

A Multimodal Fusion Algorithm Based on FRR and FAR Using SVM

Yong Li¹, Meimei Shi², En Zhu³, Jianping Yin³, Jianmin Zhao⁴

¹ Department of Information Engineering,
Engineering University of CAPF, Xi'an China

² Department of Science, Engineering University of CAPF, Xi'an, China

³ School of Computer, National University of Defense Technology,
Changsha, Hunan Province, China

⁴ Top Key Discipline of Computer Software and Theory in Zhejiang Provincial
Colleges, Zhejiang Normal University, China

¹liyong@nudt.edu.cn, ²meimeishi2003@yahoo.com.cn, ³{enzhu,jpyin}@nudt.edu.cn,
⁴zhaojm0310@163.com

Abstract

Remarkable improvements in recognition can be achieved through multibiometric fusion. Among various fusion techniques, score level fusion is the most frequently used in multibiometric system. In this paper, we propose a novel fusion algorithm based on False Reject Rate (FRR) and False Accept Rate (FAR) using Support Vector Machine (SVM). It transfers scores into corresponding FRRs and FARs, thus avoiding calculating posteriori probability of a certain score, as well as be capable of illustrating distribution of matching scores. The proposed method takes full advantages of both capabilities of FRR and FAR to describe the order of score and classification of SVM. Experimental results show that the proposed method outperforms existing representative approaches and can effectively improve the performance of multibiometric system.

Keywords: Biometrics, Multibiometric, Score level fusion, Multi-modal, SVM, False Reject Rate, False Accept Rate

1. Introduction

Biometric recognition refers to the process of automatically confirming the identity of a person through physiological or behavioral characteristics. A high security level system always demands for high performance, such as low FRR (False Reject Rate) and FAR (False Accept Rate). Unibiometric system, using a single biometric trait, with its insufficient information and easily influenced by collection noises, is no longer able to meet the requirements of high level system [1]. A possible solution is multibiometric fusion [14-16]. According to the level of information fused, the fusion scheme can be classified into sensor level, feature level, score level and decision level fusion. Among them, score level fusion is the most frequently researched for it shields both the diversity of bottom biometric characteristic data and complexity of recognition process, as well as preserves similarity metrics of individual traits to differentiate samples from genuine or intruder. Already existing score level fusion approaches can be categorized into three classes: transformation-based, density-based and classifier-based fusion [2].

Transformation-based fusion firstly normalizes the matching scores and then acquires a new score through a certain fusion rule to make final decision. This method takes into consideration of the two factors, one is normalization function, and the other is fusion rule [2,

3-4]. In density-based fusion scheme, matching scores are firstly transformed into posteriori probability and final decision is made according to Bayes rules [5-6]. Classifier-based fusion takes N matching scores as an N-dimensional feature vector and transfers fusion problem into classification of the N-dimensional vector [8-9].

In conclusion, transformation-based fusion technique, with no training process and few consideration of distribution of matching scores, is easy to implement. On the contrary, density based fusion, which requires accurate estimation of density and huge number of training samples, is hard to carry out for the following reasons: Firstly, positive samples, namely genuine matching scores are limited in today's multi-biometrics system. Secondly, it is difficult to estimate the density of matching scores in that they may not obey a certain distribution model. Besides, the time and space cost of this method is considerable. Classifier based fusion has its advantage of freeing from the restriction of different distribution of matching scores. However, it can neither directly produce a matching score nor obtain optimal FRR by certain FAR. Also, it needs sufficient training samples and new training for a different system.

Based on the above analysis of the advantages and disadvantages of existing methods, we propose a novel approach to describe the distribution of matching scores by FRR and FAR. As two important parameters of illustrating performance of a recognition system, FRR and FAR avoid estimation of probability density when used as descriptor of matching score distribution. It is similar to integral of matching score density, thus makes the original discrete density continuous. Tronci [7] utilized FRR-FAR as an important standard to make the final decision, but with the assumption of normal distribution when calculating its value. However, no matter how FRR and FAR are combined, loss of information is inevitable. Besides, the recognition performance of sum rule is not good enough. In this context, we consider directly using FRR and FAR as features. With more features introduced, available information is much more abundant. It firstly calculates FRR and FAR based on training samples, then computes FRR and FAR of each matching score through interpolation based on testing samples, and makes final decision by SVM. Compared with existing methods, the algorithm presented in this paper can greatly improve the recognition performance of multibiometric system.

