Fast and Accurate Biometric Identification Using Score Level Indexing and Fusion

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Abstract

Biometric identification provides a very convenient way to authenticate a user because it does not require the user to claim an identity. However, both the identification error rates and the response time increase almost in proportion to the number of enrollees. A technique which decreases both of them using only scores has the advantage that it can be applied to any kind of biometric system that outputs scores. In this paper, we propose such a technique by combining score level fusion and distance-based indexing. In order to reduce the retrieval error rate in multibiometric identification, our technique takes a strategy to select the template of the enrollee whose posterior probability of being identical to the claimant is the highest as a next to be matched. The experimental evaluation using the Biosecure DS2 dataset and the CASIA-FingerprintV5 showed that our technique significantly reduced the identification error rates while keeping down or even reducing the number of score calculations, compared to the unimodal biometrics.

1. Introduction

A biometric authentication system can operate in the following two modes: verification and identification [4]. In verification, a user claims an identity along with his / her biometric sample (referred to as a query sample) and the system matches the sample with a biometric template corresponding to the claimed identity (i.e. one-to-one matching). In identification, a user only inputs a query sample and the system matches the sample with many templates in the database (i.e. one-to-many matching) to identify the user. The latter provides a very convenient way to authenticate a user because it does not require the user to enter ID / password nor to present a card. The user does not even need to do anything if, for example, his / her face or iris is captured at a distance [19].

However, biometric identification has problems with the accuracy and the response time: both the identification error rates and the one-to-many matching time increase as the number of enrollees increases. These two problems make biometric identification quite challenging to apply to the large-scale applications.

There are several strategies to improve the accuracy in biometric identification: (a) improving modules such as (a1) sensors, (a2) feature extractors, and (a3) matchers; (b) adopting multimodal biometric techniques [17]. Multimodal biometric techniques use multiple biometric sources of information (such as fingerprint, face, and iris) and can be classified into three categories [17]: (b1) feature level fusion, (b2) score level fusion, and (b3) decision level fusion. They combine the multiple biometric features, scores (similarities or distances), and final outputs (identification results), respectively.

Strategies to improve the response time in biometric identification are as follows: (i) improving matching algorithms; (ii) using classification / indexing techniques at the feature level [11]; (iii) using distance-based indexing techniques [7] which have been developed in the area of similarity search. The first strategy reduces the one-to-one matching time (time to match one query sample with one template), while the second and third strategies reduce the number of templates to be matched with a query sample. Distance-based indexing techniques reduce the number of objects to be matched with a query only using distances between objects. Thus, they can be applied to biometric identification as a speed-up technique at the score level.

Figure 1 shows the strategies to improve the accuracy and the response time in biometric identification (we refer to the user who inputs a query sample as a claimant). Among
In biometric identification, two kinds of error rates are defined: FRR (False Reject Rate) and FAR (False Accept Rate). FRR is the probability that a genuine individual is rejected as an impostor, while FAR is the probability that an impostor is accepted as a genuine individual. Similarly, $FRR(N)$ and $FAR(N)$ are defined in identification [4]. $FRR(N)$ is the probability that an enrollee is rejected as a non-enrollee, and $FAR(N)$ is the probability that a non-enrollee is accepted as some enrollee. Although EFAR (Enrollee False Accept Rate), the probability that an enrollee is accepted as another enrollee, is also defined in [12], it is not used in this paper for simplicity (we evaluated the $FRR(N)$ - EFAR curves along with the $FRR(N)$ - FAR(N) curves in our experiment, and confirmed the similar trade-offs were obtained). $FRR(N)$ and $FAR(N)$ can be written as follows [4]:

$$FRR(N) = FRR$$

(1)

$$FAR(N) \approx N \times FAR.$$  

(2)

That is, $FAR(N)$ increases almost in proportion to the number of enrollees $N$.

