Can the Utility of Anonymized Data be used for Privacy Breaches?

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ABSTRACT

Group based anonymization is the most widely studied approach for privacy preserving data publishing. This includes k-anonymity, l-diversity, and l-closeness, to name a few. The goal of this paper is to raise a fundamental issue on the privacy exposure of the current group based approach. This has been overlooked in the past. The group based anonymization approach basically hides each individual record behind a group to preserve data privacy. If not properly anonymized, patterns can actually be derived from the published data and be used by the adversary to breach individual privacy. For example, from the medical records released, if patterns such as people from certain countries rarely suffer from some disease can be derived, then the information can be used to imply linkage of other people in an anonymized group with this disease with higher likelihood. We call the derived patterns from the published data the foreground knowledge. This is in contrast to the background knowledge that the adversary may obtain from other channels as studied in some previous work. Finally, we show by experiments that the attack is realistic in the privacy benchmark dataset under the traditional group based anonymization approach.

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1. INTRODUCTION

A major technique used in privacy preservation data publishing is group based anonymization, whereby records in the given relation are partitioned into groups and each group must ensure some property such as diversity so as to satisfy the privacy requirement while maintaining sufficient data utility. There are many privacy models associated with group based anonymization such as k-anonymity [24], l-diversity [21], l-closeness [17], (k, e)-anonymity [30], Injector [18] and m-confidence [27]. It seems that this technique is sound for privacy preserving data publishing. However, when examined more carefully, they all suffer from one fundamental privacy violation problem, which is overlooked in the past. The main cause of this problem is that the utility that is maintained in the anonymized table can help the adversary to breach individual privacy.

In the literature, background knowledge [21, 15, 22, 27, 18] such as the rarity of a disease among a certain ethnic group or the pattern of age or gender for a disease can be used by the adversary to breach individual privacy. In this paper, we show that such knowledge can be mined from the published data or the anonymized data to compromise individual privacy. In fact, one of the main purposes of data publishing is data mining which is mainly about the discovery of patterns from the published data.

Let us illustrate the problem with an example. Suppose a table T is to be anonymized for publication. Table T has two kinds of attributes, the quasi-identifier (QI) attributes and the sensitive attribute. The QI attributes can be used as an identifier in the table. [24] points out that in a real dataset, most individuals can be uniquely identified by three QI attributes, namely sex, date of birth and 5-digit zip code. The sensitive attribute contains some sensitive values. In our example, Table 1 is the given table T where one of the QI attributes is “Nationality” and the sensitive attribute is “Disease” containing sensitive values such as Heart Disease and HIV. Note that there can be other QI attributes in this table such as sex and zip code. For the sake of illustration, we list attribute “Nationality” only. Assume that each tuple in the table is owned by an individual and each individual owns at most one tuple.

Suppose that we want to anonymize T and publish the anonymized dataset T’ to satisfy some privacy requirements. Typically, T’ consists of a set of anonymized groups (in short, A-groups), where each A-group is a set of tuples with a multi-set of sensitive values that are linked with the A-group. Depending on the anonymization mechanism, each A-group may correspond to either a set of quasi-identifier
Table 1: An example

| Nationality | GID | Disease |
|-------------|-----|---------|
| American    | L1  | Heart Disease |
| Japanese    | L2  | Flu |
| French      | L3  | Stomach Virus |
| Japanese    | L4  | Heart Disease |
| American    | L5  | Diabetes |

Table 2: A 2-diverse dataset anonymized from Table 1

(QI) values or a single generalized QI value. An attribute GID is added for the ID of the A-group. Such an anonymized dataset is generated as a result of group-based anonymization commonly adopted in the literature of data publishing [3, 16, 29, 27, 18, 17] (including k-anonymity, l-diversity, l-closeness and a vast number of other privacy models).

For illustration, a simplified setting of the l-diversity model [21] is used as a privacy requirement for published data \( T' \). An A-group is said to be l-diverse or satisfy l-diversity if in the A-group the number of occurrences of any sensitive value is at most \( 1/l \) of the group size. A table satisfies l-diversity (or it is l-diverse) if all A-groups in it are l-diverse. Table 2 satisfies 2-diversity. The intention is that each individual cannot be linked to a disease with a probability of more than 0.5. However, does this table protect individual privacy sufficiently?

Let us examine the A-group with GID equal to \( L_1 \) as shown in Table 2. We also refer to the A-group by \( L_1 \). In \( L_1 \), Heart Disease and Flu are values of the sensitive attribute Disease. It seems that each of the two individuals, Alex and Bob, in this group has a 50% chance of linking to Heart Disease (Flu). The reason why the chance is interpreted as 50% is that the analysis is based on this group locally without any additional information.

However, from the entire published table containing multiple groups, the adversary may discover some interesting patterns globally. For example, suppose the published table consists of many A-groups like \( L_2 \) with all Japanese with no occurrence of Heart Disease. At the same time, there are many A-groups like \( L_3 \) containing some Japanese without Heart Disease. The pattern that Japanese rarely suffer from Heart Disease can be uncovered. Note that it is very likely that such an anonymized data is published by conventional anonymization methods, given the fact that Heart Disease occurs rarely among Japanese. With the pattern uncovered, the adversary can say that Bob, being a Japanese, has less chance of having Heart Disease. S/he can deduce that Alex, being an American, has a higher chance of having Heart Disease. The intended 50% threshold is thus violated.

1.1 Foreground Knowledge Attack

The anonymized data can be seen as an imprecise or uncertain data [8, 9], and an adversary can uncover interesting patterns since the published data must maintain high data utility [29, 30, 27]. We call the uncovered patterns the foreground knowledge (which is implicitly inside the table) in contrast to the background knowledge, studied by existing works [21, 17, 30, 27], which the adversary requires much effort to obtain from somewhere outside the table. Since it is easy to obtain the foreground knowledge from the anonymized dataset, all existing works suffer from privacy breaches.

In Table 2, there are only two local possible worlds for assigning the disease values to the two individuals in \( L_1 \): (1) \( w_1 \) : Alex is linked to Heart Disease and Bob is linked to Flu and (2) \( w_2 \) : Alex is linked to Flu and Bob is linked to Heart Disease. To construct a probability distribution over the domain of the real world, a simplest definition is based on the assumption that all the possible worlds are equally likely, or each world has the same probability.

If we publish a group \( L_1 \) alone, the random world assumption is a good principle in the absence of other information. However, when several groups are published together as typically the case, the groups with Japanese contribute to a statement that their members are not likely linked to Heart Disease. This statement means that the probability (or weight) of the possible world \( w_1 \) is much greater than that of \( w_2 \).

