Anonymization by Local Recoding in Data with Attribute Hierarchical Taxonomies

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Abstract—Individual privacy will be at risk if a published data set is not properly deidentified. k-Anonymity is a major technique to deidentify a data set. Among a number of k-anonymization schemes, local recoding methods are promising for minimizing the distortion of a k-anonymity view. This paper addresses two major issues in local recoding k-anonymization in attribute hierarchical taxonomies. First, we define a proper distance metric to achieve local recoding generalization with small distortion. Second, we propose a means to control the inconsistency of attribute domains in a generalized view by local recoding. We show experimentally that our proposed local recoding method based on the proposed distance metric produces higher quality k-anonymity tables in three quality measures than a global recoding anonymization method, Incognito, and a multidimensional recoding anonymization method, Multi. The proposed inconsistency handling method is able to balance distortion and consistency of a generalized view.

Index Terms—k-anonymization, local recoding, generalization distance, inconsistency.

1 Introduction

A vast amount of operational data and information has been stored by different vendors and organizations. Most of the stored data is useful only when it is shared and analyzed with other related data. However, this kind of data often contains some personal details and sensitive information. The data can only be allowed to be released when individuals are unidentifiable. K-anonymity has emerged as an effective approach in anonymization [18], [19], [20].

1.1 K-anonymization and Various Methods

The key idea of k-anonymization is to make individuals indistinguishable in a released table. A tuple representing an individual within the identifiable attributes has to be identical to at least $(k-1)$ other tuples. The larger the value of k is, the better the protection. One way to produce k identical tuples within the identifiable attributes is to generalize values within the attributes, for example, removing day and month information in a Date-of-Birth attribute. A general view of attribute generalization is the aggregation of attribute values. K-anonymity has been extensively studied in recent years [4], [7], [9], [10], [22].

Various approaches for generalization have been studied, such as global recoding generalization [4], [7], [9], [18], [19], [22], multidimensional recoding generalization [10], and local recoding generalization [6], [15], [24]. Global recoding generalization maps the current domain of an attribute to a more general domain. For example, ages are mapped from years to 10-year intervals. Multidimensional recoding generalization (or multidimensional global recoding generalization by LeFevre et al. [10]) maps a set of values to another set of values, some or all of which are more general than the corresponding premapping values. For example, {male, 32, divorce} is mapped to {male, [30,40), unknown}. Local recoding generalization modifies some values in one or more attributes to values in more general domains. We will illustrate the differences between multidimensional recoding generalization and local recoding generalization in the following.

A general view of k-anonymity is clustering with the constraint of the minimum number of objects in every cluster. Data records are mapped to data points in a high dimensional space. When a region partitioned by attribute values has fewer than k data points, individuals represented by data points are at risk of being identified. The region needs to be merged with other regions by generalizing attribute values so that the merged region contains at least k data points.

Global, multidimensional, and local recoding generalization can be explained in this way. Consider the 2D example in Fig. 1a and let $k=5$. Attribute values (a,b,c,d) and (α,β,γ) partition the data space into 12 regions in Fig. 1a. Two regions, $[a,\alpha]$ and $[b,\beta]$, contain less than five but more than zero data points. Individuals in these two regions are likely to be identified. Therefore, they need to be merged with other regions to make the number of data points at least five. In the global recoding generalization scheme, a merged region stretches over the range of other attributes. For example, the merged rectangle in Fig. 1b covers all values of Attribute 1 since all occurrences of α and β in Attribute 2 have to be generalized. The merged regions and the summary of the corresponding generalized table are

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Manuscript received 16 Dec. 2006; revised 20 Sept. 2007; accepted 17 Jan. 2008; published online 4 Mar. 2008.
For information on obtaining reprints of this article, please send e-mail to: tkde@computer.org, and reference IEEECS Log Number TKDE-0570-1206.
Digital Object Identifier no. 10.1109/TKDE.2008.52.

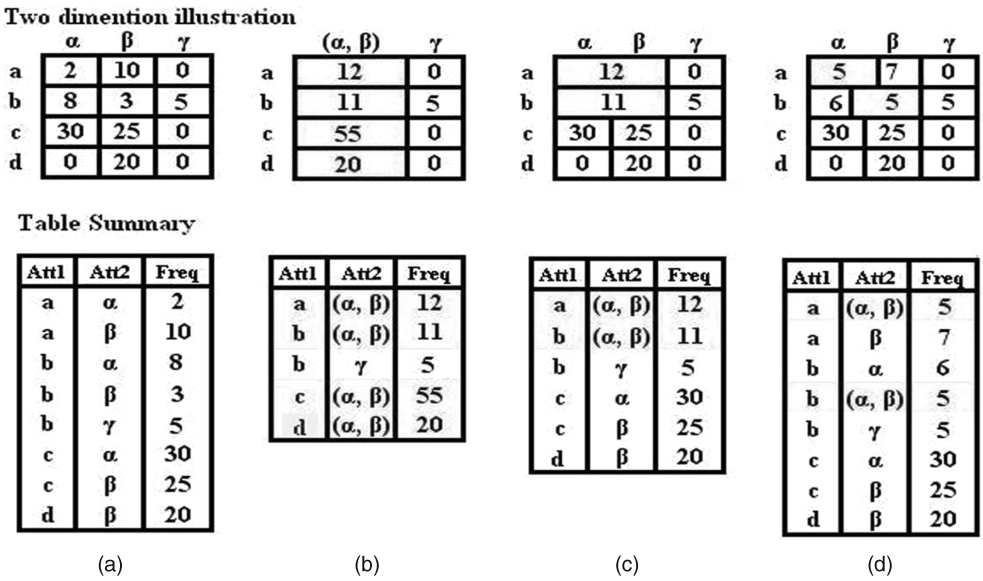

Fig. 1. An illustration of different methods to achieve k-anonymity. A table has two attributes Att1 and Att2. $\{a, b, c, d\}$ and $\{\alpha, \beta, \gamma\}$ are the original domains for Att1 and Att2. Top tables summarize the number of data points in separate regions of the 2D space. The bottom tables summarize frequencies of identical tuples. (a) The original data. (b) Generalization by a global recoding approach. (c) Generalization by a multidimensional recoding approach. (d) Generalization by a local recoding approach.

listed in Fig. 1b. In a table view, domain (α, β, γ) is mapped to domain $(\alpha, [\beta, \gamma])$. The global recoding generalization causes some unnecessary mergers, for example, regions $[c, (\alpha, \beta)]$ and $[d, (\alpha, \beta)]$. This is the overgeneralization problem of global recoding generalization. For the multidimensional generalization scheme, any two or more regions can be merged as long as the aggregated attribute value such as $[\beta, \gamma]$ makes sense. For example, regions $[a, \alpha]$ and $[a, \beta]$ merge into region $[a, (\alpha, \beta)]$, and regions $[b, \alpha]$ and $[b, \beta]$ merge into region $[b, (\alpha, \beta)]$. Regions $[c, \alpha]$, $[c, \beta]$, $[d, \alpha]$, and $[d, \beta]$ keep their original areas, see Fig. 1c. In a table view, all tuples (a, α) and (a, β) are mapped to $(a, [\alpha, \beta])$ and all tuples (b, α) and (b, β) are mapped to $(b, [\alpha, \beta])$, but tuples (c, α), (c, β), and (d, β) remain unchanged. A local recoding generalization method is even more flexible, see Fig. 1d. It does not merge whole regions. A dense region can be split into two or more overlapping regions, and some merge with other regions. For example, region $[a, \beta]$ is split into two overlapping regions containing three and seven data points each. The three-data point region is merged with region $[a, \alpha]$ to form region $[a, (\alpha, \beta)]$ with five data points. Both multidimensional and local recoding approaches do not overgeneralize a table. In a table view, some tuples of (a, α) and (a, β) are mapped to $(a, [\alpha, \beta])$, and some tuples of (b, α) and (b, β) are mapped to $(b, [\alpha, \beta])$, but some remain unchanged in their original forms.

