Randomized Addition of Sensitive Attributes for I-diversity

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Keywords: Privacy, Data mining, Anonymization.

Abstract: When a data holder wants to share databases that contain personal attributes, individual privacy needs to be considered. Existing anonymization techniques, such as *l*-diversity, remove identifiers and generalize quasiidentifiers (QIDs) from the database to ensure that adversaries cannot specify each individual's sensitive attributes. Usually, the database is anonymized based on one-size-fits-all measures. Therefore, it is possible that several QIDs that a data user focuses on are all generalized, and the anonymized database has no value for the user. Moreover, if a database does not satisfy the eligibility requirement, we cannot anonymize it by existing methods. In this paper, we propose a new technique for *l*-diversity, which keeps QIDs unchanged and randomizes sensitive attributes of each individual so that data users can analyze it based on QIDs they focus on and does not require the eligibility requirement. Through mathematical analysis and simulations, we will prove that our proposed method for *l*-diversity can result in a better tradeoff between privacy and utility of the anonymized database.

1 INTRODUCTION

In recent years, numerous organizations have begun to provide services related to Cloud computing that collect a great deal of personal information. This personal information can be shared with other organizations so that they can subsequently create new services. However, the data holder should not publish any information that identifies an individual's sensitive attributes.

A lot of research studies regarding anonymized databases of personal information have been proposed (e.g., (Samarati, 2001; LeFevre et al., 2008; Wu et al., 2013)). Most of existing methods consider that the data holder has a database of the form *explicit identifiers*, *quasi-identifiers* (*QIDs*), *sensitive attributes*, where explicitly identifiers are attributes that explicit identify individuals (e.g., name and phone number), QIDs are attributes that could be potentially combined with public directories to identify individuals (e.g., zip code, age), and sensitive attributes are personal attributes of private nature (e.g., disease) (Fung et al., 2010).

The *l*-diversity technique (Machanavajjhala et al., 2007), which enhances *k*-anonymity (LeFevre et al., 2006), is one of the major anonymization techniques. This technique removes explicit identifiers and generalizes QIDs to ensure that the adversaries cannot

specify each individual's sensitive values with confidence greater than 1/l. For example, Table 1 shows the original patient database that a hospital wants to publish. Consider that Name is the explicit identifier, Sex, Age, Address, and Job are the QIDs, and Disease is the sensitive attribute. Suppose that an adversary knows that Becky is included in the database and knows Becky's QIDs. From the database, the adversary can identify Becky's sensitive value as Sty with 100% confidence, even if we remove all the Names from Table 1.

Table 2 shows one result of the *l*-diversity technique where *l* is set to 2. Even if the adversary knows that Becky is included in Table 2 and knows Becky's QIDs, he cannot know whether Fever or Sty is Becky's disease. That is, he cannot identify Becky's sensitive value with greater than 50% (=1/2) confidence. Table 3 is another result of the *l*-diversity technique. If Tables 2 and 3 are both published, the adversary can identify Becky's disease as Sty with 100% confidence, so the data holder usually anonymizes Table 1 once and publishes the anonymized table (i.e., either Table 2 or Table 3 only) to the all data users.

Therefore, the data holder should anonymize the database based on one-size-fits-all measures. Suppose that two data users, A and B, receive Table 2, and suppose that data user A wants to know the difference between male and female, while data user B wants to

Table 1: Patient table.

Name	Sex	Age	Address	Job	Disease
Alex	М	41	13000	Artist	Fever
Becky	F	41	17025	Artist	Sty
Carl	Μ	50	13021	Writer	Cancer
Diana	F	51	14053	Nurse	HIV
Edward	Μ	68	15000	Writer	Chill
Flora	F	69	16022	Nurse	HIV
Greg	Μ	72	13001	Artist	Cut
Hanna	F	77	17001	Artist	Cancer

Table 3: 2-diversity by existing method (2).

Sex	Age	Address	Job	Disease
М	41-72	13*	Artist	Fever
F	41-77	17*	Artist	Sty
Μ	50-68	13*-15*	Writer	Cancer
F	51-69	14*-16*	Nurse	HIV
Μ	50-68	13*-15*	Writer	Chill
F	51-69	14*-16*	Nurse	HIV
Μ	41-72	13*	Artist	Cut
F	41-77	17*	Artist	Cancer

know the differences among age. Although data user B may know the differences among age from Table 2, data user A cannot know any differences between sexes because the values of sex are all generalized. On the other hand, suppose that data users A and B receive Table 3 rather than Table 2. In this case, data user A can analyze Table 3, but data user B cannot analyze it effectively because ages are too generalized.

In this paper, we deal with this specific problem. Our proposed method keeps QIDs unchanged and adds l-1 dummy values into sensitive attributes in order to satisfy *l*-diversity. The resulting anonymized database is shown in Table 4. Because all QIDs are not changed, all data users can analyze the anonymized database in their preferred ways. We propose a protocol that estimates the original data distribution of sensitive values according to each data user's preferred QIDs from the anonymized database, as well as an anonymization protocol for the data holder. If the number of records in the table is large, data users can analyze it with a high degree of accuracy by the proposed method.

