# Seeded Distribution-Agnostic Database De-Anonymization Under Synchronization Errors

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Abstract-Recently, there has been an increased scientific interest in the de-anonymization of users in anonymized databases containing user-level microdata via multifarious matching strategies utilizing publicly-available correlated data. Existing literature has either emphasized practical aspects where underlying data distribution is not required, at the expense of theoretical guarantees, or theoretical aspects with limited practicality due to the assumptions on the availability of underlying distributions. In this work, we reconcile these two lines of work, by investigating the de-anonymization of random correlated databases, without prior knowledge of data distribution, ensuring theoretical guarantees. Motivated by time-indexed microdata, database deanonymization is considered under both synchronization errors (column repetitions) and obfuscation (noise). By modifying the existing replica detection algorithm to accommodate for the incognizance of the underlying distributions, proposing a new seeded deletion detection algorithm, and employing statistical and information-theoretic tools, sufficient conditions for successful matching are derived. Our findings demonstrate that a doublelogarithmic seed size relative to row size ensures successful deletion detection. More importantly, we show that sufficient conditions we derive are the same as in the distribution-aware setting, negating any asymptotic loss of performance due to unknown underlying distributions.

## I. INTRODUCTION

With the accelerating growth of smart devices and applications, there has been a colossal collection of user-level microdata in private companies' and public institutions' possession. And inevitably this microdata is often shared and/or sold for multifarious purposes. Although this data transfer is performed after removing the explicit user identifiers, a.k.a. anonymization, and coarsening of the data through noise, a.k.a. obfuscation, there has been a growing concern from the scientific community [1]. These concerns were further validated by the success of a series of practical attacks on real data by researchers [2]–[6]. In the light of these successful experimental work, recently there has been an increasing effort on the information-theoretic and statistical foundations of database de-anonymization, a.k.a. database alignment/matching/recovery [7]–[16].

More recently, we have focused on the database deanonymization problem under synchronization errors. In [13], we investigated the matching of Markov databases under synchronization errors, with no subsequent obfuscation/noise. We showed that the synchronization errors could be detected

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with no seeds through a histogram-based detection scheme. Furthermore, we found the noiseless matching capacity to be equal to the erasure bound. More relevantly, in [14], we considered the de-anonymization of databases under noisy synchronization errors. We proposed a noisy replica detection algorithm and a seeded deletion detection algorithm to detect synchronization errors. We proposed a joint-typicality-based matching algorithm and derived achievability results, which we subsequently showed to be tight, given a seed size logarithmic with the row size of the database. Then in [15], we improved this sufficient seed size to one double logarithmic with the row size. Albeit successful in deriving detecting and matching results, in these works, the availability of information on the underlying distributions was assumed and the proposed algorithms were tailored for these known distributions.

Motivated by most practical settings where the underlying distributions are not readily available, but only could be estimated from the available data, in this paper, we investigate the de-anonymization problem without any a priori knowledge of the underlying distributions. We focus on a noisy random column repetition model borrowed from [14], as illustrated in Figure 1. We modify the noisy replica detection algorithm proposed in [14] which was tailored for the underlying distribution in a distribution-agnostic way. Then we propose a novel outlier-detection-based deletion detection algorithm and show that when seeds whose size grows double logarithmic with the number of users (rows) in the database, the underlying repetition pattern could be inferred. Finally, through a typicality-based de-anonymization algorithm that relies on the estimated distributions, we show that database de-anonymization could be performed with no asymptotic loss of performance compared to when all the information on the distributions is available a priori.

The structure of the rest of this paper is as follows: Section II introduces the formal statement of the problem. Section III contains our proposed algorithms, states our main result, and contains its proof. Finally, Section IV consists of the concluding remarks.

*Notation:* We denote a matrix **D** with bold capital letters, and its  $(i, j)^{\text{th}}$  element with  $D_{i,j}$ . A set is denoted by a calligraphic letter, e.g.,  $\mathfrak{X}$ . [n] denotes the set of integers  $\{1,\ldots,n\}$ . Asymptotic order relations are used as defined in [17, Chapter 3]. All logarithms are base 2. H(.) denotes the Shannon entropy [18, Chapter 2].

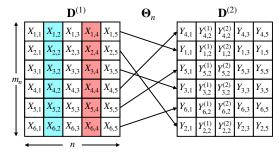


Fig. 1: An illustrative example of database matching under column repetitions. The column coloured in red is repeated zero times, *i.e.*, deleted, whereas the column coloured in blue is repeated twice, *i.e.*, replicated.  $Y_{i,2}^{(1)}$  and  $Y_{i,2}^{(2)}$  denote noisy copies/replicas of  $X_{i,2}$ . Our goal is to estimate the row permutation  $\Theta_n = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 \\ 2 & 6 & 4 & 1 & 3 & 5 \end{pmatrix}$ , by matching the rows of  $\mathbf{D}^{(1)}$  and  $\mathbf{D}^{(2)}$ .

#### II. PROBLEM FORMULATION

We use the following definitions, most of which are borrowed from [14] to formalize our problem.

**Definition 1.** (Anonymized Database) An  $(m_n, n, p_X)$  anonymized database  $\mathbf{D} = \{X_{i,j} \in \mathfrak{X}\}$  is a randomly generated  $m_n \times n$  matrix with  $X_{i,j} \stackrel{\text{i.i.d.}}{\sim} p_X$ , where  $p_X$  has a finite discrete support  $\mathfrak{X} = \{1, \dots, |\mathfrak{X}|\}$ .