Most previous privacy works such as l-diversity [21], t-closeness [17], (k, e)-anonymity [30] and m-confidentiality [27] adopt the random world assumption locally. In this paper, the source of attack of the adversary is to apply the more complete model of the weighted possible worlds. We call this kind of attack foreground knowledge attack.

1.2 Contributions

Our contributions can be summarized as follows. Firstly, we define and study data anonymization issues in data publication with the consideration of foreground knowledge attack, which is ignored in the privacy literature. Secondly, we show how an adversary can breach privacy by computing the probability that an individual is linked to a sensitive value by using foreground knowledge.

Finally, we have conducted experiments to show how the adversary can succeed in foreground knowledge attack for four recent privacy models, namely Anatomy [29], MASK [27], Injector [18] and t-closeness [17].

We emphasize that, similar to l-diversity, all privacy models using group-based anonymization [29, 27, 18, 17] also suffer from possible privacy breaches due to the utility of the published table. We believe that this work is significant in pointing out this overlooked issue, and that all followup works should need to deter foreground knowledge attack.

The rest of the paper is organized as follows. Section 2 formulates the problem. Section 3 describe how the adversary can breach individual privacy with the foreground knowledge obtained from the anonymized data. Section 4 shows how the adversary can obtain the foreground knowledge from the anonymized data. An empirical study is reported in Section 5. Section 6 reviews the related work. The paper is concluded in Section 7.

2. PROBLEM DEFINITION

Let \( T \) be a table. We assume that one of the attributes is a sensitive attribute \( X \) where some values of this attribute should not be linkable to any individual. The value
of the sensitive attribute of a tuple $t$ is denoted by $t.X$. A quasi-identifier (QI) is a set of attributes of $T$, namely $A_1, A_2, ..., A_9$, that may serve as identifiers for some individuals. Each tuple in the table $T$ is related to one individual and no two tuples are related to the same individual.

Let $P$ be a partition of table $T$. We give a unique ID called GID to this partition $P$ and append an additional attribute called GID to this partition where each tuple in $P$ has the same GID value. Existing group-based anonymization defines a function $\beta$ on $P$ to form an $\Lambda$-group such that the linkage between the QI attributes and the sensitive attribute in the $\Lambda$-group is lost. There are two ways in the literature for this task. One is generalization by generalizing all QI values to the same value. The other is bucketization by forming two tables, called the QI table and the sensitive table, where $P$ is projected on all QI attributes and attribute GID to form the QI table, and on the sensitive attribute and attribute GID to form the sensitive table. A table $T$ is anonymized to a dataset $T^*$ if $T^*$ is formed by first partitioning $T$ into a number of partitions, then forming an A-group from each partition by $\beta$ and finally inserting each A-group into $T^*$. For example, Table 1 is anonymized to Table 2 by bucketization.

In known voter registration lists, the QI values can often be used to identify a unique individual [24, 16]. We assume that there is a mapping which maps each tuple in $T$ to an A-group in $T^*$. For example, the first tuple $t_1$ in Table 1 is mapped to A-group $L_1$.

In the following, for the sake of illustration, we focus on discussing the anonymized table generated by bucketization, instead of generalization. The discussion for generalization is same as that for bucketization. Specifically, generalization is similar to bucketization but generalization changes all QID values in a partition to the same “generalized” values. If the table is generated by generalization, each A-group contains the same “generalized” values. In the worst case scenario (which is a basic assumption in the privacy literature [22, 27, 19]), the adversary can uniquely map each individual in an A-group by an external table such as a voter registration list. After the mapping, each A-group contains individuals with the original QID values, which becomes the case of bucketization. Thus, the discussion for bucketization still applies in the case for generalization. The worst case scenario assumption is essential in data publishing. Nobody can afford if the privacy of an individual is breached [19]. AOL published the dataset about search logs in 2006. After it realized that a single 62 year old woman living Georgia can be re-identified from the search logs by New York Times reporters, it withdraws the search logs and fired two employers responsible for releasing the search logs [5].

In the literature [29, 27, 18, 17], it is assumed that the knowledge of the adversary includes (1) the published dataset $T^*$, (2) the QI value of a target individual, (3) an external table $T^*$ such as voter registration list that maps QIDs to individuals [24, 16]. We also follow these assumptions in our analysis.

The aim of privacy preserving data publishing is to deter any attack from the adversary on linking an individual to a certain sensitive value. Specifically, the data publisher would try to limit the probability that such a linkage can be established. Let us consider an arbitrary sensitive value $x$ for the analysis. We denote any value in $X$ which is not $x$ by $\overline{x}$.

| $p()$ | Heart Disease | Not Heart Disease |
|-------|---------------|--------------------|
| American | 0.1           | 0.9                |
| Japanese | 0.003         | 0.997              |
| French   | 0.65          | 0.95               |

Table 3: A global distribution of attribute “Nationality” for our motivating example

In this paper, we consider that an adversary can obtain additional information from the published dataset $T^*$ in the form of global distribution, which can lead to individual privacy breach. In the example in Section 1, we can mine from the published table that the chance of Japanese suffering from Heart Disease is low compared with American. This pattern is from the global distribution for the attribute set \{“Nationality”\}.

Consider an arbitrary sensitive value “Heart Disease”. Table 3 shows the global distribution of attribute set \{“Nationality”\}, which consists of the probabilities that a Japanese, an American or a French is linked to Heart Disease. Each probability in the table is called a global probability. The sample space for each such probability consists of the possible assignments of the values $x$ and $\overline{x}$ to an individual with the particular nationality.

Each possible value in attribute “Nationality” is called a signature. There are three possible signatures in our example: “Japanese”, “American” and “French”. In general, there are other attribute sets, such as \{“Sex”, “Nationality”\}, with their correspondence global distributions. We define the signature and the global distribution for a particular attribute set $A$ as follows.

**Definition 1 (Signature).** Let $T^*$ be the published dataset. Given a QI attribute set $A$ with $r$ attributes $A_1, ..., A_r$. A signature $s$ of $A$ is a set of attribute-value pairs $(A_i, v_i), ..., (A_r, v_r)$ which appear in the published dataset $T^*$, where $A_i$ is a QI attribute and $v_i$ is a value. A tuple $t$ in $T^*$ is said to match $s$ if $t.A_i = v_i$ for all $i = 1, 2, ..., r$.

For example, a signature $s$ can be \{ (“Nationality”, “American”), (“Sex”, “Male”) \} if the attribute set $A$ is \{ “Nationality”, “Sex” \}. For convenience, we often drop the attribute names in a signature, and thus we refer to \{ “American”, “Male” \} instead of \{ (“Nationality”, “American”), (“Sex”, “Male”) \}. The first tuple $t_1$ in Table 2(a) matches \{ “American” \} but the second tuple does not.