It is worth noting that we need not protect QIDs when we use *k*-anonymity or *l*-diversity as privacy models. Although QIDs of databases may be anonymized as a result of anonymization, most of major privacy models such as *k*-anonymity, *l*-diversity and *t*-closeness offer no guarantee of anonymizing QIDs because their aims are not to protect QIDs but to protect sensitive attributes.

Moreover, one major limitation of existing techniques for l-diversity is the eligibility requirement,

Table 2: 2-diversity by existing method.

Sex	Age	Address	Job	Disease
*	41	13*-17*	Artist	Fever
*	41	13*-17*	Artist	Sty
*	50-51	13*-14*	*	Cancer
*	50-51	13*-14*	*	HIV
*	68-69	15*-16*	*	Chill
*	68-69	15*-16*	*	HIV
*	72-77	13*-17*	Artist	Cut
*	72-77	13*-17*	Artist	Cancer

Table 4: 2-diversity by proposed method.

Sex	Age	Address	Job	Disease
Μ	41	13000	Artist	{Fever, Flu}
F	41	17025	Artist	{Fever, Sty}
М	50	13021	Writer	{Cold, Cancer}
F	51	14053	Nurse	{HIV, Pus}
Μ	68	15000	Writer	{Chill, Cut}
F	69	16022	Nurse	{Cold, HIV}
Μ	72	13001	Artist	{Cut, Fever}
F	77	17001	Artist	{Cancer, Flu}

which requires that "at most |T|/l records of T carry the same sensitive value" where |T| represents the number of records of an original database T (Xiao et al., 2010). Our proposed method does not require the eligibility requirement, therefore our method can be applied to any databases when l is less than the number of distinct sensitive values.

The rest of this paper is organized as follows. Section 2 presents the models of applications and attacks. Section 3 defines privacy and utility as used in this paper. Section 4 discusses the related methods. Section 5 presents the design of our algorithm. The results of a mathematical analysis and our simulations are presented in Section 6, and Section 7 concludes the paper.

2 ASSUMPTIONS

2.1 Application Model

A data holder has a database that contains personal information. Such information consists of explicit identifiers, QIDs, and sensitive attributes as described in Section 1. The database can contain non-sensitive attributes that are not explicit identifiers, QIDs, or sensitive attributes. We can publish these non-sensitive attributes without them being anonymized if they are important for data analysis.

We assume that the data holder wants to publish the database for collaborating with data users. Be-

Sex	Age	Address	Job	Disease
М	31	13000	Artist	Fever
Μ	31	13000	Artist	Sty
Μ	52	13021	Writer	Cancer
Μ	52	13021	Writer	HIV

Table 5: *l*-diversity does not protect any values of QIDs when the original database satisfies *l*-diversity (here, l=2).

cause of privacy concerns, the data holder wants to anonymize the database in order to ensure that any adversaries cannot identify each individual's sensitive attribute.

In this paper, we assume that the data user wants to know what kinds of people tend to have certain sensitive values. As a result, we might find that older men are more likely to get lung cancer than young women if the anonymized table contains age and sex as QIDs (or non-sensitive attributes) and disease as a sensitive attribute.

We assume that we must protect sensitive attributes, but we do not need to protect QIDs. This assumption is widely accepted in research studies related to k-anonymity, l-diversity, and so on. If there are l records that have the same values of QIDs, these records are not anonymized in any methods for l-diversity. For example, if a data holder want to anonymize Table 5, the values of QIDs are not anonymized at all when l=2.

If we want to protect some of the QIDs, then we can treat them as *sensitive attributes*.

2.2 Attack Model

We assume that the data holder is an honest entity, but the data users may be malicious entities. Moreover, we assume that the data users may collude with each other to identify each individual's sensitive attributes.

3 NOTATIONS AND MEASUREMENTS

3.1 Notations

Let *T* and T^* denote the original and anonymized database respectively. Let *N* denote the number of records of *T* or T^* and let r_i and r_i^* denote the *i*-th record of *T* and T^* , respectively.

S represents the domain of possible sensitive attributes that can appear in the database and s_i means the *i*-th value of *S* (i = 0, ..., |S| - 1). Let \mathfrak{Q} be the set of QIDs that a data user wants to analyze and let $\mathfrak{Q}(i)$ be the *i*-th QID of \mathfrak{Q} ($i = 0, ..., |\mathfrak{Q}| - 1$).

Let Q(i) denote the domain of possible values that can appear in $\mathfrak{Q}(i)$ and let $q(i)_j$ denote the *j*-th value of Q(i).

For example, *S* is {Fever, Sty, ...} in Table 1. \mathfrak{Q} is {Sex}, $\mathfrak{Q}(0)$ is Sex, $\mathcal{Q}(0)$ is {M, F} and $q(0)_0$ is M and $q(0)_1$ is F if a data user wants to know the difference between the sexes (male and female). In this case, the data user might find that people who are men have the highest risk of getting cancer.

