Model-based Differentially Private Data Synthesis

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Abstract
We propose model-based differentially private synthesis (modips) in the Bayesian framework for releasing individual-level surrogate data sets for the original with strong privacy guarantee. The modips technique integrates differential privacy (DP) – a concept discussed largely in the theoretical computer science community – into microdata synthesis in statistical disclosure limitation. The modips guarantees individual privacy protection at a given privacy budget without making assumptions about data intruder’s behaviors and knowledge. The privacy budget can be used as tuning parameters in the trade-off between privacy protection and original information preservation in synthesized surrogate data. The uncertainty from the sanitization and synthetic process in the modips can be accounted for by releasing multiple synthetic data sets and by applying the proposed variance combination rule. We also characterize the conditions for the consistency of estimators based on released synthetic data. The modips method provides a viable alternative to the currently limited choice set of microdata synthesis approaches in statistical disclosure limitation.

keywords: (Bayesian) sufficient statistics, sanitization, (truncated and BIT) Laplace mechanism, multiple release, surrogate data

1 Introduction
Statistical approaches to protecting data privacy are known as statistical disclosure limitation (SDL). SDL techniques aim to provide protection for individual sensitive information when releasing data for research and public use. Data synthesis (DS) is a SDL technique that releases pseudo individual-level data. Both parametric and nonparametric Bayesian and frequentist approaches have been proposed for DS [Rubin 1993, Liu and Little 2002, Little et al. 2004, Reiter 2005a, An and Little 2007, Caiola and Reiter 2010, Drechsler and Reiter 2011, Burgette and Reiter 2013]. To reflect the uncertainty introduced during the synthesis process, multiple sets of synthetic data are often released. Inferential methods are available to combine information from multiple synthetic data sets to yield valid inferences [Raghunathan et al. 2003, Reiter 2003]. A long-standing research problem in SDL (including DS) is the lack of a universally applicable and robust measure of disclosure risk in released data. Most existing disclosure risk assessment approaches rely on strong and ad-hoc assumptions on the background knowledge and behaviours of data intruders [Fienberg et al. 1997, Domingo-Ferrer and Torra 2001, 2004, Reiter 2005b, Domingo-Ferrer and Saygin 2008, Manrique-Vallier and Reiter 2012, Reiter et al. 2014].

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Differential privacy (DP), a concept developed in theoretical computer science, has gained enormous popularity since its debut in 2006 (Dwork et al., 2006b; Dwork and Smith, 2010; Dwork, 2011). An attractive feature of DP is that it formalizes privacy in mathematical terms without making assumptions about data intruders; in other words, DP guards against the worst disclosure scenarios. DP has spurred a great amount of work in developing mechanisms to release statistics that satisfy DP in general settings and for specific types of queries or statistical analyses. The Laplace mechanism (Dwork et al., 2006b), the Exponential mechanism (McSherry and Talwar, 2007), and the Gaussian mechanism (Dwork and Roth, 2014; Liu, 2016a) are common differentially private sanitizers for general purposes. Differentially private versions of various statistical analyses are also available, such as point estimators (Smith, 2011; Lei, 2011), principle components analysis (Chaudhuri et al., 2013), linear and penalized regression (Chaudhuri et al., 2011; Kifer et al., 2012), model selection (Smith and Thakurta, 2013), release of functions (Hall et al., 2013), the $\chi^2$ test in genome-wide association studies (Yu et al., 2014), and deep learning (Shokri and Shmatikov, 2015; Abadi et al., 2016), among others.

In addition to the sanitization of aggregates statistics, there are also approaches for differentially private synthesis of individual-level data (dips). An obvious advantage of dips over query-based sanitization is that dips releases surrogates for the original data set which allow data users to run statistical analysis of their own as if they had the original data. Dips also eliminates the need to continuously monitor submitted queries and design differentially private algorithms to sanitize query results in interactive settings, especially considering that it is unlikely for data curators to anticipate the types of queries submitted to a database beforehand. Finally, due to the sequential composability of DP (McSherry, 2009), only a certain number of queries submitted to the same set of data can be answered before a pre-specified privacy budget is exhausted. We focus on dips that releases individual-level data rather than aggregate statistics in this discussion.

Most available dips approaches are nonparametric and distribution-free in nature, and require some degree of discretization if the original data contains numerical attributes. Barak et al. (2007) generated synthetic data via the Fourier transformation and linear programming in low-order contingency tables. Blum et al. (2008) discussed the possibility of dips from the perspective of the learning theory in a discretized domain. Abowd and Vilhuber (2008) examined releasing predictive tabular data in the Bayesian framework by imposing a “differentially private” prior on cell proportions (the Multinomial-Dirichlet/MD synthesizer), later implemented in the commuting data of the US population in Machanavajjhala et al. (2008). The MD synthesizer was applied in Charest (2010) to investigate the statistical inferences on proportions in synthetic binary data. McClure and Reiter (2012) implemented a similar technique for synthesizing binary data with a different specification of the differentially private prior. Wasserman and Zhou (2010) proposed several paradigms to sample from differentially private perturbed or smoothed histograms, or empirical distribution functions, and examined the rate at which the empirical distribution of synthetic data converges to the true distribution of the original data. The technique developed in Hall et al. (2013) can be used to release differentially private kernel density estimator from which synthetic data can be simulated and released. Hardt et al. (2012) developed the iterative MWEM (multiplicative weights exponential mechanism) algorithm to synthesize discrete data via “matching” on linear queries. DualQuery by Gaboardi et al. (2013) also employed the MW technique to handle a large number of linear queries in the discrete domain. Zhang et al. (2014) proposed PrivBayes to release high-dimensional data from Bayesian networks with binary nodes and low-order interactions among the nodes. Li et al. (2014) proposed DPCopula to sample synthetic data from differentially private copula functions for multi-dimensional data. There are also dips approaches developed for specific types of data such as graphs (Proserpio et al., 2012); mobility data from GPS trajectories (He et al., 2015), and edge data.
based on exponential random-graph models in social networks (Karwa et al., 2016). While all the work on dips is encouraging and sheds light in releasing differentially private synthetic individual-level data, there are limitations. First, many dips methods require discrete attributes (an exception is the DPCopula method) and discretizes numerical attributes prior to DS. How the bins are constructed on continuous attributes will affect the utility of synthetic data. In addition, high-order cross-tabulations among categorical attributes and bins of histogram on continuous attributes can lead to a large amount sparse and empty cells, especially in high-dimensional data.

Motivated by the need for alternative dips approaches, we propose the model-based differential private synthesis (modips) approach for individual-level DS. Data sets generated via modips contain the same structure as the original data. DP of the modips is achieved at the step of sanitizing the (Bayesian) sufficient statistics of the synthesis model, and is preserved in all subsequent synthesis steps and in the released surrogate data sets. We recommend releasing multiple synthetic data sets so that the uncertainty of the sanitization and synthesis processes can be conveniently quantified and accounted for when inferring from the released data sets. We examine the consistency of the inferences based on synthesized data and provide a theoretical framework to combine inferences from multiple released surrogate data sets. Unlike the existing nonparametric dips approaches, the modips approach does not discretize continuous variables and aims to sanitize a low-dimensional set of statistics yet sufficient in summarizing original information given a synthesis model. Compared to the traditional DS approaches in SDL, the modips approach provides a robust solution to the long-standing issue of disclosure risk quantification with privacy protection guaranteed through DP at a pre-specified level of privacy budget.

