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Efficient Known-Sample Attack for Distance-Preserving Hashing Biometric Template Protection Schemes

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Abstract—The rapid deployment of biometric authentication systems raises concern over user privacy and security. A biometric template protection scheme emerges as a solution to protect individual biometric templates stored in a database. Among all available protection schemes, a template protection scheme that relies on distance-preserving hashing has received much attention due to its simplicity and efficiency in offering privacy protection while archiving decent authentication performance. In this work, we introduce an efficient attack called known sample attack and demonstrate that most state-of-art template protection schemes that utilize distance-preserving hashing can be compromised in practice (within few seconds), especially when the output is significantly smaller than the original input sample size. These findings further motivated our subsequent work in proposing a secure authentication mechanism to resist such an attack with proper study over the distribution of the input samples. Furthermore, we conducted revocability, unlinkability analysis to demonstrate the satisfactory of general biometric template protection requirements; and showed the resistance of various security and privacy attacks, i.e., false acceptance attack, and attack via record multiplicity.

Index Terms—Biometric, Known-Sample attack, secure authentication.

I. INTRODUCTION

BIOMETRICS refers to the automatic verification or identification process using the physiological or behavioral characteristics of humans. Some typical biometric traits include fingerprint, face, and iris, which are inherently and permanently associated with individuals. Due to its attractive features such as token/ID card-free and ease of use (e.g., no need to remember the complex password), the biometric authentication system is widely deployed in many applications that demand identity management [1]. However, since

biometric is permanently associated with individuals, direct exposure of personal biometric data to a third party may lead to security and privacy issues. Specifically, once the database that utilized to store individual biometric data (i.e., template) is compromised, the attacker could transform the stored template to its original form, which leads to severe privacy invasion and permanent identity loss for individual users.

Therefore, the security and privacy issues of biometric template storage are of great concern. As a remedy, biometric template protection (BTP), which is a protection scheme, is put forward by researchers to address the concerns mentioned above [2].

Briefly, BTP is designed with the primary goal of transforming an unprotected biometric template into a protected biometric template using a parameterized function. An effective biometric template protection scheme should satisfy the following four requirements: *non-invertibility*, *revocability*, *unlinkability*, and *performance preservation* [3].

In this paper, we focus on distance-preserving hashing BTP: a BTP scheme that utilizes a heuristic hash function $f: \mathbb{R}^k \rightarrow \{0, 1\}^n$, with distance-preserving property, to generate a hashed template over the hashed domain $\{0, 1\}^n$. Most conventional distance-preserving hashing BTPs fulfill the properties of non-invertibility, revocability, and unlinkability. However, to realize performance preservation, such BTP must preserve the relative distance between different biometric templates after the BTP applied. Such a goal is necessary to ensure that similar templates render high similarity scores for better recognition utility. Nonetheless, the distance preserving property induces information leakage and jeopardizes the system security. We introduce an *efficient* security attack for existing distance-preserving hashing BTP. We show that without proper designation of the hash function, such distant preservation property could lead to a severe security breach, hence leaving the security of the system in doubt for practical use. Subsequently, we propose a countermeasure to resist such an attack while preserving the original authentication performance.

The rest of this paper is organized as follows: a literature survey on existing research on BTP is covered in Section II. Our motivations and contributions of this paper are highlighted in Section III. An efficient attack, which is robust against the current state-of-the-art distance preserving hashing BTP schemes, is put forward in Section IV. A proposal of solution

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78 to resist against the attack is given in V. Our experiments and
 79 evaluations are covered in Section VI. A concluding remark
 80 is given in Section VII.

81 II. RELATED WORK

82 A. Distance-Preserving Hashing BTP

83 One of the representative approaches to construct a
 84 BTP scheme is by ‘hashing’. In different with the con-
 85 ventional cryptographic one-way hashing, e.g., SHA-512,
 86 the term ‘hashing’ in BTP context relies on heuristic
 87 distance-preserving hash function $f : \mathbb{R}^k \rightarrow \{0, 1\}^n$ to gener-
 88 ate a hashed template $y = f(x) \in \{0, 1\}^n$ from its original
 89 biometric template $x \in \mathbb{R}^k$. The hashed template obtains
 90 its non-invertible characteristic through information loss via
 91 dimensional reduction, where $n < k$. Follow the studies in [4],
 92 [5], reconstructing the input x from y is equivalent to solving
 93 an under-determined linear system, which is computationally
 94 hard if $n \ll k$.

95 In general, there are two main categories where
 96 distance-preserving hashing is utilized for BTP in the liter-
 97 ature, namely, Bio-hashing and Locality Sensitive Hashing
 98 (LSH).

99 1) *Bio-Hashing*: The earliest attempt of applying such
 100 technique to biometric is Bio-hashing [6] for protecting human
 101 fingerprint template. In Bio-hashing, the hashing operation is
 102 performed by using randomly generated orthogonal matrices
 103 which are implemented as dimension-reducing mapping to
 104 project the original fingerprint template to a random string of
 105 lower dimension. The projection supports distance-preserving
 106 property, where the pairwise distance of the fingerprint tem-
 107 plates is preserved in the hashed domain. There are some
 108 similar lines of work on Bio-hashing applied to different
 109 biometric modalities, including palm [7], iris [8], and human
 110 speech [9].

111 2) *Locality Sensitive Hashing (LSH)*: On the other hand,
 112 recent approaches (including the state-of-the-art works)
 113 [10]–[12] use LSH for BTP. Briefly, LSH refers to the use
 114 of multiple hash functions h_i over a LSH hashing family
 115 $H = \{h_i : \mathbb{R}^k \rightarrow U\}_{i=1}^n$, where individual hash function
 116 h_i is designed to hash the input $x, y \in \mathbb{R}^k$ to an output
 117 hash space $U = \{0, 1\}$ where $n < k$. LSH ensures the input
 118 pair x, y with small distance (viz., high similarity) renders
 119 a higher probability of collision in the hashed domain and
 120 vice versa. There are few reported ways for designing the
 121 hash function $h_i \in H$. For instances, Lai *et al.* [11] construct
 122 a LSH family $H = \{h_i : \{0, 1\}^k \rightarrow \{0, \dots, q - 1\}\}_{i=1}^n$
 123 for iris template protection, while Jin *et al.* [10] construct
 124 a LSH family $H = \{h_i : \mathbb{R}^k \rightarrow \{0, \dots, q - 1\}\}_{i=1}^n$ for
 125 fingerprint template protection. Both constructions utilize a
 126 set of randomly generated projection matrices of dimension
 127 $q \times k$ for h_i to project the input features into q dimensional
 128 subspace, where the index of maximum value selected over
 129 $\{0, \dots, q - 1\}$ is returned.

130 Formal speaking, Bio-hashing and LSH exploit the random
 131 projection process to preserve the original inputs’ distance in
 132 the hashed domain.

Specifically, the random projection could be viewed as a
 multiplicative data perturbation such that $y = A \cdot x$ for a
 random matrix A and input x .

Theorem 1 [13]: Given two vectors $x, x' \in \mathbb{R}^k$. Let $A \in \mathbb{R}^{n \times k}$ be a $n \times k$ random matrix whose elements A_{ji} (where $j = 1, \dots, n$ and $i = 1, \dots, k$) are i.i.d. drawn from some distributions with $\mathbb{E}[A_{ji}] = \mu$ and $\text{Var}(A_{ji}) = 1$. Recall that random projection computes $y = \frac{1}{n}A \cdot x$ and $y' = \frac{1}{n}A \cdot x'$. Then for x and x' such that $\|x\| \leq 1$ and $\|x'\| \leq 1$, it follows that

$$(1 + \mu^2) \mathbb{E}[\|y - y'\|^2] - \|x - x'\|^2 \leq 2\mu^2 k. \quad (1)$$

Eq (1) of the above theorem implies that regardless of which type of random matrix, the corresponding output distance, i.e., $\|y - y'\|^2$, would inevitably increase with the increment of the input distance $\|x - x'\|^2$, and vice versa. This demonstrates that the Bio-hashing and LSH distance exhibit distance-preserving property, and they can be generally named as distance-preserving hashing, categorized under the distance-preserving transformation (DPT).

152 B. Related Works in Privacy Preservation Using DPT

The studies of distance-preserving property for privacy-preserving data mining in a broad sense have been an area of research since 1991 [14]. The main goal is to protect user data privacy from a database via DPT. Some notable literature refer to the works by Kim and Winkler [15], Tendick [16], and Evans *et al.* [17]. However, the question of how well is x being hidden in y remains unclear, which deserves a careful study. Potential attackers without any prior knowledge can only do very little (if any) in recovering the original sample x . However, it is unrealistic for such zero prior knowledge to happen in many practical situations. Motivated by such reasoning, a lot of works have been done by considering the vulnerability of distance-preserving transformation. We briefly highlight some notable literature as follow. For a more general survey, we direct the interested reader to [18].

First, Liu *et al.* [19] reported that the attacker could exploit the distance-preserving property in reverting the original sample x . They realized the principal component analysis (PCA) could be a useful tool for a reasonable estimation of the original and transformed covariance matrices, which later leads to the recovery of the original data. Their work has inspired Turgay *et al.* [20] to recover the original data values with very high confidence for PCA based attack. A more robust type of attack extended from PCA based attack is proposed by Guo *et al.* [21] to show security breach in projection-based transformation (isometric). They applied traditional independent component analysis (ICA) over a set of known samples and perturbed samples. Information leakage allows the derivation of a transformation matrix that could lead to a close approximation of the original sample. Chen *et al.* [22] have also pointed out the security concern over distance preserving transformation such as geometric data perturbation, including random rotation perturbation, random translation perturbation, and noise addition. Subsequently, Wong *et al.* [23] have shown

188 that the original input data is uniquely recoverable when one
 189 can solve the K -independent linear equation systems.

190 For the biometric line of research, recent works by Gal-
 191 bally *et al.* [24] reported the utilization of some heuristic
 192 algorithms to revert the original biometric template (human
 193 iris) through the exploitation of the preserved distances among
 194 hashed template. Specifically, they utilized a genetic algorithm,
 195 which aimed to minimize the ‘fitness’ function corresponding
 196 to the pairwise hashed template distance. The minimization
 197 process performs iteratively with several guesses defined by a
 198 population of synthetic iris data. Apart from using a genetic
 199 algorithm, another attack carried out by Feng *et al.* [25]
 200 incorporated multiple layers of perceptron learning to mini-
 201 mize the hashed distance over the set of synthetic real-value
 202 templates. Their results demonstrated the close reconstruction
 203 of human face images from the synthetic real-value template
 204 by utilizing the hill-climbing technique [26]. Recent work by
 205 Kaplan *et al.* [27] have shown that any distance-preserving
 206 transformation is also relation-preserving. Even under the
 207 scenario where only the relative order of the distance or
 208 similarity is preserved, the data breach is still inevitable due
 209 to similarity information leakage.

210 The schemes mentioned above have identified severe secu-
 211 rity threats to distance-preserving transformation, leading to
 212 doubts and curiosity about non-invertibility.

213 C. Optimal Distance-Preserving Hashing

214 Upon closer look, all the attacks mentioned in the previous
 215 sub-section rely on the information leakage due to DPT.

216 Follow the works in [13], to resist this kind of attacks,
 217 one must reduce such information leakage, which can be
 218 described as the mutual information, denoted as $I(D_I|D_o)$,
 219 where D_o is the distribution of the original interclass distance,
 220 and D_I is the distribution of the interclass distance d_I after
 221 hashing with $f(\cdot)$. In our context, we refer the term *dissim-*
 222 *ilarity* when D_o and D_I are normalized to $[0, 1]$. Because
 223 optimizing the mutual information $I(D_I|D_o)$ is NP-complete,
 224 it is more practical for one to optimize the upper bound
 225 of $I(D_I|D_o)$. Specifically, let $H(W)$ denote the entropy of
 226 distribution W . It follows that $I(D_I|D_o) \leq H(D_I) \leq H(D_o)$.
 227 Then, by assuming that D_I asymptotically follows unimodal
 228 distribution, where small distribution’s variance presumably
 229 leads to small entropy [28], the term $H(D_I)$ can be replaced
 230 with the variance of D_I , denoted as $\text{Var}(D_I)$. Optimizing
 231 $I(D_I | D_o)$ can be done via minimizing $\text{Var}(D_I)$. In other
 232 words, the inter-class distance over the hashed domain shall
 233 be made as small as possible with equidistance to reduce the
 234 mutual information leakage. Doing this is sufficient to show
 235 the resistance against the aforementioned attacks over DPT.