**Definition 2.** (Column Repetition Pattern) The *column* repetition pattern  $S^n = \{S_1, S_2, ..., S_n\}$  is a random vector with  $S_i \stackrel{\text{i.i.d.}}{\sim} p_S$ , where  $p_S$  has a finite integer support  $\{0, ..., s_{\text{max}}\}$ .

**Remark 1.** We note the fact that  $X_{i,j} \stackrel{\text{i.i.d.}}{\sim} p_X$  and  $S_i \stackrel{\text{i.i.d.}}{\sim} p_S$  can be checked through the Markov order estimation algorithm of [19] with a vanishing probability of error. Thus from now on, we can assume the aforementioned relations are known, while the distributions  $p_X$  and  $p_S$  are not.

**Definition 3.** (Anonymization Function) The *anonymization* function  $\Theta_n$  is a uniformly-drawn permutation of  $[m_n]$ .

**Definition 4.** (**Labeled Correlated Database**) Let  $\mathbf{D}^{(1)}$ ,  $S^n$  and  $\Theta_n$  be a mutually-independent  $(m_n, n, p_X)$  anonymized database, repetition pattern and anonymization function triplet. Let  $p_{Y|X}$  be a conditional probability distribution with both X and Y taking values from  $\mathfrak{X}$ . Given  $\mathbf{D}^{(1)}$ ,  $S^n$ ,  $\Theta_n$  and  $p_{Y|X}$ ,  $\mathbf{D}^{(2)}$  is called the *labeled correlated database* if the respective  $(i,j)^{\text{th}}$  entries  $X_{i,j}$  and  $Y_{i,j}$  of  $\mathbf{D}^{(1)}$  and  $\mathbf{D}^{(2)}$  have the following relation:

$$Y_{\Theta_n(i),j} = \begin{cases} E, & \text{if } S_j = 0\\ Z^{S_j} & \text{if } S_j \ge 1 \end{cases} \quad \forall i \in [m_n], \, \forall j \in [n]$$
 (1)

where  $Z^{S_j}$  is a row vector consisting of  $S_j$  noisy replicas of  $X_{i,j}$  with the following conditional probability distribution

Pr 
$$\left(Z^{S_j} = z^{S_j} | X_{i,j} = x\right) = \prod_{l=1}^{S_j} p_{Y|X}\left(z_l | x\right)$$
 (2)

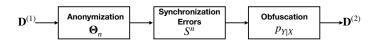


Fig. 2: Relation between the unlabeled database  $\mathbf{D}^{(1)}$  and the labeled noisy repeated one,  $\mathbf{D}^{(2)}$ .

where  $z^{S_j} = z_1, \dots, z_{S_j}$  and  $Y_{\Theta_n(i),j} = E$  corresponds to  $Y_{\Theta_n(i),j}$  being the empty string.

Note that  $S_j$  indicates the times the  $j^{th}$  column of  $\mathbf{D}^{(1)}$  is repeated. When  $S_j = 0$ , the  $j^{th}$  column of  $\mathbf{D}^{(1)}$  is said to be *deleted* and when  $S_j > 1$ , the  $j^{th}$  column of  $\mathbf{D}^{(1)}$  is said to be *replicated*.

The  $i^{\text{th}}$  row  $X_i$  of  $\mathbf{D}^{(1)}$  and the  $\Theta_n(i)^{\text{th}}$  row  $Y_{\Theta_n(i)}$  of  $\mathbf{D}^{(2)}$  are called *matching rows*.

The relationship between  $\mathbf{D}^{(1)}$  and  $\mathbf{D}^{(2)}$ , as described in Definition 4, is illustrated in Figure 2.

**Remark 2.** As stated above, unlike [16], in this work, we assume a non-adversarial random noise and repetition model. Furthermore, we will assume that the fact that  $S^n \perp \!\!\! \perp \!\!\! \mathbf{D}^{(1)}$  and that the conditional independence of the noisy replicas stated in (2) are known.

As often done in both the graph matching [20] and the database matching [14] literatures, we will assume the availability of a set of already-matched row pairs called *seeds*, to be used in the detection of the underlying repetition pattern.

**Definition 5.** (Seeds) Given a pair of anonymized and labeled correlated databases  $(\mathbf{D}^{(1)}, \mathbf{D}^{(2)})$ , a *seed* is a correctly-matched row pair with the same underlying repetition pattern. A *batch* of  $\Lambda_n$  seeds is a pair of seed matrices of respective sizes  $\Lambda_n \times n$  and  $\Lambda_n \times \sum_{j=1}^n S_j$ .

For the sake of notational brevity, we assume that the seed matrices  $\mathbf{G}^{(1)}$  and  $\mathbf{G}^{(2)}$ ) are not submatrices of  $\mathbf{D}^{(1)}$  and  $\mathbf{D}^{(2)}$ . Throughout this work, we will assume a seed size  $\Lambda_n = \omega(\log n) = \omega(\log\log m_n)$  which is double-logarithmic with the number of users  $m_n$ .

Similar to [8], [12]–[14], in this paper, our goal is to characterize the sufficient and the necessary conditions for the almost-perfect recovery of the anonymization function  $\Theta_n$  when the underlying distributions are not provided a priori. More formally, "almost-perfect recovery" corresponds to the construction of the estimate  $\hat{\Theta}_n$  such that

$$\lim_{n\to\infty} \Pr\left(\Theta_n(J) \neq \hat{\Theta}_n(J)\right) \to 0 \tag{3}$$

where  $J \sim \text{Unif}([m_n])$ .

