Near-collisions and Their Impact on Biometric Security

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Abstract: Biometric recognition encompasses two operating modes. The first one is biometric identification which consists in determining the identity of an individual based on her biometrics and requires browsing the entire database (*i.e.*, a 1:*N* search). The other one is biometric authentication which corresponds to verifying claimed biometrics of an individual (*i.e.*, a 1:1 search) to authenticate her, or grant her access to some services. The matching process is based on the similarities between a fresh and an enrolled biometric template. Considering the case of binary templates, we investigate how a highly populated database yields near-collisions, impacting the security of both the operating modes. Insight into the security of binary templates is given by establishing a lower bound on the size of templates and an upper bound on the size of a template database depending on security parameters. We provide efficient algorithms for partitioning a leaked template database in order to improve the generation of a master-template-set that can impersonates any enrolled user and possibly some future users. Practical impacts of proposed algorithms are finally emphasized with experimental studies.

1 INTRODUCTION

With the continuous growth of biometric sensor markets, the use of biometrics is becoming increasingly widespread. Biometric technologies provide an effective and user-friendly means of authentication or identification through the rapid measurements of physical or behavioral human characteristics. For biometric identification and authentication schemes, biometric templates of users are registered with the system. The first operating mode consists in determining the identity of an individual based on similarity scores calculated from all the enrolled templates and the fresh provided template. The latter corresponds to the verification of the claimed identity based on a similarity score calculated from the assigned enrolled template and a fresh template. As a consequence, service providers need to manage biometric databases in a manner similar to managing password databases.

The leak of biometric databases is more dramatic since, unlike passwords, biometric data serve as long term identifiers and cannot be easily revoked. The consequences of stolen biometric templates are impersonation attacks and the compromise of privacy. Essential security and performance criteria that must be met by biometric recognition systems are identified in (ISO, 2011) and (ISO, 2018): *Irreversibility*, *unlinkability*, *revocability* and *performance preservation*.

Biometric templates are generated from biometric measurements (*e.g.*, a fingerprint image). They result from a chain of treatments, an extraction of the features (*e.g.*, using Gabor filtering (Manjunath and Ma, 1996; Jain et al., 2000)) followed eventually by a Scale-then-Round process (Ali et al., 2020) to accommodate better handled representations, *i.e.,* binary or integer-valued vectors. These templates are then protected either through their mere encryption, or using a Biometric Template Protection (BTP), *e.g.,* a cancelable biometric transformation such as Biohashing (Jin et al., 2004; Lumini and Nanni, 2007) or any other salting method. For more details on BTP schemes, the reader is referred to the surveys (Nandakumar and Jain, 2015; Natgunanathan et al., 2016; Patel et al., 2015). The use of a BTP scheme is in general preferred since its goal is to address the aforementioned criteria. However, note that cancelable biometric transformations are prone to inversion attacks, at least in the sense of second-preimages (Durbet et al., 2021). They even lead sometimes to the compromise of privacy with a good approximation of a feature vector (Lacharme et al., 2013; Ghammam et al., 2020).

Recent works have also demonstrated that recog-

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nition systems are vulnerable to dictionary attacks based on master-feature vectors (Roy et al., 2017; Bontrager et al., 2018). A master-feature vector is a set of synthetic feature vectors that can match with a large number of other feature vectors. This can naturally be extended to the problem of generating master-templates and masterkeys. The notion of masterkey has recently been addressed in (Gernot and Lacharme, 2021) to produce backdoors with the aim of implementing biometric-based access rights. In the same topic, the present paper analyses the security of biometric databases by making some recommandations, and by proposing attacks using the notions of master-template, master-feature and masterkey.

Contributions. Our main contribution is an efficient partitioning algorithm which accelerates attacks aiming to generate master-key or master-feature vector. Numerical studies on implementations of the proposed algorithm show a reduction of the computational time by a factor of up to 38 in certain settings. In addition, we show a link with the closest string problem with an arbitrary number of words, for which we provide a solution using Simulated ANNealing (SANN). Moreover, we determine a bound on the size of a database in function of the template space dimension and the decision threshold, thus preventing near-collisions with a high probability. Specifically, for a secure database, the recommanded template size is $n = 512$ bits with a threshold of the order of 10% of n, *i.e.,* around 50 bits. Setting these paramaters in this way rules out attacks based on master-templates and ensures a good recognition accuracy. Finally, some indications are provided for handling basic database operations such as addition or deletion of users.

