual-level data. In the former case, satisfying the prespecified $\epsilon$ when releasing multiple queries while maintaining some level of data utility becomes an issue due the allocation of the overall privacy budget per the sequential composition (or, equivalently speaking, the increased GS with multiple queries). Once the privacy budget is exhausted from answering queries, the data curator must refuse to accept any more queries. Another issue with query-based data release is that the data user might not know all the statistics they would like to get from the data or might just prefer to conduct analysis on their own instead of relying on the data curator. DIPS methods resolve these challenges by producing differentially private individual-level synthetic data with a prespecified level of privacy.

2.2 STatistical Election to Partition Sequentially (STEPS)

STEPS synthesizes individual-level data by injecting noises to the full histogram of all the attributes in a data set sequentially, the order of which is guided by a statistical procedure, followed by a post-processing procedure similar to the UH approach. There are some new concepts in the context of STEPS, including 1) statistical differentiability metric (SDM) that quantifies the marginal contribution of an attribute in explaining the variability in a data set. Any routine metrics for comparing models or measuring goodness of fit of a model can be used, such as AIC or a deviance statistic; 2) the most statistically differentiable attribute (MoSDA) that explains the most variability in a data set marginally, such as the attribute with the largest decrease AIC if used as a predictor in the model compared to the intercept-only model. The opposite to MoSDA is the least statistically differentiable attribute (LeSDA) that explains the least variability marginally in a data set.

The original UH approach sanitizes count data. If a data set contains numerical variables, then they will first need to be binned to create histograms before applying the UH procedure. The full histogram (or cross-tabulation) of the attributes in a data set is constructed in a hierarchical manner by first forming low-dimensional histograms and then keeping partitioning adding more dimensions until it reaches the individual cells from the full histogram. Denote the hierarchical tree generated this way by $\mathcal{P}$. Let $v$ denote a node in $\mathcal{P}$ and $\text{succ}(v)$ be the set containing all $v$’s children. For example, a node could present the level “white” in attribute “race”, and its children, partitioned further by gender, could be “white female” and “white male”. There is a count associated with each node. The $l_1$ GS of releasing the tree $\mathcal{P}$ is the tree height, $L$, per the sequential and parallel composition theorems. Denote all the node counts in $\mathcal{P}$ by $\mathbf{n}$, then the sanitized counts are $\mathbf{n}^* = \mathbf{n} + \mathbf{e}$, where each entry in $\mathbf{e}$ is drawn from Lap($0, L\epsilon^{-1}$). The UH algorithm leverages the inherent consistency constraint in $\mathcal{P}$ (that is, the sum counts in $\text{succ}(v)$ is equal to the count of their parent node $v$). To correct the inconsistency caused by the sanitation, the UH procedure first calculates the inconsistent node counts $\mathbf{z}$ via Eqn (2) in a bottom-up manner,

$$z[v] = \begin{cases} n^*[v], & \text{if } v \text{ is a leaf node} \\ \frac{b^{L-1}}{b^{L-1}} n^*[v] + \frac{b^{L-1}}{b^{L-1}} \sum_{u \in \text{succ}(v)} z[u], & \text{otherwise} \end{cases}$$

where $b$ is the number of children per node, which is a constant in $\mathcal{P}$, and then applies the
top-down scan to compute the final released count $\bar{n}^*$ via Eqn (3), where $u$ is $v$’s parent.

$$\bar{n}^*[v] = \begin{cases} z[v], & \text{if } v \text{ is the root node} \\ z[v] + \frac{1}{b} (\bar{n}^*[u] - \sum_{w \in \text{succ}(u)} z[w]), & \text{otherwise} \end{cases}$$ (3)

The constant number of children per node $b$ can be set by the data user ($b \geq 2$). Qardaji et al. (2013b) examined how $b$ and the total number of cells $N$ in the full histogram/crosstabulation affect the MSE of queries based on $\bar{n}^*$ via the UH algorithm relative to the one-step Laplace sanitizer. The UH procedure is mostly studied in the context of a single attribute, where the high-level nodes will be some combinations of the categories/bins of the attribute and the leaf nodes in the lowest level are the finest categories/bins for the attribute. Though The UH procedure can be applied to multidimensional data, its benefit over the one-step Laplace sanitizer seems to diminish over increasing dimensionality (Qardaji et al. 2013a,b).

Compared to the regular UH algorithm, our proposed STEPS procedure leverages the inherent information in the data and uses a statistical criterion to decide the sequence for partitioning. In addition, STEPS deals with multidimensional data with $p$ attributes and partitions by attributes. Though in theory different levels of an attribute can span across more than one layers in the STEPS tree, this does not seem to be necessary given that all levels of the attribute are treated equally from a statistical perspective. In other words, once an attribute is used for splitting on a particular layer in a particular branch, the attribute is no longer available for future partition into lower-level layers in that branch. Given this feature of the STEPS procedure, the requirement of the UH algorithm that $b$ (which would become the number of bins/categories per attribute in STEPS) is a constant seems to be a stringent criterion to satisfy for many real-life data sets. To utilize the UH framework, we designed a workaround by creating *phantom* categories to make each attribute have the same number categories as the attribute with the most categories (corresponding to $b$ in the UH procedure). These phantom categories are only working categories with zero counts and created solely for the purposes of applying the UH procedure, and should be removed once the synthetic data are generated. The attributes selected for partitioning onto the next layer do not have to the same across the parents in the current layer.

