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Biometric Masterkeys

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Abstract

Biometric authentication is used to secure digital or physical access. Such an authentication system uses a biometric database, where data are sometimes protected by cancelable transformations. This paper introduces the notion of biometric masterkeys. A masterkey is a feature vector such that the corresponding template matches with a significant number of templates stored in a cancelable biometric database. Such a masterkey is directly researched from a cancelable biometric database, but we also investigate another scenario in which the masterkey is fixed before the creation of the cancelable biometric database, providing additional access rights in the system for the masterkey's owner. Experimental results on the fingerprint database FVC and the face image database LFW show the effectiveness and the efficiency of such masterkeys in both scenarios. In particular, from any given feature vector, we are able to construct a cancelable database, for which the biometric template matches with all the templates of the database.

Keywords— Biometric Authentication, Cancelable Biometric Transformation, Masterkey

1 Introduction

Nowadays, biometrics is more and more used in many applications, from access control on smartphones to payment on the Internet. Biometrics is generally based on physical characteristics such as fingerprints, face, iris or voice. Several ways are used for biometric data protection, as cryptography or cancelable biometric transformations. These transformations should respect several security properties as revocability, unlinkability and non-invertibility while maintaining good performance. They use a secret parameter, called token or seed, but the most used security model considers that this secret can be known by an attacker (stolen token model).

During the enrollment step, one or several biometric data is transformed into a biometric template and stored in a database with biometric templates of other people. During the authentication step, a person sends a biometric data and the seed to the matcher, the corresponding template is computed and compared with templates of the database. If the matching is correct, the person is authenticated.

The performance of the cancelable scheme is expected close to the original scheme without transformations, which means similar biometric data are mapped to similar templates with high probability.

In this paper, we are interested in the creation of feature vectors for which the corresponding templates match with the greatest number of templates of the cancelable database. Such feature vectors, called masterkeys, can be used to attack the system, in the stolen token model, or provide some additional access rights for the system administrator. In this case, the cancelable transformation is used not for the security of biometric data, but for the creation of efficient masterkeys, by considering the secret seed as a public salt. More precisely, masterkeys are computed in the two following scenarios:

- The cancelable database and the corresponding seeds are known. The goal is to create a synthetic feature vector for which the corresponding templates, computed with the seeds, matches with the maximal number of templates of the database.
- The biometric database is known, and a feature vector is fixed. The goal is to find the seeds for which the corresponding templates, computed with the seeds, match with the maximal number of templates, computed with the same seeds.

Experiments use a random projection, with or without a binarization step, for transformation, applied on two biometric databases: the FVC database (fingerprints) and the LFW database (face images).

In the second scenario, a brute force strategy is used for the computation of seeds, providing successful masterkeys for all the biometric database, with no significant performance degradation in these cancelable biometric databases. This second scenario proposes a new paradigm in biometric authentication, with the creation of biometric databases with specific access rights. It can also be seen as a backdoor placed in the system. Seeds are also computed for a set of masterkeys's candidate, providing partial masterkeys for other feature vectors.

Section 2 proposes generic definitions on biometric systems and presents the works close to this paper. Section 3 formalizes the concept of masterkey with several definitions on the effectiveness of such masterkeys. Experiments and results are given in Section 4, whereas conclusion and future works are in Section 5.

2 Definitions and related works

A biometric authentication scheme is realized into two phases. One (or several) feature vector is extracted from a biometric data during the enrollment process and is stored into a biometric database. During the authentication phase, a second feature vector is extracted from a biometric data and these two vectors are compared.

Definition 2.1. Let (\mathcal{M}_A, D_A) be a metric space. A biometric authentication scheme for two biometric data b and b' is a pair of algorithms (E, V) , where

- E takes biometric data b as input, and returns a feature vector $x \in \mathcal{M}_A$.
- V takes two feature vectors $x = E(b)$, $x' = E(b')$, and a threshold τ_A as input, and returns *True* if $D_A(x, x') < \tau_A$, and *False* otherwise.

It is expected that feature vectors x and x' of the same individual, extracted from two measurements are sufficiently close to verify $D_A(x, x') < \tau_A$. This paper uses the Euclidean distance for D_A , defined for feature vectors $x, x' \in \mathcal{M}_A = \mathbb{R}^N$ by:

$$D_A(x, x') = \sqrt{\sum_{i=1}^N (x_i - x'_i)^2}.$$

Definition 2.2. Let $B = \{x_i\}_{i=1, \dots, n}$ be a biometric database, composed of feature vectors. A biometric authentication scheme for B is an algorithm that takes a feature vector x and a threshold τ_A as inputs and returns *True* if $\exists i$ between 1 and n such that $V(x, x_i, \tau_A)$ returns *True* and *False* otherwise. In the first case, x is successfully authenticated by x_i .

The quality of a biometric database is estimated with two rates: the False Match Rate (FMR) that provides the percentage of impostors authenticated by the system and the False Non Match Rate (FNMR) that provides the percentage of genuine peoples rejected by the system. These rates depend on τ_A and in case of equality these rates correspond to the Equal Error Rate (EER).