The rest of the paper is organized as follows. Section 2 introduces the modips technique, establishes DP in released synthetic data, and investigates the inferential properties of synthetic data. Section 3 presents a simulation study to illustrate the application the modips method in a data set and obtain inferences from synthetic data and to examine the effects of number of released data sets on inferences. The paper concludes in 4 with final remarks and plans for future works.

2 Model-based Differentially Private Data Synthesis (modips)

2.1 concepts and notations

We denote the target data for protection by $x_{n \times p} = \{x_{ij}\}$, where $x_{ij}$ is the $j^{th}$ variable/attribute in individual $i$ ($j = 1, \ldots, p$ and $i = 1, \ldots, n$), and assume $x$ is bounded in each of its $p$ attributes because first, it is difficult to extend DP to unbounded domains, and second, real-life data are hardly unbounded. For example, it is safe to say human height is bounded within $(0, 300)$ cm, and personal annual income is bounded within $\$$[0, c]$, where $c$, the maximum income, is a finite number. Categorical attributes can be coded with binary indicators and thus be made “bounded”.

Definition 1. (Dwork, 2006; Dwork et al., 2006b) A sanitization algorithm $R$ is $\epsilon$-differentially private if for all data sets $(x, x')$ that is $\Delta(x, x') = 1$ and all possible result subset $Q$

$$\left| \log \left( \frac{\Pr(R(s(x)) \in Q)}{\Pr(R(s(x')) \in Q)} \right) \right| \leq \epsilon. \quad (1)$$

$\Delta(x, x') = 1$ denotes that data $x'$ differs from $x$ by one individual, $\epsilon > 0$ is the privacy budget parameter, $s$ contains the set of functions/queries sent to $x$, and $s(x)$ refers to the query results or statistics (we sometimes abuse the notations and equate $s(x)$ with $s$). Eq. (1) states that the probabilities of obtaining the same query result from $x$ and $x'$ after the sanitization are similar – the ratio between the two probabilities is in $[e^{-\epsilon}, e^\epsilon]$. In layman’s terms, DP implies the chance that
a participant in the data set will be identified based on sanitized query results is very low since the query results are about the same with or without that participant in the data set. The smaller $\epsilon$ is, the more protection will be executed on the individuals in the data set. DP provides a strong and robust privacy guarantee in the sense that it does not make assumptions regarding the background knowledge or behaviors on data intruders; in other words, DP guarantees privacy at privacy cost $\epsilon$ in the worst case scenario. There are also softer versions of DP that guarantee privacy in a “weak” sense, including the $(\epsilon, \delta)$-approximate DP (aDP) \cite{Dwork2006}, the $(\epsilon, \delta)$-probabilistic DP (pDP) \cite{Machanavajjhala2008}, the $(\epsilon, \delta)$-random DP (rDP) \cite{Hall2012}, and the $(\epsilon, \tau)$-concentrated DP (cDP) \cite{Dwork2015}. In all the relaxed versions of DP, an extra parameter is employed to characterize the amount of relaxation on top of the privacy budget $\epsilon$. The $(\epsilon, \delta)$-aDP and the $(\epsilon, \delta)$-pDP reduce to $\epsilon$-DP when $\delta = 0$. To release a query result with DP, differentially private mechanisms or sanitizers are used. The Laplace mechanism and the Exponential mechanism are two popular sanitizers of $\epsilon$-DP for general purposes.

**Definition 2.** \cite{Dwork2006} In the Laplace mechanism of $\epsilon$-DP, sanitized $s^*$ is defined as $s^* = s + e$, where $e$ comprises $r$ independent random draws from Laplace distribution $\text{Lap}(0, \delta_1 \epsilon^{-1})$.

$\delta_1$ is the $l_1$ global sensitivity (GS) of $s$, a special case of $l_p$-GS $\delta_p$ when $p = 1$ \cite{Liu2016}, where $\delta_p = \max_{x,x',\Delta(x,x')} \|s(x) - s(x')\|_p = \max_{x,x',\Delta(x,x')} (\sum_{i=1}^r |s(x) - s(x')|^p)^{1/p}$. The sensitivity is “global” since it is defined for all possible data sets and all possible ways of two neighboring data sets differing by one record. The larger the GS is, the more spread out the Laplace distribution, and the more perturbation is needed for $s$ to offset the large sensitivity. The mean of the Laplace distribution in Definition 2 is $s$ and the variance is $2 (\delta_1 \epsilon^{-1})^2$, implying that the larger $\delta_1$ or the smaller $\epsilon$ is, the more spread out the Laplace distribution is, and the more likely to have $s^*$ deviates further away from $s$. When $s$ is bounded, the noninformative truncated Laplace mechanism or the boundary-inflated truncated (BIT) Laplace mechanism can be employed \cite{Liu2016}.

**Definition 3.** \cite{McSherry2007} The Exponential mechanism of $\epsilon$-DP generates $s^*$ from

$$p(s^*|x) = \frac{\exp \left( u(s^*|x) \frac{\epsilon}{2\delta_u} \right)}{\sum_{s^* \in S} \exp \left( u(s^*|x) \frac{\epsilon}{2\delta_u} \right)} \quad \text{if } S \text{ is discrete; } p(s^*|x) = \frac{\exp \left( u(s^*|x) \frac{\epsilon}{2\delta_u} \right)}{\int_{s^* \in S} \exp \left( u(s^*|x) \frac{\epsilon}{2\delta_u} \right)} \quad \text{if } S \text{ is continuous},$$

where $S$ is the set containing all possible outputs $s^*$, $u(s^*|x)$ is the utility score of $s^*$ given data $x$, and $\delta_u = \max_{x,x',\Delta(x,x')} |u(s^*|x) - u(s^*|x')|$ is the maximum change in score $u$ between neighboring data sets $x$ and $x'$. In the Exponential mechanism, the probability of returning a particular $s^*$ is exponentially proportional to its utility score.

In addition to the Laplace mechanism and the Exponential mechanism, the Gaussian mechanism is another mechanism commonly used in theoretical research and practical applications. The Gaussian mechanism sanitizes statistics with additive Gaussian noises to satisfy $(\epsilon, \delta)$-aDP or $(\epsilon, \delta)$-pDP \cite{Dwork2014, Liu2016}. The generalized Gaussian mechanism (GGM) includes the Laplace mechanism and Gaussian mechanism as special cases \cite{Liu2016}.

2.2 the modips algorithm

The steps of modips are presented in Algorithm 1 and a diagrammatic description is given in Figure 1. $f(x|\theta)$ is the likelihood of the model assumed on the original data $x$, $f(\theta)$ is the prior, and $f(\theta|x) = f(\theta|s)$ is the posterior distribution of $\theta$. The modips mechanism is presented in the Bayesian framework to satisfy the pure $\epsilon$-DP. It is possible to extend modips to the non-Bayesian
framework by drawing $\tilde{x}^{(k)*}$ directly from $f(\tilde{x}^{(k)*}|s^{(k)*})$ if the distribution is easy to compute and sample from, and to softer versions of DP by replacing sanitizers of $\epsilon$-DP in the sanitization step of the modips algorithm with sanitizers that deliver other versions of DP such as $(\epsilon,\delta)$-pDP. In

\begin{align*}
\textbf{Input:} & \text{ number of released data sets } m, \\
& \text{ overall privacy budget } \epsilon, \\
& \text{ Bayesian sufficient statistics } s \text{ in the Bayesian model assumed on original data } x
\end{align*}

