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Correlation-based identification approach for multimodal biometric fusion

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Abstract

Information fusion is a key step in multimodal biometric systems. The feature-level fusion is more effective than the score-level and decision-level method owing to the fact that the original feature set contains richer information about the biometric data. In this paper, we present a multiset generalized canonical discriminant projection (MGCDP) method for feature-level multimodal biometric information fusion, which maximizes the correlation of the intra-class features while minimizes the correlation of the between-class. In addition, the serial MGCDP (S-MGCDP) and parallel MGCDP (P-MGCDP) strategy were also proposed, which can fuse more than two kinds of biometric information, so as to achieve better identification effect. Experiments performed on various biometric databases shows that MGCDP method outperforms other state-of-the-art feature-level information fusion approaches.

Keywords correlation analysis, multimodal biometric information, information fusion

1 Introduction

Biometric refers to the use of the physical characteristics of the human body as the identity of the technology, which essentially is a pattern recognition technology through special identity. At present, the most widely used biometric technology mainly relies on a single biometric information, such as face, fingerprint, palm vein, voice, iris, etc. Because the use of these methods alone may result in poor recognition rates, therefore, the use of multimodal biometric fusion technology for identification has become the focus of research in this field.

Multimodal biometric fusion technology can be divided into feature-level, score-level and decision-level mode. In feature-level mode, data obtained from multi-sensor is used to compute a single feature vector. In score-level mode, each sensor provides a matching score indicating the proximity of the feature vector with the corresponding template vector. In decision-level mode, each sensor can capture multimodal biometric information and the resulting feature vectors individually classified into accept or reject class [1–2].

The feature-level fusion method is more effective than the score-level and decision-level method in multimodal biometric recognition, the reason is that it fuse more original biometric information into a single vector before dimensional reduction procedure [3]. Traditional parallel [4] and serial [5] strategy provide the technical support for feature-level fusion. The serial fusion strategy is simply connecting two original feature vectors, so the dimension of fused new feature vector is the sum of the two original vectors. The parallel fusion strategy convert two original feature vector into a complex vector, therefore the dimension of fused new vector is equal to the maximal dimension in original feature vector.

In recent years, the application of canonical correlation analysis (CCA) in multimodal biometric field attracted a growing number of researchers [6]. CCA convert the correlation of random vectors into a pair of variables, which are uncorrelated. The kernel CCA (KCCA) method [7] using non-linear method project two non-separable sets to a high dimensional linear separable

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space. The discriminative CCA (DCCA) method [8] takes into account the feature between intra-class samples and between-class samples, it minimizes the difference of intra-class while maximizes the difference of between-class. The generalized CCA (GCCA) method [9] makes use of both the supervised information and the intra-class distribution matrix information.

In this paper, we propose MGCDP method for multimodal biometric information fusion, which maximizes the correlation of the intra-class features within the modal while minimizing the correlation of the between-class between the modal.

2 Basic concept of CCA

CCA is an effective multi class data processing method, which is widely used in the analysis of the relationship between the two sets of data. Assuming that there are two sets of data matrix $\boldsymbol{X}\in\mathbb{R}^{p\times n}$ and $\boldsymbol{Y}\in\mathbb{R}^{q\times n}$, the dimensions of $\boldsymbol{X}$ and $\boldsymbol{Y}$ are p and q respectively, and all of them contain n training feature vectors. CCA is to find a set of optimal direction vector $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$, so that maximum the correlation between $\boldsymbol{a}_1=\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{X}$ and $\boldsymbol{b}_1=\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{Y}$. After determining the first set of canonical vector $(\boldsymbol{a}_1,\boldsymbol{b}_1)$, CCA will continue to search the second pairs of canonical vector $(\boldsymbol{a}_2,\boldsymbol{b}_2)$, in which $\boldsymbol{a}_2=\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{X}$ and $\boldsymbol{b}_2=\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{Y}$ not only uncorrelated with $(\boldsymbol{a}_1,\boldsymbol{b}_1)$, but also is the largest correlation between $\boldsymbol{a}_2$ and $\boldsymbol{b}_2$. In the same way, CCA can iteratively find all the d groups of canonical vector $(\boldsymbol{a}_d,\boldsymbol{b}_d)$.