The steps of the STEP procedure are given in Algorithm 1. The nodes in layer $l$ (for $l = 0, 1, \ldots, L$) are denoted by $v^{(l)}$. $v^{(0)}$ is the whole data. $K^{(l)}$ denotes the maximum number of nodes in layer $l$. Per the discussion above, once a node is used in partitioning data along a branch in $P$, it is no longer available. We denote the availability set for node $k \in v^{(l)}$ layer $l$ by $A^{(l)}_{v^{(l)}[k]}$. $A^{(0)}_{v^{(0)}[1]}$ contains all $p$ attributes in the data.

**Remark 1.** In the regular UH framework, $L$ is computed as $\log_b N$, where $N$ is total number cells in the cross-tabulation. In the STEPS algorithm, if the tree splits by all $p$ attributes, then $L = p$; but it does not have to be and can be set at a value $< p$, unless we allow different levels of an attribute to span across multiple level (there does not seem to exist such a need from a statistical perspective as mentioned above). The regular UH approach has an exponential time complexity $O(b^L)$ in $L$ for a given $b$, implying a large $L$ would dramatically increase the computational time (Qardaji et al. 2013b). Lastly, the larger $L$ is, the less privacy budget each layer will receive for sanitization, implying more noises are injected into the individual nodes in each layer. However, since the counts in
Algorithm 1: STatistical Election to Partition Sequentially with \( L \) layers (STEPS-L)

**Input:** number of partition layers \( L(\leq p) \); overall privacy budget \( \epsilon \); allocation scheme \( C \); number of synthetic sets \( m \); original data \( D \) (see **Remark 1**).

Set \( l = 0 \)

1. **while** \( l < L \) **do**
   - for \( k = 1 \) to \( K^{(l)} \)
     - Apply a loglinear model separately to the one-way table formed by each attribute in \( A^{(l)}_{v^{(l)}[k]} \) and calculate the SDM associated with each of the attributes in \( A^{(l)}_{v^{(l)}[k]} \) and identify the MoSDA \( X_j \).
     - Partition the data by the MoSDA \( X_j \) (see **Remark 2**).
     - Let \( A^{(l)}_{v^{(l)}[k]} \leftarrow A^{(l)}_{v^{(l)}[k]} \setminus X_j \) and \( v^{(l)} \leftarrow v^{(l)} \setminus v^{(l)}_j \), where \( v^{(l)}_j \) denotes all the levels of \( X_j \).
     - \( l \leftarrow l + 1 \)
   **end do**

2. **If** \( A_{v^{(L)}} = \emptyset \), **go to Step 3 directly**; **otherwise** \( (A_{v^{(L)}} \) is not an empty set), apply the full cross-tabulation over all the attributes in \( A_{v^{(L)}} \) for each node in layer \( L \) \( v^{(L)}[1], \ldots, v^{(L)}[K^{(L)}] \) (see **Remark 3**).

3. Sanitize all nodes in the generated tree \( P \) via the Laplace mechanism with the allocation scheme \( C \) in the sanitization of the layers in \( P \). Suppose layer \( l \) receives a fraction of \( c_l \) of the privacy budget \( \epsilon/m \), then the nodes in layer \( l \) are sanitized by the Laplace mechanism with scale parameter \( (c_l\epsilon/m)^{-1} \) (see **Remark 4**).

4. Apply the UH procedure in Eqns (2) and (3) to obtain the sanitized counts \( \bar{n}^* \). If all attributes are categorical, \( \bar{n}^* \) can be released directly; otherwise, an extra step of uniform sampling is applied draw numerical attributes from the histogram bins.

**Output:** \( m \) synthetic sets \( \bar{D}^{(1)}, \ldots, \bar{D}^{(m)} \)

earlier layers are weighted averages of multiple nodes per Eqn (3), the loss in privacy budget in per layer could be offset by the information aggregation over multiple nodes. Therefore, in theory, there exists an optimal \( L \) by a certain data utility criterion (such as \( l_1 \) error, mean squared error of certain queries). We would suggest users try different values of \( L \) and pick the optimal one for satisfying a certain data utility criterion (e.g., the SPECK metric), within computational limit. For future work, we will also look into devising a stopping rule to choose \( L \) adaptively, such as by defining a threshold on SDM. If the SDM associated with the MoSDA at layer \( l \) is smaller than the threshold, then the partitioning stops. More discussion on this are provided in Section 4.

