Parallel versus Serial Classifier Combination for Multibiometric Hand-Based Identification

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Abstract. This paper presents an approach for optimizing both recognition and processing performance of a biometric system in identification mode. Multibiometric techniques facilitate bridging the gap between desired performance and current unimodal recognition rates. However, traditional parallel classifier combination techniques, such as Score sum, Borda count and Highest rank, cause further processing overhead, as they require a matching of the extracted sample with each template of the system for each feature. We examine a framework of serial combination techniques, which exploits ranking capabilities of individual features by reducing the set of possible matching candidates at each iteration, and we compare its performance with parallel schemes. Using this technique, both a reduction of misclassification and processing time in identification mode will be shown to be feasible for a single-sensor hand-based biometric system.

Keywords: Multibiometrics, serial combination, hand biometrics.

1   Introduction

Recently, a number of biometric systems have exploited advantages of multi-instance and multi-algorithm approaches to biometric recognition based on single-sensor input. In particular, such systems benefit of increased matching accuracy, more difficult biometric attacks, reduced enrollment errors in case of failures to extract single biometric traits and, finally, a less complex acquisition procedure [1,2,3]. For single-sensor fusion of iris and face a combined feature achieved 99.75% Genuine Acceptance Rate (GAR) compared to 97.35% GAR for face and 95.42% GAR for iris at 0.1% False Acceptance Rate (FAR) in [1]. A similar result was obtained for fusion of hand-based modalities with reported perfect classification compared to 91.5% GAR at 0.01% FAR for palmprints only and 95-99.9% GAR for individual fingers in [2] and good separation with 0.08% Total Error Rate (TER) compared to 0.24% TER for the best single feature (Minutiae) in [3]. All these studies combined matching scores by employing min-max score normalization and (weighted) sum of scores. While this technique seems to be a good choice outperforming many other alternatives [4,5], processing time requirements are not optimized.

In a system with m biometric matchers M_i, $1 \leq i \leq m$ in identification mode, each sample B is matched against the whole system database $D =$

$\{T_1, T_2, \ldots T_t\}$. In case of parallel fusion methods based on the outcome of comparisons $M_i(B, T_j)$, an identification involves $m \cdot t$ matches, i.e. for the total processing time T_p in a single-processor environment we have:

$$T_p = \sum_{j=1}^{t}(C_p + \sum_{i=1}^{m} P_{ij}) \tag{1}$$

where P_{ij} denotes the processing time required for the comparison $M_i(B, T_j)$ and C_p is the time needed for parallel combination. Even if C_p is insignificant, still this term increases linear in the number of users t with a potentially large factor m. You et al. [6] identified this problem and proposed a 4-level hierarchical multifeature coding scheme to facilitate coarse-to-fine matching for palmprints. In this scheme, levels 1-3 reduce the initial set $D_1 := D$ of possible candidates (leading to candidate sets $D_{i+1} \subset D_i \; \forall i < m$) and level 4 performs final matching on D_m. With the preclassification capabilities of fast geometry-based features and final decision by an accurate (but costly) texture-based feature, processing time compared to sequentially executed parallel schemes were reduced from 6.7 seconds to 2.8 seconds in [6]. A similar idea was used in [7] for face detection, where simpler, yet fast classifiers rejected a majority of sub-windows before more complex, but accurate cascaded classifiers guaranteed a low false detection rate.

We extend the approach in [6] and formulate a framework of serial combinations, which, apart from the reduction of candidates, introduces additional information flow between levels by accumulating matching information according to the fusion rule. Serial processing time T_s can be estimated as follows:

$$T_s = \sum_{i=1}^{m}(C_s(i) + \sum_{j \in I(D_i)} P_{ij}) \tag{2}$$

where $I(D_i)$ denotes the index set of templates in D_i and $C_s(i)$ is the time needed for serial combination at level i. With this modification, as will be shown, both a reduction of processing time and increased accuracy can be achieved at the same time. Another contribution of this work is a performance comparison with respect to processing time and accuracy of well-known fusion rules Sum, Borda count and Highest rank in parallel form and (to be defined) serial application using a hand-based multibiometric system. The third contribution of this work is an assessment of individual Minutiae and Eigenfinger-based classifiers in identification mode when operating on single-sensor data, as motivated in [8]. Finally, we present an optimal solution for the employed hand-biometric system minimizing a cost function $C = \omega_1 * (1 - RR) + \omega_2 * T$ with RR being the Rank-1 Recognition Rate, T the processing time, and ω_1, ω_2 weights for misclassification and processing costs.