If the sample space $\Omega=\{\boldsymbol{\xi}\,|\,\boldsymbol{\xi}\in\mathbb{R}^n\}$ has two vectors with mean value of zero $\boldsymbol{X}=\{\boldsymbol{x}\,|\,\boldsymbol{x}\in\mathbb{R}^p\}$ and $\boldsymbol{Y}=\{\boldsymbol{y}\,|\,\boldsymbol{y}\in\mathbb{R}^q\}$, where $\boldsymbol{x}$ and $\boldsymbol{y}$ are different biometric modal sample from same person $\boldsymbol{\xi}$, assume that $\boldsymbol{S}_{\mathrm{XX}}\in\mathbb{R}^{p\times p}$ and $\boldsymbol{S}_{YY}\in\mathbb{R}^{q\times q}$ are covariance matrix of the unimodal $\boldsymbol{X}$ and $\boldsymbol{Y}$ respectively, and that $\boldsymbol{S}_{\mathrm{XY}}\in\mathbb{R}^{p\times q}$ is covariance matrix of the multimodal $\boldsymbol{X}$ and $\boldsymbol{Y}$, (note that $\boldsymbol{S}_{\mathrm{XY}}=\boldsymbol{S}_{\mathrm{YX}}^{\mathrm{T}}$), then the covariance matrix $\boldsymbol{S}$ contains all feature information of the person $\boldsymbol{\xi}$:

$$\boldsymbol{S}=\begin{bmatrix}\mathrm{var}(\boldsymbol{x}) & \mathrm{cov}(\boldsymbol{x},\boldsymbol{y})\\ \mathrm{cov}(\boldsymbol{y},\boldsymbol{x}) & \mathrm{var}(\boldsymbol{y})\end{bmatrix}=\begin{bmatrix}\boldsymbol{S}_{\mathrm{XX}} & \boldsymbol{S}_{\mathrm{XY}}\\ \boldsymbol{S}_{\mathrm{YX}} & \boldsymbol{S}_{\mathrm{YY}}\end{bmatrix} \tag{1}$$

Let $\boldsymbol{\alpha}\in\mathbb{R}^p$ and $\boldsymbol{\beta}\in\mathbb{R}^q$ are two non-zero vector, then the linear combination of $\boldsymbol{x}$ and $\boldsymbol{y}$ can be expressed as:

$$\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x}=a_1x_1+a_2x_2+\ldots+a_px_p \tag{2}$$

$$\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y}=b_1y_1+b_2y_2+\ldots+b_qy_q \tag{3}$$

In order to maximize the correlation between $\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x}$ and $\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y}$, CCA uses Eq. (4) to find the projection in $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$ directions:

In order to maximize the correlation between $\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x}$ and $\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y}$, CCA uses Eq. (4) to find the projection in $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$ directions:

$$J(\boldsymbol{\alpha},\boldsymbol{\beta})=\frac{\mathrm{cov}(\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x},\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y})}{\sqrt{\mathrm{var}(\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x})\mathrm{var}(\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y})}} \tag{4}$$

Because:

$$\mathrm{var}(\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x})=\boldsymbol{\alpha}^{\mathrm{T}}\mathrm{var}(\boldsymbol{x})\boldsymbol{\alpha}=\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{XX}}\boldsymbol{\alpha} \tag{5}$$

$$\mathrm{var}(\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y})=\boldsymbol{\beta}^{\mathrm{T}}\mathrm{var}(\boldsymbol{y})\boldsymbol{\beta}=\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{YY}}\boldsymbol{\beta} \tag{6}$$

$$\mathrm{cov}(\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{x},\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{y})=\boldsymbol{\alpha}^{\mathrm{T}}\mathrm{cov}(\boldsymbol{x},\boldsymbol{y})\boldsymbol{\beta}=\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{XY}}\boldsymbol{\beta} \tag{7}$$

Therefore, the optimization criterion of CCA is:

$$J(\boldsymbol{\alpha},\boldsymbol{\beta})=\frac{\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{XY}}\boldsymbol{\beta}}{\sqrt{\boldsymbol{\alpha}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{XX}}\boldsymbol{\alpha}\boldsymbol{\beta}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{YY}}\boldsymbol{\beta}}} \tag{8}$$