The one-to-many matching time also increases almost in proportion to the number of enrollees $N$. Especially, when a score level fusion technique which combines scores from $M$ modalities is used to improve the accuracy, the system is required to calculate $MN$ scores in total. Thus, if $MN$ is very large, or it takes much time to calculate one score, the response time is $O(MN)$. A classification / indexing technique [7, 11] can be used to reduce the number of score calculations. The performance of such a technique is measured by the probability that the system fails to match the template of the enrollee identical to the claimant and the percentage of templates the system has to match with the query sample. They are referred to as the retrieval error rate and the penetration rate, respectively [11].

3. Related Work

3.1. Score Level Fusion

Although some score level fusion techniques were proposed in biometric identification, we focus on the techniques based on the Bayes decision rule [12, 14]. The Bayes decision rule minimizes the identification error rate in multi-class classification by selecting the class whose posterior probability of being a correct answer is the highest [8]. Nandakumar et al. [14] proposed a fusion technique in identification which calculates for each enrollee the posterior probability of being identical to the claimant after calculating all scores. They also demonstrated that the technique can handle the missing data in the form of missing templates, query samples, or incomplete score lists from the individual matchers. Another example is a sequential fusion technique proposed by Murakami and Takahashi [12] which calculates the posterior probabilities and makes a decision each time the claimant inputs a query sample. It was shown that this technique improved the accuracy while keeping down the number of biometric inputs in identification.
3.2. Distance-based Indexing

Maeda et al. [10] proposed a distance-based indexing technique to improve the response time in biometric identification. This technique calculates the score between every pair of templates and constructs the \( N \times N \) score matrix in advance. During the one-to-many matching process, it calculates the correlation between the vector comprising the scores with the query sample and each row of the matrix, selecting the template whose correlation is the highest as a next to be matched. This technique can be regarded as a modification of AESA (Approximating and Eliminating Search Algorithm) [21] to skip the elimination step based on the triangle inequality. Although AESA can significantly reduce the number of objects to be matched with a query [7], it requires an index space quadratic with the number of objects (i.e. the \( N \times N \) matrix). Glenn and Potts [2] proposed another technique in biometric identification, where \( P (\leq N) \) templates (referred to as pivots) are randomly selected from \( N \) templates in the database, and the query sample is matched with all pivots. The obtained scores are used as a feature vector for clustering to reduce the number of remaining templates (referred to as non-pivots) to be matched.

In this paper, we use the permutation-based indexing technique [1, 6] which is one of the state-of-the-art distance-based indexing techniques. It is simple to implement, requires an index space linear with the number of objects, and has been shown to outperform other techniques in some cases by a wide margin [6].

3.2.1 Permutation-based Indexing

Let us explain the algorithm of the permutation-based indexing technique [1, 6]. It belongs to the category where non-pivots are matched with a query in ascending (or descending) order of some values which are easily calculated and highly relevant to the true scores. In this paper we refer to such a value as a pseudo-score.

To begin with, the index is constructed as follows: (1) \( P \) \((\leq N)\) pivots are selected from \( N \) objects in the database (at random [6], for example); (2) For each non-pivot, a permutation where the pivot IDs are written in ascending (or descending) order of similarity scores (or distances) with the non-pivot is obtained and stored. The index is a set of \( N - P \) permutations, and the index space is \( O(N) \).

At query time, the distance between two permutations is used as a pseudo-score, and the search is carried out as follows: (1) Scores between the query and all pivots are calculated, and a query’s permutation is obtained; (2) Pseudo-scores between the query and all non-pivots are calculated; (3) Scores between the query and non-pivots are calculated in ascending order of pseudo-scores, until the number of score calculations with non-pivots reaches the threshold \( T \) \((\leq N - P)\); (4) The result of either range queries or K-

![Figure 2. Permutation-based indexing (\( P = 4 \) and \( N = 10 \)).](image)

NN queries is output. As a distance measure between two permutations, Spearman Rho, for example, can be used [6]. Spearman Rho sums up the squares of the differences in the positions of each pivot ID in two permutations. Figure 2 shows the example of the permutation-based indexing technique when \( P = 4, N = 10 \) and Spearman Rho is used as a distance measure between two permutations.