As done in [8], [12]–[14], [16], we utilize the database growth rate, defined below, as the main performance metric.

**Definition 6.** (Database Growth Rate) The *database growth* rate R of an  $(m_n, n, p_X)$  anonymized database is defined as

$$R = \lim_{n \to \infty} \frac{1}{n} \log m_n \tag{4}$$

# III. DE-ANONYMIZATION ALGORITHM AND ACHIEVABILITY

In this section, we present our main result on the achievable database growth rates when no a-priori information is provided on  $p_{X,Y}$  and  $p_S$ . We state the main result in Theorem 1 and prove it.

**Theorem 1.** (Main Result) Consider an anonymized and labeled correlated database pair, with underlying database distributions  $p_{X,Y}$  and a column repetition distribution  $p_S$ . Then, given a seed size  $\Lambda_n = \omega(\log n)$ , any database growth rate R satisfying

$$R < I(X; Y^S | S) \tag{5}$$

is achievable with no prior information on  $p_{X,Y}$  and  $p_S$ . Here  $S \sim p_S$ ,  $X \sim p_X$  and  $Y^S = Y_1, \dots, Y_S$  with  $Y_i | X \overset{i.i.d.}{\sim} p_{Y|X}$ .

In order to demonstrate the tightness of the achievability result stated in Theorem 1, we now compare it to the distribution-aware results derived in [14, Theorem 1].

**Remark 3.** (Converse of [14, Theorem 1]) Consider an anonymized and labeled correlated database pair, with underlying database distributions  $p_{X,Y}$  and a column repetition distribution  $p_S$ . Then, a necessary condition for the existence of a successful de-anonymization scheme is:

$$R < I(X; Y^S | S) \tag{6}$$

Theorem 1 and Remark 3 imply that given a seed size  $\Lambda_n = \omega(\log n) = \omega(\log \log m_n)$  we can perform matching as if we knew the underlying distribution  $p_{X,Y}$  and the actual column repetition pattern  $S^n$  a priori. Hence in the asymptotic regime, not knowing the distributions causes no loss in the matching capacity.

The rest of this section is on the proof of Theorem 1. In Section III-A, we present our detection of noisy replicas algorithm and prove its asymptotic performance. Then in Section III-B, we propose a seeded deletion algorithm and derive a sufficient seed size that guarantees its asymptotic performance. Finally in Section III-C, we present our deanonymization algorithm.

# A. Noisy Replica Detection

Similar to [14], as a permutation-invariant future of the labeled correlated database we use the running Hamming distances between the consecutive columns  $C_j^{(2)}$  and  $C_{j+1}^{(2)}$  of  $\mathbf{D}^{(2)}$ , denoted by  $H_j$ ,  $j \in [K_n - 1]$ , where  $K_n \stackrel{\triangle}{=} \sum_{j=1}^n S_j$ . More formally,

$$H_{j} \triangleq \sum_{t=1}^{m_{n}} \mathbb{1}_{\left[D_{t,j+1}^{(2)} \neq D_{t,j+1}^{(2)}\right]}, \qquad \forall j \in [K_{n} - 1]$$
 (7)

We first note that

$$H_{j} \sim \begin{cases} \operatorname{Binom}(m_{n}, p_{0}), & \text{if } C_{j}^{(2)} \perp L_{j+1}^{(2)} \\ \operatorname{Binom}(m_{n}, p_{1}), & \text{otherwise} \end{cases}$$
(8)

# Algorithm 1: Noisy Replica Detection Algorithm

```
Input: (\mathbf{D}, m_n, K_n)

Output: isReplica

H \leftarrow \text{RunningHammingDist}(\mathbf{D}); /* \text{Eq. } (7) */

(\hat{p}_0, \hat{p}_1) \leftarrow \text{EstimateParams}(H); /* \text{See } [21] */

\tau \leftarrow \frac{\hat{p}_0 + \hat{p}_1}{2};

isReplica \leftarrow \varnothing;

for j = 1 to K_n - 1 do

if H[j] \leq m_n \tau then

| isReplica[j] \leftarrow \text{TRUE};

else

| isReplica[j] \leftarrow \text{FALSE};

end

end
```

where

$$p_0 \triangleq 1 - \sum_{y \in \mathfrak{X}} p_Y(y)^2 \tag{9}$$

$$p_1 \triangleq 1 - \sum_{x \in \mathfrak{X}} p_X(x) \sum_{y \in \mathfrak{X}} p_{Y|X}(y|x)^2 \tag{10}$$

From [16, Lemma 1], we know that as long as the databases are correlated, *i.e.*,  $p_{X,Y} \neq p_X p_Y$ , we have  $p_0 > p_1$  for any  $p_{X,Y}$ . Thus, as long as  $p_{X,Y} \neq p_X p_Y$ , replicas can be detected based on the Hamming distances  $H_j$  similar to [16]. However, the algorithm in [14] depends on a threshold chosen with a priori knowledge on  $p_{X,Y}$ . In Algorithm 1, we propose the following modification: We first construct the estimates  $\hat{p}_0$  and  $\hat{p}_1$  for the respective parameters  $p_0$  and  $p_1$  through the moment estimator proposed by Blischke in [21]. Then we proceed with the algorithm proposed in [14]. This modification removes any dependence on a-priori knowledge of  $p_{X,Y}$ .