2. Transform the Score to FRR and FAR

Matching scores coming from different recognition systems are not comparable directly. At the same time, FRR and FAR can be obtained by setting threshold as each score. They can well describe the score distribution of genuine and imposter. Therefore, we firstly calculate FRR and FAR of each matching score based on training samples, then compute FRR and FAR of each matching score through interpolation based on testing samples.

2.1. FRR and FAR calculation based on training set

Suppose an M-matcher fusion system has N training samples. For i th training sample, the template feature is $U = \langle u_i^1, \dots, u_i^M \rangle$, input feature is $V = \langle v_i^1, \dots, v_i^M \rangle$ and output score is $S_i = \langle s_i^1, \dots, s_i^M \rangle$. Here, u_i^k, v_i^k, s_i^k respectively represents template feature, input feature and matching score of i th training sample by k th matcher. In addition, we use z_i to note when i th training sample is genuine or imposter. Namely, if the i th training sample is genuine, then $z_i = 1$; if it is imposter, then $z_i = 0$. Then, FRR and FAR of k th ($1 \leq k \leq M$) matcher based on training samples are respectively calculated as follows.

$$FAR_k(t) = \left| \left\{ i \mid s_i^k \geq t, z_i = 0 \right\} \right| / \sum_{i=1}^N (1 - z_i) \quad (1)$$

$$FRR_k(t) = \left| \left\{ i \mid s_i^k < t, z_i = 1 \right\} \right| / \sum_{i=1}^N z_i \quad (2)$$

2.2. FRR and FAR calculation based on testing set

According to the above analysis, calculation of transformation function based on FRR and FAR requires all the matching scores, which is impossible in a real system. So we can only make the calculation based on training samples. Generally, training and testing samples follow the same distribution, which means that if one score appears in the training samples, it will probably appear in the testing samples as well. Thus, using each matching score as threshold t , we can get transformation value. For the newly appearing scores, we use interpolation to obtain its transformation value. At most N discrete matching scores are generated by each matcher for N training samples in training set. Generally, score obtained in testing process is not absolutely identical to that attained in training process. So the transformational scores in testing process can be calculated through interpolation based on scores from training samples. Suppose in the training process, n_k ($n_k \leq N$) different matching scores are generated by k th matcher based on N samples and ranked in ascending order as $\{t_1^k, t_2^k, \dots, t_{n_k}^k\}$. Substitute these scores into $FAR_k(t)$ and $FRR_k(t)$, we can obtain $\{FAR_k(t_i^k) \mid 1 \leq i \leq n_k\}$ and $\{FRR_k(t_i^k) \mid 1 \leq i \leq n_k\}$. For matching score x generated by k th matcher in testing process, $FAR_k(x)$ and $FRR_k(x)$ are calculated in the four situations as follows.

1. If $x < t_1^k$, then use t_1^k and t_2^k as control points, and calculate $FRR_k(x)$ and $FAR_k(x)$ through extrapolation.

Suppose

$$FRR'_k(x) = \frac{t_2^k - x}{t_2^k - t_1^k} FRR_k(t_1^k) + \frac{x - t_1^k}{t_2^k - t_1^k} FRR_k(t_2^k) \quad (3)$$

$$FAR'_k(x) = \frac{t_2^k - x}{t_2^k - t_1^k} FAR_k(t_1^k) + \frac{x - t_1^k}{t_2^k - t_1^k} FAR_k(t_2^k) \quad (4)$$

Then

$$FRR = \begin{cases} FRR' & FRR' > 0 \\ 0 & FRR' \leq 0 \end{cases} \quad (5)$$

$$FAR = \begin{cases} FAR' & FAR' < 1 \\ 1 & FAR' \geq 1 \end{cases} \quad (6)$$

2. If $x > t_{n_k}^k$, then use $t_{n_k}^k$ and $t_{n_k-1}^k$ as control points, and calculate $FRR_k(x)$ and $FAR_k(x)$ through extrapolation.