**Definition 2 (Global Distribution).** Given an attribute set $A$, the global distribution $G$ of $A$ contains a set of entries $(s : x, p)$ for each possible signature $s$ of $A$, where $p$ is equal to $p(s : x)$ which denotes the probability that a tuple matching signature $s$ is linked to $x$ given the published dataset $T^*$.

For example, if $G$ contains \{ (“Japanese”:“Heart Disease”, 0.003) and (“American”:“Heart Disease”, 0.1) \}, then the probability that a Japanese patient is linked to Heart Disease is equal to 0.003 while that of an American patient is 0.1.

The global distribution $G$ derived from the published dataset $T^*$ is called the foreground knowledge. We will describe how the adversary derives $G$ from the published table.

**Problem 1 (Foreground Knowledge).** Given any arbitrary attribute set $A$, we want to find the global distribution $G$ of $A$ from published dataset $T^*$.
From Section 1, we show that with the global distribution \( G \) of attribute set \{"Nationality"\}, we can deduce that the chance of Alex, an American, suffering from Heart Disease is high. Let \( t \) be Alex and \( x \) be Heart Disease. The chance can be formulated by \( p(t : x) \), the probability that \( t \) is linked to \( x \) given \( G \).

**Problem 2 (Privacy Breach).** Given a published dataset \( T^* \), for any individual \( t \), any sensitive value \( x \) and any attribute set \( A \), we want to determine whether the probability that \( t \) is linked to \( x \) denoted by \( p(t : x) \) is greater than 1/r. Individual \( t \) is said to suffer from privacy breaches if the probability is greater than 1/r.

In this paper, we first study Problems 1 and 2. In Section 3, we will first give how we solve Problem 2 assuming that we are given the foreground knowledge. Then, in Section 4, we will describe how we can mine the foreground knowledge from the published dataset \( T^* \) for Problem 1. We shall show that the two problems are intertwined, since the global probability is derived based on the published table, and thus depends on the probability \( p(t : x) \) for each tuple \( t \).

Given \( G \), the formula for \( p(t : x) \), the probability that a tuple \( t \) is linked to sensitive value \( x \), is derived here. Suppose \( t \) belongs to \( A \)-group \( L_k \). For the ease of reference, let us summarize the notations that we use in Table 6. We shall need the following definitions.

**Definition 3 (Primitive events, Projected events).** A mapping \( t : \gamma \) from an individual or tuple \( t \) to a sensitive value \( \gamma \) (\( x \) or \( \overline{x} \)) is called a primitive event. Suppose \( t \) matches signature \( s \). Let us call an event for the corresponding signature, \( "s : \gamma" \), a projected event for \( t \).

Hence, a primitive event is an event in the sample space for \( p(t : x) \), which is the probability of the interest for the adversary. A projected event is an event for \( p(s : x) \) which appears in the global distribution \( G \).

**Definition 4 (Possible world).** Consider an \( A \)-group \( L_k \) with \( N \) tuples, namely \( t_1,t_2,...,t_N \), with sensitive values \( \gamma_1,\gamma_2,...,\gamma_N \), where \( \gamma_i \) is either \( x \) or \( \overline{x} \) for \( i = 1,2,...,N \). A possible world \( w \) for \( L_k \) is a possible assignment mapping the tuples in set \( \{t_1,t_2,...,t_N\} \) to values in multi-set \( \{\gamma_1,\gamma_2,...,\gamma_N\} \) in \( L_k \).

Given an \( A \)-group \( L_k \) with a set of tuples and a multi-set of sensitive values. For each possible world \( w \), according to the global distribution \( G \) based on attribute set \( A \), we compute the probability \( p(w) \) that \( w \) occurs. The sample space for \( p(w) \) consists of all the possible assignments of \( x \) or \( \overline{x} \) to a set of \( N \) tuples with the same signatures as those in \( L_k \).

Suppose that in a possible world \( w \) for \( L_k \), tuple \( t_j \) is linked to \( \gamma \), where \( \gamma \) is either \( x \) or \( \overline{x} \). Let \( p_{j,w} \) be the probability that \( t_j \) is linked to \( \gamma \).

Like [21, 29, 27], we assume that the linkage of a sensitive value to an individual is dependent on the linkage of the sensitive value to another individual. For example, whether an American suffers from Heart Disease is independent of whether a Japanese suffers from Heart Disease. Thus, for a possible world \( w \) for \( L_k \), the probability that \( w \) occurs is the product of the probabilities of the corresponding projected events for the tuples \( t_1,...,t_N \) in \( L_k \).

\[
p(w) = p_{1,w} \times p_{2,w} \times ... \times p_{N,w}
\]

(1)

Suppose \( t_j \) matches signature \( s_i \). If \( t_j \) is linked to \( x \) in \( w \), then \( p_{j,w} = f_i \). Otherwise, \( p_{j,w} = \overline{f_i} \).

\( p(w) \) corresponds to the weight of \( w \), which we mentioned in the introduction.

The probability of \( L_k \) given \( T^* \) is the sum of the probabilities of all the possible worlds consistent with \( T^* \) for \( L_k \). Let the set of these worlds be \( W_k \). For \( w \in W_k \), we have

\[
p(w|L_k) = p(w) \sum_{w \in W_k} p(w)
\]

(2)

It is easy to verify that \( \sum_{w \in W_k} p(w|L_k) = 1 \).

Our objective is to find the probability that an individual \( t_j \) in \( L_k \) is linked to a sensitive value \( x \). This is given by the sum of the conditional probabilities \( p(w|L_k) \) of all the possible worlds \( w \) where \( t_j \) is linked to \( x \).

\[
p(t_j : x) = \sum_{w \in B_x} p(w|L_k)
\]

(3)

where \( B_x \) is a set of all possible worlds \( w \) in \( W_k \) in which \( t_j \) is assigned value \( x \).