A biometric database contains some feature vectors that strongly influence these indicators. Doddington et al. [9] sorted them in 4 categories: sheep, goats, lambs and wolves, where wolves are able to usurp many users, causing false acceptances. These individuals appear to have generic characteristics. Similarly, Yager et al. [41] described 4 categories of animals representing the relationship between genuine and impostor match scores: worms, chameleons, phantoms and doves, where chameleons combine both high genuine and impostor match scores. In these categories, chameleons obtain scores belonging to the first quarter of the best scores.

Ine et al. defined a wolf as a feature vector that has a successful authentication probability greater than the FMR and evaluate the security of a given database with the notion of Wolf Attack Probability (WAP) in [36]. Countermeasures against this attack is investigated by Inuma et al. in [15] and tested on fingerprints by Murakami et al. in [20]. Wolf attacks have been realized on the voice by Okhi et al. in [24], then by Ohki and Otsuka [25].

Recently, Roy et al. investigated masterprints, partial fingerprints that usurp a large number of users [29] in a multi-enrollment process. They worked with small sensors of smartphones which acquire a lot of partial minutiae-based feature vectors. It was later improved with machine learning based approaches in [31, 30, 4] and recently applied on face recognition in [23].

For security reasons, feature vectors are not always directly stored in the database, but are used as input of a cancelable biometric transformation. These transformations were first proposed by Ratha et al. for face recognition [27]. There are many works on cancelable transformations, as presented in the surveys [28, 22] on biometric templates protection.

Definition 2.3. Let \mathcal{K} be a token (seed) space and (\mathcal{M}_B, D_B) be a metric space. A cancelable biometric scheme is a set of algorithms $(\mathcal{T}, \mathcal{V})$, where

- \mathcal{T} takes a secret seed $s \in \mathcal{K}$, and a feature vector $x \in \mathcal{M}_A$ as input, and returns a biometric template $u = \mathcal{T}(s, x) \in \mathcal{M}_B$.
- \mathcal{V} takes two biometric templates $u = \mathcal{T}(s, x)$, $u' = \mathcal{T}(s, x')$, and a threshold τ_B as input, and returns *True* if $D_B(u, u') < \tau_B$, and *False* otherwise.

Definition 2.4. Let $D = \{u_i\}_{i=1,\dots,n}$ be a cancelable biometric database, composed of biometric templates $u_i = \mathcal{T}(s_i, x_i)$. A cancelable biometric authentication scheme for D is an algorithm that takes a biometric template $u = \mathcal{T}(s, x)$ and a threshold τ_B as inputs and returns *True* if $\exists i$ between 1 and n such that $s = s_i$ and $\mathcal{V}(u, \mathcal{T}(s_i, x_i), \tau_B)$ returns *True* and *False* otherwise. In the first case, x is successfully authenticated by x_i .

It is expected that the cancelable biometric transformation \mathcal{T} does not significantly decrease the performance of the original biometric system, in terms of EER. This paper uses the Hamming distance for D_B , defined for biometric templates $u, u' \in \mathcal{M}_B = \{0, 1\}^M$ by:

$$D_B(u, u') = \sum_{i=1}^M u_i \oplus u'_i,$$

where \oplus is exclusive or (xor) bitwise operator.

Cancelable biometric transformations are generally based on locality sensitive hashing [5, 2, 39] or robust perceptual hashing [38, 37], ensuring the performance of the transformation. The transformations used in this paper are based on random projection, possibly with a binarization step. These cancelable transformations were first proposed in [34, 33] with the biohashing algorithm. Other projections have been later proposed, as in [12, 26, 40].

Let M_s be a real matrix with N rows and M columns, generated pseudo-randomly from the random seed s , x a feature vector of size N and $D : \mathbb{R}^M \rightarrow \{0, 1\}^M$ defined by $D(t_1, \dots, t_M) = (u_1, \dots, u_M)$ where

$$u_i = \begin{cases} 0 & \text{if } t_i < 0 \\ 1 & \text{if } t_i \geq 0 \end{cases}$$

In this case, the cancelable transformation \mathcal{T} is defined by $\mathcal{T}(x, s) = D(xM_s)$. In the biohashing algorithm, the pseudorandom matrix M_s is orthonormalized with the Gram-Schmidt algorithm.

The security of a cancelable biometric scheme is evaluated on several attack models, generally in the stolen token attack model, which considers that the token s is known by the attacker.

Definition 2.5. Let $x \in \mathcal{M}_A$ be a feature vector, $u = \mathcal{T}(s, x) \in \mathcal{M}_B$ is a biometric template, computed from a seed s and τ_A is a threshold. A nearby-feature preimage of u with respect to s is a feature vector x^* such that $V(x, x^*, \tau_A) = \text{True}$.

There are several methods for the construction of nearby-feature preimages. Genetic algorithms are a generic strategy for this, used in the case of biohashing on fingerprints in [17], in the iris case in [13], in the case of minutiae templates in [32] or recently on several transformations in [10]. A genetic algorithm is a set of operators on a population, depending on a fitness function. At each step, the population is updated with three operators: selection, crossing-over and mutation. Selection chooses the best subpart of the population. Crossing-over generates new individuals in the population from the selected population. Mutation modifies the new individuals generated during crossing-over. In the case of cancelable biometric transformations, individuals are candidates for masterkey and the fitness function

is defined by the distance D_B between the corresponding template and a target template.