Outline. In Section 2, we introduce some notations, background material as well as definitions of new notions such as master-template and ε-covering-template. In Section 3, we describe an algorithm which provides a segmentation of a database in order to focus on potential master-templates. In Section 4, we show how this algorithm can be used to improve the computation of masterkey-set and master-feature-set. Moreover, we describe how near-collisions can be used to define a secure parameter k which depends on the template space dimension and a threshold. We also explain why the secure parameter is a countermeasure and, the case of a user which is added or removed from the database are studied. In Section 5, we provide some experimentations in order to assess the performance of the proposed algorithm and to detail in practice how the near string problem is solved. All proofs are in the long version of this paper.

2 PRELIMINARIES

A biometric system is a method of authentication or identification based on biometric data. The main idea is to transform the biometric data into a template to match the four aforementioned criteria, i.e., irreversible, unlinkable, revocable and performance preservation. It must be able to compare template and determine if they belong to the same person. The template is constructed by combining a feature vector derived from the biometric data and a secret parameter named token which can be for example a password. A biometric authentication or identification system always starts by using a *feature extraction scheme* to extract some information from the biometric image to construct a feature vector (Ratha et al., 2001). A database partitioning method can be applied to each biometric system for this. In this paper, we focus on templates expressed as binary vectors, but the results below can be adapted to every template representations.

In the following, we let $(\mathcal{M}_I, \mathrm{Dist}_I)$, $(\mathcal{M}_F, \mathrm{Dist}_F)$ and $(\mathcal{M}_T, \mathrm{Dist}_T)$ be three metric spaces, where $\mathcal{M}_I$, $\mathcal{M}_F$ and $\mathcal{M}_T$ represent the image space, the feature space and the template space, respectively; and Dist_I, Dist_F and Dist_T are the respective distance functions. Note that Dist_I and Dist_F are instantiated with the Euclidean distance, while Dist_T is instantiated with the Hamming distance.

Definition 2.1 (Feature Extraction Scheme)**.** *A biometric* feature extraction scheme *is a pair of deterministic polynomial time algorithms $\Pi := (E, V)$, where:*

- *E is the feature extractor of the system, that takes biometric data $I \in \mathcal{M}_I$ as input, and returns a feature vector $F \in \mathcal{M}_F$.*
- *V is the verifier of the system, that takes two feature vectors $F = E(I)$, $F' = E(I')$, and a threshold τ_F as input, and returns True if $\mathrm{Dist}_F(F, F') \leq \tau_F$, and returns False if $\mathrm{Dist}_F(F, F') > \tau_F$.*

For the sake of privacy, biometric data (the feature vector) should be designed in a such way that it prevents information leakage. This motivates the use of a cancelable biometric transformation scheme.

Definition 2.2 (Cancelable Biometric Transformation Scheme)**.** *Let $\mathcal{K}$ be the token (seed) space, representing the set of tokens to be assigned to users. A* cancelable biometric scheme *is a pair of deterministic polynomial time algorithms $\Xi := (\mathcal{T}, \mathcal{V})$, where:*

- *$\mathcal{T}$ is the transformation of the system, that takes a feature vector $F \in \mathcal{M}_F$ and the token parameter $P \in \mathcal{K}$ as input, and returns a biometric template $T = \mathcal{T}(P, F) \in \mathcal{M}_T$.*

- $\mathcal{V}$ *is the verifier of the system, that takes two biometric templates* $T = \mathcal{T}(P,F)$, $T' = \mathcal{T}(P',F')$, *and a threshold* τ_T *as input; and returns True if* $\mathrm{Dist}_T(T,T') \leq \tau_T$, *and returns False if* $\mathrm{Dist}_T(T,T') > \tau_T$.