One can verify that \( p(t_j : x) + p(t_j : \overline{x}) = 1 \).

| Table 6: Notations |
|---------------------|
| \( L_k \) | an \( A \)-group (anonymized group) in the anonymized dataset |
| \( A \) | set of attributes e.g. \{"Nationality", "Sex"\} |
| \( t_1,...,t_N \) | tuples in an \( A \)-group |
| \( s_1,...,s_m \) | signatures for \( A \), e.g.\{"American", "Male"\} |
| \( x \) | a sensitive value |
| \( \bar{x} \) | any value not equal to \( x \) |
| \( p(t_j : x) \) | probability that tuple \( t_j \) is linked to value \( x \) |
| \( p(s_i : x) \) | probability that signature \( s_i \) is linked to \( x \) |
| \( f_i \) | a simplified notation for \( p(s_i : x) \) |
| \( \overline{f_i} \) | \( 1 - f_i \) |
| \( w \) | a possible world: an assignment of the tuples in \( A \)-group \( L_k \) to the sensitive values \( x \) and \( \bar{x} \) |
| \( W_k \) | set of all possible worlds \( w \) for \( L_k \) |
| \( B \) | set of all possible worlds \( w \) in \( W_k \) in which \( t_j \) is assigned value \( x \) |
| \( p(w) \) | probability that \( w \) occurs given the anonymized dataset and based on \( A \) |
| \( p(w|L_k) \) | conditional probability that \( w \) occurs given \( A \)-group \( L_k \) |
| \( p_{j,w} \) | let \( t_j \) be linked to \( \gamma \) in \( w \), where \( \gamma \) is either \( x \) or \( \overline{x} \) |
| \( L_{s_i} \) | the set of tuples in \( L_k \) matching \( s_i \) |
| \( L_k(s_i) \) | the expected number of tuples which match \( s_i \) and are linked to \( x \) in the \( A \)-group \( L_k \) |
| \( p(w) \) | corresponds to the weight of \( w \), which we mentioned in the introduction. |

**Finding Privacy Breaches**

We assume that the attack is based on the linkage of an attribute set \( A \) to a sensitive value \( x \). We denote by \( \bar{x} \) any value not equal to \( x \). In this section, we assume that the global distributions \( G \) for \( A \) and \( x \) have been determined and we show how an adversary can use \( G \) to find privacy breaches. How the global distributions can be derived is explained in Section 4.

Suppose there are \( m \) possible signatures for attribute set \( A \), namely \( s_1, s_2, ..., s_m \). The global distribution \( G \) of \( A \) is shown in Table 4. To simplify our presentation, the probability that \( s_i \) is linked to \( x \) (\( \overline{x} \)), \( p(s_i : x) \) (\( p(s_i : \overline{x}) \)), is denoted by \( f_i (\overline{f_i}) \).
**Table 4: Global distribution**

|   | $x$ | $\overline{\pi}$ | $\overline{p}$ |
|---|-----|-------------------|-----------------|
| $s_1$ | 0.5 | 0.5               | 0.2             |
| $s_2$ | 0.2 | 0.8               | 0.8             |

**Table 5: An example illustrating the computation of $p(t_1:x)$**

| $w$ | $t_1$ | $t_2$ | $t_3$ | $t_4$ | $p(w)$ | $p(w|L_k)$ |
|-----|------|------|------|------|--------|------------|
| $w_1$ | $x$ | $x$ | $\overline{\pi}$ | $\overline{\pi}$ | $0.5 \times 0.5 \times 0.8 \times 0.8 = 0.16$ | $0.16/0.33 = 0.48$ |
| $w_2$ | $x$ | $\overline{\pi}$ | $x$ | $\overline{\pi}$ | $0.5 \times 0.5 \times 0.2 \times 0.8 = 0.04$ | $0.04/0.33 = 0.12$ |
| $w_3$ | $\overline{\pi}$ | $\pi$ | $x$ | $\overline{\pi}$ | $0.5 \times 0.5 \times 0.8 \times 0.2 = 0.04$ | $0.04/0.33 = 0.12$ |
| $w_4$ | $\overline{\pi}$ | $\pi$ | $x$ | $\overline{\pi}$ | $0.5 \times 0.5 \times 0.2 \times 0.8 = 0.04$ | $0.04/0.33 = 0.12$ |
| $w_5$ | $\overline{\pi}$ | $\pi$ | $x$ | $\overline{\pi}$ | $0.5 \times 0.5 \times 0.8 \times 0.2 = 0.04$ | $0.04/0.33 = 0.12$ |
| $w_6$ | $\overline{\pi}$ | $\pi$ | $x$ | $\overline{\pi}$ | $0.5 \times 0.5 \times 0.2 \times 0.2 = 0.01$ | $0.01/0.33 = 0.03$ |

**Example 1.** Consider an A-group $L_k$ in a published table $T'$. Suppose there are four tuples, $t_1, t_2, t_3$, and $t_4$, and four sensitive values, $x, x, \overline{\pi}$, and $\pi$ in $L_k$. Suppose the published table $T'$ satisfies 2-diversity.

Consider the global distribution $G$ based on a certain QI attribute set $A$ which contains two possible signatures $s_1$ and $s_2$ as shown in Table 5(a).

Suppose $t_1, t_2, t_3$, and $t_4$ match signatures $s_1, s_1, s_2$, and $s_2$, respectively. There are six possible worlds $w$ as shown in Table 5(b). For example, the first row is the possible world $w_1$ with mapping $(t_1:x, t_2:x, t_3:\overline{\pi}, t_4:\overline{\pi})$. The table also shows the probability $p(w)$ of the possible worlds. Take the first possible world $w_1$ for illustration. From the global distribution in Table 5(a), $p(s_1:x) = 0.5$ and $p(s_2:\overline{\pi}) = 0.8$. Hence, $p(w_1) = 0.5 \times 0.5 \times 0.8 \times 0.8 = 0.16$. The sum of probabilities $p(w)$ of all possible worlds from Table 5(b) is equal to $0.16 + 0.04 + 0.04 + 0.04 + 0.04 + 0.01 = 0.33$. Consider $w_1$ again. Since $p(w_1) = 0.16$, $p(w_1|L_k) = 0.16/0.33 = 0.48$.

Suppose the adversary is interested in the probability that $t_1$ is linked to $x$. We obtain $p(t_1:x)$ as follows, $w_1, w_2$ and $w_3$, as shown in Table 5(b), contain “$t_1:x$”. Thus, $p(t_1:x)$ is equal to the sum of the probabilities $p(w_1|L_k), p(w_2|L_k)$ and $p(w_3|L_k)$, i.e., $p(t_1:x) = 0.48 + 0.12 + 0.12 = 0.72$ which is greater than 0.5, the intended upper bound for 2-diversity that an individual is linked to a sensitive value.

Let $|L_k|$ be the size of the A-group containing $t_1$ and $|W_k|$ be the number of possible worlds in an A-group $L_k$. We will generate $|W_k|$ possible worlds. For each possible world, we calculate $p(w)$ and $p(w|L_k)$ in $O(|L_k|)$ time. Thus, the time complexity is $O(|L_k| \cdot |W_k|)$.