1.2 Existing Problems and Our Contributions

Multidimensional and local recoding methods can improve the quality of anonymization by reducing the amount of generalization. A number of research works have been conducted in this direction [1], [6], [10], [15], [24]. However, most works focus on numerical and ordinal attributes. Two works [1], [15] handle unordered categorical attributes, but both employ a simplified suppression model: values either exist or are unknown. They do not consider attribute hierarchical structures. Work in [24] touches upon attribute hierarchical structures, but the approach is fundamentally a numerical one. More discussions on the work are given in Section 2.

There is an opportunity for studying multidimensional and local recoding k-anonymization in attribute hierarchies. When attributes are numerical or ordinal, their distances can be measured by the euclidean distance or other similar metrics. However, not every attribute can be ordered. Attribute hierarchical taxonomies provide meaningful groups in a released table. Two immediate questions will be: How can we measure distances of data objects in attribute hierarchies? How can we link the metric to the quality objective of k-anonymization? This paper will discuss these problems.

One major drawback of multidimensional and local recoding generalization methods is that they produce tables with inconsistent attribute domains. For example, generalized values (α, β) and ungeneralized values α and β coexist in Attribute 2 in Figs. 1c and 1d. This may cause difficulty when analyzing the table in many real-world applications. We will initiate discussions of inconsistency problem of local recoding generalization and study an approach to handle inconsistent domains of a generalized table.

This paper extends our work reported in [13]. In addition to defining a distance metric and splitting an equivalence class to a stub and a trunk for local recoding, we add comprehensive discussions on the inconsistency problem of local recoding and possible solutions. We also upgrade the experimental comparisons from comparing with a global recoding method based on one quality metric to comparing with both global and multidimensional recoding methods based on four quality metrics.

2 Related Work

In general, there are three categories of privacy preserving methods in the data mining literature. The first category

consists of perturbation methods, typified by [2], [3], and [17]. These methods make use of randomized techniques to perturb data and statistical techniques to reconstruct distribution of data. The second category comprises of cryptographic methods, such as [14], [21], and [23]. Cryptographic techniques have been used to encrypt data so that neither party can see other parties' data when they share data to work out common interesting solutions. The third category includes k-anonymity methods, such as [18] and [20]. A k-anonymity method deidentifies a data set so that individuals in the data set cannot be identified. Our study belongs to this category.

K-anonymization methods are generally divided into two groups: task-specific and nonspecific methods. For task-specific k-anonymization, the released tables are undergoing some specific data mining processes (e.g., building decision tree models). The purpose of anonymization is to keep sufficient protection of sensitive information while maintaining the precision for data mining tasks, such as classification accuracy. There have been a number of proposals in this group [7], [8], [22]. In most cases, data owners do not know the ultimate use of the released tables. Therefore, a general anonymization goal should not be associated with a specific data mining task but should minimize distortions in the released table. The methods in this category are called nonspecific k-anonymization methods (e.g., [1], [4], [9], [15], [18], [19]).

An alternative taxonomy of k-anonymization methods includes three groups: global, multidimensional, and local recoding methods. LeFevre et al. [10] divide multidimensional recoding methods into global and local methods. In this paper, multidimensional recoding means multidimensional global recoding. Local recoding includes multidimensional and single dimensional local recoding. Justifications for our classification are provided in Section 3.

Global recoding methods generalize a table at the domain level. Many works of k-anonymization are based on the global recoding model, such as [4], [7], [8], [9], [18], [19], and [22]. A typical global recoding generalization method is Incognito [9]. Incognito produces minimal full-domain generalizations. Incognito is the first algorithm for the minimal full-domain generalization on large databases. A global recoding method may overgeneralize a table. For example, to protect a male patient in a specific region, postcodes of thousands of records are generalized even though there are a lot of male patients in other regions, which can have their original postcodes.

Both multidimensional and local recoding methods generalize a table at cell levels. They do not overgeneralize a table and, hence, may minimize the distortion of an anonymity view. LeFevre et al. first studied the multidimensional recoding problem [10] and proposed an efficient partition method, Multi, for multidimensional recoding anonymization. Aggarwal et al. [1] and Meyerson and Williams [15] analyzed the computational complexity of local recoding methods on a simplified model: suppressing values only. Both conclude that optimal k-anonymization, minimizing the number of cells being suppressed, is NP-hard. Some new local recoding works are reported in [6] and [24]. These works mainly deal with numerical and ordinal attributes. Although work in [24] touches on hierarchical attributes, its quality metric for hierarchical attributes is a direct extension of that for numerical attributes. The quality of generalizing categorical values in [24] is determined by the number of distinct values in a generalized category and the total number of distinct values of the attribute but not by hierarchical structures. Consider two attributes with the same number of distinct values. Information losses of two generalizations are the same if the generalized categories include the same number of distinct values, although their hierarchical structures are different. In contrast, the generalization distance in this paper is determined by hierarchical structures.

Other typical approaches to achieve k-anonymity are through clustering [2], [5]. These methods normally handle numerical and ordinal attributes and are not global recoding methods. They use different representations, such as mean values instead of intervals as in generalization. For data sets with numerical attributes, there are rarely identical tuples in the quasi-identifier attribute set, defined in Section 3 (overlapping data points in a data space), since there are too many distinct values in each attribute. Therefore, there is not a point to distinguish local recoding and multidimensional recoding. In general, most k-anonymity methods can be interpreted as variant clustering approaches, either through division or agglomeration. Local and multidimensional recoding methods are differentiated by whether overlapping clusters are allowed.

3 Problem Definitions

The objective of k-anonymization is to make every tuple in identity-related attributes of a published table identical to at least $(k-1)$ other tuples. Identity-related attributes are those which potentially identify individuals in a table. For example, the record describing a middle-aged female in the suburb with the postcode of 4,352 is unique in Table 1, and hence, her problem of stress may be revealed if the table is published. To preserve her privacy, we may generalize Gender and Postcode attribute values such that each tuple in attribute set {Gender, Age, Postcode} has at least two occurrences. A view after this generalization is given in Table 1b. We provide running examples based on Table 1.

Since various countries use different postcode schemes, in this paper, we adopt a simplified postcode scheme, where its hierarchy {4201, 420*, 42**, 4***, *} corresponds to {suburb, city, region, state, unknown}, respectively. A tuple for an attribute set in a record is an ordered list of values corresponding to the attribute set in the record.

Definition 1 (Quasi-identifier attribute set). *A* quasi-identifier attribute set *(QID) is a set of attributes in a table that potentially identify individuals in the table.*

For example, attribute set {Gender, Age, Postcode} in Table 1a is a quasi-identifier. Table 1a potentially reveals private information of patients (e.g., the problem of stress of the middle-aged female). Normally, a quasi-identifier attribute set is specified by domain experts.

Definition 2 (Equivalence class). *An* equivalence class *of a table with respect to an attribute set is the set of all tuples in the table containing identical values for the attribute set.*

TABLE 1
(a) A Raw Table. (b) A Two-Anonymity View by Global Recoding. (c) A Two-Anonymity by Multidimensional Recoding. (d) A Two-Anonymity by Local Recoding

No.	Gender	Age	Postcode	Problem
1	male	middle	4350	stress
2	male	middle	4350	obesity
3	male	middle	4350	obesity
4	female	middle	4352	stress
5	female	old	4353	stress
6	female	old	4353	obesity

(a)

No.	Gender	Age	Postcode	Problem
1	*	middle	435*	stress
2	*	middle	435*	obesity
3	*	middle	435*	obesity
4	*	middle	435*	stress
5	*	old	435*	stress
6	*	old	435*	obesity

(b)

No.	Gender	Age	Postcode	Problem
1	male	middle	4350	stress
2	male	middle	4350	obesity
3	male	middle	4350	obesity
4	female	*	435*	stress
5	female	*	435*	stress
6	female	*	435*	obesity

(c)

No.	Gender	Age	Postcode	Problem
1	male	middle	4350	stress
2	male	middle	4350	obesity
3	*	middle	435*	obesity
4	*	middle	435*	stress
5	female	old	4353	stress
6	female	old	4353	obesity

(d)

For example, tuples 1, 2, and 3 in Table 1a form an equivalence class with respect to attribute set {Gender, Age, Postcode}. Their corresponding values are identical.