For another example, if the data user wants to analyze sensitive attributes based on the combination of sexes and categories of age ([0-9], [10-19], ..., [90-99]), \mathfrak{Q} is {Sex, Age}, Q(0) is {M, F} and Q(1) is {[0-9], ..., [90-99]}. In this case, the data user might find that men ages between 30-39 have the highest risk of getting cancer.

The value of a sensitive attribute of a record r is represented by E(r). For example, $E(r_0)$ returns Fever in Table 1. In a similar way, $E(r_0^*)$ returns {Fever, Flu} in Table 4.

Let *C* denote all the combinations of the elements of $Q(0), \dots, Q(|\mathfrak{Q}| - 1)$: $C = Q(0) \times Q(1) \times \dots \times Q(|\mathfrak{Q}| - 1).$ (1)

Let c_i denote the *i*-th element of C (i = 0, ..., |C| - 1). For example, if the data user wants to analyze sensitive attributes based on sexes and categories of age ([0-9], ..., [90-99]), c_0 is (M, [0-9]), c_1 is (M,

3.2 Measurement of Privacy

 $[10-19]), ..., c_{|C|-1}$ is (F, [90-99]).

Many existing papers use l-diversity as a privacy measurement (Machanavajjhala et al., 2007; Xiao et al., 2010; Cheong, 2012). Although there are several variations of l-diversity, we use a simple interpretation.

Definition 1 (QID group): We denote a set of records that has same values of all QIDs as a QID group.

For example, the first and second records in Table 2 are a QID group because their values of QIDs are the same (*, 41, 13*-17*, Artist).

Definition 2 (*l*-diversity): The anonymized table T^* satisfies *l*-diversity if the relative frequency of each of the sensitive values does not exceed 1/l for each QID group of T^* .

This definition of *l*-diversity is also widely used, such as in the cases of (Kenig and Tassa, 2011; Xiao and Tao, 2006; Nergiz et al., 2013).

For example, all QID groups of Tables 2 and 3 have 2 records and 2 distinct sensitive values. Therefore, these tables satisfy 2-diversity. Then, see Table 4. Each QID group has only one record, but each record has 2 distinct sensitive values. We consider Table 4 also satisfies 2-diversity in this paper.

3.3 Measurement of Utility

A data user estimates the distribution of sensitive attributes for each c_i (i = 0, ..., |C| - 1) as described in Section 2. Let $V_{i,j}$ denote the number of records that are categorized to c_i according to their QIDs and have a sensitive attribute s_j in the original table. Also, let $\widehat{V_{i,j}}$ denote the estimated number of values of $V_{i,j}$ for the data user.

Let N_i denote the number of records that are categorized to c_i according to their QIDs. We can use the Mean Squared Errors (MSE) between $\widehat{V_{i,j}}/N_i$ and $V_{i,j}/N_i$ to quantify the utility for category c_i :

$$\sigma^{2}(i) = \frac{1}{|S|} \sum_{j=0}^{|S|-1} \left(\frac{V_{i,j}}{N_{i}} - \frac{\widehat{V_{i,j}}}{N_{i}}\right)^{2}$$
(2)

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This utility measurement is widely used in many studies (Xie et al., 2011; Huang and Du, 2008; Groat et al., 2012).

4 RELATED WORK

Many algorithms for *k*-anonymity have been proposed. The basic definition of *k*-anonymity is as follows:

If one record in the table has some value QID, at least k - 1 other records also have the value QID (Fung et al., 2010).

Due to the fact that finding an optimal *k*-anonymity is NP-hard (Meyerson and Williams, 2004), many existing algorithms for *k*-anonymity search for better anonymization through heuristic approaches.

Datafly (Sweeney, 2002) is a bottom-up greedy approach and it generalizes QIDs until all combinations of QIDs appear at least k times. Mondrian (LeFevre et al., 2006), which is an efficient top-down greedy approach, is widely used in many other studies as a base method.

Although *k*-anonymity can protect individual identities, there are times when it cannot protect individuals' sensitive attributes. For example, the fourth and sixth rows in Table 3 are an equivalence class because their QIDs are all the same (F, 51-69, 14*-16*, Nurse). Suppose that an adversary knows Diana's QIDs and she is included in Table 3. The adversary cannot identify which row of the fourth and sixth rows is Diana's, but the adversary can identify Diana's sensitive attribute is HIV because the sensitive attributes of both the rows are HIV.

l-diversity (Machanavajjhala et al., 2007) ensures that the probability of identifying an individual's sensitive attribute is less than or equal to 1/l. There are many research studies related to *l*-diversity (e.g., (Kabir et al., 2010; Cheong, 2012)).

Although many algorithms for *k*-anonymity or *l*diversity other than the research studies previously mentioned have been proposed, most of all algorithms keep sensitive attributes unchanged and generalize QIDs. Changing QIDs leads to the problems mentioned in Section 1.

If all data users analyze the anonymized table in the same way or if we believe that all data users do not collude with each other for identifying an individual's sensitive attributes, then we can use workload-aware anonymization techniques (LeFevre et al., 2008). However, in the situation described in Section 2, we need other anonymization techniques that do not rely on those assumptions.