The time complexity depends on two factors. One is $|W_k|$ and another is $|L_k|$. (1) $|W_k|$ is equal to $C^n_5$ where $n$ is the number of tuples with $x$ in this A-group of size $N$ and $C^n_5$ denotes the total number of possible ways of choosing $n$ objects from $N$ objects. Note that $W_k$ is typically small because $n$ is usually equal to a small number. For $l$-diversity, algorithm Anatomy [29] restricts that each A-group contains either $l$ or $l+1$ tuples and each sensitive value $x$ appears at most once. Here, $n$ is equal to 1. Thus, for each possible world $w$, $|W_k|$ is at most $l+1$. For Algorithm MASK [27], in our experiment with $l=2$, the greatest frequency of $x$ in an A-group is 8. The size of this A-group is 23. $|W_k|$ is equal to $C^8_4 = 70$. When $l=10$, the greatest possible value of $|W_k|$ is $140,364,532$. These values are small compared with the excessive number of possible worlds studied in uncertain data [14, 8, 9, 4, 11] (e.g., $10^{109}$ in [4])). In the experimental setups in existing works [21, 29, 17, 27, 18], $l \leq 10$. In other words, $W_k$ can be generated within a reasonable time. (2) $|L_k|$ is bounded by the greatest size of the A-group which depends on the anonymization techniques. For example, $|L_k|$ is equal to $l$ or $l+1$ for algorithm Anatomy [29] restricting that each A-group contains either $l$ or $l+1$. In our experiment, $|L_k|$ is at most 23 for algorithm MASK [27] where $l=2$.

**4. MINING FOREGROUND KNOWLEDGE**

We first describe how we find the global distribution $G$ of a certain attribute set $A$ from the anonymized data in Section 4.1. Next, we introduce a pruning strategy to prune our search space of attribute sets in Section 4.2. Finally, we describe the algorithm for finding the global distribution of multiple attribute sets and discuss its complexity in Section 4.3.

**4.1 Foreground Knowledge**

In the previous section, we assume that the values of $f_i$ are given. Here we consider how to derive $f_i$ from the published table $T'$. We will develop $m$ equations involving the $m$ variables $f_i$, $1 \leq i \leq m$.

Let the set of A-groups in $T'$ be $L_1, ..., L_n$. Let $L_k(s_i)$ be the set of tuples in $L_k$ matching signature $s_i$. For example, in Table 2, let $s_i = \{"American"\}$. Then, $L_1(s_i)$ contains only the first tuple.

Let $L_{s_i}$ be a set of A-groups containing tuples which match $s_i$. That is, $L_{s_i} = \{L_k|L_k(s_i) \neq \emptyset\}$. 


Thus, we have two equations with two variables, namely \( f_1 \) and \( f_2 \), the probabilities in the global distribution \( G \) of \( A \) as shown in Table 4.

Consider \( f_1 \). Since only \( A \)-groups \( L_1 \) and \( L_2 \) contain the tuples matching \( s_1 \), \( L_1 = \{ L_1, L_2 \} \).

\[
f_1 = \frac{[\sum_{L_k \in C_{s_1}} c_k(s_1 : x)] / [\sum_{L_k \in C_{s_1}} |L_k(s_1)|]}\]

\( L_1 \) contains one tuple \( t_1 \) matching \( s_1 \) and \( L_2 \) contains two tuples \( t_3, t_4 \) matching \( s_1 \), \( |L_1(s_1)| = 1 \) and \( |L_2(s_1)| = 2 \). Thus,

\[
f_1 = \frac{1 \times p(t_1 : x) + 2 \times p(t_3 : x)}{1 + 2} \quad (7)
\]

Consider \( L_1 \). There are only two possible worlds, \( w_1 = \{ t_1 : x, t_2 : x \} \) and \( w_2 = \{ t_1 : x, t_2 : x \} \). Note that \( t_1 \) and \( t_2 \) match signatures \( s_1 \) and \( s_2 \), respectively. \( p_{w_1} = f_1, p_{w_2} = \overline{f_1} \) and \( p_{w_2} = f_2 \) for \( t_1 \) and \( t_3 \). Thus, \( p(w_1) = f_1, p(w_2) = f_1 \times f_2, p(w_3) = f_1 \times \overline{f_1} \). We derive that

\[
p(t_1 : x) = p(w_1|L_1) = f_1 f_2 / (f_1 f_2 + \overline{f_1} f_2) = 1/2
\]

Similarly, \( L_2 \) contains one tuple \( t_2 \) matching \( s_2 \) and \( L_3 \) contains two tuples \( t_3, t_4 \) matching \( s_2 \),

\[
f_2 = \frac{[\sum_{L_k \in C_{s_2}} c_k(s_2 : x)] / [\sum_{L_k \in C_{s_2}} |L_k(s_2)|]}\]

\( L_3 \) contains one tuple \( t_3 \) matching \( s_2 \) and \( L_4 \) contains two tuples \( t_4, t_5 \) matching \( s_2 \), \( |L_3(s_2)| = 1 \) and \( |L_4(s_2)| = 2 \). Thus,

\[
f_2 = \frac{1 \times p(t_2 : x) + 2 \times p(t_5 : x)}{1 + 2} \quad (7)
\]

From (7), we obtain

\[
f_1 = \frac{f_1 f_2}{f_1 f_2 + \overline{f_1} f_2} + 1/3 \]

\[
= \frac{f_1 (1 - f_2)}{f_1 (1 - f_2) + (1 - f_1) f_2} + 1/3
\]

Similarly, since \( L_1 \) contains one tuple \( t_2 \) matching \( s_2 \) and \( L_3 \) contains two tuples \( t_3, t_4 \) matching \( s_2 \),

\[
f_2 = \frac{[1 \times p(t_2 : x) + 2 \times p(t_5 : x)] / (1 + 2)}{1 + 2} \]

\[
= \frac{f_1 f_2}{f_1 f_2 + \overline{f_1} f_2} + 0/3 \]

\[
= [(1 - f_1) f_2 / f_1 (1 - f_2) + (1 - f_1) f_2) / 3
\]

With the above two equations involving two variables, we adopt Newton’s method to solve for these variables.

Finally, we obtain \( f_1 = 0.666667 \) and \( f_2 = 0.000000 \). Thus, we derive \( f_1 = 0.333333 \) and \( f_2 = 1.000000 \). □

### 4.2 Pruning Attribute Sets

The adversary may choose to attack with as many attribute sets as possible. Although there are many attribute sets in the anonymized data, it is not always true that the global distribution of each attribute set is reliable because if the global distribution derived is based on a small sample or a small set of tuples matching the same signature, the distribution is not accurate. For example, consider attribute set \( A = \{\text{"Nationality"} \} \) and the signature \( \{\text{"American"}\} \). Suppose there are only a few Americans, say 10 Americans, in the published table \( T^* \). Intuitively, 10 Americans cannot represent a meaningful global distribution. We will make use of the sample size studied in the literature of statistics to determine whether the distribution is reliable or not. The adversary can launch an attack only based on reliable distributions.