In this paper, the template space is, unless otherwise specified, $\mathbb{F}_2^n = \left(\mathbb{Z}/2\mathbb{Z}\right)^n$, equipped with the Hamming distance denoted by d_H. As the template space is a metric space, we denote it as $(\mathbb{F}_2^n, d_H)$. In our case, the verifier is the Hamming distance, but the transformation does not need to be specified. As we work on a set of template, we denote it as *Template DataBase* (*TDB*).

Definition 2.3 (Template Database or TDB)**.** *Let* (Ω, d) *be the template space equipped with the distance* d. *A subset* $L \subset \Omega$ *such that* $L \neq \emptyset$ *and* $L \neq \Omega$ *is a* template database (TDB)*, or just a database.*

As with hash functions, an antecedent of a transform can be searched in order to steal a password or a pass tests using this hash function. This preimage can be the exact feature vector or a nearby preimage.

Definition 2.4 ({Nearby} Template Preimage)**.** *Let* $I \in \mathcal{M}_I$ *be a biometric image, a threshold* ε_B, *and* $T = \Xi.\mathcal{T}(P,\Pi.E(I)) \in \mathcal{M}_T$ *for some secret parameter* P. *A* template preimage *of* T *with respect to* P *is a biometric image* I^* *such that* $T = \Xi.\mathcal{T}(P,\Pi.E(I^*))$, *and a* nearby template preimage *is such that* $d(T,\Xi.\mathcal{T}(P,\Pi.E(I^*))) < \varepsilon_B$.

The goal of an attacker can be to create a masterkey-set. This is a set of tokens that allow to build all the templates of a targeted database using the same feature vector. Another goal of an attacker can be to create a master-feature-set. This is a set of feature that allow to build all the templates of a targeted database using preferably the same token.

Definition 2.5 (Masterkey and Master-feature)**.** *Let* $D = \{v_i\}_{i=1,\dots,n}$ *be a template database where* $v_i := \Xi.\mathcal{T}(x_i,s_i)$ *generated with distinct tokens* $S = \{s_i\}_{i=1,\dots,n}$ *and distinct biometric features* $X = \{x_i\}_{i=1,\dots,n}$, *and let* τ_B *be a threshold. Then,* m *is a masterkey for* D, *with respect to* τ_B, *if* $\forall i \in [\![1,n]\!], \Xi.\mathcal{V}(\Xi.\mathcal{T}(x_i,m),\Xi.\mathcal{T}(x_i,s_i),\tau_B) = True$, *and in addition,* m *is a* master-feature *if* $\forall i \in [\![1,n]\!], \Xi.\mathcal{V}(\Xi.\mathcal{T}(m,s_i),\Xi.\mathcal{T}(x_i,s_i),\tau_B) = True$.

Targeting random template to find a masterkey are often not efficient, thus, to maximize the efficiency of the research of a masterkey-set, we suggest to focus on ε-covering templates and ε-master-templates (ε-MT).

Definition 2.6 (ε-cover-template and ε-master-template)**.** *Let* (Ω, d) *be the template space and* D *be a template database. An* ε-cover-template *of* D *is* x *such that* $d(x,a) \leq \varepsilon, \forall a \in D$. *Moreover, a template* $t \in \Omega$ *is an* ε-master-template *if* $\forall t' \in D, d(t,t') \leq \varepsilon$.

Note that, there are cases for which there is no possible ε-cover-template. In addition, an ε-master-template-set is a non-empty set: D is an ε-master-template-set of itself but an ε-master-template of D could be empty. Moreover, an ε-cover-template is an ε-master-template and an ε-master-template-set is a set of ε-cover-templates which are not in the same ε-cover-template-set. We define a near-collision and more precisely multiple-near-collision.

Definition 2.7 (Near Collision)**.** *Let* (Ω, d) *be the template space and a threshold* ε . *There exists a* near-collision *if* $\exists a,b \in \Omega \mid d(a,b) \leq \varepsilon$.

Thus, the search of an ε-cover-template of D a database corresponds to the search of an at least $|D|$-near-collision for which each template of D is related to the collision.

3 DATABASE PARTITIONING

The aim of this part is to determine the smallest ε-covering-template-set for a given database D.