Although the permutation-based indexing technique uses the distance between two permutations as a pseudo-score, other techniques use the different value as a pseudo-score: the distance between two vectors comprising the distances with all pivots [6]; the estimate of the distance to the query [9]; the posterior probability of being a correct answer in range queries [13].

4. Biometric Identification Using Score Level Indexing and Fusion

We propose a technique which combines the score level fusion technique based on the Bayes decision rule and the permutation-based indexing technique (although other fusion or indexing techniques can be used instead, it is outside the scope of this paper). In order to reduce the retrieval error rate in multibiometric identification, our technique takes a strategy to select the non-pivot of the enrollee whose posterior probability of being identical to the claimant is the highest as a next to be matched.

Although this strategy selects non-pivots based on the posterior probabilities in the same way as [13], it differs from [13] in two points: (1) it calculates the posterior probability using not only pseudo-scores but scores obtained up to then; (2) it calculates the posterior probability of being identical to the claimant, for each enrollee (not for each non-pivot). The reason for the second point is that our aim is to quickly find the enrollee identical to the claimant (i.e. to reduce the retrieval error rate) and such an enrollee can be quickly found by combining multiple sources of information (i.e. scores and pseudo-scores of multiple modalities) about the enrollee.
4.1. The Proposed Algorithm

Let us explain our algorithm. First of all, our technique focuses on multiple different biometrics (or multiple fingers) [4] that use \( M \) different modalities (or fingers), because we assume all scores are independent in Section 4.2. Table 1 defines the notation used in the proposed algorithm. Before authentication, \( N \) enrollees are divided into \( P \) enrollees who have \( M \) pivots and \( N - P \) enrollees who have \( M \) non-pivots. Then, the index is constructed for each modality in the same way as the permutation-based indexing technique (see Section 3.2.1). The number of permutations stored in the database is \( M(N-P) \) in total.

Figure 3 shows the flowchart of the proposed one-to-many matching and identification process, where \( P(u_k \mid \cdot) \) (0 \( \leq k \leq N \)) denotes the posterior probability that the claimant is \( u_k \). Figure 4 shows the example of the matching flow. The order of modalities in which non-pivots are matched is fixed in advance. After the claimant inputs all query samples, the process of the one-to-many matching and identification is carried out as follows.

1. All pivots are matched (\( \mathcal{S}_P \) is obtained), and the claimant’s permutations (\( M \) permutations in total) are obtained.

2. All pseudo-scores are calculated (\( \tilde{\mathcal{S}}_N \) is obtained).

### Table 1. Notations used in the proposed algorithm.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>( N )</td>
<td>number of enrollees</td>
</tr>
<tr>
<td>( P )</td>
<td>number of enrollees who have pivots</td>
</tr>
<tr>
<td>( M )</td>
<td>number of modalities</td>
</tr>
<tr>
<td>( T )</td>
<td>threshold for the number of score calculations with non-pivots</td>
</tr>
<tr>
<td>( u_i, u_0 )</td>
<td>i-th enrollee / non-enrollee</td>
</tr>
<tr>
<td>( s_n )</td>
<td>score with the i-th enrollee’s m-th template</td>
</tr>
<tr>
<td>( \tilde{s}_n )</td>
<td>pseudo-score with the i-th enrollee’s m-th template</td>
</tr>
<tr>
<td>( M_n(t) )</td>
<td>number of n-th enrollee’s non-pivots already matched after matching non-pivots for ( t ) times</td>
</tr>
<tr>
<td>( U_N^{(t)} )</td>
<td>set of enrollees who have one or more non-pivots not matched yet after matching non-pivots for ( t ) times</td>
</tr>
<tr>
<td>( \mathcal{S}_P )</td>
<td>set of scores with pivots</td>
</tr>
<tr>
<td>( \tilde{\mathcal{S}}_N )</td>
<td>set of pseudo-scores with non-pivots</td>
</tr>
<tr>
<td>( \mathcal{S}_N^{(t)} )</td>
<td>set of scores with non-pivots after matching non-pivots for ( t ) times</td>
</tr>
</tbody>
</table>