Suppose

$$FRR'_k(x) = \frac{t_{n_k}^k - x}{t_{n_k}^k - t_{n_k-1}^k} FRR_k(t_{n_k-1}^k) + \frac{x - t_{n_k-1}^k}{t_{n_k}^k - t_{n_k-1}^k} FRR_k(t_{n_k}^k) \quad (7)$$

$$FAR'_k(x) = \frac{t_{n_k}^k - x}{t_{n_k}^k - t_{n_{k-1}}^k} FAR_k(t_{n_{k-1}}^k) + \frac{x - t_{n_{k-1}}^k}{t_{n_k}^k - t_{n_{k-1}}^k} FAR_k(t_{n_k}^k) \quad (8)$$

Then

$$FRR = \begin{cases} FRR' & FRR' < 1 \\ 1 & FRR' \geq 1 \end{cases} \quad (9)$$

$$FAR = \begin{cases} FAR' & FAR' > 0 \\ 0 & FAR' \leq 0 \end{cases} \quad (10)$$

3. If there exists i which makes $x = t_i^k$,

$$FRR_k(x) = FRR(t_i^k), \quad FAR_k(x) = FAR(t_i^k) \quad (11)$$

4. If there exists i which makes $t_i^k < x < t_{i+1}^k$, then calculate $FRR_k(x)$ and $FAR_k(x)$ through interpolation.

$$FRR_k(x) = \frac{t_{i+1}^k - x}{t_{i+1}^k - t_i^k} FRR_k(t_i^k) + \frac{x - t_i^k}{t_{i+1}^k - t_i^k} FRR_k(t_{i+1}^k) \quad (12)$$

$$FAR_k(x) = \frac{t_{i+1}^k - x}{t_{i+1}^k - t_i^k} FAR_k(t_i^k) + \frac{x - t_i^k}{t_{i+1}^k - t_i^k} FAR_k(t_{i+1}^k) \quad (13)$$

In step (3) and (4), binary searching is adopted to find corresponding $(t_i^k, t_{i+1}^k (1 < i < n_k))$. The time complexity of binary search is $O(\log_2 N)$, thus effectively reducing time complexity of the whole algorithm. So far, we have attained FRR and FAR for each matching score in testing samples.

2.3. An example for computation of FRR and FAR

To better demonstrate how our algorithm works, we give an example in this section. Table 1 is one part of the experiment based on training samples, where matching scores are ranked in ascending order. From the above analysis, we know that computation of matching score transformation of a certain simple classifier is irrelevant to other classifiers. So we just choose one simple classifier for illustration. Also, in the training set, there is no other matching score among the existing ones, and FRR and FAR are calculated by taking matching score as threshold based on training samples.

Table 2 is one part of the experiment based on testing samples, where matching scores are among those in Table 1. We use calculation formula of $FAR_k(t)$ and $FRR_k(t)$ based on testing samples. Take the fourth matching score $x=1.4797$ as example, as we have $t_4^k < x < t_5^k$, then

$$FRR_k(x) = \frac{t_5^k - x}{t_5^k - t_4^k} FRR_k(t_4^k) + \frac{x - t_4^k}{t_5^k - t_4^k} FRR_k(t_5^k) \quad (14)$$

$$FAR_k(x) = \frac{t_5^k - x}{t_5^k - t_4^k} FAR_k(t_4^k) + \frac{x - t_4^k}{t_5^k - t_4^k} FAR_k(t_5^k) \quad (15)$$