The following lemma states that this algorithm has a vanishing error probability.

**Lemma 1.** (Noisy Replica Detection) Algorithm 1 has a vanishing probability of detection error, as long as  $m_n = \omega(\log n)$ .

*Proof.* Let  $\alpha$  be the mixing parameter. In other words,

$$\Pr(H_j = h) = \binom{m_n}{h} [\alpha p_0^h (1 - p_0)^{m_n - h}]$$
 (11)

$$+(1-\alpha)p_1^h(1-p_1)^{m_n-h}$$
 (12)

for  $h = 0, ..., m_n$ . Start by noting that in order for this estimator to work, the mixing parameter  $\alpha$  needs to be bounded away from 0 and 1 with high probability. Note that  $\alpha$  can be rewritten as

$$\alpha = \frac{1}{K_n - 1} \left( n - \sum_{j=1}^n \mathbb{1}_{[S_j = 0]} \right)$$
 (13)

It can easily be verified that  $\alpha \xrightarrow{p} \frac{1-\delta}{\mathbb{E}[S]}$ , which is bounded away from both 0 and 1, and in turn that the algorithm can be used in our problem. More formally, for any  $\varepsilon > 0$ .

$$\lim_{n \to \infty} \Pr\left(\left|\alpha - \frac{1 - \delta}{\mathbb{E}[S]}\right| > \varepsilon\right) = 0 \tag{14}$$

The estimator proposed in [21] works as follows: Define the  $k^{\text{th}}$  sample factorial moment  $F_k$  as

$$F_k \triangleq \frac{1}{K_n} \sum_{i=1}^{K_n} \prod_{i=0}^{K_n} \frac{H_j - i}{m_n - i}, \quad \forall k \in [m_n]$$
 (15)

and let

$$A \triangleq \frac{F_3 - F_1 F_2}{F_2 - F_1^2} \tag{16}$$

Then the respective estimators  $\hat{p}_0$  and  $\hat{p}_1$  for  $p_0$  and  $p_1$  can be constructed as:

$$\hat{p}_0 = \frac{A + \sqrt{A^2 - 4AF_1 + 4F_2}}{2} \tag{17}$$

$$\hat{p}_1 = \frac{A - \sqrt{A^2 - 4AF_1 + 4F_2}}{2} \tag{18}$$

From [21], we get  $\hat{p}_i \stackrel{p}{\to} p_i$  and in turn  $\tau \stackrel{p}{\to} \frac{p_0 + p_1}{2}$ . Thus for large n,  $\tau$  is bounded away from  $p_0$  and  $p_1$ . Finally from [15, Lemma 1], we have

$$\lim_{n \to \infty} \Pr(\text{Noisy replica detection error}) = 0 \tag{19}$$

Note that the condition in Lemma 1 is automatically satis field since  $m_n$  is exponential in n (Definition 6). Finally, we stress that as opposed to deletion detection, discussed in Section III-B, no seeds are necessary for replica detection.

#### B. Deletion Detection

In this section, we propose a deletion detection algorithm that utilizes the seeds available. Since the replica detection algorithm of Section III-A (Algorithm 1) has a vanishing probability of error, for notational simplicity we will focus on a deletion-only setting throughout this subsection. Let  $G^{(1)}$ and  $G^{(2)}$  be the seed matrices with respective sizes  $\Lambda_n \times n$  and  $\Lambda_n \times \tilde{K}_n$ , and denote the  $j^{\text{th}}$  column of  $\mathbf{G}^{(r)}$  with  $G_j^{(r)}$ , r = 1, 2where  $\tilde{K}_n \triangleq \sum_{j=1}^n \mathbb{1}_{[S_j \neq 0]}$ . Furthermore, for the sake of brevity, let  $L_{i,j}$  denote the Hamming distance between  $G_i^{(1)}$  and  $G_j^{(2)}$ for  $(i, j) \in [n] \times [\tilde{K}_n]$ . More formally, let

$$L_{i,j} \triangleq \sum_{t=1}^{\Lambda_n} \mathbb{1}_{\left[G_{t,i}^{(1)} \neq G_{t,j}^{(2)}\right]} \tag{20}$$

Observe that

$$L_{i,j} \sim \begin{cases} \text{Binom}(\Lambda_n, q_0), & G_i^{(1)} \perp \!\!\! \perp G_j^{(2)} \\ \text{Binom}(\Lambda_n, q_1), & \text{otherwise} \end{cases}$$
 (21)

where

$$q_{0} = 1 - \sum_{x \in \mathfrak{X}} p_{X}(x) p_{Y}(x)$$

$$q_{1} = 1 - \sum_{x \in \mathfrak{X}} p_{X,Y}(x,x)$$
(22)

$$q_1 = 1 - \sum_{x \in \mathfrak{X}} p_{X,Y}(x,x)$$
 (23)