For $k = 1, \ldots, m$,
1. sanitize $s$ via a differentially private mechanism with privacy budget $\epsilon/m$ to generate $s^{(k)*}$
2. draw $\theta^{(k)*}$ from the sanitized posterior distribution $f(\theta|s^{(k)*})$
3. draw $\tilde{x}^{(k)*}$ from $f(x|\theta^{(k)*})$

\begin{align*}
\textbf{Output:} & \text{ surrogate data sets: } \tilde{x}^{(1)*}, \ldots, \tilde{x}^{(m)*}
\end{align*}

\textit{Algorithm 1: modips}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{modips.png}
\caption{modips}
\end{figure}

Algorithm 1, all privacy budget $\epsilon$ is spent in the sanitization of Bayesian sufficient statistics $s$ and is preserved in subsequent steps. Identification of $s$ in a Bayesian model is critical in the modips algorithm. Generally speaking, classical sufficiency implies Bayesian sufficiency. There are examples of Bayesian sufficient statistics which are not classically sufficient but those are unusual situations (Blackwell and Ramamoorthi [1982], Bernardo and Smith [1994], Nogales et al. [2000]). In Algorithm 1, each synthetic data set is sanitized with $1/m$ of the overall privacy budget $\epsilon$, to ensure the actual total privacy cost from releasing $m$ sets of synthetic data is kept at $\epsilon$. This is known formally as the \textit{sequential composition} (McSherry [2009]), which states that the total privacy cost from querying the same data set $m$ times, with a privacy cost of $\epsilon_i$ for the $i^{th}$ query, equals to the sum of individual privacy costs $\sum_{i=1}^{m} \epsilon_i$. Since perturbation increases with decreased privacy budget, $1/m$ of the overall budget $\epsilon$ per synthesis implies each set for $m > 1$ is always noisier than when $m = 1$. However, the totality of released original information across the $m$ released sets for $m > 1$ is not necessarily less than that when $m = 1$. More importantly, releasing multiple sets provides an effective and convenient way to quantify the uncertainty and randomness introduced during the sanitization and synthesis that is necessary for valid inferences, if no others sources or approaches are available to data users to quantify the uncertainty.

2.3 differential privacy of modips

The $\epsilon$-DP of the modips algorithm is established in Theorem 4 (the proof is provided in Appendix A). Theorem 4 also suggests that all the privacy budget $\epsilon$ is spent at the sanitization of $s$, and the subsequent steps are “free” without incurring any additional privacy cost.

\textbf{Theorem 4.} In the modips algorithm in Algorithm 1 if the Bayesian sufficient statistics $s$ is sanitized with $(m^{-1}\epsilon)$-DP to generate $s^{(k)*}$ for $k = 1, \ldots, m$, then $\theta^{(k)*}$ drawn from the posterior
distribution \( f(\theta | s^*) \) also enjoys \((m^{-1}\epsilon)\)-DP, so does the synthetic data \( \tilde{x}^{(k)*} \) sampled from \( f(\tilde{x} | \theta^*) \). By the sequential composition principle, the \( m \) sets of released data satisfy \( \epsilon \)-DP.

### 2.4 statistical inferential in sanitized data via modips

A DS method in SDL should balance privacy protection and information loss incurred by the protection procedure. We established DP of the modips sanitizer in the previous section, we now investigate the properties of statistical inferences based on the synthetic data \( \tilde{x}^* \) generated by the modips. There exists work that proposes inferential approaches on differentially private synthetic data and examines the asymptotic inferential properties of differentially private estimators, but most of the work focuses on a specified type of analysis or a special type of data. \cite{Charest} explicitly modelled the differentially private mechanism in univariate binary data to incorporate the sanitization uncertainty in the Bayesian inferences based on synthetic data; \cite{Karwa} modelled the Laplace mechanism as a measurement error on the sufficient statistics of the \( \beta \)-model of random graphs and established the conditions for the existence of the private maximum likelihood estimator (MLE) that achieves the same rate of convergence as nonprivate estimators for the degree sequence; \cite{Karwa} applied MCMC techniques to fit exponential family random-graph models to social networks with differentially private synthetic edges. \cite{Smith} proposed a differentially private estimator via the “subsample-and-aggregate” technique with a differentially private \( \alpha \)-Winsorized mean over the subsamples. The private estimator applies to a large class of original estimators, and approximates the original average as long as the estimators from the subsamples are i.i.d. from an approximately Gaussian distribution with bounded third moment, for sufficiently large \( n \). In what follows, we characterize the conditions that lead to the consistency of inferences based on single and multiple synthetic data sets via the modips without having to explicitly model the sanitizer; and present a variance combination rule that aggregates information across multiple released synthetic sets.

**Lemma 5.** Denote the parameter of interest by \( \theta \), and a single synthetic data set generated via Algorithm 1 by \( \tilde{x}^* \). Assume the model used for obtaining inferences on \( \theta \) from original data \( x \) (if \( x \) were to be released) is the same as the one used to infer \( \theta^* \) based on \( \tilde{x}^* \). If estimator \( \hat{\theta}^* \) based on \( \tilde{x}^* \) is consistent for \( \theta^* \) and sanitized \( s^* \) is consistent for \( s \), then \( \hat{\theta}^* \) is consistent for \( \theta \).

The proof is given in Appendix B. The condition that \( \hat{\theta}^* \) is consistent for \( \theta^* \) is mild and can be easily satisfied via the maximum likelihood or Bayesian inferential approaches. Regarding the requirement that \( s^* \) is consistent for \( s \), generally speaking, if the disclosure risk from releasing \( s \) decreases with \( n \), so would be the amount of noise needed to sanitize \( s \), and consistency of \( s^* \) for \( s \) can be established for that sanitizer. For example, \( s^* \overset{\epsilon}{\rightarrow} s \), where \( s^* \) is sanitized via the Laplace mechanism (or its altered versions such as the truncated and BIT Laplace mechanisms), holds if the scale parameter of the Laplace distribution \( \rightarrow 0 \) as \( n \rightarrow \infty \) \cite{Liu}

Lemma 5 states the consistency of \( \hat{\theta}^* \) for \( \theta \) in a single synthetic data set. To obtain valid inferences for \( \theta \), the variabilities introduced during the process of sanitization and synthesis need to be taken into account. A legitimate yet convenient way to achieve the goal is to release multiple synthetic data sets. Theorem 6 presents how to obtain inferences from multiple synthetic data sets.

**Theorem 6.** Denote the parameter of interest by \( \theta \). \( \tilde{x}^{(k)*} \) is the \( k \)th synthetic data set and \( \tilde{s}^{(k)*} \) is the Bayesian sufficient statistics associated with the model assumed on \( \tilde{x}^{(k)*} \) for \( k = 1, \ldots, m \). Denote the posterior mean and variance of \( \theta^{(k)*} \) given \( \tilde{x}^{(k)*} \) by \( \hat{\theta}^{(k)*} = g(\tilde{s}^{(k)*}) \) and \( v^{(k)*} = v(\tilde{s}^{(k)*}) \), respectively. Assume \( \hat{\theta}^{(k)*} \overset{\epsilon}{\rightarrow} \theta^{(k)*} \), sanitized \( s^{(k)*} \overset{\epsilon}{\rightarrow} s \), and the model to infer \( \theta \) based on original \( x \) (if \( x \) were to be released) is the same as the one for inferring \( \theta^{(k)*} \) from \( \tilde{x}^{(k)*} \), then
a) \( \hat{\theta} = m^{-1} \sum_{k=1}^{m} \hat{\theta}^{(k)} \) is a consistent estimator for \( \theta \);

b) the posterior variance of \( \theta \) given \( \tilde{x}^{(1)}, \ldots, \tilde{x}^{(m)} \) is given by

\[
u = \bar{\nu} + m^{-1} b, \text{ where } \bar{\nu} = m^{-1} \sum_{k=1}^{m} v^{(k)} \text{ and } b = m^{-1} \sum_{i=1}^{m} (\hat{\theta}^{(k)} - \bar{\theta})^2 = b_1 + b_2; \quad (2)
\]