**Remark 2.** The rationale for choosing the MoSDA for partition in STEPS is that it is the most important attribute for understanding the variability in counts in a particular subset (partition) of the original data and thus “deserves” more privacy budget so that less noise will be injected and more original information on that variable can be preserved. This also relates to how \( \epsilon/m \) is allocated across the layers. Users can choose to divide by the LeSDA, and allocate smaller fractions of the privacy budget to the layers split by LeSDA.
Remark 3. When $L < p - 1$, there will more than one attributes left in $\mathcal{A}^{(L)}_{v(L)}$ after Layer $L$. Per the STEPS procedure in Algorithm 1, no more partitioning will be applied to $\mathcal{A}^{(L)}_{v(L)}$ and the leaf nodes will be made of the cells from the full cross-tabulation over all the remaining attributes in $\mathcal{A}^{(L)}_{v(L)}$ under each parent in layer $L$.

Remark 4. Different allocation scheme $C$ can be specified by users. For an equal allocation scheme, $C = (1/L, \ldots, 1/L)$ if Step 2 is skipped, and $C = (1/(L+1), \ldots, 1/(L+1))$ otherwise. An unequal allocation scheme can also be used, such as $1/2$ to layer $(L + 1)$ that contains the full cross-tabulation over remaining attributes; and $1/2$ to layers 1 to $L$ that is further split among the $L$ layers, results in the following allocation scheme in sanitizing the layers $C = (\epsilon/(2mL), \ldots, \epsilon/(2mL), \epsilon/(2m))$.

2.3 Evaluating DIPS with SPECKS

Sakshaug & Raghunathan (2010) proposed an approach to assess the covariate balance between the synthetic and actual observed data. Specifically, the actual and synthetic data are combined with an indicator variable created to indicate which group (synthetic vs actual) each record belongs to. A logistic regression model is then fitted to the combined data and an estimate of the propensity score (PS) of a record belonging to the actual data as opposed to the synthetic data is obtained. The PSs are then sorted and classified into deciles and the proportions of synthetic and actual records within each deciles are compared using a chi-squared test with 9 degrees of freedom (if deciles are used). If the synthetic and actual covariates are fully balanced, then the proportion of synthetic versus actual data should be similar in each decile group.

We extended the above approach to compare the similarity between the differentially private synthetic and actual data by constructing the empirical CDFs of the PSs in the synthetic and actual group respectively, and then measuring the distance of the two CDFs using the Kolmogorov-Smirnov (KS) distance. We call our diagnostic approach SPECKS based on the steps of Synthetic Data Generation; Propensity Score Matching; Empirical CDF Comparison via the Kolmogorov-Smirnov (KS) distance. The specific procedures executed in each step of SPECKS are given below.

1. Combine the original or synthetic data, each of size $n$. Create a indicator variable $T$ where $T_i = 1$ if record $i$ is from the actual data and $T_i = 0$ otherwise for $i = 1, \ldots, 2n$.
2. Calculate the PS for each record $i$, $e_i = Pr(T_i = 1 | x_i)$, through a logistic regression model, where the predictors are the variables of $x$.
3. Calculate the empirical CDFs of the PS, $\hat{F}(e)$ and $\tilde{F}(e)$, for the actual and the synthetic groups, separately.
4. Compute the KS distance $d = \sup_{e} |\hat{F}(e) - \tilde{F}(e)|$ between the two empirical CDFs (If multiple synthetic data are generated, the average KS distance over the multiple sets will be calculated).

If the synthetic data preserves the original information well, then the observations from the two groups are indistinguishable and a small KS distance between the original and synthetic empirical CDFs is expected. SPECKS is a general method and can be used to compare
the similarity of two data sets of the same structure of any dimension, without making assumptions on the distributions of the attributes. The procedure used in each step is standard statistical procedure and can be implemented using any standard software. Compared to the original approach in Sakshaug & Raghunathan (2010), SPECKS is different in two aspects. First, there is no need to discretize the continuous PS. Discretization introduces arbitrariness into the process and could have an impact on the subsequent chi-square test depending how to bin the cases. Second, SPECKS does not rely on a statistical test to make a binary decision on the similarity between two data sets, and is more suitable for comparing DIPS methods in original information preservation. Since some deviation in the synthetic data from the original data will always be expected for a DIPS method due to the injected noise, a relative measure such as SPECKS might makes more sense in the DP setting.