Xiao et al. (Xiao and Tao, 2006) and Sun et al. (Sun et al., 2009) proposed an algorithm based the Anatomy technique. Their algorithms publish two tables; one is a non-sensitive table that contains QIDs without change and the other is a sensitive table. By joining of the two tables, data users can analyze them. Because the resulting table have many dummy records (e.g., several times of the number of original records), such anonymized data may become useless for data analysis.

TP (Xiao et al., 2010) is the algorithm with a non-trivial bound on information loss. The authors compared TP with other techniques for *l*diversity (single-dimensional generalization method TDS (Fung and Yu, 2005) and multi-dimensional generalization method Hilbert (Ghinita, 2007)) and they proved that TP outperforms these single- or multidimensional methods.

We compare Anatomy and TP with our proposed method in Section 6.

To the best of our knowledge, all existing techniques for *l*-diversity requires the eligibility requirement as described in Section 1. Therefore, if more than |T|/l records of original database *T* have the same sensitive value, we cannot anonymize the database.

The privacy measure of *t*-closeness (Li et al., 2007) is stronger than *l*-diversity. It requires that the distribution of sensitive values in each set of records that have the same QID values should be close to the distribution of the whole database.

Differential privacy (Dwork, 2006; Domingo-Ferrer, 2013) makes user data anonymous by adding noise to a dataset so that an attacker cannot determine whether or not a particular point of user data is included. Although differential privacy represents one of the strongest privacy models (Nikolov et al., 2013), the data holder cannot publish the anonymized database. The data holder should manage the original database and respond to each data user's query every time. Therefore, the data holder's cost is high, data users cannot analyze the anonymized database freely, and it is vulnerable to malicious intrusion (Clifton and Anandan, 2013). In this paper, we assume that we need anonymization techniques other than differential privacy because of these limitations.

5 PROPOSAL

Our proposed method consists of two steps; randomization for the data holder and reconstruction for the data user.

For the data holder, we generate and add l-1 values randomly for a sensitive attribute of each record in the original database.

For the data user, the user first determines which QIDs should be analyzed in terms of the relationships between the QIDs and the sensitive attributes. Then, the number of records is estimated in each combination of the QIDs and the sensitive attribute. For example, suppose that the domain of the sensitive attribute contains HIV, Fever, and Cancer. Also, suppose that the data user wants to analyze the difference between male and female. In this case, we should estimate each number of records in which a sensitive attribute is HIV, Fever, and Cancer, and where Sex is Male and Female, respectively.

5.1 Anonymization Protocol

We generate and add distinct l-1 values randomly for a sensitive attribute of each record in the original database for the data holder. Algorithm 1 shows the anonymization protocol.

The function rand(S) returns an element of S randomly. The data holder executes Algorithm 1 for each record.

THEOREM 5.1. Algorithm 1 can always generate *l*-diversity Table T^* from an original Table T if |S| is larger than or equal to *l*.

Proof. After conducting Algorithm 1 for Table *T*, the algorithm generates an anonymized Table T^* in which each record has *l* distinct sensitive values. Suppose that a QID group has δ ($\delta = 1, ..., N$) records of T^* . The possible maximum number of occurrences of each sensitive value within the δ records is δ because each sensitive value does not appear more than once in a record. On the other hand, the total number of sensitive values in the QID group is $\delta \times l$ if we use

- **Input:** Domain of a sensitive attribute *S*, Privacy level *l*
- **Output:** Set of anonymized sensitive values for record *r*
- 1: Creates empty set R
- 2: $R \leftarrow R \cup \{E(r)\}$
 - /*Generates and adds dummy sensitive attributes*/
- 3: while |R| < l do
- 4: $R \leftarrow R \cup \{rand(S)\}$
- 5: end while

6: **return** *R*

Algorithm 1 because each record has l sensitive values, thus, the possible maximum relative frequency of each of the sensitive values in the QID group is 1/l.

5.2 Estimation Protocol

The data user who received the anonymized table estimates the distribution of sensitive attributes for each c_i (i = 0, ..., |C| - 1). We use $V_{i,j}$ to represent the *ac*-*tual* number of records, which are categorized to c_i and have a sensitive attribute s_j . Let $\widehat{V_{i,j}}$ denote the *estimated* $V_{i,j}$.