Nearby-feature preimages can also be constructed using a specific attack on the transformation. For example, random projection based schemes are vulnerable to linear programming approaches [21, 11, 35].

3 Biometric masterkeys

A biometric masterkey x is a synthetic feature vector such that the corresponding biometric template u is close to several biometric templates in the database. The first part of this section is a generalization of concepts of the previous section (wolves, masterprints) to cancelable biometric database. The second part proposes an alternative by constructing a cancelable biometric database that matches with a given masterkey. In this case, the cancelable transformation is introduced to provide such masterkeys efficiently.

Definition 3.1. Let $D = \{u_i\}_{i=1,\dots,n}$ be a cancelable biometric database and τ_B a threshold. x is a masterkey for D , by respect to τ_B , if $\forall i$ between 1 and n , $\mathcal{V}(\mathcal{T}(s_i, x), \mathcal{T}(s_i, x_i), \tau_B) = True$, with $\mathcal{T}(s_i, x_i) = u_i$.

Obviously, x is a masterkey for the database $\{\mathcal{T}(s, x)\}$, but the research of a masterkey for a large database is not necessarily an easy task. A less restrictive goal is the research of a minimal number of masterkeys such that all templates of the database are close to at least one template corresponding to one masterkey.

Definition 3.2. Let $D = \{u_i\}_{i=1,\dots,n}$ be a cancelable biometric database and τ_B a threshold. D is said covered by a set of r masterkeys $\{x^1, \dots, x^r\}$ by respect to τ_B if $\forall i$ between 1 and n , $\exists k$ between 1 and r such that $\mathcal{V}(\mathcal{T}(s_i, x^k), \mathcal{T}(s_i, x_i), \tau_B) = True$.

The minimum number R such that D is covered by a set of R masterkeys is called optimal dictionary size.

In the previous definition, each masterkey $x_i \in \{x_1, \dots, x_r\}$ is a masterkey for a subset $D_i \subset D$ and we have $\cup_{i=1}^r D_i = D$. Nevertheless, the number of templates in each subset D_i is generally different.

Definition 3.3. A cancelable biometric database $D = \{u_i\}_{i=1,\dots,n}$ is said ϵ -covered by a masterkey x , with $0 < \epsilon \leq 1$ if there exists a subset D' of D of ϵn persons such that x is a masterkey for D' . The optimal coverage percentage of D is the maximal number E such that D is E -covered by a masterkey $x \in \mathcal{M}_A$.

Such a set of masterkeys can be used for attacks on the cancelable biometric database, similarly to the work of Roy et al. on minutiae [29], called dictionary attack, using a set of carefully chosen masterkeys. Nevertheless these masterkeys could provide other applications. For example, a masterkey could be used for a system of delegation of biometric authentication, with the possibility for one person to be authenticated as herself and also as other person, similarly to proxy signatures [19] or group signatures [6] in cryptography.

A second approach of the biometric masterkey problem is the construction of a cancelable biometric database from a feature vector x and n feature vectors

extracted from n peoples, such that x is a masterkey for the cancelable database. It means that, in this second approach, the seeds used by peoples are constructed, with the knowledge of x , contrary to the previous approach.

Definition 3.4. Let x be a feature vector, τ_B be a threshold, and $B = \{x_i\}_{i=1,\dots,n}$ be a biometric database. A cancelable biometric database D is said compliant with x by respect to τ_B if there exists s_1, \dots, s_n such that $D = \{\mathcal{T}(s_i, x_i)\}$ and x is a masterkey for D by respect to τ_B .

This second approach uses not the cancelable biometric transformation for security but uses it for the construction of masterkeys. It makes possible to adjust the choice of seeds to allow super access, i.e., a vector usurping the entire base. This can allow an administrator to have the same access as its users without adding another authentication channel. If an insecure transformation is used, an additional security layer should be added in the template storage.

It can also allow an attacker active in the enrollment phase to build a backdoor in the authentication system, without adding suspicious code or making the database dubious, as in the following definition.

Definition 3.5. Let $B = \{x_i\}_{i=1,\dots,n}$ a biometric database and $D = \{\mathcal{T}(s_i, x_i)\}$ a cancelable biometric database compliant with a masterkey x . Then x is a backdoor if there exists no polynomial algorithm that distinguishes $s_1, \mathcal{T}(x_1, s_1), \dots, s_n, \mathcal{T}(x_n, s_n)$ from $s'_1, \mathcal{T}(x_1, s'_1), \dots, s'_n, \mathcal{T}(x_n, s'_n)$, where s'_1, \dots, s'_n are randomly generated from the set of seeds (x is unknown).