This paper is structured as follows: An introduction to system design for both parallel and serial setups and employed features is given in Sect. 2. Section 3 presents an overview of implemented parallel and serial combination methods. Employed biometric databases, performance indicators and experimental results are summarized and discussed in Sect. 4. Finally, Sect. 5 forms the conclusion.

2   System Setup

In order to evaluate both serial and parallel classifier combination, our multi-biometric identification system [3] employs exclusive modules for each of the examined combination schemes, see Fig. 1.
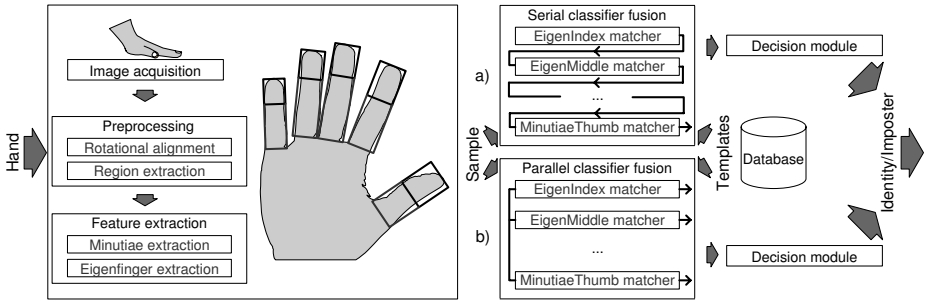
Fig. 1. Experimental setup using a) serial and b) parallel combinations of classifiers

2.1   Proprocessing

At image acquisition stage, each palmar hand is sensed using a HP Scanjet 3500c flatbed scanner sensor. After binary segmentation using Otsu's method and localization of the hand within the image, visible parts of the arm are removed. Translational and rotational invariance are achieved using an iterative algorithm, which aligns each hand based on a hand coordinate system. Its origin is defined as the inter-finger valley between ring and middle finger and the direction of the least-squares approximated outer palm boundary is used for alignment. This method provides better results than traditional moment-based best-ellipse fitting [9], as it is less degraded by different spreadings of fingers, partially visible arms or jewelery in the image. However, if applied to individual fingers, moment-based fitting can improve inter-finger valley and finger tip detection rates.

2.2   Feature Extraction

Results of the preprocessing stage are rectilinear finger images at 100 dpi resolution and contrast-limited adaptive-histogram equalized high-resolution 500 dpi images of the finger tips, illustrated as bounding boxes aligned to each finger in Fig. 1. The task of feature extractors, operating each on a single region, is to extract a feature vector representation. Each extractor contributes its representation to a common augmented template, individual matchers are designed to extract the corresponding features from the common representation and return a scalar value for each match, as defined in Sect 1. Finally, the first rank of the combined ranking vector is used for identity determination within the decision module.

Minutiae Feature Extraction and Matching. Ridge bifurcation and termination points (position, orientation and quality) are extracted from finger-tip images using NIST's *mindtct* [10]. Main processing steps for Minutiae extraction comprise [11]: generation of image maps (e.g. ridge orientation maps), Minutiae detection (by local binarization and pattern matching), and filtering (removing false Minutiae in specific configurations). As Minutiae sets are not pre-aligned by this feature extractor, an optimal pairing between Minutiae sets has to be performed at matching stage (we use NIST's *bozorth3* [10] matcher for this task). Unfortunately this task requires significantly more processing time than just distance-based matching. The processing overhead becomes even more visible in our experiment, as we employ *bozorth3* in 1:1 comparison mode.

Eigenfingers Feature Extraction and Matching. For the Eigenfingers feature, which is based on principal component analysis, we adopt the algorithm proposed by Turk and Pentland [12], which also works well for fingers [13]. Feature extraction requires a pre-calculation of a so-called eigenspace for each finger type, spanned by the most significant eigenvectors obtained from the covariance matrix of mean-normalized training samples (we used a separate dataset of 25 hand-prints and also selected 25 as feature size). The feature vector is composed of the projection coefficients of the normalized finger images projected onto their eigenspace. Therefore, it represents low-resolution 128×384 index, middle, ring fingers and 128×256 thumb and little fingers in an optimal way. In order to obtain matching scores, Manhattan distance is employed in the feature space.