Definition 3 (k-anonymity property). *A table is k-anonymous with respect to a quasi-identifier attribute set if the size of every equivalence class with respect to the attribute set is k or more.*

k-Anonymity requires that every tuple occurrence for a given quasi-identifier attribute set has a frequency of at least k. For example, Table 1a does not satisfy the two-anonymity property since the tuple {female, middle, 4352} occurs once.

Definition 4 (k-anonymization). K-anonymization *is a process to modify a table to a view that satisfies the k-anonymity property with respect to the quasi-identifier.*

For example, Table 1b is a two-anonymity view of Table 1a since the size of all equivalence classes with respect to the quasi-identifier {Gender, Age, Postcode} is at least 2.

A table may have more than one k-anonymity view, but some are better than others. For example, we may have other two-anonymity views of Table 1a as in Tables 1c and 1d. Table 1b loses more detail than Tables 1c and 1d.

Therefore, another objective for k-anonymization is to minimize distortions. We will give a definition of distortion later in Section 4. Initially, we consider it as the number of cells being modified.

There are three ways to achieve k-anonymity, namely *global recoding*, *multidimensional recoding*, and *local recoding*. LeFevre divided multidimensional recoding as having two subtypes [10]: global and local methods. Though the multidimensional global recoding contains the word global, its generalized tables are quite different from those of the global recoding generalization but are closer to those of the local recoding generalization. Both multidimensional and local recoding methods produce tables with mixed values from different domains in a field, whereas all values are from the same domain in a field of a globally generalized table. To avoid confusion, we use the terminology "multidimensional recoding" instead of "multidimensional global recoding." It is not significant to distinguish multidimensional and single dimensional local recoding since it does not lead to different approaches to generalize one value or more values in a tuple for local recoding. We call both local recoding.

Another name for global recoding is *domain generalization*. The generalization happens at the domain level. A specific domain is replaced by a more general domain. There are no mixed values from different domains in a table generalized by global recoding. When an attribute value is generalized, every occurrence of the value is replaced by the new generalized value. A global recoding method may *overgeneralize* a table. An example of global recoding is given in Table 1b. Two attributes Gender and Postcode are generalized. All gender information has been lost. It is not necessary to generalize the Gender and the Postcode attribute as a whole. So, we say that the global recoding method overgeneralizes this table.

Multidimensional and local recoding methods generalize attribute values at cell level. They generalize cell values when necessary for k-anonymity. Values from different domains coexist in a field of a generalized table. They do not overgeneralize a table, and hence, they may minimize the distortion of an anonymous view. Tables generalized by multidimensional and local recoding methods are given in Tables 1c and 1d. Another interpretation of multidimensional and local recoding is that they map a set of values to another set of values. The difference between multidimensional recoding and local recoding generalization is that the former does not allow an equivalence class to be mapped to two or more equivalence classes while the latter does. For example, three equivalence classes in Table 1a are generalized to two equivalence classes in Table 1c. The two

equivalence classes {female, middle, 4352} and {female, old, 4353} are generalized to one equivalence class {female, *, 435*}. No equivalence class is split, and this is a result of multidimensional recoding. Three equivalence classes in Table 1a are generalized to three equivalence classes in Table 1d. The equivalence class {male, middle, 4350} is split into two identical equivalence classes. One contains the first two tuples, t_1 and t_2, and the other contains the third tuple, t_3. The equivalence class containing t_3 is generalized with the equivalence class containing t_4. The equivalence class containing t_1 and t_2 remains ungeneralized. Therefore, Table 1d is a result of local recoding. A large equivalence class may be generalized into a number of equivalence classes in local recoding.

There are many possible ways for local recoding generalization. Aggarwal et al. [1] and Meyerson and Williams [15] analyze a simplified local recoding model where values either exist or are suppressed. When the optimization goal is to minimize cells being suppressed, both papers conclude that optimal k-anonymization by local recoding is NP-hard. Therefore, heuristic methods are typically employed in local recoding generalization.

4 Measuring the Quality of K-anonymization

In this section, we discuss metrics for measuring the quality of k-anonymization generalization.

There are a number of quality measurements presented in previous studies. Many metrics are utility based, for example, model accuracy [7], [11] and query quality [10], [24]. They are associated with some specific applications. Two generic metrics have been used in a number of recent works.

The Discernability metric was proposed by Bayardo and Agrawal [4] and has been used in [10] and [24]. It is defined in the following:

$$\mathrm{DM} = \sum_{\text{EquivClasses E}} |\mathrm{E}|^2,$$

where $|E|$ is the size of equivalence class E. The cost of anonymization is determined by the size of equivalence classes. An optimization objective is to minimize discernability cost.

Normalized average equivalence class size was proposed by LeFevre et al. [10], and has been used in [24]. It is defined as the following.

$$\mathrm{CAVG} = \left(\frac{\text{total\_records}}{\text{total\_equiv\_classes}}\right)/(k).$$

The quality of k-anonymization is measured by the average size of equivalence classes produced. An objective is to reduce the normalized average equivalence class size.

These measurements are mathematically sound but are not intuitive to reflect changes being made to a table. In this paper, we use the most generic criterion, called distortion. It measures changes caused by generalization.

A simple measurement of distortion is the *modification rate*. For a k-anonymity view V of table T, the *modification rate* is the fraction of cells being modified within the quasi-identifier attribute set. For example, modification rate from Tables 1a to 1b is 66.7 percent and modification rate from Tables 1a to 1c is 33.3 percent.

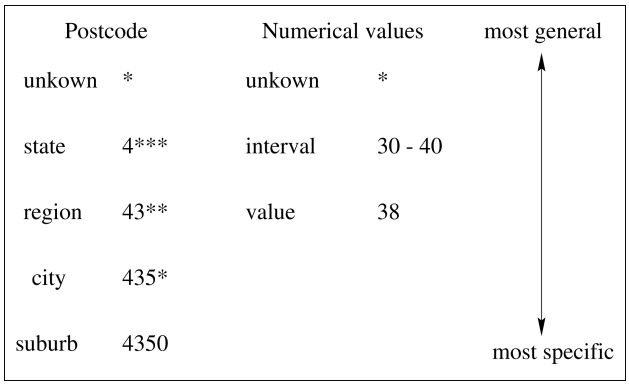

Fig. 2. Examples of domain hierarchies.

This criterion does not consider attribute hierarchical structures. For example, the distortion caused by the generalization of Postcode from suburb to city is significantly different from the distortion caused by the generalization of Gender from male/female to *. The former still keeps some information of location, but the latter loses all information of sex. The modification rate is too simple to reflect such differences.

We first define a metric measuring the distance between different levels in an attribute hierarchy.

Definition 5 [Weighted Hierarchical Distance (WHD)]. *Let h be the height of a domain hierarchy, and let levels $1, 2, \ldots, h-1$, h be the domain levels from the most general to most specific, respectively. Let the weight between domain level j and $j-1$ be predefined, denoted by $w_{j,j-1}$, where $2 \le j \le h$. When a cell is generalized from level p to level q, where $p > q$, the WHD of this generalization is defined as*

$$\mathrm{WHD}(p,q) = \frac{\sum_{j=q+1}^{p} w_{j,j-1}}{\sum_{j=2}^{h} w_{j,j-1}}.$$

Fig. 2 show two examples of attribute hierarchies, and Fig. 3 shows the numbering method of hierarchical levels and weights between hierarchical levels. Level 1 is always the most general level of a hierarchy and contains one value, unknown.

We have the following two simple but typical definitions for weight $w_{j,j-1}$ in generalization.

1. **Uniform weight**: $w_{j,j-1} = 1$, where $2 \le j \le h$. In this scheme, WHD is a ratio of the steps a cell being generalized to all possible generalization steps (the height of a hierarchy). For example, let the Date-of-Birth hierarchy be {day/month/year, month/year, year, 10-year interval, child/youth/middle-age/old-age, *}. WHD of the generalization from day/month/year to year is $\mathrm{WHD}(6,4) = (1+1)/5 = 0.4$. In a Gender hierarchy, {male/female, *}, WHD from male/female to * is $\mathrm{WHD}(2,1) = 1/1 = 1$. This means that distortion caused by the generalization of five cells from day/month/year to year is equivalent to distortion caused by the generalization of two cells from male/female to *.