In this paragraph, we consider the theoretical complexity to find masterkeys. We suppose that the metric space (\mathcal{M}_B, D_B) is $\{0, 1\}^M$ with the Hamming distance and that the biometric transformation \mathcal{T} is pseudorandom. Thus, given a biometric template u , a feature vector x and a threshold τ , the probability p that the distance $D_B(\mathcal{T}(x, s), u) < \tau$ for a random seed s is $p = \frac{1}{2^M} \sum_{i=0}^{\tau-1} \binom{M}{i}$. Let $D = \{u_i\}_{i=1,\dots,n}$ be a cancelable biometric database of n binary templates. A feature vector x , such that D is ϵ -covered by x , is expected after $1/p^{\epsilon n}$ trials. Let $B = \{x_i\}_{i=1,\dots,n}$ be a biometric database of n feature vectors and x a feature vector. A set of n seeds s_1, \dots, s_n , such that the corresponding cancelable biometric database D is compliant with x (Definition 3.4) is expected after n/p trials. Thus, the research of a masterkey given a biometric database is clearly easier than given a cancelable database.

4 Experiments

Effectiveness of masterkeys research is investigated on the fingerprint database FVC and the face database LFW. All experiments are processed on a Dell Latitude 7400 laptop with an Intel® Core™ i7-8665U CPU @ 1.90 GHz quad-core processor and 16 Gb of RAM, using python for the first part and C for the second one.

4.1 Biometric Databases

The first biometric database is the FVC2002 database [18], which contains $t = 8$ biometric images of $n = 100$ peoples obtained from fingerprints. The second one is the sub LFW database [14] used in Dong et al. experiments [10], which contains $t =$

10 biometric images of $n = 158$ peoples obtained from face pictures. This database is noted LFW10 in this section. A third database, named LFW8, is extracted from LFW10 by taking the first 100 peoples, with the first 8 biometric images, for comparison with the FVC2002 database.

Feature vectors are extracted from FVC using Gabor filters [3]. Each biometric feature vector is composed of $N = 512$ real values of 64 bits and the EER of the biometric database is 10% with a threshold $\tau_A = 240.7$. Feature vectors extracted from LFW are obtained using the deep network InsightFace [8]. Each biometric feature vector is composed of $n = 512$ real values of 64 bits and the EER of the biometric database is 0.2% with a threshold $\tau_A = 1.227$.

4.2 Masterkeys from Cancelable Biometric Database

The cancelable biometric transformation used in this subsection is the biohashing algorithm, mapping \mathbb{R}^N into $\{0, 1\}^M$ where $M = 128$, described in Section 2. The binary size of the seed is 128 bits. After transformation the EER of the cancelable biometric database is around 16.5% with a threshold $\tau_B = 17$ for FVC2002 and around 1.9% with a threshold $\tau_B = 51$ for LFW10 and LFW8.

The research of a masterkey, as presented in Definition 3.1, from a cancelable biometric database uses genetic algorithm where the fitness function is not the number of people who are authenticated by the masterkey, because it does not provide the best results. Two other fitness functions have been investigated, the first one based on the average of the minimal Hamming distance obtained for each person and the second one based on the sum of the minimal Hamming distance of not authenticated peoples by the masterkey. The second fitness function (*sum*) provides the best results on both databases and is used in next experiments.

We only consider the first biometric template for each person of the cancelable biometric database during the evaluation of the best optimal coverage percentage and for the best optimal dictionary size.

Table 1 gives the best optimal coverage percentage (OCP), as described in Definition 3.3, and the best optimal dictionary size (ODS), as described in Definition 3.2. For both cancelable biometric databases, we use thresholds τ_B at EER.

db	OCP	ODS
FVC	73	5
LFW8	21	12
LFW10	15.2	18

Table 1: Optimal coverage percentage / Optimal dictionary size

The genetic algorithm is processed on a population of 200 peoples during 500 iterations. Figure 1 shows that coverage does not increase from 350 iterations.

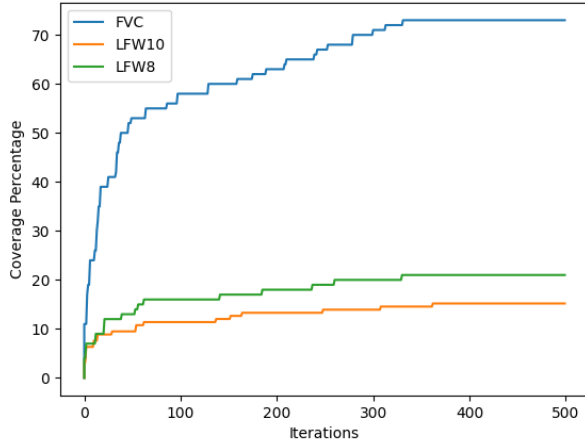


Figure 1: Evolution of coverage during iterations

The EER of the FVC database being important, lower thresholds for FVC are presented in table 2 for a more accurate comparison of the OCP with LFW.