Based on studies in statistics [25], we use the following theorem to determine the acceptable sample size (i.e., the size of the set which contains the tuples matching the same signature \( s \)). Let \( S \) be a random sample of tuples for a signature \( s \), and \( p \) be the expected fraction of tuples in \( S \).
with the sensitive value $x$. Let $\tilde{p}$ be the observed fraction of tuples with the sensitive value $x$ in the sample $S$. Then the following theorem applies.

**Theorem 1 (Sample Size [25]).** Given an error parameter $\epsilon \geq 0$ and a confidence parameter $\sigma \geq 0$, if random sample $S$ has size $|S| \geq \frac{1}{2\epsilon^2} \ln \frac{1}{\sigma}$, the probability that $|\tilde{p} - p| > \epsilon$ is at most $\sigma$.

In case the sample size is not enough to satisfy the error bound, then uniform distribution will be assumed. The sample size satisfies the monotonicity property. Formally, without loss of generality, assume that there are $u$ attributes, namely $A_1, ..., A_u$. Let $v_1 \in A_1, ..., v_u \in A_u$. Let $y(v_1, ..., v_u)$ be the number of tuples with attributes $(A_1, ..., A_u)$ equal to $(v_1, ..., v_u)$. Given a positive integer $J$, if $y(v_1, ..., v_u) < J$, then $y(v_1, ..., v_i, v_{i+1}) < J$. With the above monotonicity property, whenever we find that the sample size of $y(v_1, ..., v_i)$ is not large enough, we do not need to count the number of the tuples with values $v_1, ..., v_{i+1}$ because $y(v_1, ..., v_i, v_{i+1})$ is also not large enough. Thus, this can help to prune the search space.

### 4.3 Algorithm

In this section, we will describe how to compute the set $G$ of all global distributions of multiple attribute sets with the use of the sample size just described. The steps are shown in Algorithm 1.

**Algorithm 1 Computation of the global distributions**

- **Step 1:** For each attribute set $A$, we first identify the set $S_A$ of signatures $s_i$ with respect to $A$ where each $s_i$ is matched by some tuples in $T$ and has sufficient sample size. For example, for $A = \{\text{"Nationality"}, \text{"Sex"}\}$, a signature equal to {\"American\", \"Male\"} is matched by the first tuple in Table 2(a). If it has sufficient sample size, it is stored in $S_A$.

- **Step 2:** For each attribute set $A$, if $S_A$ is non-empty, we calculate the global distribution of $A$ according to $S_A$ for each sensitive value $x$.

In the algorithm, Step 1 is to find all signatures with sufficient sample size for each attribute set $A$. Similar to frequent pattern mining, this step is typically computed within a reasonable time. Let $\alpha$ be the time for this step. After we have determined the sample sizes, $G$ is used to store the global distributions of all attribute sets each of which contains signatures with sufficient sample size.

Step 2 is to calculate the global distribution of $A$ according to non-empty $S_A$ for each attribute set $A$. In other words, it is to find each global distribution in $G$. As described in Section 4.1, for a particular global distribution, we formulate $m$ equations with $m$ variables where $m$ is the total number of signatures for $A$. The average number of terms in each equation is $O(N \cdot |W_k| \cdot |L_k|)$ where $N$ is the average $A$-group size, $|W_k|$ is the average number of possible worlds in an $A$-group $L_k$ and $|L_k|$ is the average number of $A$-groups with tuples matching a signature $s_i$. If Newton’s method takes $\beta$ time to find a solution, the computation for a global distribution takes $O(m \cdot N \cdot |W_k| \cdot |L_k| + \beta)$ time. Since there are $|G|$ global distributions, Step 2 takes $O(|G| \cdot (m \cdot N \cdot |W_k| \cdot |L_k| + \beta))$ time.

Thus, the total running time is $O(\alpha + |G| \cdot (m \cdot N \cdot |W_k| \cdot |L_k| + \beta))$. Note that the values of $m$, $N$, $|W_k|$ and $|L_k|$ are small and the complexity is dominated by $|G|$ and $\beta$. But, as the attribute set size increases, the sample size quickly becomes insufficient, and so $|G|$ is typically well-behaved.

From our experiments, in all of our cases, Step 2 with the system of $m$ equations can be solved in a relatively short time. So, $\beta$ is also a reasonable value. For the benchmark dataset, adult, foreground knowledge can be mined within 12 minutes in all our experiments.

The probabilistic analysis is similar in nature to that studied for uncertain databases [8, 9, 4] The computation complexity above is in fact much smaller than these previous works. In [4], all results are returned within 3 hours. The reason is that [8, 9, 4] analyze the possible worlds based on the entire uncertain table (which can be regarded as a single large $A$-group) while we analyze the possible worlds based on a single small $A$-group (which is typically smaller than the entire table).

### 4.4 Discussion

We have just discussed how to find the global distribution from the published table. One may argue that the global distribution $\mathcal{G}$ found from the published table is just an approximation of the true global distribution $\mathcal{G}_o$ found from the original table. Thus, the privacy breaches found in Section 3 according to $\mathcal{G}$ are invalid. However, we disagree with this argument with the following reasons.

Firstly, since the adversary does not have the true global distribution $\mathcal{G}_o$ (because s/he has not seen the original table), the best adversary’s knowledge about the global distribution is $\mathcal{G}$.

Secondly, an adversary with $\mathcal{G}$ is more powerful and more sophisticated than another adversary without any knowledge about the global distribution. The former adversary is what we are studying in this paper and can breach individual privacy discussed in Section 3 while the latter adversary is the normal adversary studied in the privacy literature [21, 29, 27] and cannot breach any individual privacy found by the former adversary.

Thirdly, the adversary $A_o$ with $\mathcal{G}_o$ (if there is) does not perform more serious privacy attacks compared with an adversary $A$ with $\mathcal{G}$. We assume that an adversary $A_o$ can have the true global distribution $\mathcal{G}_o$. This means that the public can also know $\mathcal{G}_o$ and $\mathcal{G}_o$ is not secret information.