2.3   Matching

Matchers can be distinguised into different groups depending on the type of information provided [14]:

1. **Measurements:** $M_i(B, D) = S_i \in \mathbb{R}^t$ is a measurement vector with its j-th element $S_i[j]$, $1 \leq j \leq t$, indicating the degree that B and T_j correspond to the same identity.
2. **Ranks:** $M_i(B, D) = I_i \in \mathbb{N}^t$ is a rank index vector, where $I_i[j] = x$ indicates, that the template $T_x \in D$, $1 \leq x \leq t$ is ranked at the j-th position. Closely related to the index vector is its corresponding rank vector R_i satisfying:

$$\forall j, x \ with \ 1 \leq j, x \leq t : I_i[j] = x \Leftrightarrow R_i[x] = j. \tag{3}$$

3. **Labels:** in case of fully-automatic systems, only the top first rank or class with the highest score is relevant.

In this paper, we focus on combination schemes at rank and measurement level (see also [15]). Furthermore, we conduct both open-set (with *reject* option [16]) and closed-set identification (system users are identified only) experiments using different ranking dimensions. Since the reject decision is facilitated by thresholding single matching results and returning only classes where the corresponding matching score exceeds a predefined threshold, we interpret a rank index vector with dimensionality zero as a reject.

3   Parallel and Serial Classifier Combinations

In our biometric identification experiments, individual classifiers are *distance classifiers* in the context of [14], i.e. each matcher calculates a distance or similarity between the given template B and each enrolment-template T_j of the system database, see Sect. 1. Following the transformation-based fusion approach [15], distance scores $y = M_i(B, T_j)$ are at first converted into similarity scores by subtraction from an empirically found maximum. Resulting values y' are then mapped to the unit interval $[0, 1]$ using *min-max* normalization [15]. Since normalized scores may be interpreted as some kind of posterior probability $P(B \equiv T_j | B)$ [14], individual matchers may be incorporated in each of the introduced combination strategies *measurement* (using the normalized score vector), *rank* (by simply ranking measurements) and *abstract*-level (using the Bayes-rule estimating the class with the highest posterior probability [14]).

Combining measurements, ranks or labels of individual classifiers has long tradition in pattern recognition. A comprehensive overview of classifier combination techniques including Average Bayes Classifiers, Voting-based schemes and classifiers based on Dempster-Shafer Theory is given in [14]. Combination rules are derived in [5] using Bayesian statistics. A framework for generalized classifier combinations is introduced in [17], with Borda count, Logistic regression and Highest rank combination methods as special cases. According to [18], classifier combination schemes can be divided into *fixed rules* (with all classifiers assumed to exhibit equal performance), *trained rules* (introducing weights to account different strengths) and *adaptive rules* (weights depend on environmental factors). We apply traditional fixed parallel rank and measurement combination rules [15], as they do not need separate training datasets, and compare their serial and parallel implementation with respect to accuracy and performance.

1. **Borda count** (BC): With this technique, rank index vectors I_i of different classifiers M_i are combined to form a consolidated rank index vector I_{BC} by estimating the sum of all ranks of individual classifiers as follows:

$$I_{\text{BC}} \in \mathcal{S}_t : \forall k, l \text{ with } 1 \leq k < l \leq t \Rightarrow \sum_{i=1}^{m} R_i[I_{\text{BC}}[k]] \leq \sum_{i=1}^{m} R_i[I_{\text{BC}}[l]], \quad (4)$$

   where $\mathcal{S}_t$ is the set of all permutations of $\{1, \ldots, t\}$. If multiple such vectors exist, one is chosen randomly [15]. This method assumes equal performance of different matchers. Strengths of BC according to [17] are simplicity and no necessity for training. However, ties constitute a problem [18], especially for open set identification, where the sum of ranks for the rank-1 entry, $\sum_{i=1}^{m} R_i[I_{\text{BC}}[0]]$, is thresholded.