Threshold τ_B	16	15	14	13	12	11	10	9	8	7
FMR (%)	12.9	9.5	6.7	4.4	2.8	1.7	1	0.5	0.2	0.1
OCP	64	58	49	42	38	29	23	19	14	11

Table 2: FMR/OCP corresponding to the thresholds (FVC)

Vulnerabilities of cancelable transformations in the stolen token scenario have been already studied. Typically, nearby-feature preimages have been already constructed on bihashing in this scenario with various methods. Nevertheless, it is the first time that these attacks are extended to the entire database by the construction of masterkeys. The strategy uses a genetic algorithm which is not related to the weaknesses of this transformation. Typically, specific techniques as linear optimization algorithms give efficient results for nearby-feature preimages on bihashing and could be used to improve the performance of our algorithm. Nevertheless, the choice of this algorithm depends on the cancelable transformation, whereas the research of masterkeys should be possible for all transformations.

4.3 Masterkeys from Biometric Database

In this second scenario, we have a biometric database and a feature vector, called candidate masterkey. The objective is the generation of seeds for which the feature vector is a masterkey for the corresponding cancelable biometric database as presented in Definition 2.4. In this scenario the transformation is chosen for the efficiency of masterkeys creation, not for data protection. Thus, the beginning of this subsection describes the choice of the transformation and its parameters.

The performance of random projection-based schemes are analyzed using the Johnson-Lindenstauss Lemma [16, 7] which establishes that for any $0 < \epsilon < 1$,

there exists a map $f : \mathbb{R}^N \rightarrow \mathbb{R}^M$ such that for all x, y in a subset of n points of \mathbb{R}^N with $M \geq O(\epsilon - 2 \log n)$

$$(1 - \epsilon) \|x - y\|_2^2 \leq \|f(x) - f(y)\|_2^2 \leq (1 + \epsilon) \|x - y\|_2^2.$$

The two following random projection $N \times M$ matrices are proposed by Achlioptas in [1]. In the first case, called JL1, coefficients of the projection matrix M_s are

$$\begin{cases} 1/\sqrt{M} & \text{with a probability } 1/2 \\ -1/\sqrt{M} & \text{with a probability } 1/2 \end{cases}$$

In the second case, called JL2, coefficients of M_s are

$$\begin{cases} \sqrt{3/M} & \text{with a probability } 1/6 \\ 0 & \text{with a probability } 2/3 \\ -\sqrt{3/M} & \text{with a probability } 1/6 \end{cases}$$

The main advantage of these transformations is the low computational time for matrix generation compared to the Gram-Schmidt algorithm.

The value of ϵ in the previous inequality is detailed in figure 2 for $N = 512$ and M between 32 and 256 using the FVC database (a random database also provides similar curves). Two transformations are used: the map composed of a random orthonormalized matrix (Gram-Schmidt), where ϵ decreases from 0.9 to 0.5 and for the two previous transformations (Achlioptas) which provides the similar results ($\epsilon \simeq 0.1$ for $M \geq 128$).

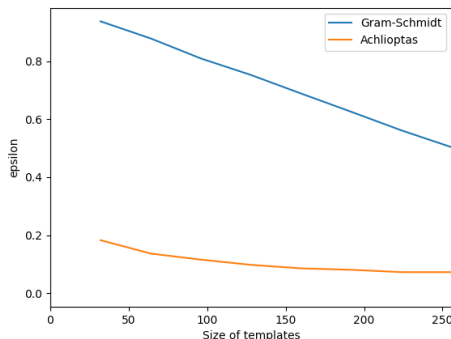


Figure 2: Estimation of ϵ for different sizes of templates (FVC)

The previous experiments on ϵ has very few consequences on the EER. The EER of the cancelable database is close to the EER of the original database in figure 3 for both transformations for $M \geq 128$. Even if the value of ϵ in the previous experiment is different, in the case of Achlioptas's transformations, the threshold is stable, whereas in the first transformation, the threshold increases. Thus, the research of masterkeys from a biometric database seems more interesting, directly in the Euclidean space, because the EER does not change compared to the original database if M is not too small (for $M = 128$, around 11% against 10% on FVC and around 1% against 0.2% for LFW). Nevertheless, the computational time for the research of masterkeys is not negligible, particularly for some feature vectors.

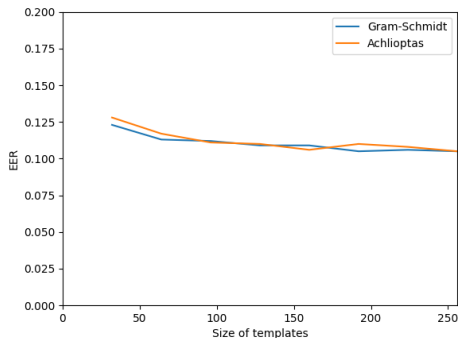


Figure 3: EER for FVC (Euclidean distance)

The EER of the cancelable database obtained with the two previous transformations and a binarization step is a little bit increased compared to the original EER: around 16.5% for FVC and 2.1% for LFW in figure 4 with $M = 128$. Consequently we investigate the research of masterkeys with transformations $\mathcal{T} : \mathbb{R}^N \rightarrow \mathbb{R}^M$ or $\{0, 1\}^M$, defined by the Achlioptas transformations, ending or not by a binarization step. Random matrices are generated from a seed of 16 bytes as previously.