\( \bar{\nu} \), the averaged within-set variance, estimates \( \mathbb{E}(V(\theta|x)|x^{(1)}, \ldots, x^{(m)}) \); \( b \), the between-set variance, estimates \( \mathbb{V}(\mathbb{E}(\theta|x)|x^{(1)}, \ldots, x^{(m)}) \); \( b_1 \) is the Monte Carlo (MC) estimate of \( \mathbb{V}(g(s)|g(s^*)) \) and represents the variability incurred by sanitization, and \( b_2 \) is the MC estimate of \( \mathbb{V}(\theta^*|g(s^*)) + \mathbb{V}(g(s^{*})|\theta^*) \) and represents the variability due to synthesis, comprising the conditional variance of \( \theta^* \) given \( s^* \) and the conditional variance of \( \tilde{x}^* \) given \( \theta^* \);

c) the inferences of \( \theta \) given \( \tilde{x}^{(1)}, \ldots, \tilde{x}^{(m)} \) are based on \( t\nu(\hat{\theta}, m^{-1}b + \bar{\nu}) \), where the degree of freedom

\( \nu = (m - 1)(1 + m\bar{\nu}/b)^2 \).

The proof of Theorem 6 is provided in Appendix C. Part b) of Theorem 6 suggests the between-set variance of \( \theta \) given \( \tilde{x}^{(1)}, \ldots, \tilde{x}^{(m)} \) is composed of the variances due to sanitization \( b_1 \) and due to synthesis \( b_2 \). Algorithm 2 does not separate \( b_1 \) from \( b_2 \) because each sanitized \( s^{*(k)} \) \( (k = 1, \ldots, m) \) leads to one synthetic set \( \tilde{x}^{*(k)} \). Though there is seldom an interest in quantifying \( b_1 \) and \( b_2 \) separately, if the need does exist it can be fulfilled via the nested modips in Algorithm 2.

**Input:**
- number of sanitizations \( m \)
- number of synthesis per sanitization \( t \)
- overall privacy budget \( \epsilon \)
- Bayesian sufficient statistics \( s \) in the Bayesian model assumed on original data \( x \)

for \( k = 1, \ldots, m, \)
- sanitize \( s \) via a differentially private mechanism with privacy budget \( \epsilon/(mt) \) to generate \( s^{(k)*} \)
- for \( l = 1, \ldots, t, \)
  1. draw \( \theta^{(k,l)*} \) from the sanitized posterior distribution \( f(\theta|s^{(k)*}) \)
  2. draw \( x^{(k,l)*} \) from \( f(x|\theta^{(k,l)*}) \)

**Output:** surrogate data sets: \( \tilde{x}^{(1,1)*}, \ldots, \tilde{x}^{(1,t)*}, \tilde{x}^{(2,1)*}, \ldots, \tilde{x}^{(2,t)*}, \ldots, \tilde{x}^{(m,1)*}, \ldots, \tilde{x}^{(m,t)*} \)

**Algorithm 2: Nested modips**

![Nested modips](image)

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Schematic presentation of which is provided in Figure 2. In brief, multiple sets of \( \theta^{(k,l)} \) per \( s^{*(k)} \) are simulated, where \( l = 1, \ldots, t, \) each of which leads to a synthetic data set. The released \( m \times t \)
sets of surrogate data $\hat{x}^{s(1,1)}, \ldots, \hat{x}^{s(1,t)}, \ldots, \hat{x}^{s(m,1)}, \ldots, \hat{x}^{s(m,t)}$ bear a 2-layer hierarchical structure. The release is not only accompanied by releasing data with increased volume, but also the analysis is more complicated with the hierarchical data structure. We suggest not employing the nested modsips unless there is an absolute need to quantify $b_1$ and $b_2$ separately.

The establishment of Eq. (2) assumes that the distribution of $g(s)$ given $g(s^{*})$, where $s^{*}$ is $g(s)$ is Gaussian. This assumption is easily satisfied by applying the CLT when $m$ is large. On the other hand, large $m$ could jeopardize the assumption $s^{*} \overset{p}{\rightarrow} s$ that is necessary for the consistency of the inferences in Theorem 6 due to allocation of the overall privacy budget to $m$ syntheses. For example, the model fitted on a data set of size $n$ contains a single sufficient statistic $s$ that is bounded within $[c_0, c_1]$ in and its $l_1$-GS is $\propto n^{-1}$ (e.g., sample means and proportions). The truncated Laplace sanitizer, $\text{Lap}(s, \propto mn^{-1})$, is employed. As $m$ increases, the truncated Laplace distribution approach the uniform distribution over the interval $[c_0, c_1]$. In other words, sanitized eventually $s^{*}$ contains no original information when $m$ is large, and $s^{* (k)} \overset{p}{\rightarrow} s$ no longer holds.

How to choose $m$ continues to be a topic for future research, and both theoretical and empirical work is needed. In the traditional non-DP DS methods, small $m$ (e.g., $\leq 10 \sim 15$) seems to work well inferentially based on the empirical studies (Reiter, 2003; Raghuathan et al., 2003). From the perspective of practical implementation, small $m$ incurs less cost in computation and storage. Another consideration is the efficiency of inferences based on synthetic data, measured by the variance estimate $\varpi + m^{-1}b$ in Eq. (2), as along as $m$ is large enough to capture the between-set variance but small enough to allocate enough privacy budget to each synthesis ($\epsilon/m$) so that the synthetic data is still good representation of the original data. Specifically, $\varpi$ remains consistent across $m$ except for the MC fluctuation, whereas $m^{-1}b$ may vary with $m$ nonmnototically. Since the privacy budget per synthesis decreases with $m$, the variance of sanitized $s^{*}$ increases, so does $b_1$, with $m$. If $s^{*}$ affects the variance of the synthesis model, $b_2$ could also vary with $m$. The first derivative of $m^{-1}b(m)$ is $m^{-1}(b'(m) - m^{-1}b(m))$ (we use $b(m)$ instead of $b$ to reflect its dependence on $m$). If $b'(m) < m^{-1}b(m)$, $m^{-1}b(m)$ decreases with $m$; else $m^{-1}b(m)$ increases with $m$. For high efficiency, we would choose an $m$ around the minimizer of $m^{-1}b(m)$, and thus $\varpi + m^{-1}b(m)$.

2.5 conjoint sanitization and individual sanitization

It is almost certain that the sufficient statistics $s$ associated with a Bayesian model on a real-life data set is multi-dimensional. At a given privacy budget, we should aim to preserve as much original information as possible when sanitizing data. At a given privacy budget, we should aim to preserve as much original information as possible when sanitizing data. Given that the sufficient statistics $s$ is multi-dimensional, we need to group the elements in $s$ according to which units/cases $s$ is calculated from: elements in the same group share at least one common case, whereas elements in different groups are calculated based on disjoint subsets of cases. The reason behind the grouping is to make the most out of the parallel composition principle (McSherry, 2009): since each group is based on a disjoint subset of $x$, then each group will receive the full budget. The next step is to sanitize the statistics in the same group with full privacy budget. We introduce conjoint sanitization and individual sanitization as two ways of sanitizing a multidimensional $s$ that shares data from the same group of individuals, and illustrate their applications in the context of the Laplace mechanism (both conjoint sanitization and individual sanitization are general concepts and can couple with other differentially private mechanisms, such as the Exponential mechanism).