3.1 Agglomerative Clustering

Consider M_D the dissimilarity matrix of a template database D, for the Hamming distance. The dissimilarity matrix M_D is used to compute template clusters, denoted by C_ε, for which the distance between two templates in the same cluster is at most s. To perform this clustering, we use the agglomerative clustering method which is a type of the hierarchical clustering. This method consists in successively agglomerating the two closest groups of templates. It begins with $|D|$ groups, one for each template, and it terminates when all the groups are merged as a unique one.

A standard post-processing is required to define at which iteration the algorithm should be terminated so that a relevant set of template clusters is obtained. However, we define a termination condition so that the clustering algorithm stop when it is not possible anymore to obtain templates cluster verifying the following required property: $\forall i \in [\![1,n]\!], \forall a,b \in C_i, max(d_H(a,b)) \leq s$. The Agglomerative Clustering algorithm we used then corresponds to a slight variation of the HACCLINK (Hierarchical Agglomerative Clustering Complete LINK) presented in (Defays, 1977).

By using the aforementioned clustering method, we obtain a set of template clusters, for which the inner-cluster distance suggests that it could exist at

least one master-template for these templates. An additional step is described below whose aim is to determine potential master-templates, if there exists some.

3.2 Master-template of a Template Group

We consider having a group of templates verifying $\forall i \in [\![1,n]\!]$, $\forall a,b \in C_i$, $max(d_H(a,b)) \leq s$, and for which we aim at finding a master-template. We emphasize that this problem can be formulated as a modified case of closest-string problem which is defined as follows.

Definition 3.1 (Modified Closest-string Problem)**.** *Given $S = \{s_1, s_2, \ldots, s_m\}$ a set of strings with length n and d a distance, find a center string t of length m such that for every string s in S, $d_H(s,t) \leq d$.*

The closest-string problem is known as an *NP*-hard problem (Frances and Litman, 1997), and there exist algorithms to solve that kind of problem, see among others (Meneses et al., 2004; Gramm et al., 2001). According to the link between both problems, we can establish that the issue addressed in this paper is a hard problem, which is specified in the following theorem.

To the best of our knowledge, this problem has not been addressed in the literature, then we propose an algorithm to solve it. Moreover, with regards to the hardness of MCSP, we deem that relying on brute force type algorithm could not be efficient and that more parsimonious algorithm must be investigated, notably stochastic algorithms. However, more efficient upcoming methods could replace this part without affecting the remainder of the database partitioning method proposed in Section 3.

We consider $D = \{v_1, \ldots, v_k\}$ be a template database and $\mathcal{C}$ the ε-cover-template-set for D (a set of ε-cover-template such that all points of D are in a ball around a point of $\mathcal{C}$). The approach described below provides a constructive definition of the elements of $\mathcal{C}$, if $\mathcal{C} \neq \emptyset$. In particular, the following result emphasizes the link between $\mathcal{C}$ and the balls $B_i = \{u \in \mathbb{F}_2^n | d_H(u,v_i) \leq \varepsilon\}$.

Theorem 3.1 ($\mathcal{C}$ Is the Intersection of the Balls of Radius ε)**.** *Let $D = \{v_1, \ldots, v_k\}$ be a template database and $\mathcal{C}$ the ε-cover-template-set for D. Then, $\mathcal{C} = \cap_{i \in \{1,\ldots,k\}} B_i$.*

We denote by $p \in \mathcal{C}$ a master-template, and Theorem 3.1 indicates that determining all the master-template p reduces to determining the intersection of k Hamming balls, which turns out to be formulated as the solutions of the following system:

$$d_H(p,v_i) \leq \varepsilon, \quad \forall i \in \{1,\ldots,k\}. \tag{1}$$

Notice that System 1 is a linear system, hence we can rely on a binary ILP (Integer Linear Programming) to solve it and then to compute $\mathcal{C}$.