3 Application of STEPS in 2002-2012 CPS youth voter data

We apply the STEPS procedure to generate the differentially private synthetic CPS youth voter data, benchmarked against the one-step Laplace sanitizer of the full histogram and the UH procedure with a random partition. The data set contains 15 variables and 44,821 observations (Table 1). In this applications, all attributes are treated as categorical. Table 2 lists the the cell sizes and frequencies from the 15-way cross-tabulation.

| Variable                        | Values            |
|--------------------------------|-------------------|
| Voted                          | 0, 1 (no, yes)    |
| Preregistration State          | 0, 1 (no, yes)    |
| Age                            | 18, 19, 20, 21, 22|
| Married                        | 0, 1 (no, yes)    |
| Female                         | 0, 1 (no, yes)    |
| Family Income                  | 14 levels         |
| College Degree                 | 0, 1 (no, yes)    |
| White                          | 0, 1 (no, yes)    |
| Hispanic                       | 0, 1 (no, yes)    |
| Registration Status            | 0, 1 (no, yes)    |
| Metropolitan Area              | 0, 1 (no, yes)    |
| Length of Residence            | 6 levels          |
| Business / Farm Employment      | 0, 1 (no, yes)    |
| In-Person Interview            | 0, 1 (no, yes)    |
| DMV Registration               | 0, 1 (no, yes)    |

Table 1: List of variables and their values from youth voter subset in the 2000-2012 CPS data.

| Cell size | 0  | 1  | 2  | 3  | 4  | 5  | >5 |
|-----------|----|----|----|----|----|----|----|
| Number of Cells | 1,268,911 | 14,061 | 3,545 | 1,508 | 740 | 425 | 1,050 |
| Proportion | 98.35% | 1.09% | 0.27% | 0.12% | 0.06% | 0.03% | 0.08% |

Table 2: Summary of cell sizes and frequencies in the full cross tabulation of the youth voter data.

Section 3.1 demonstrates the step-by-step implementation of the STEPS procedure in
the voter data. Section 3.2 shows how STEPS performs against the one-step Laplace sanitizer and the UH procedure with a random partition by the SPECKS metric, which also validates SPECKS as a tool/metric for assessing the quality of synthetic data against the original. Sections 3.3 assesses the practical utility of the STEPS synthetic data by applying three types of statistical analyses to the voter data.

3.1 STEPS

We applied Algorithm 1 and used the AIC from the loglinear model as the SDM. To demonstrate the advantage of the STEPS procedure of using the MoSDA to split when constructing the tree, we had STEPS using the LeSDA to split and splitting by a random set of attributes. In determining the tree length $L$, we tried both $L = 2$ and $3$. We started to experience computational limitations when $L \geq 4$. In addition, the results at $L = 3$ were similar to $L = 2$ in preserving original information, but was computationally more expensive. We also examined a couple of the privacy budget allocation schedules as described in Remark 4 for STEPS-2-MoSDA and STEPS-3-MoSDA: 1) equal allocation of $\epsilon$ among the $L + 1$ layers of the tree; and 2) $(1/2 + 1/L)$ split: half of $\epsilon$ to layer $L + 1$ that contains the full cross-tabulation of the remaining attributes; and the other half to layers $1 \sim L$, which is further split equally among the $L$ layers. Overall, we ran STEPS-2-MoSDA, STEPS-2-LeSDA, Random Partition-2, and STEPS-3-MoSDA, benchmarked against the one-step Laplace sanitizer applied to the full cross-tabulation.

Tables 3 show the partitioning in STEP-2-MoSDA and STEPS-2-LeSDA, respectively. STEPS-3-MoSDA further split the nodes in Layer 2 listed for STEPS-2-MoSDA in Tables 3 (not presented due to the large size of the table). In STEP-2-MoSDA, the first-layer variable “family income” was the one with the smallest AIC among the 15 univariate log-linear models. Within the subset of observations whose “family income = 1”, “length of residence” was associated within the smallest AIC among the 14 univariate log-linear models; similarly for other levels of “family income”. On the contrary, in STEP-2-LeSDA, the first-layer variable “Voted” was associated within the largest AIC among the 14 univariate log-linear models, and so on. Figure 1 presents a sketch on the tree built in STEP-2-MoSDA. The root node (layer 0) was the overall sample, which was not sanitized since we assumed the sample size is public knowledge. The next layer (layer 1) contained the 14 nodes, one per level of “family income”. In the node containing all samples with “family income = 1”, the MoSDA was “Length of Residence”, meaning the children of “family income = 1” would be split by “Length of Residence”; similarly, in the node containing all samples with “family income = 4”, the next layer MoSDA was “Married”. In layer 3, there was no more partitioning, the leaf nodes would be the cells from the full cross-tabulation of the remaining attributes not used in layers 1 and 2 in each branch of the tree. Figure presents a sketch for the constructed tree in STEP-2-MoSDA. After the tree was generated, the next step was to apply the UH procedure to the tree. The UH procedure as mentioned in Section 2 requires the number of children per parent node to be constant while the attributes in the voter data, as observed from Table 1, have different levels with “family income” having the most categories (14). To accommodate the requirement of the UH algorithm, we created phantom categories to make each attribute having 14 categories as “family income”. These phantom categories were only
working categories that always had zero counts and were created solely for the purposes of applying the UH procedure. The phantom categories should be removed once the synthetic data were generated. The GS for layer 1 and 2 was $1/L$ per the UH algorithm. For layer 3, the GS was 1 since we sanitized the full cross-tabulation counts of the remaining attributes.