2. **Highest rank** (HR): This method assigns each user its minimum rank value (i.e. highest rank) of all classifiers, again with collisions removed randomly.

$$I_{\text{HR}} \in \mathcal{S}_t : \forall k, l \text{ with } 1 \leq k < l \leq t \Rightarrow \min_{i=1}^{m} R_i[I_{\text{HR}}[k]] \leq \min_{i=1}^{m} R_i[I_{\text{HR}}[l]].$$

$$(5)$$

Since neither rank index vectors reveal information for successful rejection of unseen objects, nor do any other measurements (like the sum of ranks for the rank-1 entry as employed for the BC) indicate genuine identification attempts for HR, we exclusively tested this mode in closed set identification.

3. **Score sum** (SS): This measurement combination method averages scores of matchers M_i, i.e. the common score vector is defined as $S_{\mathrm{SS}} := \frac{1}{m} \sum_{i=1}^{m} S_i$.

   If this measurement vector is to be converted into a rank vector, again we have to break up ties randomly. However, as the set of scores is dense, we further expect strengths of this matcher in open set identification.

For serial classifier combination, these rules remain unchanged, but input and output interfaces for single matchers change. The order of matchers, their dimensionality and the combination rule define a serial classifier combination.

1. **Sequential order of matchers:** The matcher M_i is applied to a subset of templates in D specified by a characteristic function c_i, i.e. $M_i(B, D, c_i)$. In order to leave introduced rules unchanged, for elements j with $c_i(j) = 0$ we technically set $R_i[j] := \infty$ in case of BC and HR and $S_i[j] := 0$ in case of SS. Let R be the rank vector of the chosen combination rule using matchers $M_1, \ldots, M_i$ and $d[i]$ be the desired output dimension, then we define:

$$\forall j \; c_i(j) := \begin{cases} 1 \; if \; i = 1 \vee (i > 1 \wedge c_{i-1}(j) = 1 \wedge R[j] \leq d[i-1]), \\ 0 \; otherwise. \end{cases} \quad (6)$$

2. **Fixed dimensionality of each matcher's output in the chain:** We define decreasing dimensionalities $d[i], 1 \leq d[i] \leq t$ for each matcher M_i, such that $\forall i : i > 1 \Rightarrow d[i] < d[i-1]$. Finally, the resulting score or index vector is a transformed version of the outcome of the combination technique using all matchers $M_1, \ldots, M_m$ accounting the final dimensionality reduction to $d[m]$ ranks. Note, that the combination method for serial classifiers is applied m times (after each matcher) instead of just once for parallel combination.

4   Experiments

In our identification mode assessments we address absolute and relative performance differences between serial and parallel combination schemes with respect to accuracy and computational cost in both closed set and open set configurations, see Table 1. We try to identify how parameter choice (e.g. rule, order of matchers) for serial combinations influences results. In order to be able to compare performance of parallel or serial schemes relative to individual matchers, we also give a short summary of identification results for single classifiers.

As performance indicators we estimate *Cumulative Match Curves* (CMC) indicating for each rank r the relative frequency of genuine test templates (i.e. templates sharing the same identity with an enrolled template) having their corresponding identity-sharing enrolled template ranked in $\{1, \ldots, r\}$ [16]. For direct comparison, we use the RR measure (evaluating the CMC at rank 1).

Table 1. Comparison of parallel and serial combination results with individual classifiers in identification mode: RR = Rank-1 Recognition (%), RR_{FAR} = Rank-1 Recognition (%) at a specific FAR (%), T = Processing time (ms)
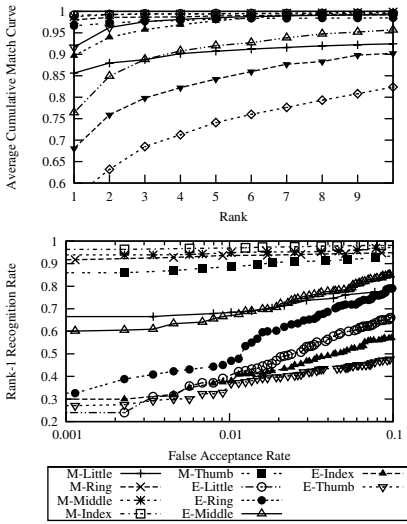
	Parallel classifier fusion			Serial classifier fusion						Minutiae		Eigenf.	
	BC	HR	SS	BC1	BC2	HR1	HR2	SS1	SS2	Index	Mid.	Mid.	Ring
Closed set identification													
RR	99.7	90.0	99.9	99.2	99.4	91.1	95.6	99.9	99.8	99.1	98.8	91.6	89.7
T	10338	10337	10338	2561	8110	2557	8108	2550	8109	5225	5111	< 1	< 1
Open set identification													
$RR_{0.1}$	95.9	–	97.4	89.6	95.0	–	–	97.6	97.4	95.6	92.6	60.1	32.6
RR_{10}	99.1	–	98.9	97.7	99.1	–	–	99.4	99.4	98.0	97.3	85.1	79.0
T	5189	–	5189	1235	4016	–	–	1232	4017	2623	2564	< 1	< 1