However, solving this system could be time-consuming in real world cases since there are as many parameters as the length of p, i.e., the dimension n of $\mathbb{F}_2^n$. Therefore, we suggest reducing System 1 by removing dependent variables and below are introduced necessary notations:

- For $K = \{k_1, \ldots, k_{|K|}\} \subset \{1,\ldots,n\}$, the Hamming distance over K is denoted by: $\forall u,v \in \mathbb{F}_2^n, d_K = d_H((u_{k_1},\ldots,u_{k_{|K|}}),(v_{k_1},\ldots,v_{k_{|K|}}))$.
- Let $\mathcal{P}_D(K)$ a statement about $K \subset \{1,\ldots,n\}$, $\mathcal{P}_D(K)$ holds if $\forall u,v \in D, d_K(u,v) \in \{0,|K|\}$.
- The smallest partition $\{(K_1,\ldots,K_{|I|}), K_i \subset \{1,\ldots,n\} \mid \forall i \in \{1,\ldots,|\,I\,|\}\}$ such that $\mathcal{P}_D(K_i)$ holds for all $i \in \{1,\ldots,n\}$ is noted I. As I is the smallest possible partition, System 1 is reduced as much as it is possible.
- For $p \in \mathbb{F}_2^n$ and $v \in D$, $n_{v,i}$ denotes $d_{K_i}(p,v)$ and n_v^I denotes the parameters vector $(n_{v,1},\ldots,n_{v,|I|})$, written $N = (n_1,\ldots,n_{|I|})$ for short when the context is clear.
- The distance vector $\big(d_H(v_1,v),\ldots,d_H(v_{|D|},v)\big)$ is denoted by $d(v)$ with $v \in D$ and $D = (v_1,\ldots,v_{|D|})$.

Then, with these notations, Theorem 3.2 can be established, specifying a smaller version of System 1.

Theorem 3.2. *For a given template database D and for a given $v \in D$, consider $L = \{p \in \mathbb{F}_2^n \,|\, AN \leq \varepsilon - d(v)\}$ with $N = n_v^I$, $\varepsilon = (\varepsilon,\ldots,\varepsilon)^T$, $n_{v,i}$ denotes $d_{K_i}(p,v)$, n_v^I denotes the parameters vector $(n_{v,1},\ldots,n_{v,|I|})$ and $A = (a_{i,j})$ a matrix of size $|I| \times |D|$ whose the $(i,j)^{th}$ element is*

$$a_{i,j} = \begin{cases} 1 & \text{if } d_{K_j}(v_1,v_i) = 0 \\ -1 & \text{if } d_{K_j}(v_1,v_i) = |K_j| \end{cases}$$

Then, $L = \mathcal{C}$ the ε-cover-template-set for D.

As I is required to reduce System 1, we assure with Lemma 3.1 that $I \neq \emptyset$, whatever the configuration of the set D is.

Lemme 3.1 (I Is Not Empty)**.** $\forall D \subset \mathbb{F}_2^n$ *such that* $|\,D\,| > 1$, $I \neq \emptyset$.

In the same vein, one can determine that $|I| \leq n$. As $|I|$ corresponds to the number of parameters, the system described in Theorem 3.2 is always smaller or equivalent to System 1.

Theorem 3.2 indicates that determining the ε-cover-template-set for D (which corresponds to an intersection of $|D|$ balls in $\mathbb{F}_n^2$ can be reduced to solving

a potentially small linear system. While the resolution of the aforementioned system can be done with powerful tools (like GUROBI (Pedroso, 2011)), we deem that simpler algorithms should be used in this case. In particular, according to the configuration of D, it is possible to obtain a such system linear that it is straightforward to determine the space of the potential solutions and to find a solution with any Markovian scanning algorithm. More precisely, if $\mathcal{N}$ denotes the set of the possible solutions N for the linear system described in Theorem 3.2, we have: $\mathcal{N} = \prod_{k=1}^{|I|}\{0,\dots,\min(\varepsilon,|K_k|)\}$ since, for $k \in \{1,\dots,|I|\}$, $n_{v,k}$ corresponds to the distance $d_{K_k}(v_k,v)$, which can not be greater than $|K_k|$, and in the other hand if $d_{K_k}(v_k,v) > \varepsilon$ then, N does not belong to L. One can then be aware that depending on the dimension of $\mathcal{N}$, finding a solution N can be efficiently done via either a brute force algorithm in case of small dimensional set $\mathcal{N}$, or via a more parsimonious algorithm if the dimension is high. As the dimension of $\mathcal{N}$ depends among other factors on D, we consider that the use of one of the both approaches should be determined with regards to pratical context-specific consideration. In this paper, we only describe an algorithm to use in case of high dimensional $\mathcal{N}$ set. We propose to rely on an efficient and simple algorithm: the Simulating Annealing algorithm (Kirkpatrick et al., 1983). Nevertheless, even if we illustrate the proposed methodology with this algorithm, it could be replaced by any optimization algorithm based on scanning the space. Below we detail features of Simulating Annealing algorithm that we tune in order to obtain good performances in our numerical study. It is composed of the following parameters:

- *Energy:* We define the following energy so that larger it is, the closer N is to solve the linear system: $E(N) = \sum_{i=1}^{|I|} f((\varepsilon - d(v) - AN)_i)$ where f is a ReLU type function: $f(x) = \min(0,x)$.
- *Cooling Schedule:* In practice, we observe that finding a solution is not sensitive to the cooling of the system, see Section 5.2. Then, we propose to choose a linear decreasing temperature. The starting temperature is fixed so that at the initial iteration, all potential move must be accepted, whatever the chosen initial point is.
- *Proposal distribution:* According to computational considerations and for the sake of numerical performance, we define a proposal distribution for which the support is the neighbors set. Moreover, we choose a non-symmetric proposal that preferentially promotes neighbors that increases the energy.
- *Termination:* The algorithm is terminated either it reaches the maximum iteration number (about $200k$ iterations), or if a solution is found, which corresponds to a vector N with a null energy.

The experimentations of this part are presented in Section 5.2.

3.3 Database Partitioning Algorithm

Using the developments of the sections 3.1 and 3.2, we propose Algorithm 1 to partition the template database. It takes as inputs D a template database and a threshold ε and returns an ε-MTS.

Algorithm 1: Database partitioning algorithm.

```
   Data: D, ε
   Result: MTS
 1 Set s to 2ε.
 2 Set MTS to [ ].
 3 while D ≠ ∅ do
 4 |   Compute cluster Cls using D and s.
 5 |   foreach cluster c in Cls do
 6 |   |   Search the cover template t for c.
 7 |   |   if a cover template t is found for
   |   |    c ∈ C then
 8 |   |   |   Set D to D\c and add t to MTS.
 9 |   |   end
10 |   |   Set s to s − 1.
11 |   end
12 end
13 return MTS.
```

4 ATTACK SCENARIO, COUNTERMEASURE AND CASE STUDIES

The aim of this section is to show that the method described Section 3 eases the computation of a masterkey-set or a master-feature-set. Their computations are straightforward in the absence of BTP scheme and are still possible if an invertible transformation is employed, like Biohashing or some other salting transformations. Moreover, that kind of attack is analyzed, and a security bound is established in Section 4.2.

4.1 Attack Scenario

Consider a pair of functions $\mathcal{T}_1^{-1}$ and $\mathcal{T}_2^{-1}$ defined as follows :

Definition 4.1 (Token (resp. Feature) Transformation Inversion Function)**.** *The* token (resp. feature)

transformation inversion function *denoted by* $\mathcal{T}_1^{-1}$ *(resp.* $\mathcal{T}_2^{-1}$*) takes* $v \in \mathcal{M}_\mathcal{T}$ *a feature vector (resp. a token) and* $t \in \Omega$ *a template and gives* p *a token such that* $\mathcal{T}(v,p) = t$.

Note that we focus on frameworks for which $\mathcal{T}_1^{-1}$ and $\mathcal{T}_2^{-1}$ can be computed in a reasonable time: at least linear and at most subexponential. These functions must be determined case-by-case according to the used biometric transformation. Furthermore, an attacker seeking to create a master-feature-set (resp. a masterkey-set) can do it using k calls to the inverse transformation function $\mathcal{T}_1^{-1}$ (resp. $\mathcal{T}_2^{-1}$), where k is the number of templates. However, the method developed in Section 3 can be used to reduce the computation complexity. Actually, the attacker can compute a master-feature-set or a masterkey-set in only ℓ step with $\ell \leq k$, where l is the number of clusters.