| STEPS-2-MoSDA | layer | 1                      | 2                      |
|---------------|-------|------------------------|------------------------|
|               | Family Income (1) | Length of Residence    |
|               | Family Income (2) | Length of Residence    |
|               | Family Income (3) | Length of Residence    |
|               | Family Income (4) | Married                |
|               | Family Income (5) | Length of Residence    |
|               | Family Income (6) | Registration Status    |
|               | Family Income (7) | Registration Status    |
|               | Family Income (8) | Registration Status    |
|               | Family Income (9) | Registration Status    |
|               | Family Income (10)| Length of Residence    |
|               | Family Income (11)| Length of Residence    |
|               | Family Income (12)| Length of Residence    |
|               | Family Income (13)| Length of Residence    |
|               | Family Income (14)| Length of Residence    |

| variable (level) | STEP2-2-LeSDA | layer | 1                      | 2                      |
|------------------|---------------|-------|------------------------|------------------------|
| Voted (1)        | Female        |       |                        |                        |
| Voted (2)        | Business / Farm Employment |       |                        |                        |

*Table 3: Sequential partitions in STEPS-2-MoSDA and STEPS-2-LeSDA.*

We generated 5 synthetic data sets to account for the synthesis variability and ran 24 repetitions. We examined privacy budget $\epsilon \in \exp\{-2,-1,0,1,2\}$ to see how the $\epsilon$ affects the quality of the synthetic data. Since we generated 5 synthetic data sets, $\epsilon/5$ was allocated to each data set per the sequential composition to ensure an overall privacy budget of $\epsilon$.

### 3.2 SPECKS

We used R package MatchIT for the PS analysis with options *method = optimal* and *distance = logit* (Ho 2011), and then applied R command `ks.test` to calculate the KS statistic between the empirical CDFs of the PS in the actual and synthetic groups, respectively. We used method *optimal* instead of the default nearest neighbor matching method because optimal matching minimizes the distance between matched pairs more than the nearest neighbor algorithm (Gu & Rosenbaum 1993).

Figure 2 depicts the results on the SPECKS analysis (the results from the equal allocation of $\epsilon$ in STEPS-2-MoSDA and STEPS-3-MoSDA were worse than $1/2 + 1/L$ allocation and are not presented). For all methods, the KS distance decreased as $\epsilon$ increased, which is expected as synthetic data is supposed to gets closer to the actual data with more privacy.
budget (less noise injected and synthetic data); this also validates the SPECKS as a reasonable metric to measure the similarity between synthetic data and original data. Overall, STEPS-2-MoSDA and STEPS-3-MoSDA performed the best (KS distance were very similar at all values of $\epsilon$) and STEPS-2-LeSDA performed the worst out of all the methods, demonstrating the importance of selecting the most statistically differentiable attributes to partition in STEPS. When $\epsilon < 1$, Random Partition-2 had a smaller KS distance all the other methods. The one-step Laplace sanitizer had similar KS distance as STEPS-2-LeSDA initially, but, the KS distance decreased quickly as $\epsilon$ increased and eventually had the same smallest value as STEPS-2-MoSDA and STEPS-3-MoSDA at $\epsilon = e^2$. Based on the results, we chose to further explore STEPS-2-MoSDA (STEPS-2-MoSDA took less computational time than STEPS-3-MoSDA) in the statistical feasibility analyses in Section 3.3, benchmarked against the one-step Laplace sanitizer.

3.3 Statistical analysis for practical feasibility

We assessed the practical feasibility of the synthetic data generated from the one-step Laplace sanitizer and STEPS-2-MoSDA (which we will refer to as STEPS-2 for now on) using three types of statistical analyses at $\epsilon = e \approx 2.72$ and $\epsilon = e^{-1} \approx 0.368$, respectively. We chose these two $\epsilon$ values since both are fairly small, implying a high level of privacy protection. In addition, the SPECKS analysis shows at $\epsilon = e^{-1}$ and $e$ yielded larger KS differences between STEPS-2-MoSDA and the other DIPS methods. From $\epsilon = e^{-1}$ to $e^1$, we expect to see an improvement in the results for both the one-step Laplace sanitizer and the STEPS-2 procedure. We released 5 synthetic data sets and appropriately combined the statistical inferences with the multiple synthesis combination rule (Liu 2016b).

For the first practical feasibility assessment, we calculated the $l_1$ distance between the
Figure 2: SPECKS analysis of the synthetic data generated from one-step Laplace sanitizer, STEPS, and UH with random partition.

The synthetic and the original cell counts in the full cross-tabulation of the 15 attributes. A smaller $l_1$ distance indicates the sanitized cell counts are closer to the original counts overall. When $\epsilon = e^{-1}$, the one-step Laplace sanitizer had a $l_1$ distance of 43,908.4 whereas STEPS-2 had a smaller $l_1$ distance of 43,065.6, averaged over the 5 synthetic sets. When $\epsilon = e$, the two methods performed similarly, where the one-step Laplace sanitizer had a $l_1$ distance of 42,068.2 and STEPS-2 had a $l_1$ distance of 42,072.7.