Consider adversary $A$. Before s/he obtains $\mathcal{G}$, individual privacy (in the published table) is protected. After s/he obtains $\mathcal{G}$ (which can be found from the published table), individual privacy breaches. There is a change of belief after s/he sees $\mathcal{G}$. There are two kinds of privacy breaches. The first one is that an adversary can guess correctly the true sensitive value of an individual. The second one is that s/he can guess incorrectly the true sensitive value of an individual. For example, even if an individual is not linked to HIV in the original table, s/he can guess that the probability that this individual is linked to HIV is very high. This is also considered as a privacy breach to this individual.

---

1If this is not true, one of the ways that adversary $A_o$ can obtain $\mathcal{G}_o$ is to steal the original table from the data publisher. Since s/he has the original table, the privacy breaches found by $A_o$ are more serious. In this paper, we are not studying that the adversary can steal the original table.
nal. The reason is that the disclosure of the high linkage between this individual and HIV hurts the reputation of the individual because the adversary can convince a certain set of people that the inference procedure about individual privacy breaches was reasonable. Thus, privacy breaches found by $A$ are also serious.

Consider adversary $A_o$. In this case, we know that $G_o$ is a public information. Thus, the data publisher must have already taken $G_o$ into the account to publish a table. The claim is true because, otherwise, no individuals are eager to disclose their information to data publisher. Thus, even if adversary $A_o$ sees $G_o$, we cannot breach any individual privacy in the published table.

5. EMPIRICAL STUDY

A Pentium IV 2.2GHz PC with 1GB RAM was used to conduct our experiment. The algorithm was implemented in C/C++. We adopted the publicly available dataset, Adult Database, from the UCIrvine Machine Learning Repository [6]. This dataset (5.5MB) was also adopted by [16, 21, 26, 12, 27]. We used a configuration similar to [16, 21, 27]. The records with unknown values were first eliminated resulting in a dataset with 45,222 tuples (5.4MB). Nine attributes were chosen in our experiment, namely Age, Work Class, Marital Status, Occupation, Race, Sex, Native Country, Salary Class and Education. By default, we chose the first five attributes and the last attribute as the quasi-identifier and the sensitive attribute, respectively. Similar to [27], in attribute “Education”, all values representing the education levels before “secondary” (or “9th-10th”) such as “1st-4th”, “5th-6th” and “7th-8th” are regarded as a sensitive value set where an adversary checks whether each individual is linked to this set more than $1/r$, where $r$ is a parameter.

There are 3.46% tuples with education levels before “secondary”. We set $\epsilon = 0.01$ and $\sigma = 0.9$ for sampling. That is, the allowed relative error of sampling is $1/3.46 = 28.90\%$, which is considered large. A larger allowed error means less attribute sets can be pruned. Since there is a set $G$ of multiple global distributions $G$, we can calculate $p(t:x)$ for different $G$’s and different $x$’s. We take the greatest such value to report as the probability that individual $t$ is linked to some sensitive value since this corresponds to the worst case privacy breach.

5.1 Privacy Breach in $t$-diverse Tables

In this section, we will show that foreground knowledge attack is successful in the published data generated from the benchmark dataset, adult, by a well-known privacy algorithm, Anatomy [29]. We set $t = r$ where $l$ is the parameter of $l$-diversity used in Anatomy. We implemented the formula in Section 3 to calculate the probability of a privacy breach and the formula in Section 4 to find the global distribution from the published data. If a tuple which appears in the published data is identified as a privacy breach by our algorithm, it is said to be a problematic tuple. The tuples linking to sensitive values in the original table are called sensitive tuples. In this case study, we evaluate privacy breaches with three measurements:

1. proportion of problematic tuples among sensitive tuples, (this is the recall in IR research).
2. proportion of non-sensitive tuples which are identified wrongly as problematic tuples by our algorithm,
3. the average probability by which individual privacy is breached among all sensitive tuples.

We have conducted experiments with the variation of $r$ and the variation of the QI size. (1) Variation of $r$: When $r = 2$ with default settings, the average probability that individual privacy breaches among all sensitive tuples is $0.8917(>1/2)$. When $r$ is increased to 4, it becomes $0.4640(>1/4)$. When $r$ increases, there is a higher chance that a tuple forms an $A$-group with other tuples. Thus, the average size of $A$-groups is larger. Thus, the average probability of privacy breaches decreases. We also studied the proportion of problematic tuples among all sensitive tuples and the proportion of non-sensitive tuples identified wrongly as privacy breaches.

We found that, in most cases, more than 99% of sensitive tuples have privacy breaches and less than 6% of non-sensitive tuples are identified wrongly. (2) Variation of the QI size: When the QI size is equal to 3 with default settings where $r = 2$, the average probability causing privacy breaches is $0.80307$. When the size is increased to 8, it becomes $0.943526$. This is because when there are more QI attributes, it is more likely that a QI attribute (or attribute set) gives a global distribution which can lead to privacy breaches.

We also have a case study in the published data generated by Anatomy. Suppose the QI attributes chosen are Age, Marital Status and Occupation and the sensitive attribute is Education. In the original data, there are the following 2 tuples.

| Age | Marital Status | Occupation | Education |
|-----|----------------|------------|-----------|
| 39  | Never-married  | Adm-clerical| Bachelors |
| 20  | Married-civ-spouse | Craft-repair | 5th-6th |

Suppose the objective of Anatomy is 2-diversity. Since “5th-6th” is a sensitive value, Anatomy forms an $A$-group containing these two tuples. However, from the global distribution derived from the published data with respect to attribute Occupation, the probability that an individual with Occupation=“Adm-clerical” is linked to a low education is only 0.02 but the probability that an individual with Occupation=“Craft-repair” is linked to a low education is 0.04. Since there is a significant difference in global distribution of attribute Occupation, the probability that the second tuple above is linked to a low education is 0.67 (which is greater than 0.5).

It is noted that the global distribution derived from the published data matches the real situation that “Adm-clerical” jobs require higher educations but “Craft-repair” jobs does not. In other words, the foreground knowledge can help the adversary to breach individual privacy.

More specifically, let us check whether the real global distribution derived from the original table is similar to the global distribution derived from the published data. From the original table, the probability that an individual with Occupation=“Adm-clerical” is linked to a low education is only 0.01 but the probability that an individual with Occupation=“Craft-repair” is linked to a low education is 0.04. We observe that this global distribution is similar to that derived from the published data.

With our default experimental setting using sufficient sample size, for 2-diversity, the average relative error of the global probabilities derived from the published data=0.7% which achieves 99.3% accuracy. For 10-diversity, the error
increases to 5.26% where the accuracy is 94.74%. It shows that statistically the accuracy is very high. In other words, the foreground knowledge derived from the published data is quite accurate compared with the knowledge derived from the original table.