As the RR refers to correct rankings of genuine samples (and therefore includes false rejects, in which case the length of the ranking vector is zero), there is a tradeoff between RR and FAR (false acceptance rate of imposter samples) in threshold-based open set identification. We visualize this tradeoff by plotting both rates against each other, varying the threshold over its entire range.

For testing purposes we use a dataset of 443 palmar scans at 4250×5850 resolution (71 males and 15 females, at least 4 different templates per person), captured in a single session at arbitrary rotations in a controlled environment (direct exposure to ambient light was avoided by placing the sensor in a box with a hole for hand insertion). A total of 4 samples were rejected due to enrollment errors and further excluded from experiments. For closed set identification tests we set up 4 different enrollment databases from this dataset using the first, second, third and fourth template of each user as enrollment template. This yields a total of 353 possible comparisons of remaining templates with each system database. For open set identification, again we set up four system databases with randomly selected 43 users for each database using the first, second, third and fourth given template, respectively, as enrolment sample. In this configuration, a total of 177 genuine and 219 imposter identification attempts can be executed per system database. The presented identification scenarios are intended to reflect biometric applications for small-sized companies, e.g. presence detection for employees (closed-set) or access control applications (open set).

4.1   Individual Classifiers

Since not all combination techniques necessarily increase overall performance, we first assess closed set (86 enroled users) and open set (43 enroled users) identification performance of unimodal Minutiae matchers (*M-Thumb, M-Index, M-Middle, M-Ring, M-Little*) and Eigenfingers matchers (*E-Thumb, E-Index, E-Middle, E-Ring, E-Little*) in order to obtain reference rates. Closed-set recognition results in form of an average CMC (averaging results over all 4 system databases) are illustrated in Fig. 2. Presumably, the most accurate feature turned out to be *M-Index* with 99.1% RR, followed by *M-Middle* (98.8%),

Fig. 2. Closed set Average CMC (top), Open set RR-FAR Tradeoff (bottom)
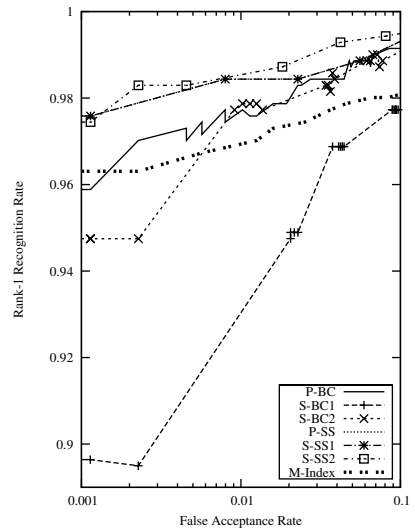
Fig. 3. Open set Recognition-Security Tradeoff for parallel/serial classifiers

M-Ring (98.0%), *M-Thumb* (96.7%), *E-Middle* (91.6%), *E-Ring* (89.7%), *M-Little* (85.6%) *E-Little* (76.4%), *E-Index* (68.1%), and *E-Thumb* (56.7%). However, whereas Minutiae features exhibit processing times of 2478 ms (*M-Little*), 4090 ms (*M-Thumb*), 4205 ms (*M-Ring*), 5111 ms (*M-Middle*) and 5225 ms (*M-Index*), all Eigenfinger-based features could create a ranking vector in almost less than 1 ms. More accurate Minutiae-based matchers tend to exhibit longer average processing times, as they usually operate on larger sets. *M-Little*'s CMC increases slowly with additional ranks, an undesired behavior for serial combination, as a dimensionality reduction may exclude the genuine identity.