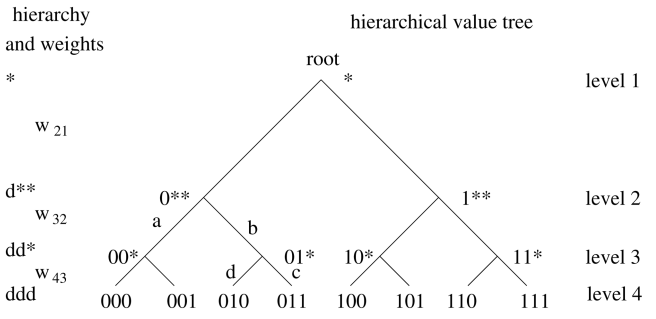

Fig. 3. An example of weights and a simplified hierarchical value tree.

This scheme does not capture the fact that generalizations at different levels yield different distortions. A generalization nearer to the root of the hierarchy distorts a value more than a generalization further away from the root. For example, in the Date-of-Birth hierarchy, the distortion caused by the generalization of a value from day/month/year to month/year is less than the distortion caused by the generalization from year to 10-year interval. This example motivates us to propose another scheme.

2. **Height weight**: $w_{j,j-1} = 1/(j-1)^{\beta}$, where $2 \leq j \leq h$ and β is a real number ≥ 1 provided by the user. The intuition is that generalization nearer the root results in larger distortion than generalization further away from the root. In this scheme, weights nearer the root are larger than weights further away from the root. For example, in the Date-of-Birth attribute, let $\beta = 1$, WHD of the generalization from day/month/year to year is

$$\begin{aligned}\mathrm{WHD}(6,5) &= (1/5)/(1/5 + 1/4 + 1/3 + 1/2 + 1)\\ &= 0.087.\end{aligned}$$

In the Gender hierarchy {male/female, *}, WHD from male/female to * is $\mathrm{WHD}(2,1) = 1/1 = 1$. The distortion caused by the generalization of one cell from male/female to * in the Gender attribute is more than the distortion caused by the generalization of 11 (i.e., 1/0.087) cells from day/month/year to month/year in the Date-of-Birth attribute. If a user wants to penalize more on the generalization close to the root, β can be set to a larger value (e.g., 2).

There are other possible schemes for various applications. An immediate enhancement is to assign weights by attribute. We adopt simple schemes for better illustration in this paper. In the following, we define distortions caused by the generalization of tuples and tables.

Definition 6 (Distortions of generalization of tuples). *Let $t = \{v_1, v_2, \ldots, v_m\}$ be a tuple and $t' = \{v'_1, v'_2, \ldots, v'_m\}$ be a generalized tuple of t, where m is the number of attributes in the quasi-identifier. Let $\mathrm{level}(v_j)$ be the domain level of v_j in an attribute hierarchy. The distortion of this generalization is defined as*

$$\mathrm{Distortion}(t, t') = \sum_{j=1}^{m} \mathrm{WHD}\Big(\mathrm{level}(v_j), \mathrm{level}(v'_j)\Big).$$

For example, let weights of WHD be defined by the uniform weight scheme, the attribute Gender be in the hierarchy of {male/female, *} and attribute Postcode be in the hierarchy of {dddd, ddd*, dd**, d***, *}. Let t_4 be tuple 4 in Table 1a and t'_4 be tuple 4 in Table 1b. For attribute Gender, $\mathrm{WHD} = 1$. For attribute Age, $\mathrm{WHD} = 0$. For attribute Postcode, $\mathrm{WHD} = 1/4 = 0.25$. Therefore, $\mathrm{Distortion}(t_4, t'_4) = 1.25$.

Definition 7 (Distortions of generalization of tables). *Let view D' be generalized from table D, t_i be the ith tuple in D, and t'_i be the ith tuple in D'. The distortion of this generalization is defined as*

$$\mathrm{Distortion}(D, D') = \sum_{i=1}^{|D|} \mathrm{Distortion}\big(t_i, t'_i\big),$$

where $|D|$ is the number of tuples in D.

For example, from Tables 1a to 1b,

$$\mathrm{WHD}(t_1, t'_1) = \ldots = \mathrm{WHD}(t_6, t'_6) = 1.25.$$

The distortion between the two tables is

$$\mathrm{Distortion}(D, D') = 1.25 \times 6 = 7.5.$$

5 Generalization Distances

In this section, we map distortions to distances and discuss properties of the mapped distances.

5.1 Distances between Tuples and Equivalence Classes

An objective of k-anonymization is to minimize the overall distortions between a generalized table and the original table. We first consider how to minimize distortions when generalizing two tuples into an equivalence class.

Definition 8 (Closest common generalization). *All allowable values of an attribute form a hierarchical value tree. Each value is represented as a node in the tree, and a node has a number of child nodes corresponding to its more specific values. Let t_1 and t_2 be two tuples. $t_{1,2}$ is the closest common generalization of t_1 and t_2 for all i. The value of the closest common generalization $t_{1,2}$ is*

$$v^i_{1,2} = \begin{cases} v^i_1 & \text{if } v^i_1 = v^i_2,\\ \textit{the value of the closest common ancestor} & \text{otherwise,}\end{cases}$$

where v^i_1, v^i_2, and $v^i_{1,2}$ are the values of the ith attribute in tuples t_1, t_2, and $t_{1,2}$.

For example, Fig. 3 shows a simplified hierarchical value tree with four domain levels and $2^{(l-1)}$ values for each domain level l. Node 0** is the closest common ancestor of nodes 001 and 010 in the hierarchical value tree. Consider another example. Let $t_1 = \{\mathrm{male}, \mathrm{young}, 4351\}$ and $t_2 = \{\mathrm{female}, \mathrm{young}, 4352\}$. $t_{1,2} = \{*, \mathrm{young}, 435*\}$.

Now, we define the distance between two tuples.

Definition 9 (Distance between two tuples). *Let t_1 and t_2 be two tuples and $t_{1,2}$ be their closest common generalization. The distance between the two tuples is defined as*

$$\text{Dist}(t_1, t_2) = \text{Distortion}(t_1, t_{1,2}) + \text{Distortion}(t_2, t_{1,2}).$$

For example, let weights of WHD be defined by the uniform weight scheme, attribute Gender be in the hierarchy of {male/female, *} and attribute Postcode be in the hierarchy of {dddd, ddd*, dd**, d***, *}. $t_1 = \{\text{male}, \text{young}, 4351\}$ and $t_2 = \{\text{female}, \text{young}, 4352\}$. $t_{1,2} = \{*, \text{young}, 435*\}$.

$$\begin{aligned}\text{Dist}(t_1, t_2) &= \text{Distortion}(t_1, t_{1,2}) + \text{Distortion}(t_2, t_{1,2}) \\ &= 1.25 + 1.25 = 2.5.\end{aligned}$$

We discuss some properties of tuple distance in the following.

Lemma 1. Basic properties of tuple distances.

1. $\text{Dist}(t_1, t_1) = 0$ *(i.e., a distance between two identical tuples is zero);*
2. $\text{Dist}(t_1, t_2) = \text{Dist}(t_2, t_1)$ *(i.e., the tuple distance is symmetric);*
3. $\text{Dist}(t_1, t_3) \leq \text{Dist}(t_1, t_2) + \text{Dist}(t_2, t_3)$ *(i.e., the tuple distance satisfies triangle inequality).*

Proof. The first two properties obviously follow Definition 9. We prove Property 3 here.

We first consider a single attribute. To make notations simple, we omit the superscript for the attribute. Let v_1 be the value of tuple t_1 for the attribute, $v_{1,3}$ be the value of the generalized tuple $t_{1,3}$ for the attribute from tuple t_1 and tuple t_3, and so forth.

Within a hierarchical value tree, $\text{Dist}(t_1, t_3)$ is represented as the shortest path linking nodes v_1 and v_3 and $\text{Dist}(t_1, t_2) + \text{Dist}(t_2, t_3)$ is represented as the path linking v_1 and v_3 via v_2. Therefore,

$$\text{Dist}(t_1, t_3) \leq \text{Dist}(t_1, t_2) + \text{Dist}(t_2, t_3).$$

The two distances are equal only when v_2 is located within the shortest path between v_1 and v_3.