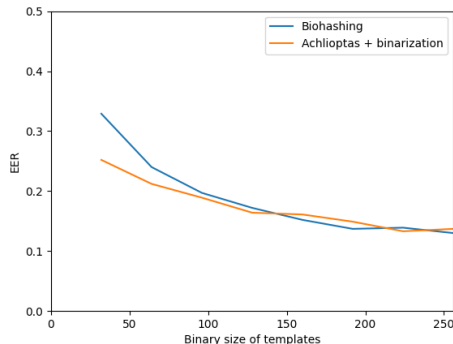


Figure 4: EER for FVC (Hamming distance)

Let $B = \{x_i^j\}_{i=1, \dots, n, j=1, \dots, t}$ be a biometric database, composed of feature vectors (n peoples with t vectors by people). In experiments, the candidate masterkey is a feature vector of a chosen people of a database. The research of seeds for a cancelable biometric database compliant with a masterkey candidate x_i^j , as presented in Definition 3.4 is realized, taking one by one the $(n-1)$ j^{th} feature vectors of each person, and choice seed, randomly generated from $\{0, 1\}^{128}$, so that the candidate masterkey is successfully authenticated. Experiments use the following algorithm, and outputs an array of $n-1$ seeds for each candidate masterkey, with the threshold at EER. The seed research is only limited by a value c_{max} , in the case of the FVC database without binarization of the transformation. If a successful seed is not founded after c_{max} trials, the output of the algorithm is *Failure* (in most of experiments, c_{max} is not achieved).

Algorithm 1 Research of seeds for masterkeys

Require: B the database, τ_B the threshold, c_{max}

```
SeedT = []
for  $i = 1$  to  $n$  and  $j = 1$  to  $t$  do
  SeedL = []
  for  $k = 1$  to  $n$ , with  $k \neq i$  do
     $cpt \leftarrow 0$ ,  $s_k \leftarrow rand(1, 2^{128})$ 
    while  $\mathcal{V}(\mathcal{T}(s_k, x_i^j), \mathcal{T}(s_k, x_k^j), \tau_B) = False$  and  $cpt < c_{max}$  do
       $s_k \leftarrow rand(1, 2^{128})$ 
    end while
    if  $\mathcal{V}(\mathcal{T}(s_k, x_i^j), \mathcal{T}(s_k, x_k^j), \tau_B) = True$  then
      SeedL.append( $s_k$ )
    else
      SeedL.append(Failure)
    end if
  end for
  SeedT.append(SeedL)
end for
Return SeedT
```

The research of seeds for masterkeys is successful for all feature vectors from FVC and LFW10 (called now LFW), for both Achlioptas’s transformations (called JL1 and JL2), with the binarization step. Figure 5 presents the number of clock required for each feature vector for both transformations on FVC database (more precisely, it is an average of the t vectors of each person), and the same results for LFW. It shows that the time is more important for some people of the FVC database, compared to the LFW database. It also shows that the second transformation provides slightly better results in both database (but the number of distance comparison is similar). The research of seeds is very efficient and only takes a few seconds for almost masterkey candidates.

The average of the EER in these $n * t$ cancelable biometric databases is around 17% for FVC (for both transformations) which is close to the EER of a cancelable database obtained with random seeds (around 16.5% for both transformations). For LFW, the average of the EER is around 2.4 % which is also close to the EER of a cancelable database obtained with random seeds (around 2.1% for both transformations).

If these transformations do not use a binarization step, the time of research increases a lot for the FVC database (more precisely for some people of this database), so we don’t detail it. In the case of LFW database, the number of clock is not significantly increased compared to the number of clock required with the binarization step. Figure 6 presents the number of clock during the research of the masterkeys for LFW (more precisely, it is an average of the t vectors of each person). In this case, the second transformation is again more efficient than the first one. The EER of these $n * t$ databases is around 1.3% which is close to the EER of the LFW database obtained with random seeds (around 1% for both transformations without binarization).

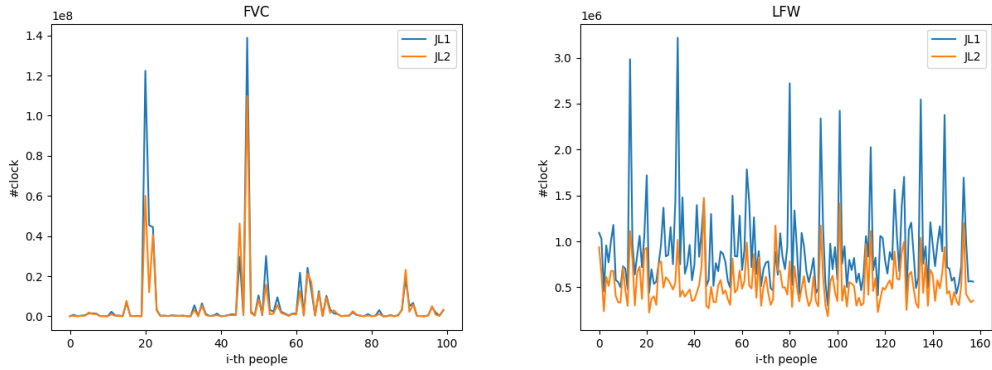


Figure 5: Average number of clock (in binary)