First, the data user counts how many records that are categorized c_i occur in the anonymized database, that is,

$$N_{i} = \sum_{h=0}^{N-1} G(r_{h}^{*}, c_{i}), \text{ where } G(r^{*}, c) =$$

$$\begin{cases} 1 \quad (r^{*'} \text{s QIDs are categorized to } c) \\ 0 \quad (otherwise) \end{cases}$$
(3)

In a similar way, the data user counts how many records that are categorized to c_i and have a set of sensitive attributes that contain s_j in the anonymized database:

$$W_{i,j} = \sum_{h=0}^{N-1} H(r_h^*, c_i, s_j), \text{ where } H(r^*, c, s) = \begin{cases} 1 & (r^{*'} \text{s QIDs are categorized to } c \text{ and } s \in E(r^*)) \\ 0 & (otherwise) \end{cases}$$

If a record *r* has s_j as its original sensitive attribute, then s_j is included in $E(r^*)$ with probability 1 and $s_{j_2}s.t., j \neq j_2$ is included in $E(r^*)$ with probability

$$P_E = \frac{l-1}{|S|-1}.$$
 (5)

Let the $W_{i,j}$ be the maximum likelihood estimate of $W_{i,j}$. Then, we have

$$\widehat{W_{i,j}} = N_i - \sum_{j_2 \neq j} (1 - P_E) \widehat{V_{i,j_2}}.$$
 (6)

The data user constructs a linear system of equations in |S| variables of $\widehat{V_{i,j}}$ (j = 0, ..., |S| - 1) from Equation 6 for each c_i . Here, we set the value of $W_{i,j}$ calculated from T^* by Equation 4 to $\widehat{W_{i,j}}$ in Equation 6. By solving the linear system of equations, the data user gets $\widehat{V_{i,j}}$ for each i = 0, ..., |C| - 1 and j = 0, ..., |S| - 1. Each value of $\widehat{V_{i,j}}$ is an unbiased maximum likelihood estimate of $V_{i,j}$.

We show this estimation protocol in Algorithm 2. A data user executes this algorithm for each c_i (i = 0, ..., |C| - 1) based on his own C.

Algorithm 2: Server protocol for c_i .

- **Input:** Anonymized database T^* , Domain of a sensitive attribute S
- **Output:** Distribution of sensitive attributes in c_i 1: Creates Array W, \hat{V}
- /*Calculates N_i*/
 2: N_i ⇐ result calculated by Eq. 3
 /*Calculates each W_{i,i}*/
- 3: **for** j = 0, ..., |S| 1 **do**
- 4: $W_{i,j} \leftarrow$ result calculated by Eq. 4
- 5: end for
- /*Calculates P_E*/
- 6: P_E ⇐ result calculated by Eq. 5 /*Creates and solves the linear system of equations*/
- 7: Creates Eq. 6 for all j = 0, ..., |S| 1

8: **for**
$$j = 0, ..., |S| - 1$$
 do

- 9: $\hat{V}_{i,j} \leftarrow$ each result calculated by the linear system of equations
- 10: end for
- 11: return $\widehat{V_{i,j}}$ (j = 0, ..., |S| 1)

5.3 Expectation of MSE

The data user should understand the expectation of the MSE between the estimated distribution and the original distribution of sensitive attributes in each category c_i (i = 0, ..., |C| - 1) for valuable data analysis. We propose the calculation method even if the data user does not have the original database.

From Equation 2, the expected value of MSE for a category c_i , i.e., $E[\sigma^2]$, is calculated by

$$E[\sigma^{2}] = \frac{1}{|S|} \sum_{j=0}^{|S|-1} E\left[\left(\frac{V_{i,j}}{N_{i}} - \frac{\widehat{V_{i,j}}}{N_{i}} \right)^{2} \right]$$
(7)

Because $\widehat{V_{i,j}}$ is the unbiased estimator of $V_{i,j}$, we have $E[\widehat{V_{i,j}}] = V_{i,j}$. Therefore, $E[(V_{i,j} - \widehat{V_{i,j}})^2]$ represents the variance of $\widehat{V_{i,j}}$. Let $Var(\widehat{V_{i,j}})$ be the variance $\widehat{V_{i,j}}$. The expected value of σ^2 is calculated by

$$E[\sigma^{2}] = \frac{1}{N_{i}^{2}} \frac{1}{|S|} \sum_{j=0}^{|S|-1} Var(\widehat{V_{i,j}}).$$
 (8)

The simultaneous equations created by Equation 6 for all j are the same as the following equation by deformation.

$$M \cdot \vec{V}^{\tau} = \vec{W}^{\tau},$$

where $M = \begin{pmatrix} 0 & 1 - P_E & \cdots & 1 - P_E \\ 1 - P_E & 0 & \cdots & 1 - P_E \\ \vdots & \vdots & \vdots & \vdots \\ 1 - P_E & 1 - P_E & \cdots & 0 \end{pmatrix},$
 $\vec{V} = (\widehat{V_{i,0}}, \widehat{V_{i,1}}, \dots, \widehat{V_{i,|S|-1}}),$
 $\vec{W} = (N_i - W_{i,0}, N_i - W_{i,1}, \dots, N_i - W_{i,|S|-1}).$ (9)

Therefore, we have

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$$\vec{V}^{\tau} = M^{-1} \cdot \vec{W}^{\tau}. \tag{10}$$