The overall distance is the sum of distances of all individual attributes. This proof is true for all attributes. Therefore, the Property 3 is proved. □

An example of Property 3 can be found in the hierarchical value tree in Fig. 3. The distance between 00* and 011 is $(a + b + c)$, the distance between 00* and 010 is $(a + b + d)$, and the distance between 010 and 011 is $(c + d)$. Therefore, $\text{Dist}(00*, 011) < \text{Dist}(00*, 010) + \text{Dist}(010, 011)$. In a special case,

$$\text{Dist}(00*, 011) = \text{Dist}(00*, 01*) + \text{Dist}(01*, 011).$$

Now, we discuss distance between two groups of tuples.

Definition 10 (Distance between two equivalence classes). *Let C_1 be an equivalence class containing n_1 identical tuples t_1 and C_2 be an equivalence class containing n_2 identical tuples t_2. $t_{1,2}$ is the closest common generalization of t_1 and t_2. The distance between two equivalence classes is defined as follows:*

$$\begin{aligned}\text{Dist}(C_1, C_2) = {} & n_1 \times \text{Distortion}(t_1, t_{1,2}) \\ & + n_2 \times \text{Distortion}(t_2, t_{1,2}).\end{aligned}$$

Note that $t_{1,2}$ is the tuple that t_1 and t_2 will be generalized if the two equivalence classes C_1 and C_2 are generalized into one equivalence class. The distance is equivalent to the distortions of the generalization, and therefore, the choice of generalization should be those equivalence classes with the smallest distances.

We consider a property of merging equivalence classes.

Lemma 2. Associative property of generalization. *Let C_1, C_2, and C_3 be equivalence classes containing single tuples t_1, t_2, and t_3, respectively, $C_{1,2}$ be the equivalence class containing two generalized tuples $t_{1,2}$ of t_1 and t_2, and $C_{2,3}$ be the equivalence class containing two generalized tuples $t_{2,3}$ of t_2 and t_3. We have the following equality,*

$$\text{Dist}(C_1, C_2) + \text{Dist}(C_{1,2}, C_3) = \text{Dist}(C_2, C_3) + \text{Dist}(C_1, C_{2,3}).$$

Proof. We start with a single attribute and consider the hierarchical value tree of the attribute. To make the notations simple, we omit the superscript for the attribute. Let v_1 be the value of tuple t_1 for the attribute, $v_{1,3}$ be the value of the generalized tuple $t_{1,3}$ for the attribute, and so forth.

Within this hierarchical tree, let node $v_{1,2,3}$ represent the closest common ancestor of v_1, v_2, and v_3. Each side of the equation is the sum of WHD from v_1, v_2, and v_3 to $v_{1,2,3}$. We use $\text{Dist}(C_1, C_2) + \text{Dist}(C_{1,2}, C_3)$ as an example to show this. $t_{1,2}$ is a descendant of $t_{1,2,3}$ (or is the same as $t_{1,2,3}$, and in this case, the proof is even simpler). $\text{Dist}(C_1, C_2)$ sums the WHDs from v_1 and v_2 to $v_{1,2}$. $\text{Dist}(C_{1,2}, C_3)$ sums the WHDs from v_3 to $v_{1,2,3}$ and twice the WHDs from $v_{1,2}$ to $v_{1,2,3}$, where one is for v_1 and the other is for v_2. Therefore, $\text{Dist}(C_1, C_2) + \text{Dist}(C_{1,2}, C_3)$ sums the WHDs from v_1, v_2, and v_3 to $v_{1,2,3}$.

The overall distance is the sum of the distances of individual attributes. The above proof is true for all attributes. The lemma is proved. □

The lemma shows that the distortions do not relate to the order of generalization but only relate to the elements in the generalized group.

6 Racing Attributes and Inconsistency

In local recoding generalization, a decision of generalization is made locally to minimize distortions. However, when there are a number of choices that cause the same amount of distortions, they lead to different outcomes. Let us start with an example. In Table 2a, attributes Gender and Marriage form the quasi-identifier. The Gender attribute is in the hierarchy of {male/female, *}, and the Marriage attribute is in the hierarchy of {married/unmarried/divorced/widowed, *}. In Table 2a, $\text{Dist}(t_1, t_2) = \text{Dist}(t_1, t_3)$. If we choose to generalize t_1 and t_3 first, the resultant two-anonymity view is in Table 2b. If we choose to generalize t_1 and t_2 first, the resultant two-anonymity view is in Table 2c. Both views have the same distortions over the original table. If users do not have preferences, both views in Table 2 are acceptable.

TABLE 2
An Example of Racing Attributes

No.	Gender	Marriage	Problem
1	male	married	stress
2	male	unmarried	obesity
3	female	married	stress
4	female	unmarried	obesity

(a)

No.	Gender	Marriage	Problem
1	*	married	stress
2	*	unmarried	obesity
3	*	married	stress
4	*	unmarried	obesity

(b)

No.	Gender	Marriage	Problem
1	male	*	stress
2	male	*	obesity
3	female	*	stress
4	female	*	obesity

(c)

(a) A raw table. (b) A two-anonymity view. (c) An alternative two-anonymity view.

TABLE 3
Another Example for Racing Attribute

No.	Gender	Marriage	Problem
1	male	married	stress
2	male	unmarried	obesity
3	female	married	stress
4	female	unmarried	obesity
5	male	divorced	stress
6	male	widowed	obesity
7	female	divorced	stress
8	female	widowed	obesity

(a)

No.	Gender	Marriage	Problem
1	*	married	stress
2	*	unmarried	obesity
3	*	married	stress
4	*	unmarried	obesity
5	male	*	stress
6	male	*	obesity
7	female	*	stress
8	female	*	obesity

(b)

No.	Gender	Marriage	Problem
1	male	*	stress
2	male	*	obesity
3	female	*	stress
4	female	*	obesity
5	male	*	stress
6	male	*	obesity
7	female	*	stress
8	female	*	obesity

(c)

(a) A raw table. (b) A two-anonymity view. (c) An alternative two-anonymity view. View (c) is more consistent than view (b).

When we consider a more complicated example as in Table 3, Table 3c is better than Table 3b. Although their distortions are identical, we may not be able to use both attributes Gender and Marriage in Table 3b since no reliable statistical or data mining results can be derived from both attributes, whereas Gender attribute in Table 3c is complete.

We call this phenomenon *racing attributes*. More precisely, we have the following definition.

Definition 11 (Racing attributes). *If*

$$\mathrm{Dist}(C_1, C_2) = \mathrm{Dist}(C_1, C_3) = \min_{\forall i,j} \mathrm{Dist}(C_i, C_j),$$

we call attributes involved in the generalization of t_1 and t_2 and the generalization of t_1 and t_3 racing attributes.

When the smallest distance is between two or more equivalence class pairs and we are going to choose one pair to generalize, the attributes involved in generalizing the tuples of equivalence classes are called racing attributes.

To facilitate the following discussions on racing attributes, we introduce a measurement.

Definition 12 (Inconsistency). *Let inconsistency of attribute i be* $\mathrm{inconsist}_i = (1 - \max_j(p_{ij}))$*, where p_{ij} is the fraction of values in domain level j of attribute i over all values in attribute i. Let the inconsistency of a data set be* $\mathrm{inconsist}_D = \max_i(p_i)$ *with $1 \leq i \leq m$, where m is the number of attributes in the quasi-identifier.*

Low inconsistency means that attribute values are mostly from one domain. High inconsistency indicates that attribute values are mixed from more than one domain. For example, inconsistency of the Gender attribute in Table 3b is 50 percent because four unknown values (*) are from domain level 1 and four values of male and female are from domain level 2. Inconsistency of the attribute Marriage in Table 3b is also 50 percent. As a result, inconsistency of Table 3b is 50 percent. Inconsistency of Table 3c is 0 percent.