236 On the other hand, for good recognition utility, the system
 237 must ensure the samples sourced from similar subjects can
 238 match successfully with high probability. Given this, it is
 239 desirable that after hashing with $f(\cdot)$, there is a large gap
 240 between the distribution of the interclass’s distance (denoted
 241 as D_I) and the distribution of the intraclass’s distance (denoted
 242 as D_g). Ideally, we wish that $\mathbb{E}[D_I] \rightarrow 1$ while $\mathbb{E}[D_g] \rightarrow 0$,
 243 where the similarity scores ($1 - D_I$ and $1 - D_g$) obtained

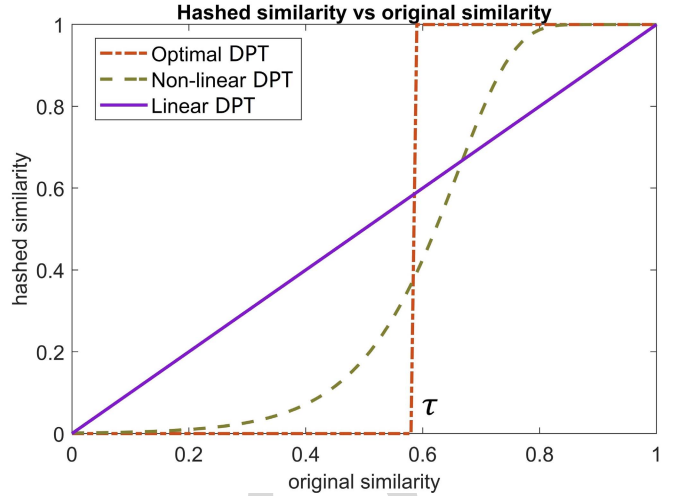


Fig. 1. Overview diagram illustrating the different relationships between the hashed similarity scores and original similarity scores.

244 between the hashed templates shall remain insensitive up to
 245 a threshold $\tau > 0$ with respect to their original similarity
 246 scores for both interclass and intraclass. The relation between
 247 the hashed similarity scores (after hashing with $f(\cdot)$) and the
 248 original similarity scores is depicted in Fig. 1. Note that an
 249 S-curve characterizes such a non-linear relationship, where
 250 the hashed similarity score is shown to remain negligibly
 251 small given the original similarity score is less than the
 252 acceptance threshold, i.e., $\tau = 0.59$ as depicted in Fig. 1.
 253 Such a non-linear relationship is sufficient to ensure negligible
 254 similarity information leakage over the hashed templates while
 255 offering correctness (i.e., authenticity) for genuine users who
 256 can present another biometric template w and show a similarity
 257 score $s(\cdot, \cdot)$ of at least τ with the enrolled template w' ,
 258 i.e., $s(w, w') \geq \tau$.

259 III. MOTIVATIONS AND CONTRIBUTIONS

260 Our motivations and contributions of this paper can be
 261 summarized as follow:

262 A. DPT-Based Attacks on BTP Schemes

263 Liu *et al.* [19] have generalized two attacks over DPT,
 264 namely, *known samples attack* (KSA), and *known input-output*
 265 *attack* (KIOA). The former attack assumes the potential
 266 attacker has acquired a small subset of the database sam-
 267 ples, while the latter assumes that the attacker has the exact
 268 knowledge over several pairs of input and their corresponding
 269 output. The known input-output attack asserts a significantly
 270 stronger assumption upon the attackers’ power in acquiring the
 271 input-output pairs. Our work emphasizes on KSA due to its
 272 popularity for DPT analysis [19]–[21], [27]. Here, we propose
 273 an attack for the BTP scheme relies on distance-preserving
 274 hashing, specifically for face biometric features. Comparatively,
 275 our attack only requires one known sample, which is
 276 indeed more realistic and practical than the 5% of the whole
 277 dataset requirement imposed by [19] and 4 ~ 6 samples men-
 278 tioned in [27]. Moreover, the attack carried out in [20] assumed

279 that the attacker has a distance matrix of the private data,
 280 which directly implies that the attacker knows the original
 281 sample's distribution. In our case, the attacker is considered
 282 much 'weaker' in that he/she has no prior knowledge of the
 283 original sample's distribution. However, we allow the attacker
 284 to model and change the input distribution iteratively by
 285 introducing additional perturbation (i.e., adding noise). We
 286 shall show later that even under such 'weaker' attacking
 287 environment, our results of attacking the BTP scheme that
 288 adopted distance-preserving hashing is prominence, where the
 289 number of iterations required to produce a valid authentication
 290 result can always describe using some polynomial ($\text{poly}(n)$)
 291 in the hashed template's length (n). These results lead to
 292 significantly less time required to launch a successful attack
 293 over a short template.

294 B. Realization of Non-Linear DPT

295 To resist against KSA, one should minimize the similarity
 296 information leakage between the original similarity scores and
 297 the hashed similarity scores [13]. To achieve this, an opti-
 298 mal, or at least non-linear, DPT is desired. As a metric for
 299 evaluation, the degree of minimization of leakage can be
 300 directly visualised from the gradient of the S -curve as depicted
 301 in Fig. 1. Clearly, steeper gradient over the S -curve indicates
 302 higher degree of minimization, hence better security and pri-
 303 vacy protection over the DPT transformed data. To realize such
 304 non-linear DPT, we therefore reformulate the design of the
 305 distance-preserving hashing for BTP. Specifically, we construct
 306 a new hashing family from the conventional locality sensitive
 307 hashing family to realize such non-linear relationship over
 308 the input and hashed domains. Besides, the new hashing
 309 family inherits the good properties of the conventional LSH
 310 hashing family such as *efficiency* and *simplicity*, and resistance
 311 against KSA as a secure distance-preserving hashing BTP
 312 scheme. Most importantly, we also conducted revocability,
 313 unlinkability analysis; and show the resistance of various
 314 security and privacy attacks, i.e. false acceptance attack, attack
 315 via record multiplicity.

316 IV. OUR ATTACK

317 A. New KSA Attack Formalization

318 We begin with the intuition of the proposed KSA attack that
 319 incorporated the structure information of the input biometric.

320 *Attack Intuition:* Let $f : \mathbb{R}^k \rightarrow \{0, 1\}^n$ be a convention
 321 distance-preserving hash function. Let $w \in \mathbb{R}^k$ be the enrolled
 322 biometric template. Given a targeted hashed template $f(w) \in$
 323 $\{0, 1\}^n$ and a dissimilarity score $\varepsilon' \in [0, 1]$, our goal is to
 324 find a sample $w^* \in \mathbb{R}^k$ s.t. $d(f(w), f(w^*)) \leq \varepsilon'$. Due
 325 to the distance-preserving property of $f(\cdot)$, if the dissimi-
 326 larity score (after transformation) is $d(f(w), f(w^*)) \leq \varepsilon'$,
 327 then the original dissimilarity score (before transformation)
 328 $d(w, w^*) \leq \varepsilon$ should hold for arbitrary $\varepsilon > 0$. Using the
 329 naive brute-force search for w^* is a practically infeasible or
 330 at least inefficient approach due to the field size $|\mathbb{R}^k|$, which
 331 increases exponentially with k . However, if we are able to look
 332 for a noise distribution \mathcal{D} and some noise samples $w_{e,i} \in \mathcal{D}$
 333 (for $i \in \{1, 2, \dots, N\}$) s.t. $d(f(w), f(w_{e,i})) \leq \varepsilon'$, then the

Algorithm 1 Proposed KSA

```

1: function ATTACK $_f(w^*, f(w), N, \varepsilon', \varepsilon, \lambda, \mathcal{S})$ 
2:    $\chi \leftarrow \{0, 1\}^k$ 
3:    $\sigma \leftarrow \mathcal{S}$             $\triangleright$  select  $\sigma$  from  $\mathcal{S}$  without repetition
4:   Set  $M = \sigma \cdot U$         $\triangleright U \in 1^k$  is vector of one
5:   for  $i = 1 : N$  do
6:      $e_i \leftarrow \chi$         $\triangleright$  select  $e_i \in \chi$  without repetition, where
      $\forall e_i \in \chi, \|e_i\| = \lfloor k\varepsilon \rfloor$ 
7:      $w_{e,i} = M \circ e_i + w^*$     $\triangleright$  where  $\circ$  denotes the
     Hadamard product of  $M$  and  $e_i$ 
8:     Compute  $d_i = d(f(w), f(w_{e,i}))$  and output
      $(d_1, d_2, \dots, d_N)$       $\triangleright$  we refer  $d(x, y) = \frac{1}{\pi} \arccos(x \cdot y)$ .
9:   end for
10:  Set  $\varepsilon_0 = \min(d_1, d_2, \dots, d_N)$ 
11:  if  $\varepsilon_0 > \lambda/\varepsilon'$  then
12:    Back to Step 3
13:  else
14:    Output  $w_{e,i}$  corresponds to  $\min(s_1, s_2, \dots, s_N)$ 
15:  end if
16: end function

```

334 searching can be reduced to look for any $w_{e,i} \in \mathcal{D}$ where
 335 $d(f(w), f(w_{e,i})) \leq \varepsilon'$ and $d(w, w_{e,i}) \leq \varepsilon$ hold. This allows
 336 us to reduce our search space for all $w_{e,i} \in \mathcal{D}$ (rather than deal
 337 with $w^* \in \mathbb{R}$) over a smaller subspace parametrized by $|\mathcal{D}|$,
 338 which is relatively easier to be modelled compared to $|\mathbb{R}^k|$.

339 Algorithmically, to look for such $w_{e,i} \in \mathcal{D}$, we have to
 340 first initialize a random distribution \mathcal{D} over \mathbb{R}^k . This can be
 341 achieved by knowing at least one sample $w^* \in \mathbb{R}^k$. More
 342 specific, we make use on the known sample's distribution to
 343 construct a smaller subset \mathcal{S} , which later is used to realize \mathcal{D} .
 344 The noisy sample can be generated by perturbing the input
 345 sample w^* using a randomly selected real values $\sigma \in \mathcal{S} \in$
 346 \mathcal{D} . Meanwhile, we also denote a distribution $\chi \in \{0, 1\}^k$ s.t.
 347 for all random sampled $e \in \chi$, the weight $\|e\| = \lfloor k\varepsilon \rfloor$ is
 348 parameterized by the original dissimilarity score $\varepsilon > 0$ s.t.
 349 $d(w, w_{e,i}) \leq \varepsilon$. The sampled e will be used to determine
 350 the position of w^* , over $0, \dots, k-1$, to be perturbed using
 351 the randomly selected σ to model \mathcal{D} precisely. More detailed
 352 discussion on how we construct \mathcal{S} and sample e are covered
 353 in the next sub-section.

354 Let $M \in \mathbb{R}^{k \times k}$ be a perturbation matrix. Given some
 355 reference hashed dissimilarity $d(f(w), f(w^*)) = \varepsilon'$, the goal
 356 of looking for $w_{e,i} \in \mathcal{D}$ can be achieved by minimizing
 357 the dissimilarity score ε' using N number of noise samples
 358 $w_{e,1}, w_{e,2}, \dots, w_{e,N}$ until one yields a dissimilarity score
 359 $\varepsilon_0 \leq \lambda\varepsilon'$ with a ratio $\lambda > 0$. Clearly, $\lambda > 0$ means the
 360 minimized dissimilarity score ε_0 is desired to be lower than
 361 the reference score ε' for meaningful minimization result.