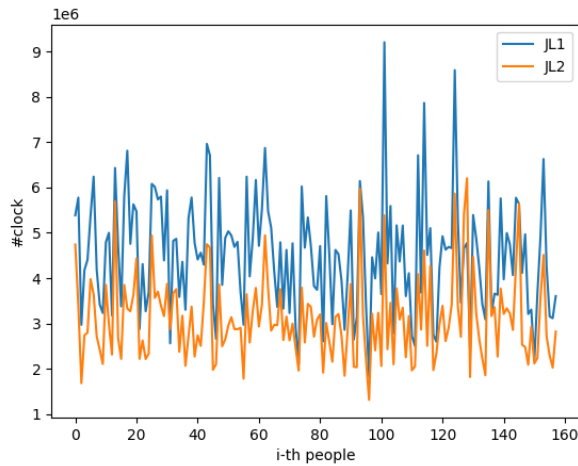


Figure 6: Average number of clock (LFW in Euclidean)

In this subsection, masterkeys have been efficiently founded for LFW in the Euclidean space. Nevertheless, due to complexity for some vectors of the FVC database, it seems more appropriate to use a transformation with binarization in the case where acquisition of feature vectors has not been perfectly realized. There is a tradeoff between performance of the cancelable database and efficiency of the research of seeds for masterkeys.

4.4 Multiple masterkeys

In this subsection, a variant of the previous scenario is investigated. The previous definition ensures for the owner's masterkey that the masterkey is successfully authenticated with enrollment data of other people. Nevertheless it does not ensure that another biometric data of the owner's masterkey is authenticated on this database. This subsection studies the percentage of the cancelable database cov-

ered by these other feature vectors.

Let $B = \{x_i^j\}_{i=1,\dots,n,j=1,\dots,t}$ be a biometric database, composed of feature vectors (n peoples with t vectors by people). Let x_1, \dots, x_t be feature vectors which are candidates for masterkey (x_1, \dots, x_t are assumed from the same people, but it doesn't mean that the distance between them is always lower than the used threshold). In a first time seeds are computed for a subset x_{t_1}, \dots, x_{t_T} , called first set (if such a seed is not founded, the seed minimizing the worst distance is kept). In a second time, we look for the coverage percentage of the database D provided by the $t - T$ other vectors, called second set. The corresponding templates of x_1, \dots, x_t , noted u_1, \dots, u_t , form the first set and the second set of templates, depending to the feature vectors.

Experiments only use the JL2 transformation, with and without binarization, on FVC and LFW, for $T = 1$ and $T = 4$. For practical reasons, we used a time limit of 5 minutes in place of c_{max} . The number of templates in D matching with the first set of T templates u_{t_1}, \dots, u_{t_T} (in blue for $T = 1$ and green for $T = 4$) and with the second set of $t - T$ other templates (in orange for $T = 1$ and red for $T = 4$) is presented in Figure 7 for FVC the Hamming space and in Figure 8 for LFW the Hamming and Euclidean space.

For example, with $T = 1$ in FVC, around 60% of templates from the second set of templates match with at less 40 templates of D (orange curve), whereas with $T = 4$, around 60% of templates from the second set of templates match with at less 75 templates of D (red curve). Moreover we have only one blue point in these figures, because 100% of templates of the first set match with all templates in the database, as seen in the previous subsection (if $T = 4$ it is not the case because the limit of 5 minutes for each seed computation).

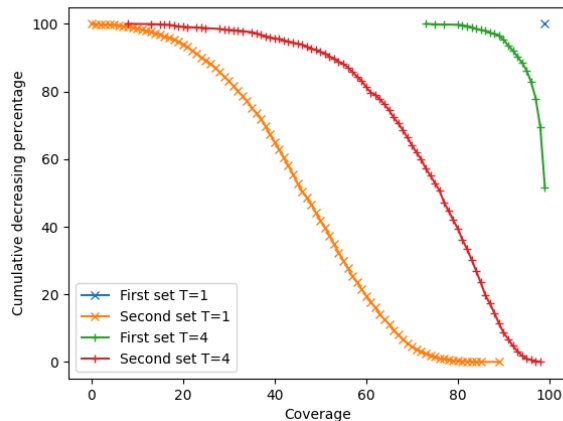


Figure 7: Cumulative decreasing percentage of successful masterkeys for $T = 1$ and 4, on FVC (Binary)

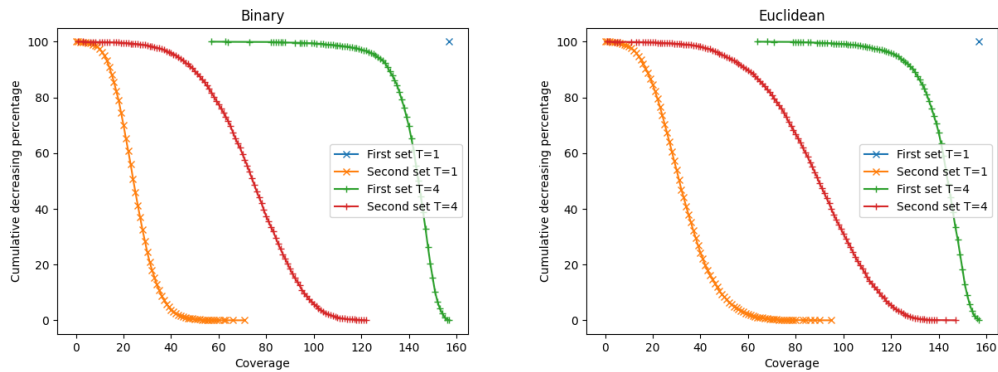


Figure 8: Cumulative decreasing percentage of successful masterkeys for $T = 1$ and 4, on LFW (Binary and Euclidean)