**Definition 7.** In the conjoint sanitization of a multi-dimensional $s$ via the Laplace mechanism, each element in $s$ is sanitized with an additive noise term drawn from $\text{Lap}(0, \delta_s \epsilon^{-1})$, where $\delta_s = \sum_{i=1}^{r} \delta_i$ is the $l_1$-GS of $s$, and $\delta_i$ is the $l_1$-GS of $s_i$. In the individual sanitization via the Laplace mechanism, element $s_i$ in $s$ is sanitized with an additive noise term drawn from $\text{Lap}(0, \delta_i (w_i \epsilon)^{-1})$, where $w_i$ is the the proportion of the total privacy budget allocated to $s_i$, and $\sum_{i=1}^{r} w_i = 1$. 
In short, all elements in \( s \) are sanitized via the same mechanism in the conjoint sanitization, while the sanitation mechanism is “individualized” for each element in the individual sanitization. The conjoint sanitization and individual sanitization can lead to different levels of perturbation for a given \( s_i \). The individual sanitization offers more flexibility since it allows users to specify the privacy budget each \( s_i \) receives. There is no restriction on specifying \( w = (w_1, \ldots, w_r)^T \) as along as the overall budget is not over-spent (\( \sum_{i=1}^{r} w_i = 1 \)). Proposition 8 presents two examples of \( w \) specification in the individual sanitization and compares the conjoint and individual sanitization under each scenario. The proof is available in Appendix D.

**Proposition 8.**

a). Define the average GS of \( s \) as \( \bar{\delta}_s = r^{-1} \sum_{i=1}^{r} \delta_i = r^{-1} \delta_s \). When \( w_i \equiv r^{-1} \) (equal allocation) in the individual sanitization, statistics with less-than-average GS are perturbed less than would be in the conjoint sanitization via the Laplace mechanism, and those with greater-than-average GS are more perturbed than would be in the conjoint sanitization.

b). The individual sanitization is equivalent to the conjoint sanitization in the Laplace mechanism when \( w_i = \delta_i (\sum_{i=1}^{r} \delta_i)^{-1} \) for \( i = 1, \ldots, r \). In other words, the conjoint sanitization can be regarded as the individual sanitization when the allocation proportion is proportional to the GS of each element in \( s \).

One could also define \( w_i \) according to how “important” \( s_i \) is from a statistical or practical perspective. For example, if the main purposes of releasing a data set is to estimate the means of its attributes, then the sample means can be given a bigger portion of \( \epsilon \) and thus be less perturbed. The definition of “importance” may vary from case to case, and thus the importance-based approach should be used with caution.

In the case of the Exponential mechanism, if the scoring function \( u \) measures the wholesome utility of \( s \) and all elements in \( s \) are sanitized simultaneously, then it belongs to the conjoint sanitization; if each element is sanitized individually with an allocated privacy budget \( w_i \epsilon \) and an element-specific scoring function \( u_i \), then it falls under the umbrella of the individual sanitization. Different from the Laplace mechanism, where the conjoint sanitization and individual sanitization are computationally equivalent (both involve drawing \( r \) independent samples from Laplace distributions), the conjoint sanitization via the Exponential mechanism can be computationally more expensive than the individual sanitization when the dimension of \( s \) is high.

### 2.6 modips vs traditional DS in SDL

Depending on the data source that synthesis is based on, traditional non-DP DS can be roughly grouped into population synthesis and sampling (Rubin, 1993; Raghunathan et al., 2003), and sample synthesis (Little, 1993). By the percentage of the synthetic component in a released data set, DS can be grouped into partial synthesis and full synthesis (Liu and Little, 2002; Little et al., 2004). Reiter (2003) suggested the variance combination rule \( u_{\bar{\theta}} = m^{-1}b + \overline{\varpi} \) for estimate \( \bar{\theta} = m^{-1} \sum_{i=1}^{m} \bar{\theta}_i \) in partial sample synthesis (PSS) where \( \overline{\varpi} \) is the averaged within-set variance and \( b \) is the between-set variance that are calculated in the same MC manner as in the Eq. (2) in Theorem 6 differing only in what \( b \) is composed of. The variance combination rule is also applicable to full sample synthesis (FSS) since it can be viewed as a special case of the PSS with a 100% synthesis proportion. The modips algorithm belongs to the FSS category but differs from its traditional counterpart with the extra step of identifying and sanitizing Bayesian sufficient statistic \( s \) to guarantee DP. The similarity in the formulation of the variance combination rules between the modips and the traditional FSS
is not a coincidence: the modips can be viewed as a “sanitized” version of FSS with an extra step of sanitizing the original $s$, the additional variability from which is absorbed into $b$.

While it is possible to apply DP in the framework of partial synthesis, we doubt the robustness and rigor of DP (which is arguably the biggest advantage of DP over other disclosure risk assessment approaches) can be maintained. Specifically, it is assumed that there is minimal disclosure risk from releasing a part of the original data, motivating the partial synthesis. In order to set apart this subset that is immune to disclosure risk from the part that is not, some kind of disclosure and reidentification risk assessment has to be in place prior to the synthesis, explicitly or implicitly, based on some data attackers’ model; this reasoning process already contradicts the concept and robustness of DP. For example, Karwa et al. (2016) proposed to synthesize edges of the exponential random graph models with DP, and treated the nodes as public information without perturbing them in the network. While the edges in a released network are differentially private, their relations with the node attributes are not. If the relations are strong, data attackers can retrieve the original edge information with high probability via unsupervised learning. In addition, perturbing only the edges could potentially lead to biased and distorted estimates of the relationship between edges and nodes if one is interested in exploring the relationship using the partially synthesized network as is with supervised learning.

### 3 A simulation study

We use this simulation study to demonstrate the application of the modips and how to obtain inferences from multiple synthesized data sets via modips, and to investigate empirically how $m$ affects the inferences. Albeit the simplicity of the simulation set-up, we obtained some interesting results and some insights on the effects of $m$ on original information preservation. More complicated simulation studies and comparison of the modips with other dips approaches and the traditional non-DP DS approach are available in Bowen and Liu (2016).

We studied sample sizes $n = 100$ and $1000$; and simulated 2000 data sets at each $n$ from $x_i \sim N(\mu = 0, \sigma = 1)$ ($i = 1, \ldots, n$). We also examined two different bounds on $X$: $[c_0, c_1] = [-4, 4]$ (symmetric around $\mu$) and $[−4, 5]$ (asymmetric around $\mu$). Given $\Pr(|x_i| > 4) = 0.0063\%$, though bounded, $X$ can still be well approximated by a Gaussian distribution. Assume $\sigma$ is known and we are interested in estimating $\mu$. With a noninformative prior $f(\mu) \propto \text{constant}$, the Bayesian sufficient statistics associated with the Gaussian likelihood is $\bar{x} = n^{-1} \sum_{i=1}^{n} x_i$ and its GS is $\delta_x = (c_1 - c_0)n^{-1}$. We examined a wide range of $m \in [2, 500]$ but focused on $m \in [2, 40]$. The overall privacy budget was set at $\epsilon = 1$, shared by the $m$ sets of synthetic data. Both the truncated Laplace and BIT Laplace mechanisms with non-informative bounding were applied to sanitize $\bar{x}$. The scale parameter in the Laplace distribution was $(c_1 - c_0)\epsilon^{-1}mn^{-1}$. $\mu$ in each synthetic set was estimated by the sample mean $\bar{x}^{(k)}$ for $k = 1, \ldots, m$; and the variance of the overall estimate $\bar{\mu} = m^{-1} \sum_{k=1}^{m} \bar{x}^{(k)}$ was calculated via Eq. [20] in Theorem 6. In single release ($m = 1$), the variance of $\bar{x}^*$ was estimated by the within-set variance without other sources or explicitly modelling the sanitization mechanism to inform the uncertainty incurred by the sanitization and synthesis. The variance estimates of $\bar{x}^*$ and $\bar{\mu}$ from the single and multiple releases were benchmarked against their respective true empirical variances $\sigma_x^2 = V(\bar{x}^*)$ and $\sigma_\mu^2 = V(\bar{\mu})$ (computed via the MC approach in this simulation).