Table 1. Computation of FRR_k and FAR_k on training set

i	t_i^k	$FRR_k(t_i^k)$	$FAR_k(t_i^k)$
1	1.4695	0.13	0.011525
2	1.47	0.13	0.0115
3	1.4701	0.13	0.011475
4	1.4715	0.13	0.01145
5	1.4721	0.13	0.011425
6	1.4728	0.13	0.0114
7	1.4736	0.13	0.011375
8	1.4742	0.13	0.011325
9	1.4765	0.13	0.0113
10	1.4769	0.13	0.011275

Table 2. Computation of FRR_k and FAR_k on testing set

x	$FRR_k(x)$	$FAR_k(x)$
1.4697	0.13	0.011515
1.4758	0.13	0.011307
1.4697	0.13	0.011515
1.4719	0.13	0.011433
1.4714	0.13	0.011451
1.4715	0.13	0.011450
1.4752	0.13	0.011314
1.4735	0.13	0.011378
1.4724	0.13	0.011414
1.476	0.13	0.011305

3. SVM Fusion Based on FRR and FAR

During score level fusion, score vector is combined to generate a single scalar score which is later used to make the final decision. Based on Section 2, one match score can be transformed to two scores which are its FRR and FAR. All the training and testing scores can be transformed into their FRRs and FARs. SVM is based on the structural risk minimization principle [12], which takes both the training error and generalization error into consideration. The SVM is to find an optimal hyper-plane that can well separate two class samples in the feature space. In our proposed multimodal biometric method, we use SVM to build a fusion function which can provide a fused score. Assume that we have N feature vectors with associated label $y_i \in \{-1, +1\}$, so the training data set is denoted as

$$\{(X_i, y_i)\}_i^N \quad X_i \in R^n, i = 1, 2, \dots, N \quad (16)$$

After transforming the match scores into FRRs and FARs, SVM is used to generate the final score. And

$$X_i = \langle FRR_1(s_i^1), FAR_1(s_i^1), FRR_2(s_i^2), FAR_2(s_i^2), \dots, FRR_1(s_i^M), FAR_1(s_i^M) \rangle \quad (17)$$

Also, the score can be first transformed by normalized methods such as Tanh, MinMax as well as T, and then SVM is used (respectively denoted as Tanh_SVM, MM_SVM, and T_SVM). In the above process, the sequential minimal optimization (SMO) training algorithm [11] is used to enhance the time efficiency. In general, the discriminate function of

an arbitrary classifier is of little probability meaning. However, the probabilistic output of SVM classifier can help in multimodal fusion post-processing. Fitting a sigmoid function to the classifier output is a solution to this problem. Platt [11] has described a method of fitting the sigmoid function.

4. Experiment Results

The XM2VTS-Benchmark database [10] consists of five face matchers and three speech matchers and was partitioned into training and evaluation sets according to the Lausanne Protocol-1 (LPI). The benchmark of LPI includes two files, one is dev.label and the other is eva.label. We use dev.label as training data and eva.label as test data. Our experiments are conducted based on this match score benchmark. We sign the face matcher as F1, F2, F3, F4 and F5 and the speech matcher as S1, S2 and S3 respectively. The Equal Error Rate (EER) is the point of the ROC curve where the two errors, *i.e.*, the FRR and the FAR, are equal. This performance measure is widely used in the biometric field to assess the performance of biometric systems [2]. In biometric recognition systems, we always try to make EER smaller.

4.1 Comparison with different fusion strategies

We firstly conducted experiments to measure the advantages of the proposed method FF_SVM over density-based algorithm LR [6], transformation-based fusion rules: Tanh and MinMax with simple sum rule [2] and the fusion methods T which was proposed in Ref.[11]. The EER of all the matchers can be found in Table 3. As shown in Table 3, among face matchers, matcher face-3 and face-5 gain the best and worst performance respectively. And among speech matchers, the performance order is speech-1, speech-3 and speech-2.