362 Our attack algorithm with input $N, \varepsilon', \varepsilon, \lambda, f(w)$ and w^*
 363 depicted in Algorithm 1. The output of Algorithm 1 is a noisy
 364 sample $w_{e,i}$ that corresponds to the minimized dissimilarity
 365 score ε_0 .

366 B. Attack Complexity and Efficiency

367 Note that the runtime complexity of Algorithm 1 is
 368 bounded by $\mathcal{O}(|\mathcal{S}|Nk^2)$. To look for $|\mathcal{S}|$, we make use of the
 369

possibility of self-enrollment of a potential attacker. Hence at least one sample $w^* \in \mathbb{R}^k$ can be obtained in reality. More precisely, the distribution of w^* can be identified by looking at the minimum and maximum value of w^* , i.e., $w^* \in [\min(w^*), \max(w^*)]$. We can define $|\mathcal{S}|$ to be the size of the subset \mathcal{S} where $\mathcal{S} \in [\min(w^*), \max(w^*)]$. Doing this will narrow our focus to a smaller subset \mathcal{S} , which is very much more manageable compared to \mathbb{R} . For any value $\sigma \in \mathcal{S}$ (chosen uniformly at random from \mathcal{S}), it should be noted that our attack is efficiently bounded over a subspace of size $|\mathcal{S}|^k$. Therefore, we should have the desired distribution $\mathcal{D} \in [2(\min(w^*)), 2(\max(w^*))]^k$ for all $\sigma \in \mathcal{S}$, and $\mathcal{S} \in [\min(w^*), \max(w^*)]$ should follow.

Formally, the dissimilarity score minimization can be conceived as a process of searching for a similar point $w_{e,i} \in \mathcal{D}$ s.t. $d(w, w_{e,i}) \leq \varepsilon$ given $d(f(w), f(w_{e,i})) \leq \varepsilon'$ holds. For each iteration, a sample from \mathcal{D} will be selected as $w_{e,i}$ to minimize $d(f(w), f(w_{e,i}))$. Trivially, for any input sample of size k over \mathbb{R} , there are at most \mathbb{R}^k different samples over the input space. If a minimization solution exists, at most \mathbb{R}^k random guesses are required. However, one needs to consider the exponentially large number of possibilities (of combinations) when k is increasing, e.g., long input length. Nonetheless, we will show that attack complexity can be relieved to $\mathcal{O}(nk^2)$ parametrized by an integer $m > 0$, the input length k , and the original dissimilarity score $\varepsilon > 0$ as shown in below.

For $\max(w^*) - \min(w^*) \leq 1$, using a parameter (integer) $m > 0$, we could construct a subset $\mathcal{S} \in [\min(w^*), \max(w^*)]$ of size

$$|\mathcal{S}| = \frac{\max(w^*) - \min(w^*)}{2^{-m}} \leq 2^m \quad (2)$$

For instance, given $m = 2$, $\max(w^*) = 2$ and $\min(w^*) = 1$, a subset \mathcal{S} can be constructed as $\mathcal{S} = \{1, 1.25, 1.5, 2\}$ with $|\mathcal{S}| \leq 2^2 = 4$.

Recall for any $\varepsilon > 0$, any random sampled e_i should have weight equal to $\|e_i\| = \lfloor k\varepsilon \rfloor$. Hence, Step 7 of Algorithm 1 is equivalent to perturbing exactly $\lfloor k\varepsilon \rfloor$ locations of w^* with M and e_i . For an input w^* of size k , it follows that by *Stirling's approximation*, we can always set (for $\varepsilon \in (1/k, 1/2)$):

$$N = 2^{\lfloor kh_2(\varepsilon) \rfloor} \leq \binom{k}{\lfloor k\varepsilon \rfloor}, \quad (3)$$

where $h_2(\varepsilon) = -\varepsilon \log(\varepsilon) - (1 - \varepsilon) \log(1 - \varepsilon)$ is the binary entropy function.

For any hashed template $f(w) \in \mathcal{D}_f$ in some random distribution \mathcal{D}_f over $\{0, 1\}^n$, let the total number of points over $\mathcal{D}_f \in \{0, 1\}^n$ be $n = 2^{\lfloor kh_2(\varepsilon) + m \rfloor} - 1$. We therefore have the intermediate results as follow $2^{\lfloor kh_2(\varepsilon) + m \rfloor} = n + 1 \leq 2^{kh_2(\varepsilon) + m}$, which leads us to the inequality below

$$kh_2(\varepsilon) + m \geq \log(n + 1). \quad (4)$$

Follow Eq (4) above, to look for $f(w_{e,i})$ (viewed as a point over $\mathcal{D}_f \in \{0, 1\}^n$) and check whether $d(f(w), f(w_{e,i})) = \varepsilon_0 \leq \lambda\varepsilon'$ using Algorithm 1, the logarithm of the number of point can be found over $\mathcal{D}_f \in \{0, 1\}^n$ must be bounded at most $kh_2(\varepsilon) + m$. In other words, the overall attack complexity is

asymptotically (for large m) described as $\mathcal{O}(nk^2) = \text{poly}(n)$, which is polynomial time. Then, we have the following claim for our attack efficiency.

Claim 1: Given $\varepsilon \in (1/k, 1/2)$ and the subset \mathcal{S} of size $|\mathcal{S}| = 2^m$ with an integer $m > 0$, for any targeted BTP transformation function $f: \mathbb{R}^k \rightarrow \{0, 1\}^n$ with output template over a random distribution $\mathcal{D}_f \in \{0, 1\}^n$ that consists of $2^{\lfloor kh_2(\varepsilon) + m \rfloor} - 1 = n$ number of points, the Algorithm 1 will halt in $\mathcal{O}(nk^2)$ with $N = 2^{\lfloor kh_2(\varepsilon) \rfloor}$.

C. Acquiring the Pre-Images

Here, we discuss the capability of our proposed attack in getting large number of similar points that are, contributed by any noisy sample $w_{e,i} \in \mathcal{D}$, close to the targeted sample w , i.e., $d(w, w_{e,i}) \leq \varepsilon$.

Given the information of \mathcal{S} and N , the distribution \mathcal{D} can be revealed and the number of points over \mathcal{D} can be known precisely. More specific, note that the perturbation value σ is chosen uniformly at random from the subset $\mathcal{S} \in [\min(w^*), \max(w^*)]$, and the random string e_i is chosen uniformly at random follows distribution χ of weight $\lfloor k\varepsilon \rfloor$. Every iteration in running Algorithm 1 will output a random noisy sample $w_{e,i} \in \mathcal{D}$ (see Step 7 of Algorithm 1) corresponding to the selected values of $\sigma \in \mathcal{S}$ and e_i . Follows Eq (2) and Eq (3), the number of possible values for $w_{e,i}$ can be expressed as $n + 1 = N|\mathcal{S}| \leq 2^{\lfloor kh_2(\varepsilon) + m \rfloor}$. Note that a point in \mathcal{D} can be revealed as $w_{e,i} \in \mathcal{D}$. Given the distribution \mathcal{D} with number of points not greater than $2^{\lfloor kh_2(\varepsilon) + m \rfloor} - 1$, at most n iterations would suffice to try all the noisy samples over \mathcal{D} using Algorithm 1. In view of this, the proposed KSA attack implicitly constructed a known distributions \mathcal{D} of at most $2^{\lfloor kh_2(\varepsilon) + m \rfloor} - 1$ number of points where each point, a.k.a. the noisy sample $w_{e,i}$, should distribute randomly and uniformly over \mathcal{D} . Therefore, it is appropriate to treat the matching in every single iteration to be independent and identically distributed. To be specific, we define

$$X = \sum_{i=1}^{n+1} X_i, \quad (5)$$

where X_i denotes the independent variable s.t. $X_i = 1$ if $d(f(w), f(w_{e,i})) \leq \varepsilon_0 \leq \lambda\varepsilon'$. Hence, X follows binomial distribution with $\Pr[X_i = 1] = p_i$ and $\Pr[X_i = 0] = 1 - p_i$ for some probability $p_i \in [0, 1]$.

Conceivably, X can be interpreted as the number of successful minimization result over the known distribution \mathcal{D} that yields $d(f(w), f(w_{e,i})) = \varepsilon_0 \leq \lambda\varepsilon'$. Without loss of generality, since $\lambda\varepsilon' \leq \varepsilon'$, hence, a successful minimization result would mean that a similar point ($w_{e,i}$) can be found over \mathcal{D} where $d(f(w), f(w_{e,i})) \leq \varepsilon'$ holds, which implies $d(w, w_{e,i}) \leq \varepsilon$.

Arguing that the number of similar points can be found is different given different input samples w^* , the exact value of X must be different as well. Hence, it is reasonable to bound the number of similar points as a variable based on their original similarity score $1 - \varepsilon$. Then by *Chernoff bound* (for $\varepsilon \in (1/k, 1/2)$):

$$\Pr[X \leq n(1 - \varepsilon)] \leq \exp(-\frac{n\varepsilon^2}{2}). \quad (6)$$

Based on the Eq (6) above, we can conclude that given an arbitrary random $\varepsilon \in (1/k, 1/2)$, for sufficiently large n , the number of similar points s.t. $d(w, w_{e,i}) \leq \varepsilon$ that can be found over \mathcal{D} is unlikely to be smaller than $n(1 - \varepsilon)$. From this point of view, after n number of iterations, the probability for Algorithm 1 in getting $n(1 - \varepsilon)$ similar points is at least $1 - \exp(-n\varepsilon^2/2)$, which is close to one if n is set to be large enough. These obtained similar points are also known as the *pre-images* of w where both $d(w, w^*) \leq \varepsilon$ and $d(w, w_{e,i}) \leq \varepsilon$ should follow. The above results also indicate that any computational unbounded attacker in running Algorithm 1 must be able to obtain at least $n(1 - \varepsilon)$ number of pre-images with high probability when n is large enough.

Given n is large, it follows that m must be set sufficiently large as well s.t. $n \leq 2^{kh_2(\varepsilon)+m} - 1$ in order to support the efficiency argument of Algorithm 1 follows Claim 1, especially under the case when ε is small. In other words, a larger m is necessary to provide more information, hence, more points can be found over \mathcal{D} . Doing so is in our favor of looking for a similar point over larger distribution \mathcal{D} , which contains more points within $\mathcal{O}(nk^2)$ operations.

Indeed, Nagar *et al.* have demonstrated that acquiring the pre-images of the enrolled sample w is sufficient to compromise the BTP schemes, i.e., Bio-hashing. (see [29], Section 5). In their works, for any targeted sample $w \in \mathbb{R}^k$, they proposed to use $t > 0$ number of known biometric samples $w_i^* \in \mathbb{R}^k$ (for $i = 1, \dots, t$), collected from a database s.t. $d_i = d(f(w), f(w_i^*)) \leq \delta$, to estimate $x \in \mathbb{R}^k$ by minimizing the 2-norm distance follows $\text{argmin} \|x - w_i^*\|_2 \leq \varepsilon$. The minimization is done by using the Matlab built-in `isqlin` function to obtain a series of estimated results x_1, \dots, x_t equivalent to the similar points that are ε -close to w . Then, the pre-image of w , denoted as \hat{x} , is computed among x_1, \dots, x_t follows $\hat{x} = \frac{\sum_{i=1}^t x_i/d_i}{\sum_{i=1}^t 1/d_i}$.

Our proposed KSA attack improved Nagar *et al.*'s approach in two perspectives. Firstly, the proposed KSA required only a single known sample of w^* , which can be trivially obtained through self-enrolment. Secondly, the proposed KSA has incorporated the input structure of the biometric distribution. Specifically, the number of pre-images obtained is described as a function of the points of distribution (\mathcal{D}). The incorporated structural information of the biometric distribution offers a better attack efficiency guarantee in looking for the similar points that are ε -close to the original biometric sample w .

V. COUNTERMEASURE FOR DPT-BASED ATTACKS

In this section, first, we present a few definitions and briefly walk through the randomized strategy, which is a crucial background study in the following subsection. Then, we put forward a countermeasure for DPT based attack, particularly to resist against KSA. We reformulate the conventional LSH hashing adopted by the BTP scheme as proposed in [10]–[12] to construct a non-linear DPT for our goal.