For the second analysis, we conducted the chi-squared tests of association in all possible 2-way tables (105 in total) across the 15 attributes to see how well the DIPS approaches preserved statistically significant 2-way associations. Note the goal is not to report which associations are statistically significance across all 105 tables, so there is no need for multiplicity adjustment. We combined the p-values across the 5 surrogate data sets via the combination rules from Li et al. (1991). Table 4 presents the confusion matrices at the significance levels $\alpha = \{0.01, 0.05, 0.10\}$ and the test consistency rate (percentage that the test conclusions were consistent between the original and synthetic data out of 105 tests). When $\epsilon = e^{-1}$, STEPS-2 outperformed the one-step Laplace sanitizer at all 3 $\alpha$ levels. When $\epsilon$ increased from $e^{-1}$ to $e$, there was a significant improvement for the one-step Laplace sanitizer; STEPS procedure also improved, but its advantages over the one-step Laplace sanitizer was less obvious.

For the third feasibility analysis, we adopted the difference-in-differences (DID) model to examine the effects of “Preregistration State” on “Voted” controlling for “Registration Status” as conducted by Holbein & Hillygus (2016a). In the DID logistic regression model, the outcome was “Vote” with all the other 14 attributes as predictors plus an interaction term between “Preregistration State” and “Registration Status”. “Age” was entered as a
$$\epsilon = e^{-1}$$

|               | \(\alpha = 0.01\) | \(\alpha = 0.05\) | \(\alpha = 0.10\) |
|---------------|---------------------|---------------------|---------------------|
| **STEPS-2**   |                     |                     |                     |
| synthetic +   | 53                  | 55                  | 60                  |
| synthetic -   | 36                  | 25                  | 34                  |
| **STEPS-2 CR**| 62/105 = 59.0%      | 64/105 = 61.0%      | 68/105 = 64.8%      |
| **Laplace**   |                     |                     |                     |
| synthetic +   | 44                  | 50                  | 59                  |
| synthetic -   | 45                  | 30                  | 35                  |
| **Laplace CR**| 53/105 = 50.5%      | 59/105 = 56.2%      | 66/105 = 62.9%      |

|               | \(\alpha = 0.01\) | \(\alpha = 0.05\) | \(\alpha = 0.10\) |
|---------------|---------------------|---------------------|---------------------|
| **STEPS-2**   |                     |                     |                     |
| synthetic +   | 77                  | 81                  | 86                  |
| synthetic -   | 12                  | 8                   | 8                   |
| **STEPS-2 CR**| 89/105 = 84.8%      | 92/105 = 87.6%      | 97/105 = 92.4%      |
| **Laplace**   |                     |                     |                     |
| synthetic +   | 78                  | 81                  | 85                  |
| synthetic -   | 11                  | 9                   | 9                   |
| **Laplace CR**| 90/105 = 85.7%      | 93/105 = 88.6%      | 94/105 = 89.5%      |

\(^\dagger\)CR: consistency rate

| Synthetic + (-): p-value from a chi-squared test based on the synthetic data < (>) \(\alpha\) |
|---------------------------------------------|
| Original + (-): p-value from a chi-squared test based on the original data < (>) \(\alpha\) |

Table 4: Confusion matrices of the Chi-Square Tests for Independence.

We averaged the coefficient estimates over 5 synthetic sets and calculated their differences from the original coefficient estimates, Table 5 lists which coefficient estimates out of 32 in the one-step Laplace sanitizer and STEPS-2 had the same sign as in the original analysis. When \(\epsilon = e^{-1}\), STEPS-2 had 17 coefficients with the same sign as the original whereas the one-step Laplace sanitizer only had 7. when \(\epsilon = e\), the number of coefficients with the same sign as the original increased to 23 for STEPS-2, and to 15 for the one-step Laplace sanitize.

Table 6 shows the 95% confidence interval (CI) of the DID coefficients from the one-step Laplace sanitizer and the STEPS-2 method. When \(\epsilon = e^{-1}\), the CI’s for the one-step Laplace sanitizer approach covered slightly fewer of the original coefficients than STEPS-2 (21 and 24, respectively). As \(\epsilon\) increased from \(e^{-1}\) to \(e\), the CI’s for the one-step Laplace sanitizer covered more coefficients (from 21 to 25 coefficients, respectively). However, when \(\epsilon\) increased from \(e^{-1}\) to \(e\), the CI’s for the the STEPS-2 approach covered less coefficients (from 24 to 21 coefficients, respectively). Overall, the one-step Laplace sanitizer and the
\[
\epsilon = e^{-1}
\]