\( (1 \leq i \leq N, P + 1 \leq n \leq N, 1 \leq m \leq M, 0 \leq t \leq T) \)

\[
\begin{align*}
4.1. & \text{ The Proposed Algorithm} \\
\text{Let us explain our algorithm. First of all, our technique focuses on multiple different biometrics (or multiple fingers) [4] that use } & \text{\( M \) different modalities (or fingers), because we assume all scores are independent in Section 4.2. Table 1 defines the notation used in the proposed algorithm. Before authentication, } \text{\( N \) enrollees are divided into } \text{\( P \) enrollees who have } \text{\( M \) pivots and } \text{\( N - P \) enrollees who have } \text{\( M \) non-pivots. Then, the index is constructed for each modality in the same way as the permutation-based indexing technique (see Section 3.2.1). The number of permutations stored in the database is } \text{\( M(N-P) \) in total.} \\
\text{Figure 3 shows the flowchart of the proposed one-to-many matching and identification process, where } & \text{\( P(u_k \mid \cdot) \) (0 \( \leq k \leq N \)) denotes the posterior probability that the claimant is } \text{\( u_k \). Figure 4 shows the example of the matching flow. The order of modalities in which non-pivots are matched is fixed in advance. After the claimant inputs all query samples, the process of the one-to-many matching and identification is carried out as follows.} \\
& 1. All pivots are matched (\( \mathcal{S}_P \) is obtained), and the claimant’s permutations (\( M \) permutations in total) are obtained. \\
& 2. All pseudo-scores are calculated (\( \tilde{\mathcal{S}}_N \) is obtained). \\
\end{align*}
\]

3. The enrollee \( u_n^* \) who satisfies the following is selected:

\[
\begin{align*}
\text{where } t \text{ denotes the number of score calculations with non-pivots. That is, the enrollee is selected whose posterior probability of being identical to the claimant, using all pseudo-scores and scores obtained up to then, is the highest. Then, the non-pivot of } u_n^* \text{ which is not matched yet is selected and matched with the query sample (} \mathcal{S}^{(T+1)}_N \text{ is obtained). Calculation of } P(u_n \mid \mathcal{S}_P, \tilde{\mathcal{S}}_N, \mathcal{S}_N^{(t)} \text{ is explained in Section 4.2. This step is repeated until } t \text{ reaches the threshold } T. \\
& 4. If the highest posterior probability } P(u_k \mid \mathcal{S}_P, \tilde{\mathcal{S}}_N, \mathcal{S}_N^{(T)}) \text{ exceeds the threshold } P_{th}, \text{ the claimant is iden-}
\end{align*}
\]
4.2. Calculation of Posterior Probabilities

The calculation of $P(u_n | S_P, S_N, S^{(t)}_N)$ ($0 \leq k \leq N, 0 \leq t \leq T$) is complicated due to the correlation among the pseudo-scores and the scores. First, $S_P$ and $S_N$ are very highly correlated with each other because $S_N$ is uniquely obtained from $S_P$. Since $S_P$ is a set of scores with pivots and $S_N$ is a set of pseudo-scores with non-pivots, they are useful in calculating the posterior probability of the enrollees who have pivots and non-pivots, respectively. Thus, we approximate the above posterior probability by $P(u_n | \tilde{S}_N, S^{(t)}_N)$ ($P + 1 \leq n \leq N$) in selecting the non-pivot to be matched, and by $P(u_n | S_P, S^{(t)}_N)$ ($0 \leq k \leq N$) in identifying the claimant.

We next consider the correlation between $\tilde{S}_N$ and $S^{(t)}_N$ in calculating $P(u_n | \tilde{S}_N, S^{(t)}_N)$. A pseudo-score can be regarded as an indirect score between two biometric samples using the distance between two permutations, while a score is a direct one between the two. That is, $\tilde{S}_N$ and $S^{(t)}_N$ can be regarded as scores from multiple matchers (one outputs $\tilde{S}_N$, and the other outputs $S^{(t)}_N$) [4], and strictly speaking, they should be assumed as independent. However, another problem in calculating $P(u_n | \tilde{S}_N, S^{(t)}_N)$ is that we have to do so very quickly in order to reduce the response time. In this paper, to simply calculate $P(u_n | \tilde{S}_N, S^{(t)}_N)$, we assume the information sources from multiple matchers (i.e. $\tilde{S}_N$ and $S^{(t)}_N$) are independent in the same way as [15].