Thus, we have a problem seemingly similar to the one in Section III-A. However, for the reasons explained below, we cannot utilize similar tools: i) Recall that the two components of the Binomial mixture discussed in Section III-A were

distinct for any underlying joint distribution  $p_{X,Y}$  as long as the databases are correlated, i.e.,  $p_{X,Y} \neq p_X p_Y$ . Unfortunately, the same idea does not automatically work here as demonstrated by the following example: Suppose  $X_{i,j} \sim \text{Unif}(\mathfrak{X})$ , and the transition matrix **P** associated with  $p_{Y|X}$  has unit trace. Then,

$$q_0 - q_1 = \sum_{x \in \mathfrak{X}} p_{X,Y}(x,x) - p_X(x)p_Y(x)$$
 (24)

$$= \frac{1}{|\mathfrak{X}|} \sum_{x \in \mathfrak{X}} p_{Y|X}(x|x) - p_Y(x) \tag{25}$$

$$=\frac{1}{|\mathfrak{X}|}(\operatorname{tr}(\mathbf{P})-1)\tag{26}$$

$$=0 (27)$$

In [14], this problem is overcome with the following modification: Based on  $p_{X,Y}$ , a bijective remapping  $\Phi \in \mathfrak{S}(\mathfrak{X})$  is picked and applied to all the entries of  $G^{(2)}$  before computing the Hamming distances  $L_{i,j}$ , where  $\mathfrak{S}(\mathfrak{X})$  denotes the symmetry group of  $\mathfrak{X}$ . Denoting the consequent version of the Hamming distance  $L_{i,j}$  by  $L_{i,j}(\Phi)$ , it was proven in [14, Lemma 2] that there as long as  $p_{X,Y} \neq p_X p_Y$ , there exists  $\Phi \in \mathfrak{S}(\mathfrak{X})$  such that the Binomial mixture distribution associated with  $L_{i,i}(\Phi)$  has two distinct components with respective success parameters  $q_0(\Phi)$  and  $q_1(\Phi)$ . In other words, we have

$$L_{i,j}(\Phi) \sim \begin{cases} \operatorname{Binom}(m_n, q_0(\Phi)), & G_i^{(1)} \perp \!\!\! \perp G_j^{(2)} \\ \operatorname{Binom}(m_n, q_1(\Phi)), & \text{otherwise} \end{cases}$$
 (28)

and  $q_0(\Phi) \neq q_1(\Phi)$ . Call such  $\Phi$  a useful remapping.

ii) In the distribution-aware settings, the useful remapping  $\Phi$  and threshold  $\tau_n$  for Hamming distances were chosen based on a-priori knowledge on  $p_{X,Y}$ . In Section III-A, this has been overcome via parameter estimation in Binomial mixtures. However, since for each retained column, we have exactly one Binom( $\Lambda_n, q_1(\Phi)$ ) component, whereas we have n-1Binom $(\Lambda_n, q_0(\Phi))$  components. Hence, it can be seen that the mixture parameter  $\beta$  of this Binomial mixture distribution approaches 1 since

$$\beta = \frac{(n-1)\tilde{K}_n}{n\tilde{K}_n} \tag{29}$$

This imbalance prevents us from performing a parameter estimation as done in Algorithm 1.

We propose to exploit the aforementioned observation that for a useful mapping  $\Phi$ , in each column of  $L(\Phi)$ , there is exactly one element with a different underlying distribution, while the remaining n-1 entries are i.i.d., rendering this entry an outlier. Note that  $L_{i,j}(\Phi)$  being an outlier corresponds to  $G_i^{(1)}$  and  $G_i^{(2)}$  being correlated, and in turn  $S_i \neq 0$ .

To detect the outliers in  $L(\Phi)$ , we propose to use the distances of  $L_{i,j}(\Phi)$  to the sample mean  $\mu(\Phi)$  of  $\mathbf{L}(\Phi)$  where

$$\mu(\Phi) \triangleq \frac{1}{n\tilde{K}_n} \sum_{i=1}^n \sum_{j=1}^{\tilde{K}_n} L_{i,j}(\Phi)$$
 (30)

As given in Algorithm 2, if these distances are lower than  $\hat{\tau}_n$ , we detect retention i.e., non-deletion.

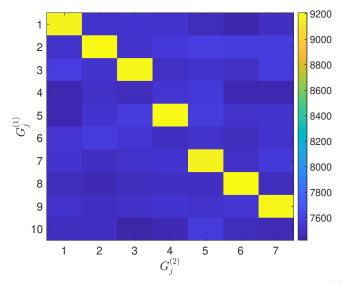


Fig. 3: Hamming distances between the columns of  $\mathbf{G}^{(1)}$  and  $\mathbf{G}^{(2)}$  with n=10,  $\tilde{K}_n=7$  and  $\Lambda_n=10^4$ . The  $(i,j)^{\text{th}}$  element corresponds to  $L_{i,j}$ , with the colorbar indicating the approximate values. It can be seen that there are no outliers in the 4<sup>th</sup>, 6<sup>th</sup> and 10<sup>th</sup> rows . Hence, it can be inferred that  $I_{\text{del}}=(4,6,10)$ .

Note that this step is equivalent to utilizing Z-scores (also known as standard scores), a well-studied concept in statistical outlier detection [22], where the distances to the sample mean are also divided by the sample standard deviation. In this section, for the sake of brevity, we will avoid such division.

The following lemma states that for sufficient seed size,  $\Lambda_n = \omega(\log n) = \omega(\log \log m_n)$ , Algorithm 2 works correctly with high probability.