4.2 Countermeasure: Managing the Database Size

Consider a biometric system set with a template space of size n and a threshold ε. Moreover, suppose that the biometric system is unbiased i.e., each template is randomly chosen in the template space. There exists a maximum size for a database at n and ε fixed which minimizes the gain of an attacker with the method presented in Section 3 and which maximizes the size of that database. Notice that the following approach can be applied to any biometric system.

Prevent an Advantage. An advantage of an attacker is significant when our database partitioning method (Section 3) reduces the complexity of the initial attack by at least one. Let k be the number of clients allowed in a database and, $\mathbb{F}_2^n$ the template space. If $k \geq \left\lceil 2^n \Big/ \sum_{i=0}^{\varepsilon} \binom{n}{i} \right\rceil$ then, there is at least one cluster containing two or more templates, according to the Dirichlet's box principle. In our case, c is at most: $\left\lceil 2^n \Big/ \sum_{i=0}^{\varepsilon} \binom{n}{i} \right\rceil$ and there are two scenarios:

1. There are enough clients to find a coverage of $\mathbb{F}_2^n$ by using their clusters and any other enrollment is already compromised.
2. There is not enough clients to find a coverage of $\mathbb{F}_2^n$ and the attacker obtains an advantage for the computation.

By using birthday problem, more particularly the probability of a near collision (Lamberger et al., 2012; Lamberger and Teufl, 2012), we can establish that, the average number of template must be about $2^{(n+1)/2} S_\varepsilon(n)^{-1/2}$ so that a cluster contained two templates, where, $\sum_{i=0}^{\varepsilon} \binom{n}{i} = S_\varepsilon(n)$. Furthermore, the number of near collisions is $N_C(\varepsilon)$ and its expected value $\mathbb{E}(N_C(\varepsilon))$ is equal to $\binom{k}{2} S_\varepsilon(n) 2^{-n}$ with k the number of templates. Thus, the number k of templates which give a collision with a probability of 50% is $\approx 2^{n/2} S_\varepsilon(n)^{-1/2}$.

Figure 1 provides numerical and graphical representations based on experimentations, enlightening on how k behaves relatively to n and ε. They show that the size of a database which can provide collisions is wide smaller than the size of n. Furthermore, if ε is bigger than 20% of n, this size dramatically decreases. To keep enough room in a safe database, n must be larger than 512 and ε smaller than 51.

5 ATTACK EVALUATION

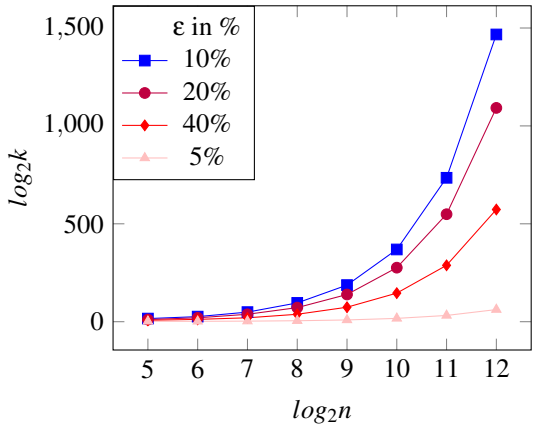
In this section we provide some experimental evaluations of Algorithm 1 and, we discuss our results. In our experiments, the passwords are assumed unique for each individual. The hashed passwords serve as seeds for the generation of the matrices. Thus, the produced templates are uniformly distributed.

To compare the efficiency of our proposal with a baseline, we propose a naive algorithm based on a greedy strategy. First, a template is picked from the template database. Then, all templates in the template database which are at a distance of at most ε from the chosen template are removed. These steps are repeated as long as there are templates in the database. As a result, the chosen templates form the MTS.

5.1 Evaluation of the Database Partitioning

Templates are randomly drawn from $\mathbb{F}_2^n$. For each configuration, experimentations are replicated 10k times and averaged results are computed. The average results are presented in Table 1 and Table 2 with the following notations: n: the space dimension, ε: the threshold, #*clients*: the number of templates in the TDB, #*clust*: the number of clusters found with Algorithm 1, #*clust*(G): the number of clusters found using the greedy Algorithm 5, $Efficiency$ is the ratio #*clust*(G)/#*clust*, $Time$ is the running time of Algorithm 1, $Time(G)$ is the running time of the greedy Algorithm 5. As the computation of the ε-cover-template 3.2 is the most expensive part of Algorithm 1, an experimentation Table 2 is dedicated to the ε-cover-template search 3.2. In fact, we remark that the gain of the attacker is greater when the value of k is greater that what we recommend in Section 4.2.