That is, we assume that each pseudo-score $\tilde{s}^m_n \in \tilde{S}_N$ and each score $s^m_n \in S^{(t)}_N$ is independent, and that genuine / impostor pseudo-scores and scores of the $m$-th modality are generated from $g^m_{gen}(\tilde{s}^m_n)$ / $g^m_{imp}(\tilde{s}^m_n)$ and $f^m_{gen}(s^m_n) / f^m_{imp}(s^m_n)$, respectively. Then, $P(u_n | \tilde{S}_N, S^{(t)}_N)$ is written using Bayes’ Theorem as follows:

$$P(u_n | \tilde{S}_N, S^{(t)}_N) = \frac{\exp \left( Y_n^{(t)} \right) P(u_n)}{\sum_{\kappa=0}^{N} \exp \left( Y^{(t)}_\kappa \right) P(u_n)}, \quad (4)$$

where

$$Y^{(t)}_\kappa = \begin{cases} \sum_{m=1}^{M} G^m(\tilde{s}^m_{\kappa}) + \sum_{\mu=1}^{M^{(t)}} F^\mu(s^\mu_{\kappa}) & (\text{if } P + 1 \leq \kappa \leq N) \\ 1 & (\text{if } 0 \leq \kappa \leq P) \end{cases} \quad (5)$$

and

$$G^m(\tilde{s}^m_{\kappa}) = \log(g^m_{gen}(\tilde{s}^m_{\kappa})/g^m_{imp}(\tilde{s}^m_{\kappa})) \quad (6)$$

$$F^m(s^m_{\kappa}) = \log(f^m_{gen}(s^m_{\kappa})/f^m_{imp}(s^m_{\kappa})) \quad (7)$$

$G^m(\cdot)$ and $F^m(\cdot)$ are log-likelihood ratio function of a pseudo-score and a score, respectively. They are trained using the templates in the database or the biometric samples collected in advance. This is done by assuming, for example, the logistic regression model which is valid in rather general cases [3] and whose effectiveness is shown in multimodal biometrics [12, 20].

Another advantage of assuming the logistic regression model is that we can calculate $Y_n^{(t)}$ very quickly. Since it models $G^m(\cdot)$ and $F^m(\cdot)$ as a linear function of a score, we can update $Y_n^{(t)}$ by only one multiplication and one addition each time a non-pivot is matched. Furthermore, if the prior probabilities $P(u_n)$ ($P + 1 \leq n \leq N$) are uniform in equation (4), we only have to calculate $Y_n^{(t)}$ instead of $P(u_n | \tilde{S}_N, S^{(t)}_N)$ because the enrollee whose $Y_n^{(t)}$ is the highest is identical to the one whose $P(u_n | \tilde{S}_N, S^{(t)}_N)$ is the highest. In our experiments, the time to calculate $Y_n^{(t)}$ and select $\hat{u}_n^*$ was negligible, compared to the time to match a query sample with one non-pivot.

$P(u_n | S_P, S^{(t)}_N)$ is written, by assuming all scores are independent, as follows:

$$P(u_n | S_P, S^{(t)}_N) = \frac{\exp \left( Z^{(t)}_\kappa \right) P(u_n)}{\sum_{\kappa=0}^{N} \exp \left( Z^{(t)}_\kappa \right) P(u_n)}, \quad (8)$$

where

$$Z^{(t)}_\kappa = \begin{cases} \sum_{m=1}^{M} F^m(s^m_{\kappa}) & (\text{if } 1 \leq \kappa \leq P) \\ \sum_{\mu=1}^{M^{(t)}} F^\mu(s^\mu_{\kappa}) & (\text{if } P + 1 \leq \kappa \leq N) \\ 1 & (\text{if } \kappa = 0). \end{cases} \quad (9)$$

This formula is equivalent to that of the score level fusion technique which handles the missing data ($M(N - P) - T$ scores are missing in total) [14].