**Lemma 2.** (Deletion Detection) Let  $I_R = \{j \in [n] : S_j \neq 0\}$  be the true retention index set and  $\hat{I}_R$  be its estimate output by Algorithm 2. Then for any seed size  $\Lambda_n = \omega(\log n)$ , we have

$$\lim_{n \to \infty} \Pr(\hat{I}_R = I_R) = 1 \tag{31}$$

*Proof.* For now, suppose that  $\Phi$  is a useful remapping. Start by observing that using Chebyshev's inequality [23, Theorem 4.2] it is straightforward to prove that for any  $\varepsilon_n > 0$ 

$$\gamma \triangleq \Pr(|\mu(\Phi) - \Lambda_n q_0(\Phi)| > \Lambda_n \varepsilon_n) \le O\left(\frac{1}{K_n n \Lambda_n \varepsilon_n}\right) \quad (32)$$

Let  $I_R = \{r_1, \dots, r_{\tilde{K}_n}\}$  and note that  $L_{i,j} \sim \text{Binom}(\Lambda_n, q_1(\Phi))$ . Thus, from the Chernoff bound [24, Lemma 4.7.2] we get

$$\beta_{r_j,j} \triangleq \Pr(|L_{r_j,j}(\Phi) - \Lambda_n q_1(\Phi)| \ge \varepsilon_n \Lambda_n)$$

$$< 2^{-\Lambda_n D(q_1(\Phi) - \varepsilon_n || q_1(\Phi))}$$
(33)

$$+2^{-\Lambda_n D(1-q_1(\Phi)-\varepsilon_n\|1-q_1(\Phi))}$$
 (34)

where D(p||q) denotes the relative entropy [18, Chapter 2.3] (in bits) between two Bernoulli distributions with respective parameters p and q.

# Algorithm 2: Seeded Deletion Detection Algorithm

```
Input: (G^{(1)}, G^{(2)}, \Lambda_n, n, \tilde{K}_n, \mathfrak{X})
Output: \hat{I}_R
\mathfrak{S}(\mathfrak{X}) \leftarrow \text{SymmetryGroup}(\mathfrak{X});
\hat{\tau}_n \leftarrow 2\Lambda_n^{2/3} (\log n)^{1/3};
for s \leftarrow 1 to |\mathfrak{X}|! do
      \hat{I}_R \leftarrow \varnothing;
       \Phi \leftarrow \mathfrak{S}(\mathfrak{X})[s];
       \mathbf{L}(\Phi) \leftarrow \text{HammDist}(\mathbf{G}^{(1)}, \mathbf{G}^{(2)}); / \star \text{ Eq. } (20) \star /
       \mu(\Phi) \leftarrow \text{SampleMean}(\mathbf{L}(\Phi)); /* \text{Eq. (30)} */
       \mathbf{M}(\Phi) \leftarrow |\mathbf{L}(\Phi) - \mu(\Phi)|;
       for j \leftarrow 1 to \tilde{K}_n do
             count \leftarrow 0;
             for i \leftarrow 1 to n do
                    if M[i][j] > \hat{\tau}_n then
                          \hat{I}_R \leftarrow \hat{I}_R \cup \{i\};
                           count \leftarrow count + 1:
                    end
             end
             if count > 1 then
                    return ERROR;
             else
                    if count = 0 then
                           Skip to next \Phi;
                    end
             end
       end
       return \hat{I}_R;
end
```

Now, for notational brevity, let

$$f(\varepsilon) \triangleq D(q - \varepsilon || q) \tag{35}$$

$$g(\varepsilon) \triangleq D(1 - q - \varepsilon || 1 - q)$$
 (36)

Then, one can simply verify the following

$$f'(\varepsilon) = \log \frac{q}{1-q} - \log \frac{q-\varepsilon}{1-q-\varepsilon}$$
 (37)

$$f''(\varepsilon) = \frac{1}{\log e} \left[ \frac{1}{q - \varepsilon} + \frac{1}{1 - q + \varepsilon} \right]$$
 (38)

$$g'(\varepsilon) = \log \frac{1 - q}{q} - \log \frac{1 - q - \varepsilon}{q + \varepsilon}$$
 (39)

$$g''(\varepsilon) = \frac{1}{\log e} \left[ \frac{1}{1 - a - \varepsilon} + \frac{1}{a + \varepsilon} \right] \tag{40}$$

Observing that

$$f(0) = f'(0) = 0 (41)$$

$$g(0) = g'(0) = 0 (42)$$

and performing second-order MacLaurin Series expansions on f and g, we get for any  $\varepsilon < 1$ 

$$f(\varepsilon) = c(q)\varepsilon^2 + O(\varepsilon^3) \tag{43}$$

$$g(\varepsilon) = c(q)\varepsilon^2 + O(\varepsilon^3) \tag{44}$$

where

$$c(q) \triangleq \frac{1}{2\log e} \left[ \frac{1}{q} + \frac{1}{1-q} \right] \tag{45}$$

Let  $\Lambda_n = \Gamma_n \log n$  and  $\varepsilon_n = \Gamma_n^{-1/3}$  and pick the threshold as  $\hat{\tau}_n = 2\Lambda_n \varepsilon_n$ . Observe that since  $\Gamma_n = \omega_n(1)$ , we get

$$\hat{\tau}_n = 2\Lambda_n \varepsilon_n = o_n(\Lambda_n) \tag{46}$$

$$\Lambda_n \varepsilon_n^2 = \Gamma_n^{1/3} \log n = \omega_n(\log n) \tag{47}$$

Then, we have

$$\beta_{r_i,j} \le 2^{1-\Lambda_n(c(q_1(\Phi))\varepsilon_n^2 + O(\varepsilon_n^3))}$$
(48)

$$= 2^{1-c(q_1(\Phi))\Gamma_n^{1/3}\log n + O(\varepsilon_n^3))}$$
 (49)