Table 3. EERs of each simple recognition system on XM2VTS-Benchmark

	S1	S2	S3	F1	F2	F3	F4	F5
EER	1.109	6.500	4.500	1.814	4.115	1.767	3.500	6.500

Table 4. EER comparison of different fusion techniques

EER(%)	F1S1	F1S2	F1S3	F2S1	F2S2	F2S3	F3S1	F3S2	F3S3	F4S1	F4S2	F4S3	F5S1	F5S2	F5S3
FF_SVM	0.250	1.000	0.750	0.500	1.250	1.250	0.462	0.901	0.750	0.446	0.958	0.750	0.500	2.500	1.750
T	0.260	0.757	0.750	0.750	1.750	1.143	0.500	1.267	0.973	0.727	1.000	0.788	0.500	3.000	1.750
LR	0.290	1.000	0.750	0.629	1.500	1.250	0.500	0.985	0.912	0.373	0.748	0.863	0.603	2.398	1.750
Tanh	0.543	1.750	0.634	0.500	1.750	1.250	0.500	1.668	1.220	0.750	1.417	1.250	1.039	3.000	2.500
MM	0.914	1.250	1.098	0.500	1.637	1.232	0.456	1.250	0.750	1.178	1.383	1.500	2.615	3.532	3.798

The experiments are conducted with 15 kind multimodal combination. Table 2 shows the EER of multi-modal fusion among FF_SVM, LR, T, Tanh and MinMax. From Table 4, we observe that FF_SVM provides the best performance 8 times and the second best performance 6 times. FF_SVM fusion method gains the best recognition performance followed by T and LR fusion algorithms. In order to evaluate the performance precisely, we give each matcher of every fusion a performance mark. The performance mark for the best matcher is 5 and followed is 4, 3, 2, 1. If the performance of two matchers are the same, for

example, both are the second best, then the two matchers get the same mark $(4+3)/2=3.5$. Table 5 is the performance mark of different fusion techniques which is measured by EER. From Table 5, we can easily find that the proposed fusion method FF_SVM shows the best performance because the total mark is the largest one. And we observe that the T and LR methods also perform well.

Table 5. Performance mark comparison of different techniques based on EER

Mark	F1S1	F1S2	F1S3	F2S1	F2S2	F2S3	F3S1	F3S2	F3S3	F4S1	F4S2	F4S3	F5S1	F5S2	F5S3	total
FF_SVM	5	4	3	4	5	2	4	5	4.5	4	4	5	4	4	4	61.5
T	4	5	4	1	1.5	5	1.5	2	2	3	3	4	5	3	4	48
LR	3	3	2	2	4	2	3	4	3	5	5	3	3	5	4	51
Tanh	2	1	5	4	1.5	2	1.5	1	1	2	1	2	2	2	2	30
MM	1	2	1	4	3	4	5	3	4.5	1	2	1	1	1	1	34.5

4.2. Comparison with SVM-based strategies

In order to verify the effect of transforming score to FRR and FAR, we compare the proposed method FF_SVM with T-based SVM fusion method T_SVM, Tanh-based SVM fusion method Tanh_SVM, MinMax-based SVM fusion method (MM_SVM) and SVM fusion directly on raw scores. From Table 6 and 7, we can observe that the proposed fusion method FF_SVM outperforms Tanh_SVM, MM_SVM, T_SVM and SVM. During 15 multimodal combinations, FF_SVM gives the best performance 10 times, and the total performance mark is larger than the other SVM-based algorithms.

Table 6. EER comparison of SVM-based Techniques

EER(%)	F1S1	F1S2	F1S3	F2S1	F2S2	F2S3	F3S1	F3S2	F3S3	F4S1	F4S2	F4S3	F5S1	F5S2	F5S3
FF_SVM	0.250	1.000	0.750	0.500	1.250	1.250	0.462	0.901	0.750	0.446	0.958	0.750	0.500	2.500	1.750
T_SVM	0.283	1.232	1.000	0.691	1.500	1.359	0.500	1.160	1.020	0.750	1.254	1.105	0.571	3.000	1.750
Tanh_SVM	0.513	1.500	0.730	0.671	1.698	1.250	0.500	1.250	0.964	0.710	1.250	1.250	0.547	2.750	2.250
MM_SVM	0.500	1.000	0.750	0.536	1.360	1.235	0.423	0.823	0.750	0.500	0.756	1.131	0.500	2.639	1.988
SVM	0.500	1.327	0.750	1.000	4.250	2.750	0.500	1.750	0.761	1.000	2.000	1.250	0.544	6.000	2.750