Fig. 3 illustrates the tradeoff between RR and FAR for all features in open set identification. The best RR performance at 0.1% FAR is 95.6% (*M-Index*), while the worst performing feature (*E-Little*) only achieves 18.4%. Generally, in this configuration, Eigenfingers perform significantly worse than Minutiae-based features. If FAR is relaxed to 10%, RR reaches $48.2 - 98\%$. Regarding performance, single Minutiae-based classifiers require up to 2623 ms, whereas Eigenfingers remain at processing times of less than 1 ms.

4.2   Parallel versus Serial Classifier Combinations

The first question arising naturally when serial and parallel classifier combination techniques are compared is the choice of parameters for the serial combination scheme. Recall, that serial combinations are defined by rule, order, count and dimensionality of each matcher. As both the number of possible choices for dimensionalities and order of matchers grow exponentially in the number of matchers, an exhaustive search within a training set to find the best parameters becomes unfeasible if the number of matchers is large. For the comparison of serial and

parallel techniques, we restrict the set of possible individual classifiers to the best two Minutiae features *M-Index*, *M-Middle* and the two best Eigenfinger features *E-Middle* and *E-Ring*. In order to be independent of training datasets, we conservatively define a class reduction factor of two, i.e. $d[0] := \frac{t}{2}, d[i+1] := \frac{d[i]}{2}$, and examine two natural choices for the order of matchers:

- **Configuration 1:** In order to exploit the intrinsic property of class reduction in serial combinations, we select fast classifiers at lower ranks followed by more costly features, i.e. the order is *E-Middle, E-Ring, M-Index, M-Middle*.
- **Configuration 2:** Here we select matchers in the order of accuracy to avoid early loss of potential matches: *M-Index, M-Middle, E-Middle, E-Ring*.

Results of all employed parallel and serial combination experiments can be found in Table 1. In a first test we assessed closed set identification performance of the introduced combination rules Borda count (BC), Highest rank (HR) and Score sum (SS) in its parallel (*P-BC, P-HR, P-SS*) and serial forms (*S-BC1, S-HR1, S-SS1* for Configuration 1, and *S-BC2, S-HR2, S-SS2* using Configuration 2). Whereas for BC serial classifiers exhibit slightly worse accuracy ($99.2 - 99.4\%$ instead of 99.7%), serial SS combinations perform almost equally well ($99.8 - 99.9\%$) and serial HR even outperforms parallel techniques (up to 95.6% instead of 90%). However, serial combination techniques could reduce required processing time of parallel schemes significantly (up to a factor of 4 using the fast configuration, and at least by over 20% using the conservative configuration). When comparing different combination rules, SS combination performs best and is at the same time least affected by serial class reduction, followed by BC and the HR method, which is no good choice for the selected classifiers, as overall accuracy even degrades compared to individual classifiers.

When assessing open set identification mode performance of the BC and SS methods in Fig. 3, again SS turns out to be highly accurate. The faster serial combination technique *S-SS1* outperforms the best individual matcher (with 97.6% RR at 0.1% FAR) and at the same time even requires less processing time (1232 ms instead of 2623 ms). Serial combination S-BC1 however seems to be more affected by the worse performance of Eigenfingers. Finally, we have applied exhaustive search using a separate (randomized) training system database, to find the best serial combination with respect to the cost function C introduced in Sect. 1 using weights $\omega_1 = 1, \omega_2 = 10^{-5}$. The best serial combination turned out to be SS considering *E-Middle, E-Ring, M-Index* with dimensions 9, 4, 1 yielding a total accuracy of 98.7% at 616 ms (99.7% at 591 ms on training set).

5   Conclusions and Future Works

We have examined parallel and serial combination techniques on classifiers of a single-sensor hand-based multimodal biometric system. Serial classifiers turned out to decrease processing time significantly at almost the same or even higher accuracy than their parallel combination counterparts. The Score sum method was found to produce the best results for both parallel and serial combination,

followed by Borda count and Highest rank. The ability to improve both accuracy and processing performance simultaneously makes serial combination techniques an excellent choice for classifier fusion. Still, the choice of parameters for serial classification influences recognition accuracy and performance and deserves further attention in future work.

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