(a) $\log_2 n$ in function of $\log_2 k$ for ε.



(b) ε in % in function of $\log_2 k$ for n.

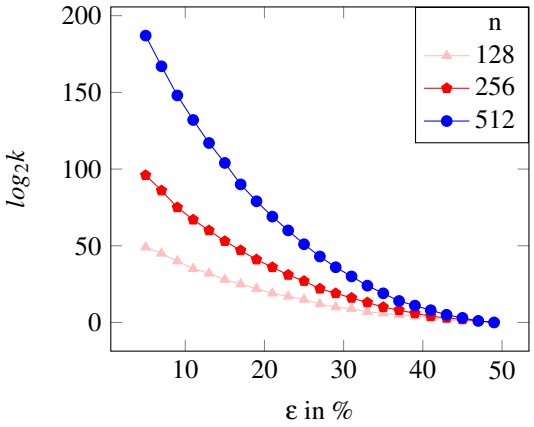


Figure 1: Link between k and n or ε.

Table 1: Summary of the experiments of the space partitioning algorithm.

n	ε	#clients	#clust	#clust(G)	Efficiency	Time (ms)	Time G (ms)
20			2.700	35.433	×**13.12**	8415.270	10.714
30	10	50	8.709	48.977	× 5.70	8775.802	18.940
40			18.087	49.986	× 2.77	6417.596	23.762
	5		200.000	200.000	× 1.00	43.969	449.166
70	15	200	90.000	200.000	× 2.22	47016.050	337.082
	25		22.109	198.982	× **9.00**	222386.614	346.420
		90	89.67	90		136.572	137.186
50	10	130	129.30	130	×1.00	428.885	251.221
		170	168.79	170		531.363	434.727

5.2 Evaluation of Simulated Annealing

Keeping the same notations, the average experimentations are stored in Table 3. In the case where the simulated annealing is used as a sub-routine of the algorithm 1, this latter is slower and less efficient. The main reason of this loss of performance is the error rate of the simulated annealing which forces doing more calculations. However, it is quicker and more efficient than solving a system to answer to the near string problem given in Section 3.1.

Moreover, we use several cooling functions (Aarts et al., 2005; Kirkpatrick et al., 1983) to determine what is preferable and we remark that finding a solution is not strongly sensitive to the cooling method.

6 CONCLUDING REMARKS

In this paper, we have performed an in-depth analysis of the Hamming space as template space. We first have introduced some formal definitions such as multiplicative near-collision, master-template, ε-covering template and some technical terms and concepts. We then have proposed an algorithm to perform a partition of the set of templates. This partitioning can be used to improve either the masterkey-set search or the master-feature-set search. The proposed center search algorithm using simulated annealing is also a result of independent interest for solving the near-string-problem.

By relying on the properties of near-collisions and the partitioning algorithm, we have also shown there exists a security bound on the size of a database that depends on both the space dimension and the decision threshold. Beyond that limit on the size, there is a high probability of a near collision that impacts both security and efficiency.

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Table 2: Summary of the experiments of the ε-cover-template search algorithm ILP version.

n	ε	#clients	Time (ms)	n	ε	#clients	Time (ms)	n	ε	#clients	Time (ms)
20			1592.213		5		24949.724			90	11087.893
30	10	50	2428.682	70	15	200	20978.806	70	10	130	18330.508
40			3887.738		25		29089.280			170	20887.950

Table 3: Summary of the experiments of the ε-cover-template search algorithm SANN version.

n	ε	#clients	Error in %	Time (ms)	n	ε	#clients	Error in %	Time (ms)	n	ε	#clients	Error in %	Time (ms)
20			0.64	17		5		0.00	36			90	0.14	12
30	10	50	0.00	1	70	15	200	0.00	36	70	10	130	0.00	22
40			0.05	1		25		0.00	40			170	0.00	31

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