Table 7. Performance mark comparison of SVM-based Techniques based on EER

Mark	F1S1	F1S2	F1S3	F2S1	F2S2	F2S3	F3S1	F3S2	F3S3	F4S1	F4S2	F4S3	F5S1	F5S2	F5S3	total
FF_SVM	5	4.5	3.5	5	5	3.5	4	4	4.5	5	4	5	4.5	5	4.5	67
T_SVM	4	3	1	2	3	2	2	3	1	2	2	4	1	2	4.5	36.5
Tanh_SVM	1	1	5	3	2	3.5	2	2	2	3	3	1.5	2	3	2	36
MM_SVM	2.5	4.5	2	4	4	5	5	5	4.5	4	5	3	4.5	4	3	60
SVM	2.5	2	3.5	1	1	1	2	1	3	1	1	1.5	3	1	1	25.5

To show the comparison of all the algorithms in multimodal biometric systems, Figure 1 shows the EERs of the 9 algorithms. The proposed FF_SVM algorithm is show in bold line. From the figure, we can conclude that the proposed algorithm can improve the performance of multimodal biometric system efficiently.

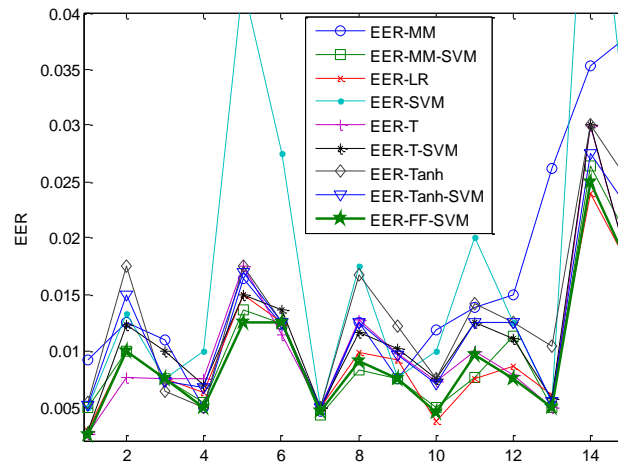


Figure 1. EERs of all Algorithms

5. Conclusion

This paper proposes a novel fusion algorithm: FF_SVM. This proposed algorithm first transforms the match scores into FRRs and FARs and then adopts SVM for classification. To be more specific, we firstly calculate FRRs and FARs based on the training set, and then use interpolation to obtain the FRRs and FARs of each score in the testing set. As well, binary searching is applied to find interpolation points in order to reduce time complexity of the whole algorithm. In addition, SVM is used to explore the relationship between the final score and FRR & FAR. The experimental results show that this FF_SVM fusion algorithm can efficiently improve performance compared with LR, T, Tanh and MinMax algorithms. Besides, in comparison with other SVM-based fusion methods, the proposed fusion method can provide better recognition performance for multimodal biometric fusion systems.

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Authors



Yong Li received his PhD degree from National University of Defense Technology of China. And now he is a lecturer at the Department of Information Engineering, Engineering University of CAPF.



Meimei Shi received her M.S. degree from Hunan University of China. And now she is a lecturer of Engineering University of CAPF.



En Zhu is an associate professor at the School of Computer, National University of Defense Technology. His research interest covers pattern recognition and image process.



Jianping Yin is a professor at the School of Computer, National University of Defense Technology. His re-search interest covers pattern recognition, artificial intelligence, and network security.



Jianmin Zhao is a professor of Zhejiang Normal University. His research interest covers information security, pattern recognition and image process.