In general, if X and Y are random variables and a and b are constant, then we have

$$Var(aX+bY) = a^{2}Var(X) + b^{2}Var(Y) + 2abCov(X,Y), (11)$$

where Cov(X, Y) represents the covariance between X and Y. Let M_{j_1,j_2}^{-1} denote the j_1 -th row and j_2 -th column element of the inverse matrix of M. Because we have $\widehat{V_{i,j_1}} = \sum_{j_2} M_{j_1,j_2}^{-1} (N_i - W_{i,j_2})$ from Equation 10, we get from Equation 11,

$$Var(\widehat{V_{i,j_1}}) = \sum_{j_2} (M_{j_1,j_2}^{-1})^2 Var(N_i - W_{i,j_2}) + \sum_{\substack{j_2,j_3\\(j_2 \neq j_3)}} M_{j_1,j_2}^{-1} M_{j_1,j_3}^{-1} Cov(N_i - W_{i,j_2}, N_i - W_{i,j_3}).$$
(12)

Let P_j denote the probability that an arbitrary $E(r^*)$ contains s_j , let P_{j_2,j_3} denote the probability that it contains s_{j_2} and s_{j_3} , let $P_{j_2,\overline{j_3}}$ denote the probability that it contains s_{j_2} but does not contain s_{j_3} , and let $P_{\overline{j_2,j_3}}$ denote the probability that it contains s_{j_3} but does not

contain s_{j_2} . We get

$$\begin{aligned} &Var(N_i - W_{i,j_2}) = E[W_{i,j_2}^2] - E[W_{i,j_2}]^2 \\ &= \sum_{h=0}^{N_i} P_{j_2}^h (1 - P_{j_2})^{N_i - h} N_i C_h \cdot h^2 - (NP_{j_2})^2 \\ &= N_i P_{j_2} (1 - P_{j_2}), \end{aligned}$$

$$Cov(N_{i}-W_{i,j_{2}},N_{i}-W_{i,j_{3}}) = E[W_{i,j_{2}}W_{i,j_{3}}] - E[W_{i,j_{2}}]E[W_{i,j_{3}}]$$

$$= \sum_{h=0}^{N_{i}} \sum_{t=0}^{N_{i}-h-N_{i}} \sum_{u=0}^{h-t} \left[P_{j_{2},j_{3}}^{h} P_{j_{2},j_{3}}^{u} P_{j_{2},j_{3}}^{u} + (1-P_{j_{2},j_{3}}-P_{j_{2},j_{3}}-P_{j_{2},j_{3}})^{N_{i}-h-t-u} + N_{i}C_{h} \cdot N_{i}-hC_{t} \cdot N_{i}-h-tC_{u} \cdot (h+t)(h+u) \right] - N_{i}P_{j_{2}}N_{i}P_{j_{3}}$$

$$= N_{i}(P_{j_{2},j_{3}} + (P_{j_{2},j_{3}}+P_{j_{2},j_{3}})(P_{j_{2},j_{3}}+P_{j_{2},j_{3}})(N_{i}-1)) - N_{i}P_{j_{2}}N_{i}P_{j_{3}}$$
(13)

If we assume that each P_i is the same and it is ∇ . The time complexity of the anonymization protocol at independent of each other, we get

$$P_{j_{2}} = P_{j_{3}} = \frac{l}{|S|}$$

$$P_{j_{2},j_{3}} = \frac{l}{|S|} \cdot \frac{l-1}{|S|-1}$$

$$P_{j_{2},\overline{j_{3}}} = P_{\overline{j_{2}},j_{3}} = \frac{l}{|S|} \cdot (1 - \frac{l-1}{|S|-1})$$
(14)

We get from Equations 8, 12, 13 and 14

$$E[\sigma^{2}] = \frac{1}{N_{i}} \left[\frac{l}{|S|} \left(1 - \frac{l}{|S|}\right) \sum_{j_{2}} (M_{j_{1},j_{2}}^{-1})^{2} - \frac{l(|S|-l)}{(|S|-1)|S|^{2}} \cdot \sum_{j_{2},j_{3},j_{2} \neq j_{3}} M_{j_{1},j_{2}}^{-1} M_{j_{1},j_{3}}^{-1} \right].$$
(15)

The inverse matrix of *M* is represented by

$$M^{-1} = \frac{1}{|S| - l} \begin{pmatrix} 2 - |S| & 1 & \dots \\ 1 & 2 - |S| & \dots \\ \vdots & \vdots & \ddots \end{pmatrix}.$$
 (16)

Therefore, we get

$$\sum_{j_2} (M_{j_1, j_2}^{-1})^2 = \left(\frac{1}{|S| - l}\right)^2 \left\{ (2 - |S|)^2 + |S| - 1 \right\},\tag{17}$$

and

$$\sum_{j_2,j_3,j_2 \neq j_3} M_{j_1,j_2}^{-1} M_{j_1,j_3}^{-1}$$

= $\left(\frac{1}{|S|-l}\right)^2 \cdot \{2(2-|S|)(|S|-1) + (|S|-1)(|S|-2)\}(18)$

As a result, from equations 15, 17, and 18, we get the expected MSE between the original and estimated distributions of sensitive attributes in c_i ;

$$E[\sigma^2] = \frac{l(|S|-1)^2}{N_i(|S|-l)|S|^2}.$$
(19)

5.4 Analysis

5.4.1 Prerequisite for Anonymization

Our proposed method does not require the eligibility requirement because our method does not generalize any QIDs nor insert dummy records. Let |S| denote the number of kinds of sensitive values. If $l \leq |S|$, we can anonymize any databases for *l*-diversity because we can add l-1 sensitive values to each user's sensitive attribute. Note that setting l > |S| is meaningless in terms of the definition of *l*-diversity.