Note that with probability at least  $1 - \gamma - \beta_{r_j,j}$  we have

$$|\mu(\Phi) - \Lambda_n q_0(\Phi)| \le \Lambda_n \varepsilon_n \tag{50}$$

$$|L_{r_i,j}(\Phi) - \Lambda_n q_1(\Phi)| \ge \Lambda_n \varepsilon_n \tag{51}$$

From the triangle inequality, we have

$$|L_{r_j,j}(\Phi) - \mu(\Phi)| \ge \Lambda_n(|q_1(\Phi) - q_0(\Phi)| - 2\varepsilon_n)$$
 (52)

$$\geq \hat{\tau}_n$$
 (53)

for large n. Therefore, from the union bound we have

$$\Pr(\exists j \in [\tilde{K}_n] : |L_{r_i,j} - \mu(\Phi)| \le \hat{\tau}_n)$$
(54)

$$\leq \gamma + \sum_{i=1}^{\tilde{K}_n} \beta_{r_j,j} \tag{55}$$

$$= \gamma + 2^{\log \tilde{K}_n - 1 - c(q_1(\Phi)) \Gamma_n^{1/3} \log n + O(\varepsilon_n^3))}$$
 (56)

Since  $\tilde{K}_n \leq n$  and  $\Lambda_n = \omega_n(\log n)$ , we have

$$\lim_{n \to \infty} \log \tilde{K}_n - c(q_1(\Phi)) \Gamma_n^{1/3} \log n = -\infty$$
 (57)

Thus we have

$$\lim \Pr(\exists j \in [\tilde{K}_n] : M_{r_i, j} \le \hat{\tau}_n) = 0$$
 (58)

Next, we look at  $i \neq r_j$ . Repeating the same steps above, we get

$$\beta_{i,j} \triangleq \Pr(|L_{i,j}(\Phi) - \Lambda_n q_0(\Phi)| \ge \varepsilon_n \Lambda_n) \tag{59}$$

$$< 2^{-\Lambda_n D(q_0(\Phi) - \varepsilon_n \| q_0(\Phi))} + 2^{-\Lambda_n D(1 - q_0(\Phi) - \varepsilon_n \| 1 - q_0\Phi))}$$
 (60)

$$= 2^{1-c(q_0(\Phi))\Gamma_n^{1/3}\log n + O(\varepsilon_n^3))}$$
(61)

Again, from the triangle inequality, we get

$$|L_{i,i}(\Phi) - \mu(\Phi)| \le 2\varepsilon_n = \hat{\tau}_n \tag{62}$$

From the union bound, we obtain

$$\Pr(\exists j \in [\tilde{K}_n] \,\exists i \in [n] \setminus \{r_j\} : |L_{i,j}(\Phi) - \mu(\Phi)| \ge \hat{\tau}_n) \tag{63}$$

$$\leq \gamma + \sum_{j=1}^{\tilde{K}_n} \sum_{i \neq r_j} \beta_{i,j} \tag{64}$$

$$\leq \gamma + n^2 2^{1 - c(q_0(\Phi))\Gamma_n^{1/3} \log n + O(\varepsilon_n^3))}$$
 (65)

Since  $\Lambda_n = \omega(\log n)$ , we have

$$\lim_{n\to\infty} \Pr(\exists j\in [\tilde{K}_n] \,\exists i\in [n]\setminus \{r_j\} : |L_{i,j}(\Phi)-\mu(\Phi)| \geq \hat{\tau}_n) = 0 \tag{66}$$

Thus, for any useful remapping  $\Phi$ , the misdetection probability decays to zero as  $n \to \infty$ .

For any *useless* remapping  $\Phi$ , following the same steps, one can prove that

 $Pr(Useless remapping \Phi is inferred as useful.)$  (67)

$$\leq \gamma + \sum_{i=1}^{n} \sum_{j=1}^{K_n} \Pr(M_{i,j} \geq \varepsilon_n \Lambda_n)$$
 (68)

$$\leq \gamma + n^2 2^{1 - c(q_0(\Phi))\Gamma_n^{1/3} \log n + O(\varepsilon_n^3))} \tag{69}$$

$$=o_n(1) \tag{70}$$

Observing  $|\mathfrak{S}(\mathfrak{X})| = |\mathfrak{X}|! = O_n(1)$  concludes the proof.  $\square$ 

#### C. De-Anonymization Scheme

In this section, we propose a de-anonymization scheme by combining the detection algorithms proposed in Section III-A-III-B, and performing a modified version of the typicality-based scheme proposed in [14]. Then using this scheme we prove the achievability of Theorem 1.

Given the database pair  $(\mathbf{D}^{(1)}, \mathbf{D}^{(2)})$  and the corresponding seed matrices  $(\mathbf{G}^{(1)}, \mathbf{G}^{(2)})$ , the de-anonymization scheme we propose is as follows:

- 1) Detect the replicas through Algorithm 1.
- 2) Remove all the extra replica columns from the seed matrix  $\mathbf{G}^{(2)}$  to obtain  $\tilde{\mathbf{G}}^{(2)}$  and perform seeded deletion detection via Algorithm 2 using  $\mathbf{G}^{(1)}, \tilde{\mathbf{G}}^{(2)}$ . At this step, we have an estimate  $\hat{S}^n$  of the column repetition pattern  $S^n$ .
- 3) Based on  $\hat{S}^n$  and the matching entries in  $\mathbf{G}^{(1)}$ ,  $\tilde{\mathbf{G}}^{(2)}$ , obtain an estimate  $\hat{p}_{X|Y^S|S}$  of  $p_{X|Y^S|S}$  where

$$\hat{p}_X(x) \triangleq \frac{1}{\Lambda_n n} \sum_{i=1}^{\Lambda_n} \sum_{i=1}^n \mathbb{1}_{[G_{i,j}^{(1)} = x]}, \quad \forall x \in \mathfrak{X}$$
 (71)

$$\hat{p}_{Y|X}(y|x) = \frac{\sum_{i=1}^{\Lambda_n} \sum_{j=1}^{\tilde{K}_n} \mathbb{1}_{[G_{i,r_j}^{(1)} = x, \tilde{G}_{i,j}^{(2)} = y]}}{\sum_{i=1}^{\Lambda_n} \sum_{j=1}^{\tilde{K}_n} \mathbb{1}_{[\tilde{G}_{i,j}^{(2)} = y]}}, \quad \forall (x, y) \in \mathfrak{X}^2$$
 (72)

$$\hat{p}_{S}(s) = \frac{1}{n} \sum_{i=1}^{n} \mathbb{1}_{[S_{j} = s]}, \qquad \forall s \ge 0$$
 (73)

and construct

$$\hat{p}_{X,Y^S|S}(x,y^s|s) = \begin{cases} \hat{p}_X(x) \mathbb{1}_{[y^s=*]} & \text{if } s = 0\\ \hat{p}_X(x) \prod_{j=1}^s \hat{p}_{Y|X}(y_j|x) & \text{if } s \ge 1 \end{cases}$$
(74)

with  $y^s = y_1 \dots y_s$ .

**4)** Using  $\hat{S}^n$ , place markers between the noisy replica runs of different columns to obtain  $\tilde{\mathbf{D}}^{(2)}$ . If a run has length 0, *i.e.* deleted, introduce a column consisting of erasure symbol  $* \notin \mathfrak{X}$ .

**5)** Fix  $\varepsilon > 0$ . Match the  $l^{\text{th}}$  row  $Y_l^K$  of  $\tilde{\mathbf{D}}^{(2)}$  with the  $i^{\text{th}}$  row  $X_i^n$  of  $\mathbf{D}^{(1)}$ , if  $X_i$  is the only row of  $\mathbf{D}^{(1)}$  jointly  $\varepsilon$ -typical with  $Y_l^K$  according to  $\hat{p}_{X,Y^S,S}$ , assigning  $\hat{\Theta}_n(i) = l$ . Otherwise, declare an error.

Let  $\kappa_n^{(1)}$  and  $\kappa_n^{(2)}$  be the error probabilities of the noisy replica detection (Algorithm 1) and the seeded deletion (Algorithm 2) algorithms, respectively. By the Law of Large Numbers, we have

$$\hat{p}_{X|Y^S|S} \xrightarrow{p} p_{X|Y^S|S} \tag{75}$$

and by the Continuous Mapping Theorem [25, Theorem 2.3] we have

$$\hat{H}(X, Y^S|S) \xrightarrow{p} H(X, Y^S|S) \tag{76}$$

$$I(\hat{X}; \hat{Y}^{\hat{S}}|\hat{S}) \stackrel{p}{\to} I(X; Y^{S}|S) \tag{77}$$

where  $\hat{H}(X,Y^S|S)$  and  $\hat{I}(X,Y^S|S)$  denote the conditional joint entropy and conditional mutual information associated with  $\hat{p}_{X,Y^S|S}$ , respectively. Thus, for any  $\varepsilon > 0$  we have

$$\kappa_n^{(3)} \stackrel{\triangle}{=} \Pr(|\hat{H}(X, Y^S|S) - H(X, Y^S|S)| > \varepsilon) \stackrel{n \to \infty}{\longrightarrow} 0$$
 (78)

$$\kappa_n^{(4)} \stackrel{\triangle}{=} \Pr(|\hat{I}(X, Y^S|S) - I(X, Y^S|S)| > \varepsilon) \stackrel{n \to \infty}{\longrightarrow} 0$$
(79)

Now, from multiple triangle inequalities conditioned on the  $|.-.| < c\varepsilon$  events (omitted here due to length concerns), by choosing adequate multiplicative constants c, the probability of error of the de-anonymization scheme can be bounded as

$$Pr(\text{error}) \le 2^{nR} 2^{-n(I(X;Y^S,S)-4\varepsilon)} + \varepsilon + \kappa_n^{(1)} + \kappa_n^{(2)} + \kappa_n^{(3)} + \kappa_n^{(4)}$$
(80)

$$\leq \varepsilon$$
 (81)

as  $n \to \infty$  as long as  $R < I(X; Y^S, S) - 4\varepsilon$ , concluding the proof of the main result.

# IV. CONCLUSION

In this work, we have investigated the distribution-agnostic database de-anonymization problem under synchronization errors and noise. We have showed that the noisy replica detection algorithm of [14] tailored for specific  $p_{X,Y}$  could be adjusted to work in tandem with a moment estimator to accommodate the incognizance of  $p_{X,Y}$ . Then, we proposed an outlier-detection-based seeded deletion detection algorithm and showed that a seed size growing double logarithmic with the number of rows is sufficient for correct estimation of the deletion pattern. Finally, we proposed a joint-typicality-based de-anonymization scheme utilizing the estimated distributions and derived an achievable rate. Furthermore, we show that this achievable database growth rate is equal to the matching capacity derived when full information on the underlying distributions is available.

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