An anonymity table is normally used for data mining or statistical analysis. Most data mining and statistical tools assume that values are drawn from the same domain of an attribute. When values are drawn from more than one domain, values from a more general domain do not provide the same detailed information as values from a more specific domain. There are two ways to handle the situation without changing data mining or statistical software tools. When the number of values from a more general domain is not too many, consider them as missing values and disregard them in the analysis process. When values from a more general domain are too many to be ignored, generalize other values in more specific domains to the more general domain to make the attribute consistent. In the latter solution, low distortion is sacrificed for high consistency.

We discuss three approaches for handling racing attributes and controlling inconsistency.

The first approach is to randomly select racing attributes to generalize. Consider a large data set where a small number of values are generalized. We wish that these generalized values, which may be considered missing values in an analysis process, are scattered across all attributes. The randomness of a small number of generalized values does not cause a big impact on any attribute and, therefore, does not affect analysis results significantly.

The second approach is to set priority attributes. More often than not, attributes have different importance in data for an application. For example, the attribute Age is usually more important than the attribute Postcode in a medical data set. We may sacrifice postcode information for the integrity of age information as much as possible. Attributes to be sacrificed are set with high priority. High priority attributes receive low weights in calculating distortions while low priority attributes receive high weights. As a result, more generalizations will occur in high priority attributes than low priority attributes. This could reduce the overall inconsistency. For example, when we set attribute Marriage in Table 3a as a higher priority than attribute Gender, Table 3a will be generalized as Table 3c, which has an inconsistency of 0 percent.

The third approach is to incorporate global recoding generalization into local recoding generalization. The inconsistency from the global recoding generalization is always zero. However, the global recoding methods may overgeneralize a table and cause high distortions. The strength and weakness of the local recoding generalization complement those of the global recoding generalization. Ideally, we wish that the consistency of a table is high and that a small number of more generalized values are scattered among attributes.

To make the inconsistency controllable, we introduce another requirement, the maximum inconsistency. We require that the inconsistency of a generalized table is smaller than *max_inconsist*.

We present the following metric to be a criterion for deciding when to choose global recoding generalization.

Definition 13 (Generalization portion). *Let values of an attribute be drawn from a number of domains* $< D_b, D_{b-1}, \ldots >$, *where* D_b *is the most specific domain. The generalization portion is defined as* $\text{genportion} = 1 - P_{D_b}$, *where* P_{D_b} *is the fraction of values in domain* D_b *over all values of the attribute.*

Values in an attribute are split into base (the most specific) and generalization portions. Note that the base portion is not necessarily from the most specific domain of an attribute hierarchy but the most specific one from domains which the attribute currently draws values from. For example, let the attribute Date-of-Birth be in domain levels {day/month/year, month/year, year, 10-year interval, *}. Assume that fractions of values drawn from each domain level are listed in the following: 0 percent from level day/month/year, 20 percent from level month/year, 40 percent from level year, 20 percent from 10-year interval, and 20 percent from *. The base domain is at domain level month/year since there are no values drawn from domain level day/month/year. As a result, $\text{genportion} = 1 - 20 \text{ percent} = 80 \text{ percent}$.

We have the following relationship between generalization portion and inconsistency.

Lemma 3. *For an attribute, when the generalization portion is less than 50 percent,* $\text{inconsist} = \text{genportion}$.

Proof. When generalization portion is less than 50 percent, the fraction of values drawn from the base domain is greater than 50 percent. As a result, the base domain has the largest fraction of values among all domains. Therefore, $\text{inconsist} = 1 - P_{D_b} = \text{genportion}$. □

The relationship between generalization portion and inconsistency is not this simple when generalization portion is greater than 50 percent. In the previous example, Date-of-Birth values are drawn from the following four domain levels: 20 percent from level month/year, 40 percent from level year, 20 percent from 10-year interval, and 20 percent from *. $\text{genportion} = 1 - 20 \text{ percent} = 80 \text{ percent}$, whereas $\text{inconsist} = 1 - 40 = 60 \text{ percent}$.

In most applications, the required maximum inconsistency is less than 50 percent. Therefore, the requirement for the inconsistency of a generalized table to be less than max_inconsist is equivalent to the requirement that the generalization portion is less than max_inconsist for every attribute.

The reason for using generalization portion instead of inconsistency is that generalization portion gives a desirable direction for generalization. See the following two examples. Attribute 1: 90 percent of values are generalized to a more general domain, and 10 percent values remain at the original domain. We have $\text{inconsist} = 10 \text{ percent}$ and $\text{genportion} = 90 \text{ percent}$. Attribute 2: 10 percent of values are generalized to a more general domain, and 90 percent of

values remain in the original domain. We have $\text{inconsist} = 10$ percent and $\text{genportion} = 10$ percent. In the former case, 10 percent of the detailed information does not improve the quality of the attribute significantly but reduces its utility. So, we generalize the 10 percent of values to the more general domain for a 100 percent consistency. In the latter case, it is worthwhile to sacrifice 10 percent values to keep 90 percent detailed information. Therefore, we do not generalize the remaining values.

We use the generalization portion as a criterion for switching on the global recoding. If the generalization portion is larger than max_inconsist, we have to generalize values in the base domain (the current most specific one) to a more general domain. In other words, we need to use a global generalization method to generalize an attribute until the portion of values to be generalized further is less than max_inconsist. The following lemma gives an indicator for this.

Lemma 4. *Let D be a table to be generalized into a k-anonymity view. Consider an attribute i in the quasi-identifier and $\text{inconsist}_i = 0$. Let f_j be the frequency of value j in the attribute. The lower bound of the generalization portion is $(\sum_{f_j<k} f_j)/|D|$.*

Proof. When the frequency of a distinct value in an attribute is less than k, this value will be generalized to satisfy the k-anonymity requirement. All such values are to be generalized. The number of generalized values is hence at least $\sum_{f_j<k} f_j$ since some other values may be involved in the generalization. Therefore, the lower bound of generalization portion is $(\sum_{f_j<k} f_j)/|D|$. □

As a result, we can generalize an attribute globally and recursively until the lower bound of the generalization portion is less than max_inconsist. Then, the data set is ready for local recoding generalization.

The objective of keeping low inconsistency contradicts the objective of minimizing distortions. The maximum inconsistency gives users a means to achieve balance between minimizing distortions and keeping the consistency of a generalized table.

7 Two Local Recoding Anonymization Algorithms

After the distortion has been mapped to a proper distance metric, it is a natural way to achieve k-anonymization by a clustering approach. An agglomerative hierarchical clustering method [12] suits k-anonymization by local recoding generalization very well. An agglomerative hierarchical clustering method works in the following way. Initially, each object is assigned as a cluster. Then, two clusters with the smallest distance are merged into one cluster. This procedure repeats until the number of clusters reaches the user's specified number. We modify the agglomerative hierarchical clustering algorithm for k-anonymization by local recoding.

One issue needs to be resolved when using a clustering algorithm for local recoding generalization. One equivalence class is initially assigned as a cluster. In multidimensional local recoding generalization, each equivalence class as a whole is to merge with another equivalence class to form a new equivalence class. In local recoding generalization, only a portion of tuples in an equivalence class merge with another equivalence class. In other words, overlapping clusters are allowed and data points in the identical position are mapped into different clusters.

The purpose of allowing overlapping clusters is to preserve partial detailed information of a large equivalence class. For example, a small equivalence class (e.g., containing one tuple) is generalized with a large equivalence class (e.g., containing 100 tuples). Should we generalize the whole large equivalence class in order to absorb the small equivalence class? We should not. A better solution is to allocate a small number of tuples, $k-1$ tuples, from the large equivalence class to generalize with the small equivalence class. As a result, information in most tuples of the large equivalence class is preserved. Data points representing tuples in the large equivalence class belong to two clusters, one for the large equivalence class and the other for merging with data points of the small equivalence class.

We propose two concepts, stub and trunk, to facilitate local recoding k-anonymization by clustering.

Definition 14 (Stub and trunk of equivalence class). *Suppose a small equivalence class C_1 and a large equivalence class C_2 are to be generalized for k-anonymity. If $|C_1| < k$ and $|C_1| + |C_2| \geq 2k$, C_2 is split into two parts, a* stub *and a* trunk. *The stub contains $(k - |C_1|)$ tuples, and the trunk contains $(|C_1| + |C_2| - k)$ tuples. The stub is to be generalized with the small equivalence class C_1.*

After this split, both the new generalized equivalence class and the remaining trunk of C_2 satisfy the k-anonymity property. The detailed information in the trunk is preserved.