| Variable                  | Laplace sanitizer | STEPS-2 | Laplace sanitizer | STEPS-2 |
|--------------------------|-------------------|---------|-------------------|---------|
| Intercept                | Y                 | Y       | Y                 | Y       |
| Age                      | N                 | Y       | N                 | Y       |
| Married                  | N                 | Y       | Y                 | Y       |
| Female                   | N                 | N       | Y                 | Y       |
| Family Income\(^\dagger\) | 1Y/13             | 9Y/13   | 3Y/13             | 10Y/13  |
| College Degree           | Y                 | N       | N                 | N       |
| White                    | N                 | N       | N                 | N       |
| Hispanic                 | N                 | Y       | Y                 | Y       |
| Metropolitan Area        | N                 | N       | Y                 | Y       |
| Length of Residence\(^\dagger\) | 2Y/5             | 0Y/5   | 4Y/5             | 4Y/5   |
| Business/Farm Employment | Y                 | N       | N                 | N       |
| In-Person Interview      | N                 | Y       | Y                 | Y       |
| DMV Registration         | N                 | Y       | Y                 | Y       |
| Preregistration State    | Y                 | N       | N                 | N       |
| Registration Status      | Y                 | Y       | Y                 | Y       |
| Interaction of Registration \(	imes\) Preregistration State | N | N | N | N |

Y and N represent the same and difference sign from the original analysis.

\(^\dagger\) “Family Income” has 14 levels, and thus 13 coefficients associated with 13 dummy variables; “Length of Residence” has 6 levels, and thus 5 coefficients

Table 5: Sign consistency on the DID regression coefficients with the original on DID coefficient estimate for the Laplace sanitizer and STEPS-2 methods.

The STEPS method did not show significant differences in this analysis and the increase in \(\epsilon\) did not seem to affect the results much either.

4 Concluding Remarks

We developed a new DIPS method STEPS to synthesize differentially private individual-level data with the goal to improve the statistical utility of the synthesized data. The STEPS approach can be used to generate differentially private synthetic data regardless of the attribute types. With numerical attributes, the STEPS will first discretize the attributes into bins before sanitization. The STEPS procedure outperformed the one-step Laplace sanitizer in the application of the youth voter data, with a smaller SPECK value across the examined range \(\epsilon\) values, as well as in some of the feasibility analyses at two practically reasonable small \(\epsilon\) values. Additionally, we devised a new diagnostic tool, SPECKS, for comparing DIPS data to the original data in general. Its application in the vote data demonstrates its straightforward implementation and effectiveness as a metric to measure similarity between data sets.