Figure 3 presents the biases, variance estimates and coverage probabilities (CP) of the 95% confidence intervals (CIs) for $\mu$ when $m \in [2, 40]$. A similar figure but with a wider range of $m \in [2, 500]$ is given in Figure S1 in the supplementary materials. Figures S2 to S9 and S16 to S23 present example synthetic data sets $\tilde{x}^{(k)}$ at $m = 5, 15, 40$, and 500 when $n = 1000$ and $n = 100$, respectively. The main findings are summarized as follows. As $m$ increased at a fixed $n$, the scale parameter ($\propto mn^{-1}$) of the Laplace distribution increased, and, as expected, the
distribution of sanitized $x^*$ via the truncated Laplace mechanism approached $\text{unif}(c_0, c_1)$, and more and more probability mass accumulated at $c_0$ and $c_1$ for the BIT Laplace mechanism (Figures S12,
S15, S26, and S29 when \( m = 500 \), implying less information in the original \( \bar{x} \) was preserved after the sanitization step. As a result, \( \bar{x}^* \) generated in the subsequent synthesis step deviated more and more from the original \( x \) (Figures S5, S9, S19, and S23 when \( m = 500 \)), and the inferences of \( \mu \) based on \( \bar{x}^{*(1)}, \ldots, \bar{x}^{*(m)} \) became meaningless and misleading. Though it appeared the bias was negligible and the CP was no lower than nominal level for large \( m \) when \( (c_0, c_1) = (-4, 4) \) (Figure S1), this was more because the bounds were symmetric around \( \mu \) rather than because \( \bar{x}^* \) preserved the original information in \( x \). Regarding the comparison between the BIT Laplace and the truncated Laplace mechanisms, there were minimal differences for small \( m \). As \( m \) increased, \( \bar{\mu} \) based on the synthetic data via the truncated Laplace mechanism was more biased and suffered from more severe undercoverage in CP at the same \( m \) when \( (c_0, c_1) \) were asymmetric around \( \mu \). In summary, \( m \) needed to be small relative to \( n \) (\( m \in [2, 8 \sim 10] \) when \( n = 100 \), and \( \in [2, 40 \sim 50] \) when \( n = 1000 \)) for the inferences based on the synthetic data to be meaningful.

The point estimates of \( \mu \) were comparable between single release and multiple release and both were accurate when \( m \) was small. However, the single release suffered from severe undercoverage because \( \omega \) was an underestimate for \( \sigma^2_1 \). In the multiple release, \( \sigma^2_m \) estimated via Eq. (2) had minimal bias and all the CPs were at the nominal level for small \( m \). Figure 3 suggests that \( \sigma^2_m > \sigma^2_1 \); in other words, if \( \sigma^2_2 \) could be correctly quantified, releasing a single synthetic data set would be more efficient from the inferential (and computational) perspective than releasing multiple sets.

\( \sigma^2_m \) increased with \( m \) for \( 2 \leq m \leq 40 \) when \( n = 1000 \) and for \( 2 \leq m \leq 10 \) when \( n = 100 \), suggesting original information accumulation could not catch up with the increase in perturbation as \( m \) increased. This was in contrast to the non-DP FSS, where \( \sigma^2_m \) is bound to decrease with \( m \) and eventually approaches \( \omega \). Figure S1 shows a non-monotonic relationship between \( \sigma^2_m \) and \( m \) across \( 2 \leq m \leq 500 \) for both \( n = 100 \) and \( n = 1000 \) (\( \sigma^2_m \) reached the maximum around \( m \) 15 to 30 when \( n = 100 \), and around 70 to 100 when \( n = 1000 \) depending on the sanitizer). The decrease in \( \sigma^2_m \) should not be taken simply as evidence for increased original information after a certain \( m \). At \( m \) so large, \( \bar{x} \) was severely perturbed via the sanitizers, the synthetic data sets were bad surrogates for the original data, and the inferences based on the synthetic data were no longer reliable.

4 Discussion

The lack of consistent and robust assessment of disclosure risk in released data is a long-standing problem in SDL, and makes it difficult to evaluate the “safety” of the released data and to compare original information preservation among different DS methods of individual-level microdata. The modips approach circumvents the need to assess disclosure risk, and guards against the worst disclosure scenarios at a specified privacy budget in a robust manner by incorporating DP in the synthesis process. No assumptions about knowledge and behaviors of data intruders or data attack models are made in modips. The privacy budget parameter can be used as a tuning parameter in balancing privacy protection and original information preservation.

We focused the discussion of the modips in the context of the pure \( \epsilon \)-DP. Extensions of modips to softer versions of DP, such as the \((\epsilon, \delta)\)-pDP are straightforward. The only step that needs modification is to replace a sanitizer of \( \epsilon \)-DP with a mechanism that satisfies a softer version of DP in the sanitization of sufficient statistics (e.g., the Gaussian mechanisms of \((\epsilon, \delta)\)-pDP). We presented modips in the context of the full sample synthesis and argued against applying DP to partial synthesis. It may be possible to extend modips to full population synthesis, which will make an interesting topic for future research, though it can technically challenging given the missing values in the unsampled set of a population and the extra sampling step to release data.

The synthesis stage of the modips algorithm has two steps: draw parameters from their posterior distribution given sanitized Bayesian sufficient statistics, and sample data given the drawn param-
eters. The two-step synthesis can be viewed as a Bayesian data augmentation scheme of sampling data directly from the exact distribution conditional on the sanitized sufficient statistics. Though the data augmentation approach involves sampling from the posterior distributions of model parameters, it is likely to be less computationally intensive than the direct sampling, which can be hard due to either the lack of a closed form of the exact conditional distribution or the satisfaction of constraints imposed by the sanitized sufficient statistics.

If a data set is mainly for exploratory data analysis and data mining with minimal involvement of statistical inferences and uncertainty quantification, releasing a single surrogate data set is workable; otherwise, multiple sets will need to be released or the sanitization mechanism has be modelled when analyzing the synthetic data in order to obtain valid inferences. We expect there exists an “optimal” $m$ in a modips mechanism that maximizes original information preservation at a prespecified privacy budget. This “optimal” $m$ may vary case by case, and may depend on sample size, number and types of sufficient statistics, and possibly sanitizers, among others. If everything is equal, it is preferable to use relatively small $m$ so that each synthesis can receive a reasonable amount of budget as long as it is large enough to capture the between-set variance. Small $m$ also helps save computational/storage cost. The simulation study was an example where smaller $m$ (3 to 5) delivered better inferential performance than larger $m$. We will continue to investigate theoretically and empirically the topic on choosing $m$ in general settings.