We modify the distance calculation between two equivalence classes C_1 and C_2, where $|C_1| < k$, in the following, to support stub and trunk splitting:

- If $(|C_1| + |C_2| < 2k)$, calculate the distance between C_1 and C_2.
- If $(|C_1| + |C_2| \geq 2k)$, calculate the distance between C_1 and the stub of C_2.

We present two algorithms. The first algorithm does not have the maximum inconsistency constraint, and the second algorithm does.

The pseudocode of the first algorithm is presented in Algorithm 1. In the algorithm, we say that an equivalence class C is generalized with another equivalence class C'. We mean that C is generalized with the stub of equivalence class C' when $(|C| + |C'| \geq 2k)$ and C is generalized with C' when $(|C| + |C'| < 2k)$.

Algorithm 1 K-Anonymization by Clustering in Attribute hierarchies (KACA1)

1: form equivalence classes from the data set
2: **while** there exists an equivalence class of size $< k$ **do**
3: randomly choose an equivalence class C of size $< k$
4: *evaluate the pairwise distance between C and all other equivalence classes
5: *find the equivalence class C' with the smallest distance to C

6: *generalize the equivalence classes C and C'
7: **end while**
(* simplified statements. Read explanation for details.)

Line 1 forms equivalence classes. Sorting data will speed up the process. One tuple is also called an equivalence class. The generalization process continues in lines 2-6 when there is one or are more equivalence classes whose size is smaller than k. In each iteration, we randomly find an equivalence class C of size smaller than k in line 3. Then, we calculate the pairwise distances between C and all other equivalence classes in line 4. Note that the distance of C and another equivalence class C' means the distance of C and the stub of C' when $(|C| + |C'| \geq 2k)$. Line 5 finds the equivalence class C' with the smallest distance to C. When there are more than one such equivalence classes, we select one randomly. Line 6 generalizes the equivalence classes C and C'. This implies that C is generalized with the stub of C' if $(|C| + |C'| \geq 2k)$. When C is generalized with the stub of C', the trunk of C' remains as an equivalence in the next round. This means that a large equivalence class can be split into a number of generalized equivalence classes. The algorithm terminates when there is no equivalence class whose size is smaller than k left.

The complexity of KACA1 is analyzed in the following. Let n be the number of tuples. All tuples are sorted and only $O(n)$ passes are needed to find all equivalence classes. The complexity of this step is $O(n \log n)$. Let $|E|$ be the number of all equivalence classes, and $|E_s|$ be the number of equivalence classes whose size is less than k. Each iteration chooses an arbitrary equivalence class, which takes $O(1)$ time, evaluates the pairwise distance, which takes $O(|E|)$ time, finds the equivalence class with the smallest distance, which takes $O(|E|)$ time, and finally generalizes the equivalence class, which takes $O(1)$ time. As there are $O(|E_s|)$ iterations, the overall runtime is $O(n \log n + |E| * |E_s|)$.

We present another algorithm that extends KACA1 by using the constraint of maximum inconsistency. The pseudocode is listed in Algorithm 2.

Algorithm 2 K-Anonymization by Clustering in Attribute hierarchies with the maximum inconsistency constraint (KACA2)

1: **for** each attribute in the quasi-identifier **do**
2: generalize the attribute by the global recoding until the lower bound of genportion $<$ max_inconsistency according to Lemma 4
3: **end for**
4: call KACA1
5: **for** each attribute i in the quasi-identifier **do**
6: **if** inconsist_$i <$ max_inconsistency **then**
7: generate the attribute until inconsist_$i <$ max_inconsistency
8: **end if**
9: **end for**

The maximum inconsistency constraint is used in KACA2 to balance consistency and distortion. KACA2 incorporates the global recoding generalization to reduce inconsistency. In line 2, the employment of global recoding generalization is determined by the lower bound of the generalization portion from Lemma 4. KACA1 is called after the lower bound of the generalization portion is less than max_inconsist for each attribute. After local recoding generalization by calling KACA1, a final generalization step is conducted when necessary to ensure the inconsistency of each attribute is less than the user-specified threshold. In this step, low distortion is sacrificed for high consistency.

The complexity of KACA2 has a similar formulation as that of KACA1. Global recoding generalization takes $O(n)$ for each generalization. The number of global generalizations has a lower bound of 0 and an upper bound of $m * (h - 1)$, where m is the number of attributes in the quasi-identifier and h is the maximum height of attribute hierarchies. In practice, some attributes do not need global generalization to satisfy Lemma 4 and some attributes only need one or two global generalizations. We estimate the complexity of this step as $O(m * n)$. In sum, the time complexity of KACA2 is $O(n \log n + m * n + |E| * |E_s|)$. The additional computational cost for global generalization $O(m * n)$ can be well compensated for by the reduction in $O(|E| * |E_s|)$ since $|E_s|$, the number of equivalence classes whose size is less than k, is significantly reduced as a result of global generalization.

TABLE 4
Description of Adult Data Set

	Attribute	Distinct Values	Generalizations	Height
1	Age	74	5-, 10-, 20-year ranges	4
2	Work Class	7	Taxonomy Tree	3
3	Education	16	Taxonomy Tree	4
4	Martial Status	7	Taxonomy Tree	3
5	Occupation	14	Taxonomy Tree	2
6	Race	5	Taxonomy Tree	2
7	Sex	2	Suppression	1
8	Native Country	41	Taxonomy Tree	3

8 Proof-of-Concept Experiments

Our proposed methods are compared with a typical global recoding method, Incognito [9], and a typical multidimensional recoding method, Multi [10]. Different methods are compared against four quality measures, distortion, discernability metric, normalized average equivalence class size, and inconsistency. Multi assumes fully ordered attributes and does not use attribute hierarchical taxonomies, and hence, we do not have distortion and inconsistency results for it.

The adult data set from the UCIrvine Machine Learning Repository [16] has become a benchmark data set for comparing k-anonymity methods. The data set has been used in most recent k-anonymity studies [6], [7], [9], [10], [11], [24]. We eliminated the records with unknown values. The resulting data set contains 45,222 tuples. Eight attributes were used as the quasi-identifier, as shown in Table 4.

Experimental results are shown in Figs. 4 and 5. In Fig. 4, the first six attributes are selected as the quasi-identifier. In Fig. 5, k is fixed to 10. Since there is random selection in our algorithms, we report the distortion, discernability, normalized average equivalence class size, and inconsistency of our methods based on the average of 10 trials. Our methods