A. Definitions

Definition 1 (Locality Sensitive Hashing): Let $d_1 < d_2$ be two distances of some distance measure $d(\cdot, \cdot)$. A family \mathcal{H}

of functions is said to be (d_1, d_2, p_1, p_2) -sensitive if $\forall h \in \mathcal{H}$ then the following hold true:

$$\Pr[h(x) = h(y)] \geq p_1, \text{ if } d(x, y) \geq d_1, \text{ and}$$

$$\Pr[h(x) = h(y)] \leq p_2, \text{ if } d(x, y) \leq d_2.$$

Given an (d_1, d_2, p_1, p_2) -sensitive family \mathcal{H} , one can construct another family \mathcal{H}' where each member of \mathcal{H}' consists of exactly k members from \mathcal{H} . We called such new family to be (d_1, d_2, p_1^k, p_2^k) -sensitive, which is defined below:

Definition 2: Given an (d_1, d_2, p_1, p_2) -sensitive family \mathcal{H} , we say another family \mathcal{H}' is (d_1, d_2, p_1^k, p_2^k) -sensitive if it consists of members of a set $\{h_1, \dots, h_k\}$ from \mathcal{H} , where $h(x) = h(y)$ (over \mathcal{H}) if and only if $h_i(x) = h_i(y)$ for $i = 1, \dots, k$ (over \mathcal{H}').

B. Randomized Strategy for LSH Family

One typical way to construct an LSH family of (d_1, d_2, p_1, p_2) -sensitive is by random projection.

Random projection has been used by Gormans *et al.* [30] in solving the relaxed version of maximum cut problem. In particular, given a graph $G(V, E)$ and nonnegative weight $z_{ij} = z_{ji}$ on the edges $(i, j) \in E$, the max-cut problem is a computational problem that aims to find the set of vertices $S \subset V$ follows a cut (S, \bar{S}) where the weight of the edges with one endpoint in S and the other in \bar{S} (the complement of S) is maximized [31]. The relaxed version of max-cut problem is to maximize the objective function described as $\frac{1}{2} \sum_{i < j} z_{ij} (1 - w_i \cdot w_j)$ where w_i and w_j are two vectors over \mathbb{R}^k . Gormans *et al.* used a random vector r (uniformly distributed on a unit sphere) to partition the set of vertices S and its complement \bar{S} into those vectors $w \in \mathbb{R}^k$ that lie above the hyperplane (i.e., the inner product $r \cdot w$ is positive) and below the hyperplane (i.e., the inner product $r \cdot w$ is negative) while maximizing the objective function $\frac{1}{2} \sum_{i < j} z_{ij} (1 - w_i \cdot w_j)$.

The Lemma below characterizes the above randomized strategy that renders a locality sensitive hashing family which is (d_1, d_2, p_1, p_2) -sensitive with the distance measure referring to the cosine distance (i.e., angle between w and w') described as $d(w, w') = \frac{1}{\pi} \arccos(w \cdot w')$.

Lemma 1 [30]:

$$\Pr[\text{sgn}(r_i \cdot w) \neq \text{sgn}(r_i \cdot w')] = \frac{1}{\pi} \arccos(w \cdot w').$$

In our case, we apply random projection to project the input biometric template (a vector) $w \in \mathbb{R}^k$ using multiple random Gaussian vectors with mean zero and variance one, and a signum function $\text{sgn}(r \cdot w) \in \{0, 1\}$, yielding an output vector $v \in \{0, 1\}^n$ described as follow $v = [\text{sgn}(r_1 \cdot w), \dots, \text{sgn}(r_n \cdot w)]$, where $\text{sgn}(r_i \cdot w) = 0$ if $r_i \cdot w \geq 0$ and $\text{sgn}(r_i \cdot w) = 1$ if $r_i \cdot w < 0$. The output vector v is a core element to be used in our proposed countermeasure for DPT based attack, and to construct a new LSH family, which are discussed in details in the next sub-section.

C. Formalization of the Proposed Technique

The formalization of our proposed countermeasure for DPT based attack adopts the LSH family constructed via

Algorithm 2 Proposed Transformation

```

1: function TRANS $f \in \mathcal{H}_r$ ( $w, r, s, u, b$ )
2:    $n = s \times u \times b$ 
3:   for  $i = 1 : n$  do
4:      $v_i = f_i(w, r_i)$ 
5:   end for
6:   Set  $v = (v_1, \dots, v_n)$ 
7:   Reshape  $v \rightarrow v \in \{0, 1\}^{s \times ub}$ 
8:   Convert every  $b$  bits into a unit of integer in range
    $\{0, \dots, 2^b - 1\}$ 
9:   Output  $v \in \{0, \dots, 2^b - 1\}^{s \times u}$ 
10: end function

```

Algorithm 3 Proposed Authentication

```

1: function AUTH( $v, w', r, s, u, b, \tau$ )
2:    $v' \leftarrow$  TRANS $f \in \mathcal{H}_r$ ( $w', r, s, u, b$ )
3:   Initialize score  $X = 0$ ;
4:   for  $i = 1, \dots, s$  do
5:     if Each row of  $v'$  and  $v$  collided in at least  $\tau$  positions
       of units then
6:       Set  $X = X + 1$ 
7:     end if
8:   end for
9:   Output  $X/s$ 
10: end function

```

584 randomized strategy. We follow Definition 1 and 2 to construct
585 a new LSH family derived from the randomized strategy,
586 which offers non-linearity for our security goal.

587 *Notation.* Suppose we are given an input sample $w \in \mathbb{R}^k$
588 (for enrolment). Let $f \in \mathcal{H}_r$ denote the hashing function over
589 the LSH family of randomized strategy \mathcal{H}_r , where $f : \mathbb{R}^k \rightarrow$
590 $\{0, 1\}^n$. In particular, we have $f_i(r_i, w) = \text{sgn}(r_i \cdot w)$ for
591 $i = 1, \dots, n$ with random Gaussian vector $r_i \in \mathcal{N}(0, 1)$ and
592 signum function $\text{sgn}(\cdot)$. We set $n = s \times b \times u$, and use s, b
593 and u to denote stripe, bit and unit, respectively.

594 *Main Idea.* Our core idea is to reformulate the LSH function
595 to generate a fixed number of points that can be directly
596 expressed using the number of stripes over the hashed domain.

597 For high recognition utility, our formulation must ensure
598 that similar points, that are ε -close together, i.e., $d(w, w') \leq$
599 ε , can be found with overwhelming probability given their
600 hashed similarity is large (i.e., the matching score is high,
601 close to one, after hashing). On the other hand, it should
602 exhibit negligible probability to look for the similar points
603 when the hashed similarity is small (i.e., the matching score
604 is negligible small, close to zero, after hashing). To achieve
605 this, we define a radius of τ for each stripe (point) over
606 the hashed domain. Such radius could be quantified by the
607 number of units in a single stripe, which consists of b number
608 of bits. With an adequately selected τ , we can tolerate the
609 errors in the similar input samples to ensure authenticity with
610 overwhelming probability. It follows that a highly non-linear
611 relationship between the original similarity scores and output
612 hashed similarity scores can be obtained, hence establishing
613 resistance against KSA while keeping high recognition utility.

614 *Overview Procedure (Transformation):* Our procedure to
615 generate the hashed template is quite simple and can be
616 summarized as follow. First, the input template $w \in \mathbb{R}^k$ is
617 being hashed by f_1, \dots, f_n with r_1, \dots, r_n to output a binary
618 vector v of size n . Next, v will be reshaped into a 2-D matrix
619 of size $s \times ub$. We called the individual row of the resulting
620 matrix - a stripe. Precisely, a stripe consists of u number
621 of units, and every unit is represented by b binary symbols
622 (bit). Each unit can be conveniently viewed as an integer
623 over the set of $\{0, \dots, 2^b - 1\}$. Let $r = (r_1, \dots, r_n)$ be the
624 collection of all random Gaussian vectors. The transformation
625 takes (w, r, s, u, b) as input, and its pseudocode is presented
626 as Algorithm 2.

627 *Overview Procedure (Authentication):* Given another input
628 template $w' \in \mathbb{R}^k$, using the same published parameters
629 (r, s, u, b) , the same transformation (Algorithm 2) is utilized
630 to generate its corresponding hashed vector $v' \in \{0, 1\}^{s \times ub}$.
631 Authentication can then be viewed as a score counting process
632 as follow: For each stripe ($i = 1, \dots, s$) in v and v' ,
633 a score count X_i is recorded if there is at least τ number
634 of colliding units. The total score count is simply $X = \sum_{i=1}^s X_i$.
635 Then, X is normalized and outputted as the similarity score,
636 i.e., $X/s \in [0, 1]$. The authentication mechanism, which takes
637 (w', r, s, u, b, τ) as the input, is presented as Algorithm 3.

D. Non-Linearity Derivation

638 Here, we derive the non-linearity property of our proposed
639 algorithm pair (TRANS, AUTH).
640

641 Let $d(w, w') = \frac{\arccos(w \cdot w')}{\pi}$ be the *dissimilarity* between w
642 and w' , which corresponds to their distance measured by the
643 angle between them. Therefore, $p = 1 - d(w, w')$ refers to
644 the *similarity* measure. By Lemma 1, we have the colliding
645 probability of single bit over a single stripe to be:

$$646 \Pr[f_i(r_i \cdot w) = f_i(r_i \cdot w')] = 1 - d(w, w') = p.$$

647 Recall that each unit consists of exactly b number of bits.
648 We shall see that for each single unit, it should come from
649 a (d_1, d_2, p_1^b, p_2^b) -sensitive family \mathcal{H}' (see Definition 2). It
650 follows that the colliding probability for one single unit is
651 equivalent to colliding exactly b number of bits. This can be
652 expressed as:

$$653 \Pr[f_i(r_i \cdot w) = f_i(r_i \cdot w') \mid i = 1, \dots, b] = p^b.$$

654 The probability of no unit colliding is $1 - p^b$. Let z be number
655 of colliding units. Clearly, z follows a binomial distribution
656 and we denote p_c the probability of *at least* τ number of
657 units colliding. Therefore,

$$658 p_c(u, b, \tau, p) = \Pr[z \geq \tau] = \sum_{i=\tau}^u \binom{u}{i} (p^b)^i (1 - p^b)^{u-i}. \quad (7)$$

659 By Eq (7) and Definition 2, each stripe is considered as an
660 $(d_1, d_2, p_{c1}, p_{c2})$ -sensitive LSH family \mathcal{H}'' constructed from
661 an (d_1, d_2, p_1^b, p_2^b) -sensitive LSH family \mathcal{H}' .

The derived p_c has direct effect on the final computed authentication score $X = \sum_{i=1}^s X_i$, where $X_i = 1$ if the i -th stripe has at least τ number of colliding units. Given all stripes are independent, then X should follow i.i.d with $\Pr[X_i = 1] = p_c$ and $\Pr[X_i = 0] = 1 - p_c$. Therefore we shall have the expected score count expressed as $\mathbb{E}[X] = sp_c$ and variance $\text{Var}(X) = s(p_c)(1 - p_c)$. Follows Eq (5), one shall notice that our proposed transformation offers well-defined number of stripe s which can be interpreted as the number of points over the hashed domain $\{0, 1\}^n$.

Note that the score count X is highly non-linear with respect to the original dissimilarity $d(w, w')$ measurement (see the functionality of p_c in Eq (7)). Fig. 2 depicts the non-linear relationship between the derived p_c and the input dissimilarity score $d(w, w')$. Observe that a larger number of bits b and τ would lead to a greater degree of non-linearity, where the gradient of the S -curve becomes steeper. Besides, a larger number of u promotes more colliding units. Therefore, the input templates with small dissimilarity $d(w, w')$ can easily attain overwhelming value for p_c (i.e., close to one). The argument above gives rise to our *correctness* claim for the genuine user with a higher value of τ .