5. Experimental Evaluation

We used the Biosecure DS2 dataset (cost-sensitive evaluation set) [16] and the CASIA-FingerprintV5 [5] to evaluate our technique in the dataset of multiple different biometrics and multiple fingers, respectively. For comparison, we evaluated the following strategies:

1. **Unimodal biometrics**: After matching all templates of a single modality ($N$ scores in total), it identifies a claimant by comparing scores to the threshold.

2. **Fusion**: After matching all templates of $M$ modalities ($MN$ scores in total), it identifies a claimant by comparing posterior probabilities to the threshold [14].

3. **Indexing and fusion (pseudo-score)**: After matching all $MP$ pivots, it selects $T$ non-pivots from $M(N - P)$
non-enrollees to be as much as possible in order to calculate FRR(\text{N}) and FAR(\text{N}). Then, it identifies a claimant by comparing \( P(u_k | S_p, S_N^{(T)}) \) to the threshold.

4. Indexing and fusion (proposed): After matching all \( MP \) pivots, it selects the non-pivot of the enrollee whose \( P(u_k | S_N, S_N^{(t)}) \) is the highest as a next to be matched, until the number of score calculations with non-pivots \( t \) reaches \( T \) (\( MP + T \) scores in total). Then, it identifies a claimant by comparing \( P(u_k | S_p, S_N^{(T)}) \) to the threshold.

The third strategy, which we devised for comparison, simply combines the permutation-based indexing technique and the score level fusion technique based on the Bayes decision rule. In the CASIA-FingerprintV5, we measured the time to identify the claimant after obtaining the input images, and controlled \( T \) in the third and fourth strategies so that the average identification time would be the desired value.

5.1. Biosecure DS2 dataset

We first used the Biosecure DS2 dataset (cost-sensitive evaluation set) [16]. This dataset contains scores of fingerprints (left and right thumb / index / middle finger), faces, and irises from 207 subjects (each subject contributed 4 samples including one template). In this paper we used scores of right index fingerprints, faces, irises (\( 3 \times 207 \times 4 \) scores in total including scores between templates).

We divided 207 subjects into 20 subjects who enrolled pivots, 160 subjects who enrolled non-pivots (\( P = 20, N = 180 \)), and 27 non-enrollees (we randomly chose 100 ways to divide). Then, we divided 3 samples of each enrollee except the template into one training sample and 2 query samples (we used 4 samples of each non-enrollee as query samples). We set the prior probabilities \( P(u_k) \) (\( 0 \leq k \leq N \)) to be uniform, used the logistic regression model to estimate \( G^m() \) and \( F^m() \), and trained for each modality the regression coefficients common to all enrollees using 180 templates and 180 training samples. We controlled \( T \) so that the penetration rate would be the desired value. We tried all of 6 (= 3!) ways with regard to the order of modalities in which non-pivots are matched. We evaluated the performance when all the enrollees and non-enrollees input all the modalities twice and four times, respectively (180 \( \times 6 \times 2 \times 100 = 216000 \) accesses by enrollees, 27 \( \times 6 \times 4 \times 100 = 62400 \) attacks by non-enrollees).

Figure 5 shows the relationship between the penetration rate and the retrieval error rate in the two combination

\begin{align*}
\text{Figure 5. Penetration rate versus retrieval error rate in the Biosecure DS2 dataset.}
\end{align*}

We secondly used the CASIA-FingerprintV5 [5] which contains 20000 fingerprint images (left and right thumb / index / middle / ring finger) from 500 subjects (each subject contributed 5 samples per finger). We selected one sample per finger as a template and calculated the scores using SourceAFIS Version 1.4 [18]. We used scores of left and right thumb / index finger (\( 4 \times 500 \times 500 \times 5 \) scores in total including scores between templates).