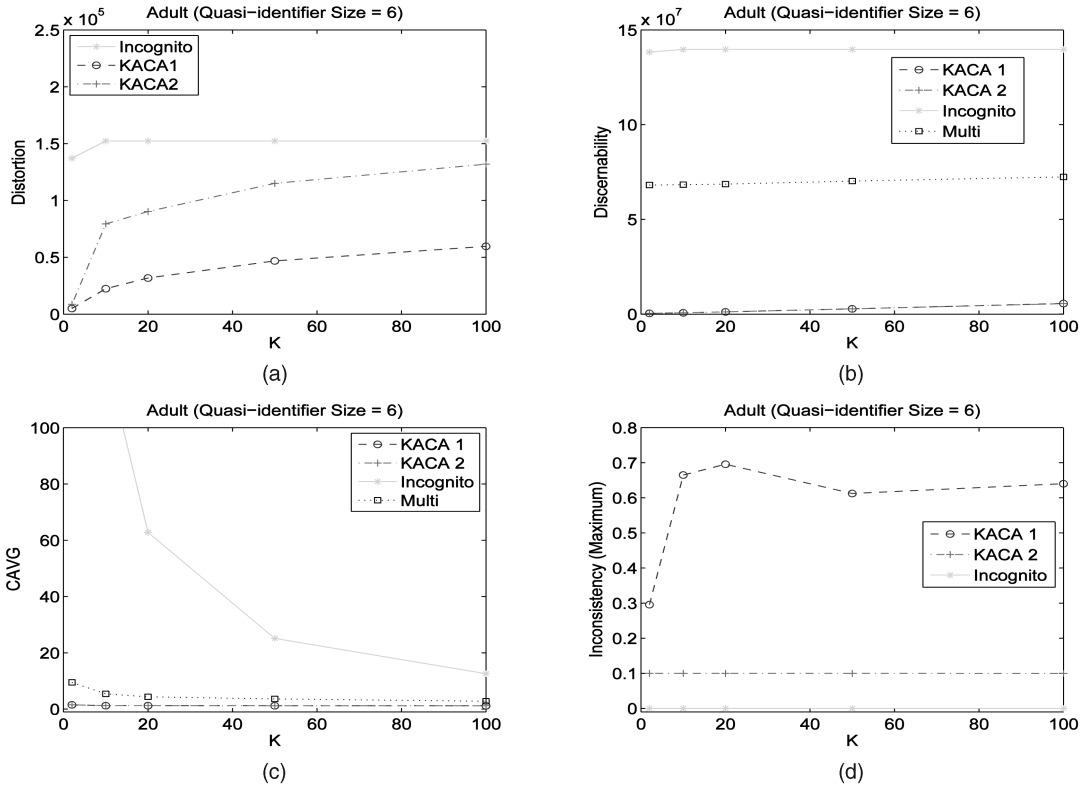

Fig. 4. Performance of different methods with variant k. (a) Distortion. (b) Discernability. (c) Normalized average equivalence class size. (d) Inconsistency.

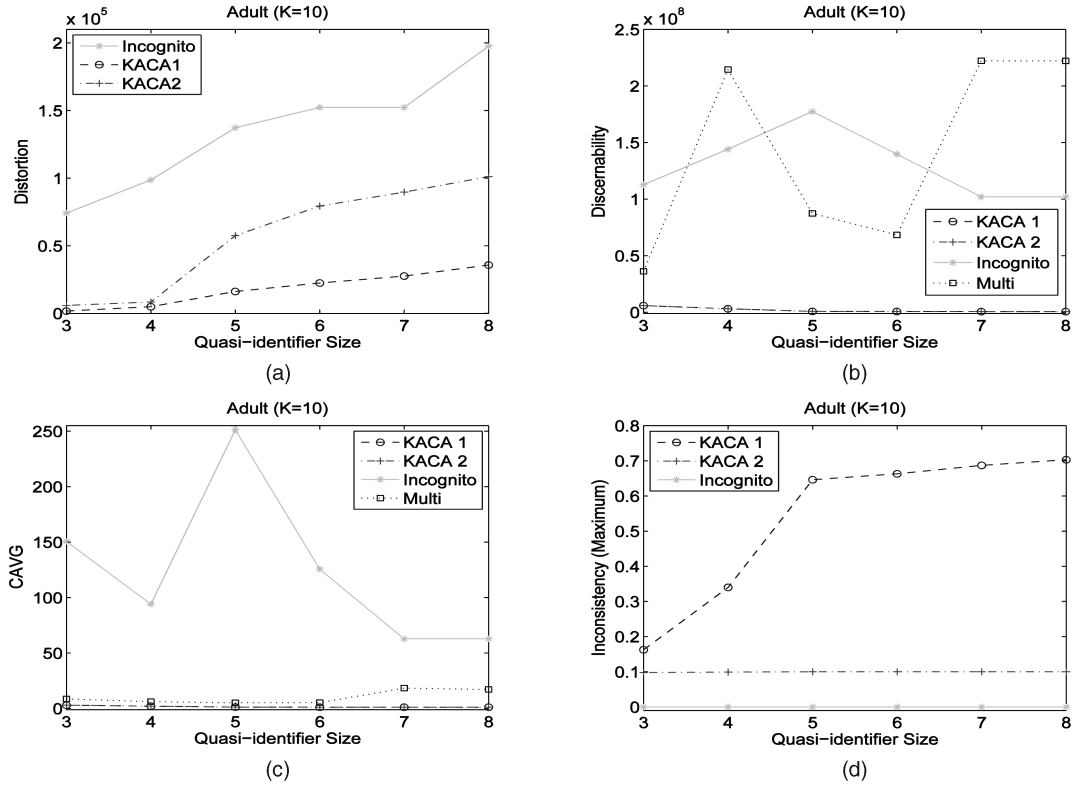

Fig. 5. Performance of different methods with variant quasi-identifier size. (a) Distortion. (b) Discernability. (c) Normalized average equivalence class size. (d) Inconsistency.

have been evaluated in both uniform and height weight schemes. Conclusions from both schemes are very similar, and here, we only show results from the height weight scheme. For the height weight scheme, $\beta = 1$. For the KACA2 algorithm, the maximum inconsistency is set as 10 percent.

Based on three quality measures, namely distortion, discernability, and normalized average equivalence class size, KACA1 performs consistently better than other methods. This shows that local recoding based on the proposed distance metric achieves good quality k-anonymity tables based on the three measures. However, its inconsistency is the highest. In some cases, the inconsistency of tables produced by KACA1 can be 70 percent. In such cases, values are drawn from every domain level in the Age attribute. This may cause difficulty in data mining applications.

Based on the inconsistency measure, Incognito performs best since its inconsistency is always zero. However, Incognito suppresses more than 50 percent of values (being generalized to the top) in some cases. Such generalized tables also cause difficulty in data mining applications. KACA2 balances distortion and consistency. Its inconsistency is capped by 10 percent, and its distortion is in between the distortions of local and global recoding methods. We note that with the increase of k, inconsistency of KACA2 is closer to that of Incognito. This is because larger k requires larger equivalence classes. Based on Lemma 4, more attributes need global recoding when k is larger. KACA2 balances distortion and inconsistency of local recoding and global recoding.

Based on discernability and normalized average equivalence class size measures, both KACA1 and KACA2 are better than Multi. Note that normalized average equivalence class sizes for the Multi in Fig. 4b look flat. This is caused by the scale in Fig. 4b. In comparison to big differences of normalized average equivalence size among different methods, differences of a method in variant k are negligible. When we drew Multi results in a separate figure, it is consistent with [10, Fig. 10]. Fluctuations in Fig. 5b are caused by different attributes in the quasi-identifier. A heuristic is used in the Multi algorithm [10] for choosing an attribute to partition the data space in the top-down greedy algorithm. A new attribute leads to a new partition. Different partitions initiated from different attributes bear little similarities.

Both KACA1 and KACA2 are not as efficient as Incognito and Multi on the Adult data set. One computational intensive part of both algorithms is to compute the distances between equivalence classes to find the closest equivalence class pair. This time complexity is quadratic to the number of equivalence classes. The employment of an advanced indexing technique to keep track of the closest equivalence classes for the efficient search of the closest equivalence class pair will improve the search efficiency significantly. This means that the current implementations of KACA1 and KACA2 are to be optimized for better efficiency.

9 Conclusions

In this paper, we have studied two major issues in local recoding k-anonymization: measuring the distance of generalization in data with attribute hierarchical taxonomies and handling the inconsistency of domains in the fields of a k-anonymity table. We define generalization distances to characterize distortions of generalizations and discuss properties of the distance. We conclude that the generalization distance satisfies properties of metric distances. We discuss how to handle a major problem in local recoding generalization, inconsistent domains in a field of a generalized table, and propose a method to approach the problem. We show by experiments that the proposed local recoding method based on the distance metric achieves better quality k-anonymity tables by three quality measures than a typical global recoding method and a typical multidimensional recoding method, and that our inconsistency handling method balances distortion and consistency of a k-anonymity table well.

Acknowledgments

The authors would like to thank the anonymous reviewers for their constructive suggestions. This research was supported by an ARC Discovery Grant DP0774450 to Jiuyong Li, in part by the RGC Earmarked Research Grants of HKSAR CUHK 4120/05E and 4118/06E to Ada Wai-Chee Fu, and an NSERC Discovery Grant to Jian Pei.

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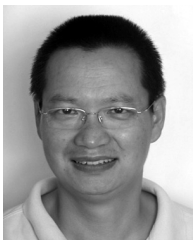

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