VI. EXPERIMENTS AND EVALUATION

Experiments Set-up and Protocol: For input biometric templates, we adopt a pre-trained convolution neural network dedicated to face recognition, namely InsightFace [32]. InsightFace employs a loss function named additive angular margin loss for learning. With InsightFace that is pre-trained with MS-Celeb-1M, a face vector with a size of $k = 256$ can be obtained. Besides, we adopt the Labelled face in the wild (LFW) dataset [33], which consists of 7,701 images of 4,281 subjects. We follow the protocol outlined in [33], where a total number of 6,000 face pairs are divided into ten disjoint subsets for cross-validation. Each subset contains 3000 genuine pairs and 3000 impostor pairs, resulting in a total number of 3000 genuine matching scores and 3000 impostor matching scores. All the while, we only consider single set of random Gaussian vector (r_1, \dots, r_n) for random projection used in (TRANS, AUTH). Equal error rate (EER) is considered as the performance metric, which is the error rate when the false acceptance rate (FAR) and false rejection rate (FRR) are equal.

For attacks using Algorithm 1, for each impostor matching, we can conveniently set the distance between the hashed templates as $\varepsilon_0 = 1$. If such distance is at most $\lambda\varepsilon'$, Algorithm 1 will halt and stop in Step 4. Otherwise, Algorithm 1 will continue to minimize ε_0 . The minimization process intending to achieve $\varepsilon_0 \leq \lambda\varepsilon'$ for all impostor matching, yielding a total number of 3000 minimized dissimilarity score ε_0 , namely the KSA attack scores, for performance evaluation of the proposed KSA attack. All experiments are conducted by using PC with processor core i5-2.50 GHz with 8GB RAM, graphic card GTX 1050 Ti, and with MATLAB Ver. R2018a.

A. Evaluation of Proposed Attack on Bio-Hashing and LSH

We evaluate the proposed known sample attack in this section. Our attack focuses on Bio-hashing and conventional

LSH. In particular, for LSH, we refer to the randomized strategy in generating the hashed vector v . Note that the randomized strategy can be viewed as a special case of the recently proposed hashing scheme [10] when the output is in binary, i.e., $q = 2$.

Parameters Control: Among all the necessary inputs $(w^*, f(w), N, \varepsilon', \varepsilon, \lambda)$, there are only four parameters, namely, N, ε', λ , and m , to be adjusted. Here, we set $\varepsilon = 10/256$, $\lambda = 1/4$, and limiting $N = 800$. The value of $m = 7$ is chosen by computing $|\mathcal{S}| = |0.2178 - (-0.1978)|/2^{-8} = 106.4 \leq 2^7$ to get a set of values for \mathcal{S} over the range of $[-0.1978, 0.2178]$. Follow Eq (4), $|\mathcal{S}| \leq 2^7 < 2^8$. Considering the attack efficiency (see Claim 1, Eq (4)), the logarithm of the number of point can be found over the hashed domain's distribution $\mathcal{D}_f \in \{0, 1\}^n$ must be bounded at most $kh_2(\varepsilon) + m$. However, without proper designation of the transformation function, one could not assure the number of points over $\mathcal{D}_f \in \{0, 1\}^n$ will be at most $2^{\lfloor kh_2(\varepsilon) + m \rfloor} - 1$. This means if Eq (4) does not hold, then the derived KSA attack efficiency is obsoleted and no guarantee on $n(1 - \varepsilon)$ (follows Eq (6)) number of similar points can be found over \mathcal{D} by using Algorithm 1. Nevertheless, a straightforward way to ensure efficiency of Algorithm 1 is to reduce the hashed output length n . In light of this, our proposed attack is highly efficient for the conventional Bio-hashing and LSH with security relying on dimensional reduction, i.e., $n < k$. Thus, our evaluation only focuses on small n .

Fig. 3 and 4 depict the results for Bio-hashing and LSH for output length of $n = 40, 60, 80$, and 100. The average time taken for obtaining a single dissimilarity attack score is observed to be 1.942851 secs and 2.04068 for Bio-hashing and LSH, respectively. Our results show that for fixed parameter m and ε' , smaller output length would lead to better attacking result in the sense that the mean of the KSA attack scores follows closer to the mean of the genuine score distribution.

B. Performance Evaluation of Proposed Transformation and Authentication

This section presents the performance evaluation of (TRANS, AUTH). With reference to (TRANS, AUTH), there are four parameters to be considered, namely s, u, b and τ . Noting the proposed authentication algorithm AUTH records the number of stripes that have at least τ number of colliding units. The authentication procedure can be perceived as a similar point searching process, where the adversary is required to look for an arbitrary number of similar points, close to w s.t. $d(w, w_{e,i}) \leq \varepsilon$, where $\varepsilon > 0$ corresponding the minimum number of colliding units between different stripes (τ). It should be noted that the generated stripes are independent of each other. Thus a larger value of s will offer higher confidence to the final score count X , where $X \rightarrow sp_c$ should converge by law of large number.

Parameters Control: Recall that, $p_c(u, b, \tau, p)$ is parameterized by u, b , and τ where $p = 1 - d(w, w') = 1 - \frac{\arccos(w \cdot w')}{\pi}$ (follows Lemma 1). Let $\varepsilon = \frac{\arccos(w \cdot w')}{\pi}$. It is convenient to define the original dissimilarity follows $d(w, w') = \varepsilon$, which means $p_c(u, b, \tau, 1 - \varepsilon)$ is now a function of ε . The value of ε

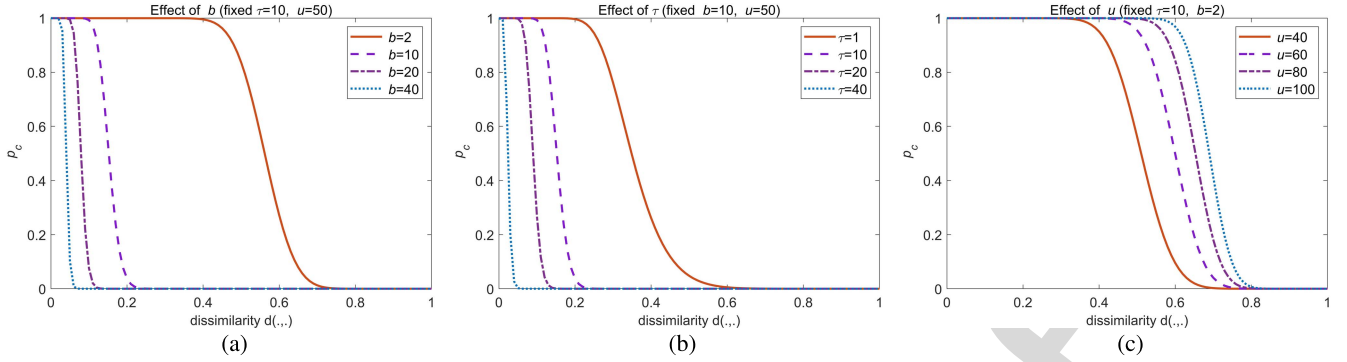


Fig. 2. Non-linearity relation parametrized by (a) $b = 5, 10, 15, 20$ (fixed $\tau = 5, u = 50$), and (b) $\tau = 5, 10, 15, 20$ (fixed $b = 10, u = 50$), and (c) $u = 40, 60, 80, 100$ (fixed $\tau = 10, b = 2$).

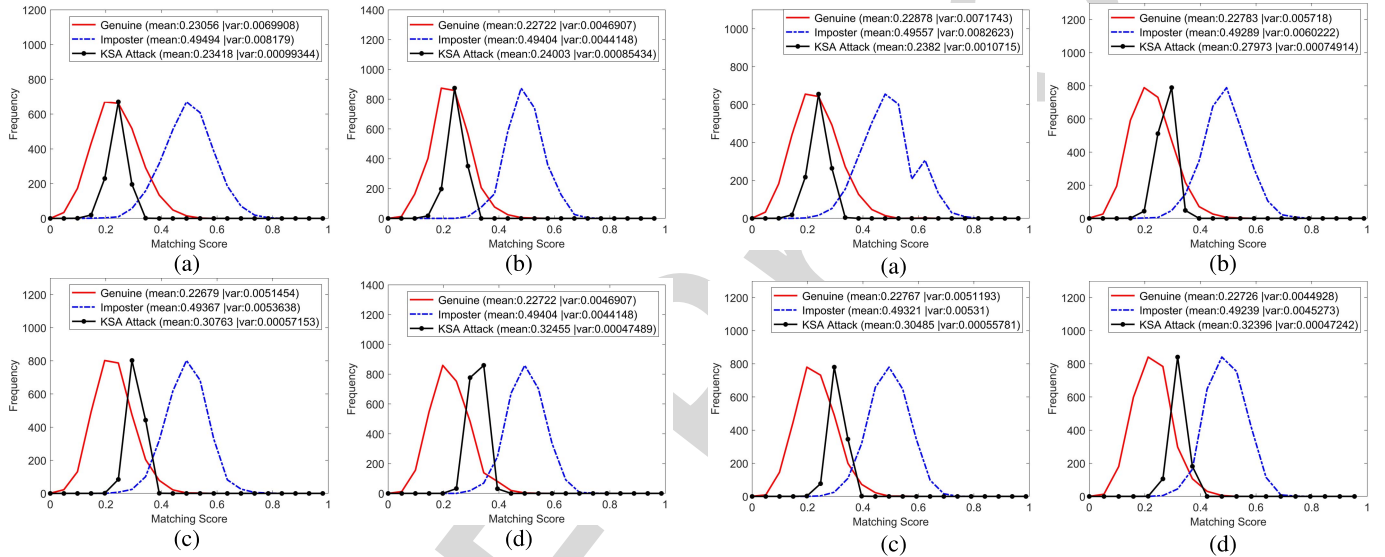


Fig. 3. Proposed KSA on Bio-hashing (a) $n = 40$, (b) $n = 60$, (c) $n = 80$, (d) $n = 100$.

Fig. 4. Proposed KSA on LSH (randomized strategy) (a) $n = 40$, (b) $n = 60$, (c) $n = 80$, (d) $n = 100$.

follows various distributions according to the input biometric template or input types, which is hard to predict. Therefore, choosing a set of values u, b, τ with optimal authentication performance and security for arbitrary value of $\varepsilon > 0$ will be our main interest. Based on Fig. 2, we know that the increment of b and τ would yield the same non-linearity effect by shifting the S-curve to the left with steeper gradient. On the other hand, the increment of u would shift the S-curve to the right with a steeper gradient. Therefore, we can choose b to be a constant to adjust the shifting of the S-curve to the left or right by increasing τ or u , respectively. Doing so would allow us to examine the non-linearity effect over the authentication performance and select the optimal parameter set corresponding to the original input distribution. All the while, we set $s = 50$ as the constant with different combinations for u, b , and τ . We set $u = 40, 60, 80, 100$, $\tau = 10, 12, 14, \dots, 30$, and repeat each setting with $b = 1, 2, 3$, and 4.

The authentication performance (in term of EER) for various settings of u, b and τ is recorded in Table I. The original performance of the input sample (without transformation) is recorded to be 0.73% of EER. The best authentication performance we could obtain after applying our proposal is

0.75% of EER. Clearly, this authentication performance is closely preserved by referring to its original one. Given $s = 50, b = 2$ and $u = 50$, the output score distributions for genuine and imposter authentication with different value of τ is shown in Fig. 5. In general, given (u, s, b) , a right choice of value τ could lead to large separation between the genuine and imposter score distributions. This scenario is mainly due to the non-linearity effect derived in Section V-D.

C. Security Evaluation of Proposed Transformation and Authentication

Here, we show how our proposal can resist against KSA. We adopt the newly proposed KSA (Algorithm 1) for our security evaluation of (TRANS, AUTH).