We divided 500 subjects into 32 subjects who enrolled pivots, 418 subjects who enrolled non-pivots (\( P = 32, N = 450 \)), and 50 non-enrollees (we randomly chose 10 ways to divide). Then, we divided 4 samples of each enrollee except the template into one training sample and 3 query samples (we used 5 samples of each non-enrollee as query samples). We set the prior probabilities \( P(u_k) \) (\( 0 \leq k \leq N \)) to be uniform, used the logistic regression model to estimate \( G^m() \) and \( F^m() \), and trained, for each finger type, the regression coefficients common to all enrollees using 450 templates and 450 training samples. We controlled \( T \) so that the average identification time would be the desired value. We tried all of 24 (= 4!) ways with regard to the order of finger types. We evaluated the performance when all the enrollees

\begin{align*}
\text{Figure 6. FRR(N) - FAR(N) curves in the Biosecure DS2 dataset (the number of score calculations was 180 in unimodal, 540 in fusion, and 162 in indexing and fusion, respectively).}
\end{align*}
and non-enrollees input all the fingers 3 times and 5 times, respectively (450 × 24 × 3 × 10 = 324000 accesses by enrollees, 50 × 24 × 5 × 10 = 60000 attacks by non-enrollees).

Figure 7 shows the relationship between the average identification time and the retrieval error rate in the two combination techniques. It took on average 13.4 [ms] to extract a feature from one image, and 1.12 [ms] to match a query sample with one template. The other processing time was negligible. Figure 8 shows the FRR(N) - FAR(N) curves where the average identification time in the combination techniques was fixed to 1.0[s] (It took on average 0.58[s] and 2.3[s] to identify the claimant in the unimodal biometrics and the fusion technique, respectively).

6. Discussions

It was found from the results that the poor performance of the unimodal biometrics was improved using indexing and fusion techniques while reducing the number of score calculations in the Biosecure DS2 dataset, and keeping the average identification time to be 1.0[s] in the CASIA-FingerprintV5, respectively. This indicates that they make possible fast and accurate biometric identification whether applied to multiple different biometrics or multiple fingers. It was also found that our proposal significantly reduced the retrieval error rate and resulted in the better performance, compared to the simple combination technique which orders non-pivots by pseudo-score. Our proposal realized the performance close to the fusion technique which calculates as much as MN scores. This demonstrates the effectiveness of selecting non-pivots based on the posterior probabilities of being identical to the claimant obtained from both pseudo-scores and scores.

However, we need a more thorough investigation. We need to investigate how discriminative information the pseudo-scores capture, and whether the log-likelihood ratios can be correctly modeled as a linear function of the scores and the pseudo-scores. Furthermore, although we tried all the order of modalities in which non-pivots are matched, it is preferable to start calculating scores from the fast or accurate modality. For example, if the system starts calculating scores from the faster modality, it can calculate more scores and reduce the retrieval error rate within the fixed response time. On the other hand, if it starts from the more accurate modality, the accuracy can be improved by combining scores which capture more discriminative information. We need to investigate the optimal order of modalities with respect to the retrieval error rate and the accuracy. We also need to evaluate our technique in the sequential fusion scenario [12] to validate whether it keeps high convenience even if the number of modalities M has to be very large to keep high accuracy in the large-scale applications.

7. Conclusion

In this paper, we proposed a technique which combines score level fusion and distance based indexing to improve both the accuracy and the response time in biometric identification. We evaluated our technique using the Biosecure DS2 dataset and the CASIA-FingerprintV5 which are the dataset of multiple different biometrics and the multiple fingers, respectively. The results showed that our technique significantly improved the accuracy while reducing the number of score calculations or keeping the average identification time to be 1.0[s], compared to the unimodal biometrics. Future work includes as follows: (1) the analysis of pseudo-scores and the validity of the logistic regression model; (2) the investigation of the optimal order of modalities in which non-pivots are matched; (3) the evaluation of our technique in the sequential fusion scenario.

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