5.4.2 Cost Analysis

the data holder is O(l). This protocol is computationally simple as we know from Algorithm 1.

Solving the linear system of equations with |S| dimensions is the most expensive step in the estimation protocol. We can solve a linear system of equations by solving a $|S| \times |S|$ matrix equation. The time complexity of solving a $|S| \times |S|$ matrix equation is $O(g|S|^2)$, where g is a parameter of the number of recursive iterations if we use the Gauss-Seidel method. Since we solved the linear system of equations for each category c, the resulting time complexity is represented by $O(g|S|^2|C|)$.

EVALUATION 6

6.1 Mathematical Analysis and **Simulations of Synthetic Data**

Figure 1 shows the results of mathematical analysis. We assume that we have N records categorized to c that are one of the combinations of elements of QIDs that a data user wants to analyze. In this subsection, we calculate MSE by Equation 2 between the distribution of original sensitive attributes and those of estimated sensitive attributes in the category c.

In the first evaluation, we set the number of records N to 1,000 and l to 5. Figure 1(a) represents the results of the MSE. We know from Fig. 1(a) that the MSE tends to be decreasing with an increase of |S|.



Figure 1: Results of mathematical analysis.

Then, we calculate the MSE by changing the privacy level *l*. The results are shown in Fig. 1(b). We changed *l* from 2 to 18 based on the settings of many existing studies (Yao et al., 2012; Nergiz et al., 2013; Hu et al., 2010). In this evaluation, we set the number of records *N* to 1,000 and the number of possible sensitive attributes |S| to 20 and 100. From the figure, we know that the MSE of our proposed method increases by increasing *l*. If we set *l* to near |S|, the MSE increases exponentially, although the MSE keeps a small value if *l* is much less than |S|. Nevertheless, we show that our proposed method can result in a small MSE even if we set *l* to very near |S| (i.e., |S| - 1) by simulations of a real data set in the next subsection.

Next, we conducted an experiment to analyze the effects of changing the number of records N. Figure 1(c) shows the results of this. In this evaluation, we set l to 5 and |S| to 20. We know that the MSE reduced relative to N.

Finally, we conducted simulations by setting parameters (|S|, l, and N) to the same values in the mathematical analysis described above. The underlying distributions of sensitive attributes were set to Uniform distribution, Gaussian distribution, and Poisson distribution. In all simulations, the results are almost the same as that of the mathematical analysis.

6.2 Real Data Set Evaluation Results

We evaluated the MSE by using real data sets, which are OCC, SAL and Adult. OCC and SAL are obtained from (Minnesota Population Center,). Many existing studies such as (Xiao et al., 2010) and (Xiao and Tao, 2006) use this data sets. OCC has an attribute *Occupation* as a sensitive attribute and has attributes *Age, Gender, Marital Status, Race, Birth Place, Education, Work Class* as QIDs. SAL has an attribute *Income* as a sensitive attribute and has the same QIDs as in OCC. The number of distinct values of each attribute is shown in Table 6.

We create 7 sets of database, OCC-1, OCC-2, ..., OCC-7 from OCC. Each database OCC-*d* has the first *d* QIDs in Table 6 and a sensitive attribute *Occupation*. For example, OCC-3 has *Age*, *Gender*, *Marital Status* as QIDs and *Occupation* as a sensitive attribute. Similarly, we also create 7 sets of database SAL-*d* (d = 1, ..., 7) from SAL.

The Adult data set consists of 15 attributes (e.g., *Age, Sex, Race, Relationship* shown in Table 7) and has 45,222 records after the records with unknown values are eliminated. Adult data set (UCI Machine Learning Repository,) used in many studies on privacy (Machanavajjhala et al., 2007; Sun et al., 2009). Wet create 15 sets of database, Adult(1), Adult(2), ..., Adult(15) from Adult. Each database Adult(*d*) has the *d*'th attribute in Table 7 as a sensitive attribute and has other attributes as QIDs. For example, Adult-2 has *Work Class* as a sensitive attribute and has *Age, Final Weight, Education,* ... as QIDs.

Following (Xiao and Tao, 2006), we consider a query involves qd random QIDs A_1, \ldots, A_{qd} , and the sensitive attribute, where qd represents the query dimensionality parameter. For example, when the database is SAL-4 and qd=3, $\{A_1, A_2, A_3\}$ is a random 3 sized subset of {Age, Gender, Marital Status, Race}. We assume that data users want to know the number of persons whose attribute A_i ($i = 1, \ldots, qd$) is the specific value. Therefore, we create random values for each A_i as the specific values in each query. Let b_i denote the size of the random values for attribute A_i . Following (Xiao and Tao, 2006), the value of b_i is calculated by the expected query selectivity s:

$$b_i = \left\lceil |A_i| \cdot s^{1/(qd+1)} \right\rceil \tag{20}$$

where $|A_i|$ represents the number of distinct values of A_i in the original database.