Recall that the matching (similarity) score outputted by AUTH (Algorithm 3) can be interpreted as the number of similar points or the amount of pair of stripes that have at least τ unit colliding. The applied KSA would have to *maximize* such a similarity score to compromise the system. In this sense, we have to reverse the stopping criteria of Algorithm 1

TABLE I
EER (%) RECORDED FOR DIFFERENT VALUE OF u , b , AND τ

$b=1$	$\tau = 10$	$\tau = 12$	$\tau = 14$	$\tau = 16$	$\tau = 18$	$\tau = 20$	$\tau = 22$	$\tau = 24$	$\tau = 26$	$\tau = 28$	$\tau = 30$
$u = 40$	1.45	1.18	1.03	0.93	0.92	1.08	1.82	3.93	14.53	31.85	44.60
$u = 60$	8.55	3.47	1.55	1.32	1.03	0.88	0.88	0.83	0.87	0.85	1.08
$u = 80$	28.03	17.42	9.88	5.07	2.47	1.42	1.08	0.93	0.80	0.88	0.87
$u = 100$	40.92	33.78	25.08	17.22	10.73	6.20	3.35	1.82	1.22	1.02	0.98
$b=2$	$\tau = 10$	$\tau = 12$	$\tau = 14$	$\tau = 16$	$\tau = 18$	$\tau = 20$	$\tau = 22$	$\tau = 24$	$\tau = 26$	$\tau = 28$	$\tau = 30$
$u = 40$	16.87	8.33	3.38	1.47	1.15	0.93	0.75	0.88	0.95	0.97	1.45
$u = 60$	43.42	37.38	29.77	21.32	13.75	8.23	4.57	2.28	1.22	1.00	0.88
$u = 80$	-	47.48	45.13	41.27	36.35	30.72	24.57	18.22	13.18	9.07	5.67
$u = 100$	-	-	48.83	47.82	46.23	43.72	40.03	36.27	31.70	26.53	21.80
$b=3$	$\tau = 10$	$\tau = 12$	$\tau = 14$	$\tau = 16$	$\tau = 18$	$\tau = 20$	$\tau = 22$	$\tau = 24$	$\tau = 26$	$\tau = 28$	$\tau = 30$
$u = 40$	41.67	33.85	23.97	14.68	7.93	3.40	1.63	1.22	0.98	0.87	0.83
$u = 60$	49.47	48.50	46.80	44.10	39.97	34.47	27.93	21.67	15.40	10.02	6.08
$u = 80$	-	-	49.58	49.15	48.37	47.12	45.37	42.52	39.30	34.88	30.42
$u = 100$	-	-	-	49.87	49.67	49.50	49.02	48.45	47.45	45.95	44.23
$b=4$	$\tau = 10$	$\tau = 12$	$\tau = 14$	$\tau = 16$	$\tau = 18$	$\tau = 20$	$\tau = 22$	$\tau = 24$	$\tau = 26$	$\tau = 28$	$\tau = 30$
$u = 40$	-	-	-	-	25.87	17.37	9.87	4.78	1.93	1.30	0.88
$u = 60$	-	-	-	-	47.78	46.08	43.58	39.30	34.77	29.12	23.18
$u = 80$	-	-	-	-	49.78	49.65	49.27	48.52	47.68	46.63	44.47
$u = 100$	-	-	-	-	-	-	-	-	-	-	-

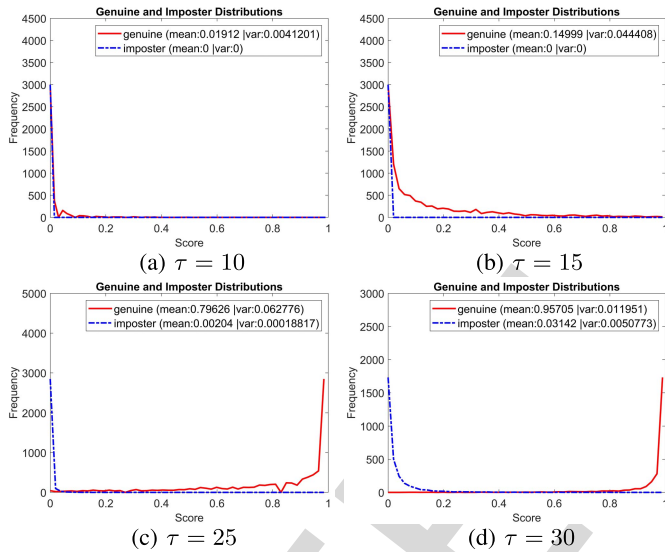


Fig. 5. Genuine and Imposter score distributions of proposed scheme with fixed $s = 50$, $b = 2$.

(i.e., line 11) and change it to $\varepsilon_0 < \varepsilon'/\lambda$. Doing that ensures the Algorithm 1 will output meaningful maximization result for all reference similarity scores ε_i (for $i = 1, \dots, N$) obtained by using AUTH.

Let $v = \text{TRANS}_{f \in \mathcal{H}_r}(w^*, r, s, u, b)$ be the transformed known sample. Our proposed KSA (Algorithm 1) can be adopted in an reverse manner with (TRANS, AUTH) described in Algorithm 4. Remark that incorporating (TRANS, AUTH) into Algorithm 4 explicitly allows the attacker to have complete knowledge over the designed system as follow the *Kerckhoffs's principle*.

Parameters Control: For evaluation, we use the same KSA setup for Bio-hashing and LSH with $N = 800$, $\varepsilon = 10/256$, $\lambda = 1/4$ and $m = 7$. The parameters considered for (TRANS, AUTH) are $s = 50$, and $b = 1$. The above setup

Algorithm 4 KSA for Proposed Scheme

```

1: function ATTACKTRANS, AUTH( $w^*, v, N, \varepsilon', \varepsilon, \lambda, s, u, b, \tau, \mathcal{S}$ )
2:    $\chi \leftarrow \{0, 1\}^k$ 
3:    $\sigma \leftarrow \mathcal{S}$   $\triangleright$  select  $\sigma$  from  $\mathcal{S}$  without repetition
4:   Set  $M = \sigma \cdot U$   $\triangleright U \in \mathbb{1}^k$  is vector of one
5:   for  $i = 1 : N$  do
6:      $e_i \leftarrow \chi$   $\triangleright$  select  $e_i \in \chi$  without repetition, where
        $\forall e_i \in \chi, \|e_i\| = \lfloor k\varepsilon \rfloor$ 
7:      $w_{e,i} = M \circ e_i + w^*$   $\triangleright$  where  $\circ$  denotes the
       Hadamard product of  $M$  and  $V_i$ 
8:     Compute  $s_i = \text{AUTH}(v, w_{e,i}, r, s, u, b, \tau)$  and output
       ( $s_1, s_2, \dots, s_N$ )
9:   end for
10:  Set  $\varepsilon_0 = \max(s_1, s_2, \dots, s_N)$ 
11:  if  $\varepsilon_0 < \lambda/\varepsilon'$  then
12:    Back to Step 3
13:  else
14:    Output  $w_{e,i}$  corresponds to  $\max(s_1, s_2, \dots, s_N)$ 
15:  end if
16: end function

```

is used for different output stripe size of $u = 40, 60, 80$, and 100 , and $\tau = 18, 24, 26$, and 30 with respect to their best authentication performance for $b = 1$ (see Table I). Fig. 6 depicted the result of KSA for (TRANS, AUTH) as described in Algorithm 4. As expected, the non-linearity property of (TRANS, AUTH) offers a strict constraint in looking for a similar point over the hashed domain. This can be explained with the function of $p_c(u, b, \tau, 1 - \varepsilon)$ (see Eq (7)) where only input with small cosine dissimilarity $\varepsilon = \frac{\arccos(w \cdot w')}{\pi}$ can show at least τ colliding units in the hashed domain with overwhelming probability. Therefore, the observed KSA attack scores follow the imposter score's distribution with small variance.

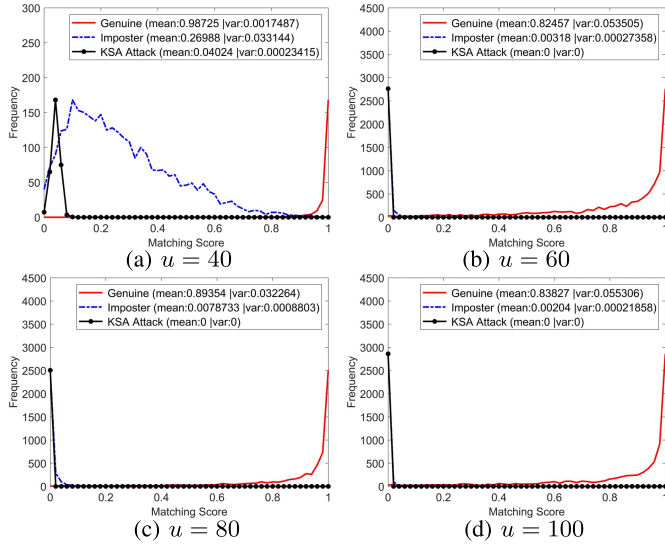


Fig. 6. Proposed KSA on algorithm pair (TRANS, AUTH).

D. Potential Security Attacks

In this subsection, we review the potential security attacks on BTP and demonstrate how our scheme resists against these attacks.

False Acceptance Attack: One of the major issues for BTP schemes relies on the false acceptance attack [34], [35]: a biometric system with high false acceptance rate is deemed as a low performing and insecure system and the transformed template stored in this system thus cannot be considered secure. False acceptance attack has been rigorously investigated in the recent works [10], [36], [37] to design a secure BTP scheme.

To be specific, let m_0 be the (minimum) entropy of a biometric source in a random distribution W . For two random k bits samples $(w, w^*) \in W$ derived from the same subject (genuine case), where w is the enrolled sample, and w^* is the query sample. To show meaningful security, the matching mechanism must only accept w^* given the hamming distance $\|w \oplus w^*\| \leq m_0$, which means that the original dissimilarity score $d(w, w^*) \leq \varepsilon \leq m_0/k$ must hold for any $\varepsilon \leq m_0/k$, where m_0/k denotes the (minimum) entropy rate of W . Otherwise, the system would accept another query sample $w' \in W'$ over a random distribution W' with dissimilarity score $d(w, w') = \varepsilon > m_0/k$, which leads to a false acceptance. It should be noted that a false acceptance would imply that the biometric source has lost all its entropy and shows no security, i.e., $m_0/k - \varepsilon < 0$.

A typical way to evaluate the false acceptance attack security is by measuring FAR. However, such measurement is crude in the sense that it does not consider the input distribution of the biometric source and cannot show meaningful security to any source that consists of a large number of errors. To further explain this, note that the FAR is depend upon the dissimilarity score of ε . Any source with a large number of errors will introduce a high dissimilarity score, which means the matcher that accepts w^* s.t. $d(w, w^*) \leq \varepsilon$ must set large ε to reduce FRR which subsequently increases

FAR. Biometric traits typically demonstrate “more error than entropy”, for instance, the human iris [38]. The human iris is believed to offer high entropy, i.e., $m_0 = 249$ bits. However the k bits binary template, namely Iriscodes, generated from human iris usually contains error ($k\varepsilon$) that is more than 249 bits, i.e., $k\varepsilon > m_0$.¹ Given above discussion, it is inevitable that a false acceptance is expected given any two Iriscodes (w, w') derived from different subjects with dissimilarity score $d(w, w') = \varepsilon > m_0/k$. Moreover, it is imprudent to believe that the distribution of the biometric source W can be modeled precisely, especially for high entropy source. The attacker might have higher computation power to model W and lead to lower attack complexity, i.e., a lower value of m_0 . Nevertheless, we can conveniently bound the entropy rate of distribution W follows $m_0/k \geq \varepsilon$ for all $w' \in W'$ that comes with a maximum dissimilarity score equal to ε . Since $m_0 \geq k\varepsilon$ is necessary to prevent a false acceptance given any sample $w' \in W'$, it follows that the false acceptance security can be claimed given the system knows the value of ε .

Based on the above reasoning, to show meaningful false acceptance security for larger class of biometric sources (including more error than entropy sources), it is desirable to design a BTP transformation as a function of the input distribution where the knowledge on the original dissimilarity score ε is perceived as a necessity. In fact, it is easy to verify that the proposed transformation and authentication algorithm pair (TRANS, AUTH) enjoys such property with the denoted p_c known as the probability of at least τ number of units colliding expressed as $p_c(u, b, \tau, p)$ where $p = 1 - d(w, w')$, and $d(w, w') = \varepsilon = \frac{\arccos(w \cdot w')}{\pi}$ corresponds to the original dissimilarity score (cosine dissimilarity) of the input samples (w, w') . Moreover, because the generated stripes (after transforming using TRANS) are independence to each other The output score X/s should asymptotically converge to p_c by law of large number (for value of $s \gg 1$). In other words, the relation in between p_c and $d(w, w')$ shown in Fig. 2 is asymptotically good for false acceptance security evaluation of (TRANS, AUTH).