In all our experiments, privacy breaches can be found within 12 minutes, which shows that foreground knowledge attack can easily be realized.

5.2 Privacy Breach in Other Privacy Models

We studied privacy breaches with four algorithms, Anatomy [29], MASK [27], Injector [18] and t-closeness [17]. They are selected because they consider t-diversity or similar privacy requirements, so we need only set \( l = r \). For Anatomy, we set \( l = r \). For MASK, the parameters \( k \) and \( m \) used in MASK are set to \( r \). For Injector, the parameters \( \text{minConf}, \text{minExp} \) and \( l \) are set to 1, 0.9 and \( r \), respectively, which are the default settings in [18]. For t-closeness, similar to [17], we set \( t = 0.2 \). We evaluate the algorithms in terms of four measurements: (1) time for mining foreground knowledge, (2) execution time, (3) the proportion of problematic tuples among all sensitive tuples, (4) the average of the greatest difference in the global probabilities in each A-group (In our figures, we label this as average value of \( \Delta \)), and (5) the relative error ratio in answering an aggregate query as in [29, 27, 18] by the published data. For each measurement, we conducted the experiments 100 times and took the average.

We do not report the time for finding privacy breaches because the time is very short (within a few minutes). For the sake of space, since the proportion of non-sensitive tuples identified wrongly for privacy breaches is small (less than 10%), we do not report here.

Let us explain measurements (4) and (5). (4) Consider an A-group \( L_k \) contains two tuples matching signatures \( s_i \) and \( s_j \), respectively. Suppose \( p(s_i : x) \) is the greatest global probabilities and \( p(s_j : x) \) is the smallest in the A-group. The value of \( \Delta \) in \( L_k \) is equal to \( p(s_i : x) - p(s_j : x) \). The average value of \( \Delta \) is taken among all A-groups and all attribute sets \( A \) with sufficient samples. (5) The relative error ratio measures the utility of the published data. We adopt all query parameters in [29, 27, 18]. For each evaluation, we performed 10,000 queries and reported the average relative error ratio.

We have conducted the experiments by varying two factors: (1) the QI size, and (2) \( r \).

Figure 1 and Figure 2 show the results when \( r \) is set to 2 and 10, respectively. Figure 1(a) shows that the time for mining foreground knowledge increases with the QI size because the algorithm needs to process more attribute sets. Figure 1(b) shows that the execution time increases with the QI size because the algorithms have to process more QI attributes.

Figure 1(c) shows that the proportion of problematic tuples among sensitive tuples increases with QI size. With a larger QI size, there is a higher chance that individual privacy breaches due to more attributes which can be used to construct the global distributions. MASK has fewer privacy breaches compared with Anatomy and Injector because the side-effect of the minimization of QI values in each A-group adopted in MASK makes the difference in the global distribution among all tuples in each A-group smaller. Thus, the number of individual with privacy breaches is smaller. It is noted that there is no violation in t-closeness. The reason why t-closeness has no privacy breaches is due to the large A-groups formed by global recoding with respect to value \( r(= 2) \). The average size of the A-group in the table satisfying t-closeness is at least 4000 and the utility of the table is low. It is noted that parameter \( t \) is independent of parameter \( r \). We will show that t-closeness has privacy breaches when \( r = 10 \).

In Figure 1(d), when the QI size increases, the average value of \( \Delta \) with respect to every attribute set increases, as shown in Figure 1(d). The average value of \( \Delta \) is the largest in Anatomy and Injector, and the third largest in MASK. This is because Anatomy and Injector does not take the global distribution directly into the consideration for merging but MASK does indirectly during the minimization of QI values.

Figure 3(a) shows that the average relative error of t-closeness is the largest since it forms large A-groups by global recoding which introduce a lot of errors and thus reduce the utility of the published data.
distribution studied here involves the probability that an individual (with any QI attribute values) is linked to a sensitive value. However, the global distribution does not give any close resemblance to the distribution in each A-group. In Figure 2(c) because there is a high chance of privacy breaches for $t$-closeness because there is a high chance of privacy breaches for $t$-closeness. For $t$-closeness, the distribution in each A-group in $T^*$ with respect to the sensitive attribute is robustly equal to the distribution of the entire table $T$. Given a real number $\alpha \in [0, 1]$ and a positive integer $k$, $(\alpha, k)$-anonymity [28] maintains that, for each A-group $L$, the number of tuples in $L$ is at least $k$ and the frequency (in fraction) of each sensitive value in $L$ is at most $\alpha$.

We emphasize that $t$-closeness is different from ours. Firstly, $t$-closeness does not have any privacy guarantee on the bound of breach probabilities. Like $l$-diversity, Anatomy, MASK, Injector and $t$-closeness suffer from serious privacy breaches in a benchmark dataset. For future work, we plan to study how to analyze the correlation between some QI attributes and the sensitive attribute. Since $t$-closeness restricts that each A-group has nearly the same distribution as the distribution of the entire table, the desired goal cannot be achieved.

In the literature, different kinds of background knowledge are considered [21, 15, 22, 27, 20, 13, 18, 2]. [15] proposes the statistics of some attributes such as age and zipcode can be also available to the public. [22] considers another background knowledge in form of implications. [27] discovers that the minimal privacy principle of the anonymization algorithm can also be used as a background knowledge. [20] proposes to use the kernel estimation method to mine the background knowledge from the original table. [13] describes that there are many tables published from different sources containing overlapping individuals.

[18] finds that association rules can be mined from the original table and thus can be used for privacy protection during anonymization. In [2], the problem of privacy attack by adversarial association rule mining is investigated. Hence, the association rules are the foreground knowledge. However, as pointed out in [23], association rules used in [18] and [2] can contradict the true statistical properties. Also, the solution in [2] is to invalidate the rules, but this will violate the data mining objectives of data publication.

A recent work [1] proposes to generate a table in form of an uncertain data model. However, this work considers $k$-anonymity which ignores any sensitive attribute.

7. CONCLUSION

In this paper, we point out a fundamental privacy breach problem which has been overlooked in the past. With the consideration of the utility of the anonymized table, group based anonymization suffers from privacy breaches. Our experiments show that existing well-known privacy models Anatomy, MASK, Injector and $t$-closeness suffer from serious privacy breaches in a benchmark dataset. For future work, we plan to study how to anonymize the data to defend against foreground knowledge attack. In our experiment, we observe that the chance of privacy breaches is lower if each group contains tuples with “similar” global probabilities. Thus, forming A-groups with “similar” tuples is one possible strategy. Another future work is to study the effect of background knowledge that may be possessed by the adversary.

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