The STEPS method is based in the general framework of the UH approach, but improves it by leveraging the inherent information in the data to determine the partitioning order. It also differs from the regular UH approach in that it partitions by attribute and will stop the
| Predictor              | Original | $\epsilon = \epsilon^{-1}$ | Laplace sanitizer | STEPS-2 | Laplace sanitizer | STEPS-2 |
|------------------------|----------|-----------------------------|------------------|---------|------------------|---------|
| Intercept              | 1.149    | (0.238, 1.080) (0.751, 1.851) | (0.354, 1.675)   | (0.710, 1.459) |
| Age                    | -0.025   | (-0.037, 0.037) (-0.029, 0.007) | (-0.031, 0.032) | (-0.019, 0.012) |
| Married                | -0.022   | (-0.047, 0.068) (-0.092, 0.008) | (-0.085, 0.027) | (-0.100, -0.004) |
| Female                 | 0.044    | (-0.047, 0.047) (-0.085, 0.082) | (-0.038, 0.048) | (-0.048, 0.058) |
| Family Income 1†       | 0.063    | (-0.332, 0.258) (-0.243, 0.056) | (-0.326, 0.264) | (-0.322, 0.237) |
| Family Income 2†       | 0.017    | (-0.357, 0.207) (-0.345, 0.537) | (-0.347, 0.207) | (-0.459, 0.442) |
| Family Income 3†       | 0.048    | (-0.254, 0.140) (-0.315, 0.244) | (-0.260, 0.148) | (-0.370, 0.360) |
| Family Income 4†       | 0.064    | (-0.209, 0.169) (-0.431, 0.518) | (-0.226, 0.200) | (-0.375, 0.417) |
| Family Income 5†       | 0.036    | (-0.233, 0.172) (-0.374, 0.415) | (-0.248, 0.201) | (-0.175, 0.227) |
| Family Income 6†       | 0.053    | (-0.369, 0.347) (-0.240, 0.151) | (-0.365, 0.368) | (-0.145, 0.259) |
| Family Income 7†       | 0.086    | (-0.240, 0.195) (-0.219, 0.296) | (-0.202, 0.188) | (-0.167, 0.262) |
| Family Income 8†       | 0.119    | (-0.406, 0.324) (-0.309, 0.341) | (-0.375, 0.330) | (-0.106, 0.183) |
| Family Income 9†       | 0.059    | (-0.240, 0.201) (-0.284, 0.270) | (-0.223, 0.212) | (-0.180, 0.232) |
| Family Income 10†      | 0.098    | (-0.163, 0.101) (-0.150, 0.189) | (-0.148, 0.128) | (-0.149, 0.174) |
| Family Income 11†      | 0.091    | (-0.235, 0.229) (-0.130, 0.217) | (-0.258, 0.283) | (-0.201, 0.213) |
| Family Income 12†      | 0.169    | (-0.240, 0.211) (-0.163, 0.242) | (-0.206, 0.246) | (-0.154, 0.155) |
| Family Income 13†      | 0.205    | (-0.212, 0.303) (-0.211, 0.241) | (-0.109, 0.384) | (-0.041, 0.205) |
| College Degree         | 0.401    | (-0.101, 0.149) (-0.039, 0.044) | (-0.139, 0.120) | (-0.144, 0.032) |
| White                  | -0.067   | (-0.066, 0.095) (-0.000, 0.039) | (-0.059, 0.122) | (-0.002, 0.078) |
| Hispanic               | -0.046   | (-0.123, 0.136) (-0.057, 0.026) | (-0.147, 0.085) | (-0.113, -0.053) |
| Metropolitan Area      | 0.038    | (-0.073, 0.035) (-0.085, 0.07) | (-0.048, 0.053) | (-0.019, 0.138) |
| Length of Residence 1† | 0.035    | (-0.152, 0.160) (-0.205, 0.141) | (-0.150, 0.194) | (-0.110, 0.204) |
| Length of Residence 2† | 0.048    | (-0.125, 0.097) (-0.158, 0.122) | (-0.124, 0.105) | (-0.200, 0.270) |
| Length of Residence 3† | 0.103    | (-0.099, 0.123) (-0.190, 0.118) | (-0.099, 0.157) | (-0.145, 0.162) |
| Length of Residence 4† | 0.137    | (-0.138, 0.132) (-0.126, 0.104) | (-0.136, 0.164) | (-0.270, 0.231) |
| Length of Residence 5† | 0.147    | (-0.121, 0.107) (-0.186, 0.128) | (-0.043, 0.175) | (-0.063, 0.199) |
| Business/Farm Employment| 0.076    | (-0.033, 0.059) (-0.069, 0.064) | (-0.060, 0.038) | (-0.072, 0.027) |
| In-Person Interview    | -0.070   | (-0.043, 0.071) (-0.076, 0.048) | (-0.064, 0.060) | (-0.100, -0.007) |
| DMV Registration       | -1.501   | (-0.112, 0.116) (-0.116, 0.085) | (-0.139, 0.091) | (-0.114, 0.016) |
| Preregistration State  | -0.025   | (-0.003, 0.002) (-0.001, 0.003) | (0.004, 0.016)  | (0.013, 0.026)  |
| Registration Status    | 3.306    | (3.238, 3.278) (2.526, 4.249) | (3.284, 3.322)  | (3.315, 3.364)  |
| Interaction of Registration | 3.306    | (3.238, 3.278) (2.526, 4.249) | (3.284, 3.322)  | (3.315, 3.364)  |
| × Preregistration State| 0.516    | (-0.663, 0.352) (-1.112, 0.700) | (-0.876, -0.946) | (-0.841, -0.549) |

† Family Income has 14 levels and thus 13 coefficients for 13 dummy variables; Length of Residence has 6 levels and thus 5 coefficients associated with 5 dummy variables.

Table 6: The 95% confidence intervals (CI) of the DID coefficients from the one-step Laplace sanitizer and STEPS-2 method.

tree building once the hierarchical histogram reaches the prespecified height or according to a stopping rule. If there are remaining attributes, then the STEPS applies a full cross-tabulation over those attributes and uses it as the lowest level of the tree. On the other hand, since the STEPS utilizes the general UH idea, such as that the released counts are weighted averages of multiple nodes in the tree given the inherent consistency constraint, we expect that the STEPS procedure shares some of the general properties of the UH procedure. For example, the UH procedure optimizes the accuracy of the sanitized nodes closer to the root (low-order marginals) with the smallest MSE (relative to the original results) among the approaches that yield unbiased sanitized estimators for the original results while satisfying
the consistency constraint, at the sacrifice of a loss of accuracy in the sanitized high-order nodes and the leaf nodes.

For future work, we will investigate the theoretical properties of the STEPS procedure by examining the mean squared error of linear queries based on the sanitized counts from the STEP procedure, in a similar manner as in Hay et al. (2010) and Qardaji et al. (2013b). We expect the theoretical investigation will shed light on and help to choose an allocation schedule for the overall privacy budget and a tree height. In addition, we will look into devising a stopping rule to choose the tree height adaptively instead of setting it a priori, such as by defining a threshold on SDM. If the SDM associated with the MoSDA at layer \( l \) is smaller than the threshold, then the partitioning stops. Since the tree generated this way might have branches of different length, Eqns (2) and (3) might no longer apply. We plan to perform theoretical and empirical researches along these lines and examine whether STEPS can be further improved with the stopping rule incorporated into its procedure.

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