We compared our method with Anatomy and TP, which were described in Section 4. All experiments were conducted on an Intel Xeon CPU E5-2687W v2 @ 3.40GHz 3.40GHz personal computer with 12 GB of RAM.



Figure 3: MSE vs. *l*.

We set l to 10, s to 0.07, and qd to 3 as a default value. In each simulation, we generated 1,000 random queries based on qd and Equation 20, and calculate MSEs based on Equation 2.

In the first simulation with OCC and SAL, we conducted an analysis to determine how the number of QIDs and qd affect the MSE. We changed the number of QIDs d from 3 to 7 and changed qd from 1 to d - 1. Figure 2 shows the results. Figures 2(a), 2(c) and 2(e) are the results of OCC, and Figs. 2(b), 2(d) and 2(f) are the results of SAL. When the number of QIDs d is 3, the MSEs of our proposed method and TP are almost the same. On the other hand, in the results of other settings, the MSEs of our proposed method is much fewer than other methods.

In the next simulation, we changed l from 5 to 15. Figure 3 shows the results. The value of l is large, the MSEs are also large. However, we know from the Figs. 3(a) and 3(b) that our proposed method has the smallest MSE among the three methods.

Then, we changed s from 0.4 to 1.0 and calculated the MSEs in each setting. The results are shown in Fig 4. The MSEs decreases as s grows higher. This is



because the number of target records of the databases becomes large when *s* is large.

In the simulations with Adult(1), Adult(2), ..., Adult(15), we changed l from 2 to 10 in each simulation. TP and Anatomy could not anonymize the database in several simulations because of the eligibility requirement. The ratio of successful anonymization is shown in Fig. 5(a). Although our proposed method (and all existing methods for ldiversity) cannot anonymize if the number of distinct sensitive attributes is less than l, our proposed method does not require the eligibility requirement.

Figure 5(b) shows the average MSEs of all simulations of Adult(1), ..., Adult(15). The figure helped us to determine that our method could realize fewer MSE.

In the following evaluation, we used an attribute of "relationship" as the sensitive attribute. S is {Wife, Hasband, Own-child, Unmarried, Not-infamily, Other-relative}.

We used an attribute of Sex as the QID, that the data user wants to analyze. That is, \mathfrak{Q} is {Sex} and Q(0) is {Male, Female}. Figure 6(a) shows the original distributions of *S* in Male and Female, respectively.

Figures 6(b), 6(c), and 6(d) present the estimated results of Proposal, TP, and Anatomy, respectively. We know from the figures that our proposed method can estimate the true distribution of *S* for Male and Female with the highest precision.

Finally, we measured the execution time of anonymization and estimation for the Adult dataset. In the proposed method, it took approximately 4 sec-

	radie of Authority and so to be and state.									
	Age	Gender	Marital Status	Race	Birth Place	Education	Work Class	Occupation	Income	
80 2 6 9 124 24 9 50 50										
	Table 7: Number of distinct values of Adult data set.									

Table 6. Number of distinct values of OCC and SAI

Age	Work Class	Final Weight	Education	Education-num	Marital Status	Occupation	Relationship
74	7	26741	16	16	7	14	6
Race	Gender	Capital Gain	Capital Loss	Hours Per Week	Country	Salary Class	
5	2	121	97	96	41	2	



anonymized database of TP anonymized database of Anatomy

Figure 6: Relationship vs. sex in l = 2.

onds. From this result, we know that our proposed method is a very efficient technique in terms of execution time.

7 CONCLUSION

An anonymization technique of *l*-diversity can achieve a privacy-preserving model where a data holder can share their data with other data users. Existing techniques generalize QIDs from the database to ensure that adversaries cannot specify each individual's sensitive attribute. However, it is possible that several QIDs that a data user focuses on are all generalized and the anonymized database has no value for the data user.

In this paper, we propose a new technique for *l*diversity, which keeps QIDs unchanged and randomizes sensitive attributes of each individual so that data users can analyze it based on QIDs that they focus on. We also proposed an estimation protocol of the original distribution of sensitive attributes for data users according to their preferred QIDs, and, we proposed the calculation method for the expected MSE between the original and estimated distribution of sensitive attributes. Moreover, our method does not require the eligibility requirement, therefore, our method can be applied to any databases when l is less than the number of distinct sensitive values. By mathematical analysis and simulations, we prove that our proposed method can result in a better tradeoff between privacy and utility of anonymized databases than existing studies.

Future work will include the evaluation of other relevant data sets. We also plan to extend our approach to other privacy measures such as *t*-closeness.

ACKNOWLEDGEMENTS

This research was subsidized by JSPS 24300005, 26330081, 26870201. The authors would also like to express their deepest appreciation to the entire staff of Professor Honiden's laboratory at the University of Tokyo and Professor Fukazawa's lab at Waseda University, both of whom provided helpful comments and suggestions.

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