Curves corresponding to the second set of templates show that, on average, seeds computed for 4 masterkey's candidate of the first set of feature vectors are better for the second set of templates than seeds computed for only one candidate of the first set of feature vectors.

Figures 9 and 10 present the correlation between the number of successful masterkeys from the first set of feature vectors (abscissa) and the number of successful matches of the other templates from the second set of feature vectors (ordinate). Red curves correspond to a linear regression of points. If the correlation is low in the case of FVC, it is really high in the case of LFW, which confirms that the seeds should be computed from several acquisitions of feature vectors. Nevertheless, with $T = 4$, the feature vectors of the first set are only masterkeys for a (large) subset of the cancelable database, which provides a new tradeoff on the value of T .

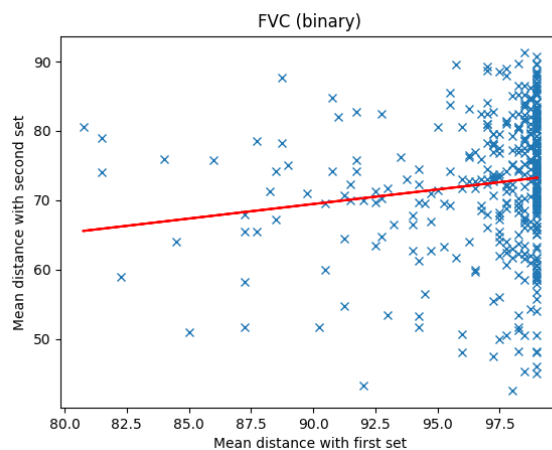


Figure 9: Correlation between successful masterkeys and other templates ($T = 4$ on FVC in Hamming space)

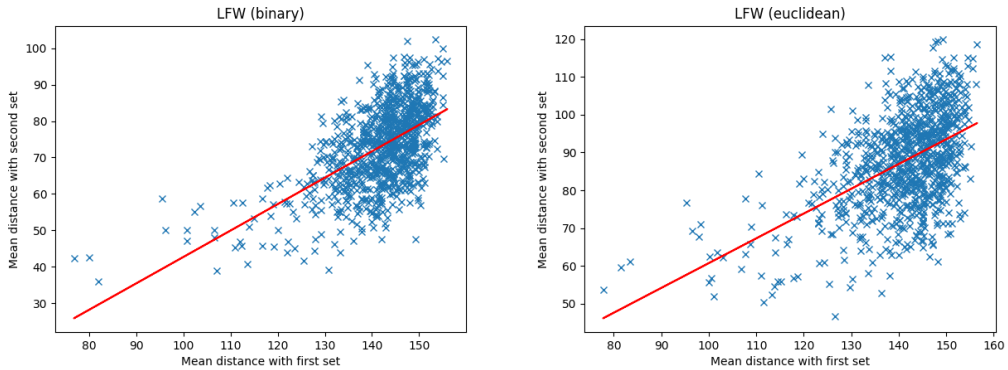


Figure 10: Correlation between successful masterkeys and other templates (T = 4 on LFW with Euclidean and Hamming space)

5 Conclusion and Future Work

This paper has introduced the concept of biometric masterkeys in two scenarios. In the first one, there exists a cancelable biometric database, and we try to find a feature vector for which the corresponding template matches with the greatest number of templates of the database. It is a formalization and a generalization of Wolf Attacks and masterprints on fingerprints, experimented with the biohashing algorithm. In the second scenario, there exists a biometric database, and we try to find a set of seeds for which the corresponding template of a given feature vector matches with the greatest number of templates of the database.

The main contribution of this work is the construction of such a cancelable biometric database covered by one of its feature vectors, with an EER similar to the original cancelable database. The research of masterkeys in this second scenario is completely different from previous works on wolves or masterprints, because it uses the transformation, not for data protection, but for the research of preimages. This work presents new opportunities for a biometric system administrator, to construct a cancelable biometric database which matches with a template obtained from its own feature vector. This masterkey only requires a public seed by template and is very easy to construct.

There are several future works and improvements of this paper, particularly in the research of seeds, providing good coverage percentage of the cancelable database for other acquisitions of feature vectors. Other applications of masterkeys, as biometric systems with fine-grained access controls, will also be investigated in the future. Finally, it would be interesting to use an efficient and secure transformation to ensure the security of templates in this context. Nevertheless, if such a transformation is not available, it is possible to combine masterkeys with any biometric protection scheme.

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