The modips algorithm can be difficult to implement when a data set contain a large number of attributes (large $p$) of various types. The difficulty resides in the construction of a parsimonious but representative model, identification and sanitization of sufficient statistics, and Bayesian computation in the high-dimensional setting. Bayesian model construction when $p$ is large can be daunting, mainly due to decreased computational efficiency in the presence of a large number of parameters. Recent development and advancement in efficient Bayesian computations such as variational Bayes, Hamitonian Monte Carlo, sequential Monte Carlo can be leveraged in the practical implementation of modips. Sometimes it might be more efficient and convenient to sanitize the likelihood (or log-likelihood) directly if it is bounded, instead of the sufficient statistics when the dimension is high or some approximation has to be employed in order to identify a set of sufficient statistics (see an example in Bowen and Liu (2016)).

Big data privacy is an exciting research topic and there is an urgent need for efficient and practically feasible privacy-protective data release methods. We hope our work on the modips helps to raise the awareness of data privacy, and make the concept of DP better known and utilized among statisticians. The immediate future work will focus on testing the modips approach in real-life data sets and developing approaches to optimize original information preservation at a prespecified privacy budget in modips.

**Supplementary Materials**

Supplementary materials that contain additional simulation results are available at [http://www3.nd.edu/~fliu2/#tools](http://www3.nd.edu/~fliu2/#tools)

**Appendix**

**A Proof of Theorem 4**

\[
\Pr(\theta^* \in Q|x) = \mathbb{E}(\mathbb{E}(1(\theta^* \in Q)|s^*)|x) = \iint 1(\theta^* \in Q) f(\theta^*|s^*) f(s^*|x) d\theta^* ds^* = \iint 1(\theta^* \in Q) f(\theta^*|s^*) f(s^*|x) d\theta^* ds^* \leq \epsilon^c \iint 1(\theta^* \in Q) f(\theta^*|s^*) f(s^*|x') d\theta^* ds^* \leq \epsilon^c \iint 1(\theta^* \in Q) f(\theta^*|s^*) f(s^*|x') d\theta^* ds^*.
\]
Since \( \int I(\theta^* \in Q) f(\theta^* | s^*) f(s^* | x') d\theta^* ds^* = E(\mathbb{E}(I(\theta^* \in Q) | s^*) | x') = Pr(\theta^* \in Q | x') \), then \( e^{-\epsilon} Pr(\theta^* \in Q | x') \leq Pr(\theta^* \in Q | x) \leq e^{+\epsilon} Pr(\theta^* \in Q | x') \), \( e^{-\epsilon} \leq \frac{Pr(\theta^* \in Q | x)}{Pr(\theta^* \in Q | x')} \leq e^{+\epsilon} \), and so \( \theta^* \) is released with \( \epsilon \)-DP. \( \Pr(\hat{x}^* \in Q | x) = E(E(I(\hat{x}^* \in Q) | \theta^*)) = \int \int I(\hat{x}^* \in Q) f(\hat{x}^* | \theta^*) f(\theta^* | x) d\hat{x}^* d\theta^* = \int \int I(\hat{x}^* \in Q) f(\hat{x}^* | \theta^*) f(\theta^* | x') d\hat{x}^* d\theta^* \). Since \( \theta^* \) is released with \( \epsilon \)-DP as proved above, that is, \( e^{-\epsilon} \leq \frac{f(\theta^* | x)}{f(\theta^* | x')} \leq e^{+\epsilon} \), \( e^{-\epsilon} \int \int I(\hat{x}^* \in Q) f(\hat{x}^* | \theta^*) f(\theta^* | x) d\hat{x}^* d\theta^* \leq \int \int I(\hat{x}^* \in Q) f(\hat{x}^* | \theta^*) f(\theta^* | x') d\hat{x}^* d\theta^* \leq e^{+\epsilon} \int \int I(\hat{x}^* \in Q) f(\hat{x}^* | \theta^*) f(\theta^* | x') d\hat{x}^* d\theta^* \). Since \( \int \int I(\hat{x}^* \in Q) f(\hat{x}^* | \theta^*) f(\theta^* | x') d\hat{x}^* d\theta^* = E(E(I(\hat{x}^* \in Q) | s^*) | x') = \Pr(\hat{x}^* \in Q | x') \), then \( e^{-\epsilon} \Pr(\hat{x}^* \in Q | x') \leq \Pr(\hat{x}^* \in Q | x) \leq e^{+\epsilon} \Pr(\hat{x}^* \in Q | x') \), and \( \hat{x}^* \) is released with \( \epsilon \)-DP.

\[ \text{Proof of Lemma 5} \]

Let \( \hat{\theta}^* \) be the consistent estimator for \( \theta^* \) based on synthetic data \( \hat{x}^* \) (e.g., MLEs, posterior means). Assume \( s^* \xrightarrow{P} s \), by the continuous mapping theorem, \( h(s^*) \xrightarrow{P} h(s) \). Denote the consistent estimator of \( \theta \) based on \( x \) by \( h(s) \), that is, \( h(s) \xrightarrow{P} \theta \). Since \( \theta^* \) is drawn from the same posterior distribution given \( s^* \) as \( \theta \) would be when given \( s \), then \( h(s^*) \) is consistent for \( \theta^* \). Therefore,

\[
\begin{align*}
E_{\hat{\theta}^* | \theta}(\hat{s}^* - \theta)^2 &= E_{\hat{\theta}^* | \theta}(E_{\hat{\theta}^* | \hat{s}^*}(\hat{\theta}^* - \theta)^2) = E_{s^* | \theta}(E_{\theta^* | s^*}(E_{\hat{\theta}^* | \theta^*}(\hat{\theta}^* - \theta)^2)) \\
&= E_{s^* | \theta}(E_{\theta^* | s^*}(E_{\hat{\theta}^* | \theta^*}(\hat{\theta}^* - \theta)^2)) \\
&= E_{s^* | \theta}(E_{\theta^* | s^*}(E_{\hat{\theta}^* | \theta^*}(\hat{\theta}^* - \theta)^2)) + E_{s^* | \theta}(E_{\theta^* | s^*}(\hat{\theta}^* - h(s^*)) + E_{s^* | \theta}(h(s^*) - h(s))^2 + E_{s^* | \theta}(h(s^*) - h(s))^2 + 2E_{s^* | \theta}(E_{\theta^* | s^*}(h(s^*) - h(s)))E_{\hat{\theta}^* | \theta^*}(\hat{\theta}^* - \theta)^2)
\end{align*}
\]

By Chebyshev’s inequality, \( \hat{\theta}^* \) is consistent for \( \theta \).

\[ \text{Proof of Theorem 6} \]

**Part a.** Let \( \hat{\theta}^{(k)} \) denote the posterior mean of \( \theta \) given \( \hat{x}^{(k)} \). By the large-sample Bayesian theorem, it is a consistent estimator for \( \theta^{(k)} \); by Lemma 5, \( \hat{\theta}^{(k)} \) is also consistent for \( \theta; \hat{\theta}^* = m^{-1} \sum_{k=1}^{m} \hat{\theta}^{(k)} \) is consistent for \( \theta \) applying the Slutzky’s theorem to \( \hat{\theta}^{(k)} \) for \( k = 1, \ldots, m \).