Generally, by using *Bayes's theorem*, the relationship of the probability $\Pr[z \geq \tau] = p_c$ given the input dissimilarity score $d(w, w') \leq \varepsilon$ can be described as:

$$\Pr[z \geq \tau \mid d(w, w') \leq \varepsilon] = \frac{\Pr[z \geq \tau] \Pr[d(w, w') \leq \varepsilon \mid \Pr[z \geq \tau]]}{\Pr[d(w, w') \leq \varepsilon]}.$$

The term $\Pr[d(w, w') \leq \varepsilon \mid \Pr[z \geq \tau]]$ is the acceptance rate, i.e., a person is identified as a valid user. In reality, the person in performing the authentication should be random (either genuine user imposter), therefore we shall let $\Pr[d(w, w') \leq \varepsilon] = 0.5$ and $\Pr[d(w, w') \leq \varepsilon \mid \Pr[z \geq \tau]] = 0.5$, yielding

$$\Pr[z \geq \tau \mid d(w, w') \leq \varepsilon] = \Pr[z \geq \tau] = p_c. \quad (8)$$

It should be noted that Eq (8) reduces the worst-case scenario, with referring to the maximum value of ε , to the

¹We direct the interested reader to refer to [39], [40] [41] for more details regarding the issues on “more error than entropy” biometric sources.

931 average-case false acceptance security of (TRANS, AUTH) 983
 932 depending on the average selection of parameter u, τ, b with 984
 933 arbitrary value of $\varepsilon > 0$. Recall that we can bound the (mini- 985
 934 mum) entropy m_0 of the biometric sources of distribution W 986
 935 follows $m_0 \geq k\varepsilon$. In such a case, it is convenient to define 987
 936 $[k\varepsilon] = -\lceil \log(1/p_c) \rceil$, as the false acceptance complexity, 988
 937 which leads us to the following claim to show meaningful 989
 938 false acceptance security for large classes of biometric sources 990
 939 with (minimum) entropy at least equal to the false acceptance 991
 940 complexity.

941 *Claim 2:* ² Given any attacker is able to sample $w' \in W'$ 992
 942 over some random distribution $W' \in \mathbb{R}^k$ s.t. the original 993
 943 dissimilarity $d(w, w')$ is at most ε , where $w \in \mathbb{R}^k$ is the 994
 944 targeted attack biometric template. The average-case false 995
 945 acceptance security of (TRANS, AUTH) is $p_c(u, \tau, b, 1 - \varepsilon)$ 996
 946 for any $\varepsilon > 0$. In particular, the input distribution $W \in \mathbb{R}^k$ 997
 947 for all $w \in W$ must possess (minimum) entropy equal to 998
 948 $m_0 \geq k\varepsilon \geq [k\varepsilon] = -\lceil \log(1/p_c) \rceil$.

949 *Attack via Record Multiplicity (ARM):* ARM refers to a pri- 1000
 950 vacy attack, which utilized multiple compromised hashed tem- 1001
 951 plates with and without the associated information, i.e., helper 1002
 952 data, parameters, etc. to reconstruct the original biometric 1003
 953 template [42], [43]. For a biometric recognition system to 1004
 954 be useful, it should allow the user to enroll in multiple 1005
 955 applications. These enrolled templates shall store in different 1006
 956 data storage, which can be easily compromised and make 1007
 957 available to the third party. Because of this, ARM is conceived 1008
 958 as a highly practical attack given a large deployment of 1009
 959 biometric recognition systems.

960 In reality, to get access to the biometric system, potential 1010
 961 attackers need not invert the hashed template completely; 1011
 962 instead, only a close approximation of the original biometric 1012
 963 template is necessary and sufficient [29]. Hence, it is desirable 1013
 964 to analyze the ARM security in terms of the attack complexity 1014
 965 to reconstruct a fraction of the original template, which is 1015
 966 sufficient to get access to the system by using an arbitrary 1016
 967 number of the hashed templates.

968 To show that the proposed algorithm pair (TRANS, AUTH) 1017
 969 resist against the ARM, we can reduce ARM to false accep- 1018
 970 tance attack: for any random sample $w' \in W'$ efficiently 1019
 971 reconstructed via ARM, i.e., within polynomial time, that is 1020
 972 ε -close to the enrolled template w , the attacker can get access 1021
 973 into the system by a false acceptance in polynomial time. 1022
 974 The above statement clearly described that if the attacker 1023
 975 can launch a successful false acceptance attack, then he/she 1024
 976 can also launch a successful ARM attack efficiently if the 1025
 977 reconstruction of the sample w' can be done efficiently, i.e., in 1026
 978 polynomial time.

979 In fact, given the proposed KSA attack, we have demon- 1027
 980 strated that the sampling process for the noisy sample $w_{e,i} \in$ 1028
 981 \mathcal{D} where $d(w, w_{e,i}) \leq \varepsilon$ can be done in polynomial time 1029
 982 (see Section IV) by only using one known sample w^* 1030

²Note that the derived false acceptance complexity does not assert any computational assumption over the attacker site. In other words, we allow the attacker to have unlimited computation power to model the biometric input distribution W and assume he/she is able to sample a $w' \in W'$ from W' where $d(w, w') \leq \varepsilon$ holds under such information-theoretical (computationally unbounded) setting.

that is trivially obtained through self enrolment. Therefore, 983
 the proposed KSA attack can be considered as a more robust 984
 notion of ARM attack without the need for the attacker to 985
 compromise multiple template storages. Argued in this way, 986
 to show resistance against ARM, a non-linear DPT is desir- 987
 able, which can be accomplished using the proposed algorithm 988
 pair (TRANS, AUTH) for transformation and authentication. 989

Non-Linear to Linear Mapping on the DPT Curve: Here we 990
 also explore the possibility of any attacker could perform a 991
 mapping from the non-linear DPT curve to a more linear one 992
 (see Fig. 1), which leads to the dispute against a system that 993
 exhibits a non-linear DPT curve looking close to the optimal 994
 DPT need not be necessarily better in security as compared to 995
 the linear case. 996

To support the justification that a non-linear DPT offers 997
 better security guaranty, we first note that the knowledge 998
 of the non-linear DPT curve need not to be kept in secret. 999
 We also note that the proposed transformation and authen- 1000
 tication (TRANS, AUTH) functions are only useful when the 1001
 value of τ is known, means a proper value of τ must be 1002
 selected to show meaningful non-linear property in such a way 1003
 that the gap between the genuine and imposter distribution is 1004
 maximized. Therefore, any attacker and system provider must 1005
 know the DPT curve, i.e., the parameter set (u, τ, b) while 1006
 designing the biometric system. 1007

Since the mapping from a non-linear DPT curve to more 1008
 linear one implies the changes in the S-curve and its gradient, 1009
 which is parameterized by the parameters (u, τ, b) . In such a 1010
 case, mapping from non-linear DPT curve to linear is possible 1011
 if there are multiple systems, say q number, where a targeted 1012
 user has generated his/her biometric samples $(w_1, \dots, w_q) \in$ 1013
 W (e.g., generated from the user's face biometric) over a 1014
 random distribution W , and enrolled w_i into the i -th system. 1015
 Clearly, a non-linear mapping would succeed if one of the 1016
 available systems (among q) behaves a linear DPT curve. 1017
 On the contrary, such mapping can be avoided if all the 1018
 systems have a proper choice of (u, τ, b) that renders a 1019
 non-linear DPT curves. Doing this is necessary to ensure the 1020
 security of the biometric samples $(w_1, \dots, w_q) \in W$ to be 1021
 enrolled into different systems for personal authentication. 1022

E. Revocability and Unlinkability 1023

Revocability Evaluation: To evaluate the revocability of 1024
 the algorithm pair (TRANS, AUTH), we follow the same 1025
 protocol mentioned in Section VI (first paragraph) to generate 1026
 3000 mated-matching scores, which are the matching scores 1027
 between different hashed templates, generated using different 1028
 set of random Gaussian vectors (r_1, \dots, r_n) , over the *same* 1029
 subject. We evaluate the revocability of the algorithm pair 1030
 (TRANS, AUTH) under different values of $b = 1, 2, 3, 4$ with 1031
 respect to different parameter settings of (u, τ, b) that render 1032
 the lowest EER as tabulated in Table I. The genuine and 1033
 imposter scores' distributions (both involved in only single 1034
 set of random Gaussian vectors) are plotted together with 1035
 the mated-scores' distribution (involved 3000 different sets of 1036
 random Gaussian vectors) in a graph. Fig. 7 depicted four 1037
 different graphs of different parameter settings with constant 1038

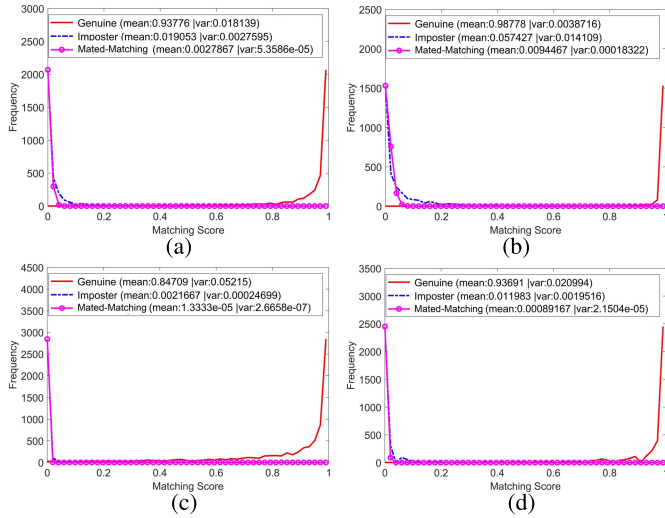


Fig. 7. Revocability evaluation: the graphs of the genuine, imposter, and mated-matching scores' distributions.

1039 $s = 50$: (a) $u = 80, \tau = 26, b = 1$, (b) $u = 40, \tau = 22, b = 2$,
 1040 (c) $u = 40, \tau = 30, b = 3$, and (d) $u = 40, \tau = 30, b = 4$
 1041 respectively. Note that a large degree of overlapping occurs
 1042 between the imposter and mated-matching scores' distributions
 1043 are observed. This result implies that the refreshed templates
 1044 are sufficiently distinctive, albeit they are generated from the
 1045 same subject. Indeed, the new transformed sample generated
 1046 with a different set of random Gaussian vectors acts as an
 1047 'imposter' to the old one since they are uncorrelated. This
 1048 verifies the revocability of (TRANS, AUTH) in generating new
 1049 templates to replace the old one with a different set of random
 1050 Gaussian vectors.

1051 *Unlinkability Evaluation:* To evaluate the unlinkability of
 1052 the algorithm pair (TRANS, AUTH), we adopted the framework
 1053 proposed by Gomez *et al.* [44]. Let $\Pr[s | M_s]$ be the prob-
 1054 ability densities of a given similarity score $s \in [0, 1]$ that
 1055 belongs mated-matching group. On contrary, let $\Pr[s | M'_s]$
 1056 denote the probability densities of score s belongs to the
 1057 non-mated group M'_s : the matching scores generated with
 1058 (TRANS, AUTH) over different hashed templates generated
 1059 using different set of random Gaussian vector (r_1, \dots, r_n)
 1060 under the *different* subjects. The unlinkability property can
 1061 be characterized by the local linkability defined as $D(s) =$
 1062 $2 \frac{\omega LR(s)}{1 + \omega LR(s)} - 1$ given $\omega LR(s) = \Pr[s | M_s] / \Pr[s | M'_s] > 1$,
 1063 where $LR(s)$ is the likelihood ratio and $\omega = \Pr[M_s] / \Pr[M'_s]$
 1064 which can be conveniently set equal to one. The system's
 1065 linkability is then defined as $D_{sys} = \int D(s) \Pr[s | M_s] ds$.
 1066 Specifically, $D_{sys} \in [0, 1]$ and the system is completely
 1067 linkable given $D_{sys} = 1$. Therefore, to attain unlinkability of
 1068 a BTP scheme, it is desirable to show that D_{sys} is negligible
 1069 small. Referring to the same parameter settings in revocability
 1070 evaluation, Fig. 8 depicted four different graphs, each contains
 1071 3000 mated-matching scores and 3000 non-mated matching
 1072 scores. The results show that the mated and non-mated scores'
 1073 distributions are significant overlapping (for all four graphs)
 1074 with small value of D_{sys} . Therefore we assert that the algo-
 1075 rithm pair (TRANS, AUTH) supports unlinkability.