**Part b.** The proof is based in a similar framework as in [Rubin (1987)] (inferences from multiple imputation) and [Reiter (2003)] (inferences from partial sample synthesis without sanitization), with necessary modifications to take into account the extra variability introduced during the sanitization process (\( s \) to \( s^* \)). Denote a synthetic data set by \( \hat{x}^{(k)} \), the sufficient statics by \( s \) and \( \hat{s}^{(k)} \) that are associated with the same model but applied to \( x \) and \( \hat{x}^{(k)} \). We aim to estimate the posterior variance of \( \theta \) given \( \hat{x}^{(1)}, \ldots, \hat{x}^{(m)} \).

\[
\begin{align*}
V(\theta | \hat{x}^{(k)}) &= V(E(\theta | x) | \hat{x}^{(1)}, \ldots, \hat{x}^{(m)}) + E(V(\theta | x) | \hat{x}^{(1)}, \ldots, \hat{x}^{(m)}) \\
&= V(g(s) | \hat{x}^{(1)}, \ldots, \hat{x}^{(m)}) + E(v(s) | \hat{x}^{(1)}, \ldots, \hat{x}^{(m)}) \\
&= V(g(s)) + g(\hat{s}^{(1)}, \ldots, g(\hat{s}^{(m)})) + E(v(s) | v(\hat{s}^{(1)}), \ldots, v(\hat{s}^{(m)})),
\end{align*}
\]

where \( g(s) \) is the posterior mean and \( v(s) \) is the posterior variance of \( \theta \) given the original data \( x \), both of which are unknown since \( x \) is not released. Since the same model is applied to \( x \) and \( \hat{x}^{(k)} \), \( g(\hat{s}^{(k)}) \) is thus the posterior mean and \( v(\hat{s}^{(k)}) \) is the posterior variance of \( \theta^{(k)} \) given \( \hat{x}^{(k)} \). By the
large-sample Bayesian theory, as $n \to \infty$,

$$\theta|s \sim N(g(s), v(s))$$  \hspace{1cm} (C.2)

$$\theta^{(k)}|s^{(k)} \sim N(g(s^{(k)}), v(s^{(k)}))$$ \hspace{1cm} (C.3)

Given Eq. (C.2), we have $g(s^{(k)})|\theta^{(k)} \sim N(\theta^{(k)}, v(s^{(k)}))$, and thus

$$m^{-1} \sum_{i=1}^{m} g(s^{(k)})|\theta^{(k)} \sim N(m^{-1} \sum_{i=1}^{m} \theta^{(k)}, m^{-2} \sum_{i=1}^{m} v(s^{(k)}))$$ \hspace{1cm} (C.4)

Based on Eq. (C.3), we have $m^{-1} \sum_{i=1}^{m} \theta^{(k)}|\bar{s}^{(k)} \sim N(m^{-1} \sum_{i=1}^{m} g(\bar{s}^{(k)}), m^{-2} \sum_{i=1}^{m} v(\bar{s}^{(k)}))$ \hspace{1cm} (C.5)

Since the sanitized $s^* \overset{P}{\to} s$ as $n \to \infty$, then by the continuous mapping theorem, $g(s^{(k)}) \overset{P}{\to} g(s)$ or $g(s^{(k)})|g(s) \overset{iid}{\sim} (g(s), v_s \to 0)$. Therefore, by the CLT as $m \to \infty$

$$g(s)|g(s^{(1)}), \ldots, g(s^{(m)}) \sim N(m^{-1} \sum_{i=1}^{m} g(s^{(k)}), m^{-1} v_s)$$ \hspace{1cm} (C.6)

Taken Eqs (C.6), (C.4) and (C.5) together, we have

$$g(s)|s^{(1)}, \ldots, s^{(m)} \sim N(m^{-1} \sum_{i=1}^{m} g(s^{(k)}), m^{-1}(v_s + m^{-1} \sum_{i=1}^{m} (v(s^{(k)}) + v(\bar{s}^{(k)}))))$$ \hspace{1cm} (C.7)

$v_s$ represents the variability of the conditional variability of $g(s^{(k)})$ given $g(s)$ during the sanitization step, and $m^{-1} \sum_{i=1}^{m} v(s^{(k)})$ and $m^{-1} \sum_{i=1}^{m} v(\bar{s}^{(k)})$ represent the variance of the conditional distribution of $\bar{x}^{(k)}$ given $\theta^{(k)}$ and the variance the conditional distribution of $\theta^{(k)}$ given $s^{(k)}$, respectively. All taken together, $v_s + m^{-1} \sum_{i=1}^{m} (v(s^{(k)}) + v(\bar{s}^{(k)}))$ is the variability of $g(s)$ given $g(s^{(1)}), \ldots, g(s^{(m)})$; in other words, the variance of $g(s^{(1)}), \ldots, g(s^{(m)})$ is the variability $V(g(s)|g(s^{(1)}), \ldots, g(s^{(m)}))$. In a similar manner, we obtain the posterior distribution of $v(s)$ given $s^{(1)}, \ldots, s^{(m)}$, which is

$$v(s)|s^{(1)}, \ldots, s^{(m)} \sim N(m^{-1} \sum_{i=1}^{m} v(s^{(k)}), m^{-1}(v_{s, s} + m^{-1} \sum_{i=1}^{m} (v_v(s^{(k)}) + v_v(\bar{s}^{(k)}))))$$ \hspace{1cm} (C.8)

Plug the conditional variance from Eq (C.7) and the conditional mean from Eq (C.8) in Eq (C.1), and Let $v_s + m^{-1} \sum_{i=1}^{m} (v(s^{(k)}) + v(\bar{s}^{(k)}))$ by $B$ and $m^{-1} \sum_{i=1}^{m} v(\bar{s}^{(k)})$ by $W$ as $m \to \infty$, then

$$V(\theta|\bar{x}^{(1)}, \ldots, \bar{x}^{(m)}) = m^{-1} B + W$$

For finite $m$, $B$ is estimated by $b = (m - 1) \sum_{i=1}^{m} (g(s^{(k)}) - \bar{\theta})^2$ and $W \sim m^{-1} \sum_{i=1}^{m} v(\bar{s}^{(k)})$. 

**Part c.** Combining the results from parts a) and b), we have $\theta|\tilde{x}^{(1)}, \ldots, \tilde{x}^{(m)} \sim N(\theta^*, m^{-1}B + W)$.

Distribution of $\theta$ given $\tilde{x}^{(1)}, \ldots, \tilde{x}^{(m)}$ for finite $m$ can be obtained in a similar manner as in Reiter [2003], which is $f(\theta|\tilde{x}^{(1)}, \ldots, \tilde{x}^{(m)}) \sim t_{\nu}(\theta^*, m^{-1} b + \bar{\omega})$ with $\nu = (m - 1)(1 + m \bar{\omega}/b)^2$.

### D Proof of Proposition 8

**Part a.** The scale parameter of the Laplace distribution in the conjoint sanitization can be written as $\lambda = \delta_s \epsilon^{-1} = r \delta_s \epsilon^{-1}$, where $\delta_s$ is the average GS. When $u_i \equiv r^{-1}$, every statistic receives the same amount of budget $\epsilon/r$ in the individual sanitization, and the scale parameter of the Laplace distribution for $s_i$ is $\lambda_i = \delta_i (\epsilon w_i)^{-1} = r \delta_i \epsilon^{-1}$, which is $< \lambda$ if $\delta_i < \delta_s$, and $> \lambda$ if $\delta_i > \delta_s$.

**Part b.** The scale parameter of the Laplace distribution for $s_i$ with individual sanitization is $\delta_i (\epsilon w_i)^{-1} = \epsilon^{-1} \delta_i (\epsilon s_i)^{-1} \sum_{i=1}^{r} \delta_i = \epsilon^{-1} \sum_{i=1}^{r} \delta_i$, which is same the as the scale parameter the Laplace distribution in the conjoint sanitization.
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