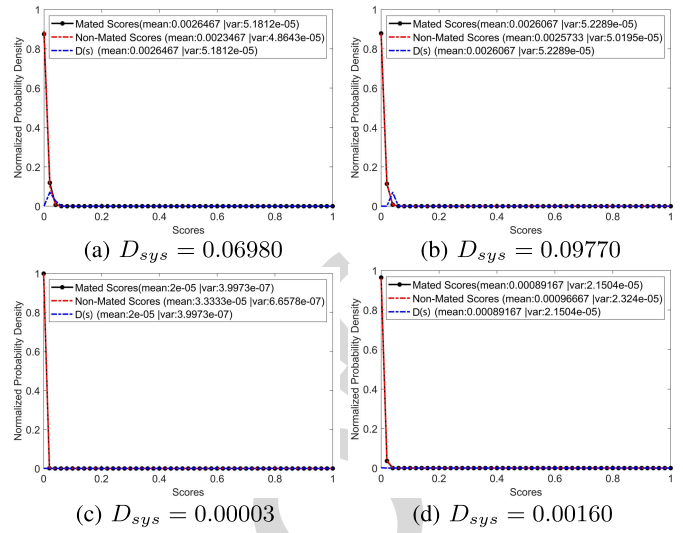


Fig. 8. Unlinkability evaluation: the graphs of the mated-matching and non-mated matching scores' distributions.

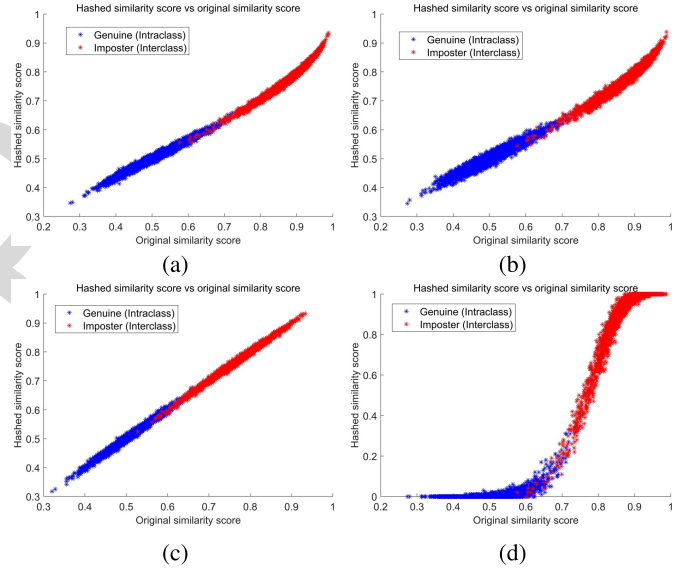


Fig. 9. Comparison of the non-linearity DPT curve of proposed technique to (a) Bio-hashing, (b) IOM-hashing, (c) IFO-hashing, (d) proposed.

F. Comparison With Existing Approaches

1076
 1077 *Non-Linearity:* We compare our proposal (best performance
 1078 setting $s = 50, u = 40, b = 2, \tau = 22$) with the best per-
 1079 formance setting for Bio-hashing [4] (0.73% EER) and other
 1080 notable LSH scheme such as Index of Max hashing (IOM) [10]
 1081 (0.75% EER) and Indexing First One hashing (IFO) [11]
 1082 (1.38% EER). Fig. 9 depicted the comparison results. Our
 1083 proposal yields a highly non-linear relationship between the
 1084 original similarity scores versus the hashed similarity scores
 1085 in comparison to others.

1086 *Decision Environment:* The degree that one can confidently
 1087 decide whether the observed sample belongs to the genu-
 1088 ine (red) or imposter distribution (blue) is as shown in Fig. 5.

1089 Note that the error rate is proportional to the overl-
 1090 apped region between the genuine and imposter distributions.

1091 The decision environment for dual distributions reveals the
 1092 extent to which the genuine and imposter distribution can be
 1093 separated, thus determining how reliable the decision can be
 1094 made for individual authentication. Following the works by
 1095 Daugman [38], for two-choice decision task such as biometric
 1096 decision making, we can measure the separation of these two
 1097 distributions by their decidability d' defined in Eq (9), where
 1098 (μ_1, μ_2) and (σ_1, σ_2) refer to the two means and standard
 1099 deviation, respectively, of two different distributions.

$$1100 \quad d' = \frac{|\mu_1 - \mu_2|}{\sqrt{(\sigma_1^2 + \sigma_2^2)/2}}. \quad (9)$$

1101 The measure of d' is independent w.r.t. any acceptance thresh-
 1102 old. Instead, it reflects the cost for the system in reducing
 1103 the FAR via increasing FRR, or vice versa. Therefore, one
 1104 can succinctly use d' to calibrate the performance of every
 1105 biometric technology.

1106 Based on the studies in the previous Section II-C, to opti-
 1107 mize the mutual information leakage, the best is to hope for
 1108 achieving $\mathbb{E}[D_I] \rightarrow 1$ and $\mathbb{E}[D_g] \rightarrow 0$ with $\text{Var}(D_I)$ is
 1109 minimized. Therefore the gap between the distribution of the
 1110 interclass's distance and the distribution of the intraclass's
 1111 distance must be large enough.

1112 Note that a large gap between the distribution of the inter-
 1113 class's distance D_I (imposter distribution) and the distribution
 1114 of the intraclass's distance D_g (genuine distribution) implies
 1115 high decidability. More precisely, the decidability can be
 1116 described in term of $\mathbb{E}[D_I]$, $\mathbb{E}[D_g]$, $\text{Var}(D_I)$, and $\text{Var}(D_g)$
 1117 as $d' = \frac{|\mathbb{E}[D_I] - \mathbb{E}[D_g]|}{\sqrt{(\text{Var}(D_I) + \text{Var}(D_g))/2}}$. Since our optimization goal is to
 1118 minimize $\text{Var}(D_I)$ while keeping $\mathbb{E}[D_I] \rightarrow 1$ and $\mathbb{E}[D_g] \rightarrow$
 1119 0 . Therefore, such goal can be achieved by maximizing d' ,
 1120 which suggests a steeper gradient of the S-curve (highly non-
 1121 linearity) depicted in Fig. 1.

1122 Follow Fig. 5 (d), the computed decidability in our proposal
 1123 is 10.03. Besides, in our experiment, the measured d' for Bio-
 1124 hashing, IOM-hashing and IFO-hashing are 4.92, 5.32, and
 1125 2.52 respectively. The comparison on the recorded d' with
 1126 the recent proposed state-of-the-art BTP schemes [37], [45],
 1127 [36], [46], [47] is tabulated in Table II. Such comparison
 1128 is performed under the scenario when the user and attacker
 1129 have complete knowledge on the transformation function and
 1130 parameters used.

1131 Observe that our proposal can achieve a higher d' value
 1132 among most of the state-of-the-art BTP schemes. The achiev-
 1133 able $d' = 10.03$ is higher as compared to a non-ideal (crossed
 1134 platform) iris recognition system, which is 7.3 as reported
 1135 in [38]. It is also worth highlighting that the non-linearity
 1136 between the original similarity scores and the hashed similarity
 1137 scores can be strengthened by increasing the parameter u
 1138 with a proper selection of b and τ , which promotes the
 1139 maximization of the system's decidability d' . This is in our
 1140 favor of reducing the mutual information leakage (i.e., min-
 1141 imizing $\text{Var}(D_I)$) to show resistance against the DPT based
 1142 attacks, while maintaining a good recognition utility (keeping
 1143 $\mathbb{E}[D_g] \rightarrow 0$) as discussed in Section II.

1144 Last but not least, we examine the performance in terms
 1145 of FRR against FAR for various distance preserving hashing

TABLE II
 COMPARISON OF SYSTEM'S DECIDABILITY WITH OTHER EXISTING BTP
 SCHEMES BASED ON THEIR RECORDED (HIGHEST) d'

BTP Schemes	Decidability, d'
Bio-hashing [6] (for fingerprint)	4.92
IOM-hashing [10] (for fingerprint)	5.34
IFO-hashing [11] (for human iris)	5.67
Kaur et al. [37] (for fingervein, palmvein, and face)	9.74
Sadhya et al. [45] (for human iris)	2.39
Qiu et al. [46] (for palm print)	9.20
Walia et al. [47] (for human iris and pericular feature)	13.47
Walia et al. [36] (for human iris, fingerprint, and face)	5.38
Proposed (for face)	10.03

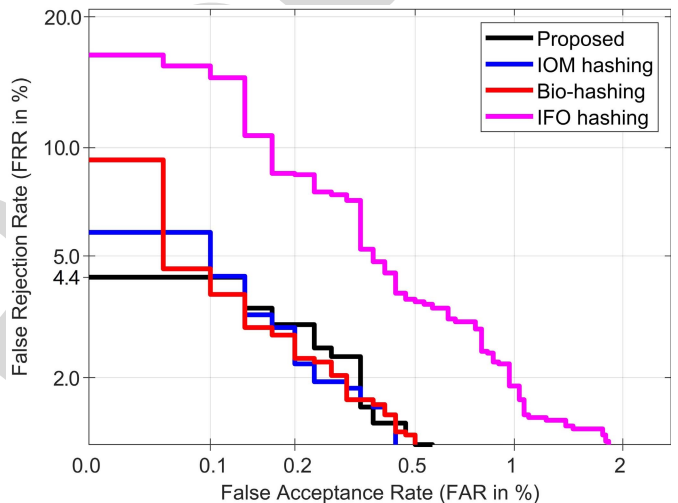


Fig. 10. DET curves for various distance preserving hashing BTP schemes.

BTP schemes using the detection error trade-off (DET) curve, as shown in Fig. 10. As it can be observed, the proposed scheme achieved superior performance with the lowest FRR (4.4%) at zero FAR (0%). On average, this implies only about 4 rejections (i.e. 4.4% FRR) over 100 trials of a genuine user to be authenticated, while no unauthorized persons is accepted incorrectly (i.e. zero FAR). This result suggests that the proposed scheme is feasible in real application scenarios.

VII. CONCLUSION

In this work, we explore the vulnerability in the existing distance-preserving hashing BTP scheme. We demonstrate an efficient security attack, i.e., KSA, for distance-preserving hashing BTP. Our results show that the potential attacker can model the input samples' distribution and obtain the pre-images of the enrolled biometric sample. This scenario is worse when the hash function's output length is set to very small, that is preferred by most distance-preserving hashing BTP schemes for irreversibility purpose via dimension reduction. We also provide some discussions over the mutual

information leakage due to the published distance-preserving hashing BTP. Noticing the non-linearity relationship between the input distance and hashed distance is crucial to provide authenticity for similar subjects while avoiding false matching for distinct subjects. The above reasons motivated our work on a pair of transformation and authentication algorithm (TRANS, AUTH) to give a highly non-linear relationship between the input and hashed domains. The algorithm pair (TRANS, AUTH) offers efficiency and simplicity for fast and secure authentication with a biometric template (we used face vector in our experiment). Most importantly, it showed resistance against KSA for polynomial-time bounded attackers under known distribution \mathcal{D} scenario and satisfied the four criteria to be used as a secure BTP scheme.

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