The goal of Eq. (8) is to find linear combinations of $\tilde{\boldsymbol{X}}=(a_1,a_2,\ldots,a_d)^{\mathrm{T}}\boldsymbol{X}=\boldsymbol{W}_{\mathrm{X}}^{\mathrm{T}}\boldsymbol{X}$ and $\tilde{\boldsymbol{Y}}=(b_1,b_2,\ldots,b_d)^{\mathrm{T}}\boldsymbol{Y}=\boldsymbol{W}_{\mathrm{Y}}^{\mathrm{T}}\boldsymbol{Y}$. In this case, $\mathrm{cov}(\tilde{\boldsymbol{X}},\tilde{\boldsymbol{Y}})=\boldsymbol{W}_{\mathrm{X}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{XY}}\boldsymbol{W}_{\mathrm{Y}}$, $\mathrm{var}(\tilde{\boldsymbol{X}})=\boldsymbol{W}_{\mathrm{X}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{XX}}\boldsymbol{W}_{\mathrm{X}}$, and $\mathrm{var}(\tilde{\boldsymbol{Y}})=\boldsymbol{W}_{\mathrm{Y}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{YY}}\boldsymbol{W}_{\mathrm{Y}}$. By using the Lagrange multiplier method to solve the optimization problem of the covariance between $\tilde{\boldsymbol{X}}$ and $\tilde{\boldsymbol{Y}}$, under the condition of $\mathrm{var}(\tilde{\boldsymbol{X}})=\mathrm{var}(\tilde{\boldsymbol{Y}})=\boldsymbol{I}$, the projection matrix $\boldsymbol{W}_{\mathrm{X}}$ and $\boldsymbol{W}_{\mathrm{Y}}$ can be determined by:

$$\left.\begin{aligned}\boldsymbol{S}_{\mathrm{XX}}^{-1}\boldsymbol{S}_{\mathrm{XY}}\boldsymbol{S}_{\mathrm{YY}}^{-1}\boldsymbol{S}_{\mathrm{YX}}\hat{\boldsymbol{W}}_{\mathrm{X}}=\boldsymbol{R}^2\hat{\boldsymbol{W}}_{\mathrm{X}}\\ \boldsymbol{S}_{\mathrm{YY}}^{-1}\boldsymbol{S}_{\mathrm{YX}}\boldsymbol{S}_{\mathrm{XX}}^{-1}\boldsymbol{S}_{\mathrm{XY}}\hat{\boldsymbol{W}}_{\mathrm{Y}}=\boldsymbol{R}^2\hat{\boldsymbol{W}}_{\mathrm{Y}}\end{aligned}\right\} \tag{9}$$

where the $\hat{\boldsymbol{W}}_{\mathrm{X}}$ and $\hat{\boldsymbol{W}}_{\mathrm{Y}}$ are eigenvectors, and the $\boldsymbol{R}^2$ is the diagonal matrix of eigenvalues.

3 MGCDP method

Based on the basic concept of CCA, we propose the MGCDP method for multimodal biometric information fusion, which maximizes the correlation of the intra-class features within the modal while minimizing the correlation of the between-class between the modals.

Assume the biometric feature set $\boldsymbol{X}$ contains n samples (n feature vectors) from C classes, each class contains k_i feature vector, let n_i denotes the ith class, $\boldsymbol{x}_{ij}$ denotes the jth feature vector from the n_i class, $\boldsymbol{X}=\bigcup_{i=1}^{C}\boldsymbol{n}_i=\bigcup_{i=1}^{C}\bigcup_{j=1}^{k_i}\boldsymbol{x}_{ij}$. Let $\boldsymbol{u}_i$ denotes the mean of $\boldsymbol{x}_{ij}$ in

n_i class, and let $\bar{\boldsymbol{\mu}}$ denotes the mean of $\boldsymbol{X}$, then $\boldsymbol{\mu}_i$ and $\bar{\boldsymbol{\mu}}$ can be determined by Eqs. (10) and (11):

$$\boldsymbol{\mu}_i = \frac{1}{n_i}\sum_{j=1}^{k_i} \boldsymbol{x}_{ij} \tag{10}$$

$$\bar{\boldsymbol{\mu}} = \frac{1}{n}\sum_{i=1}^{C}\sum_{j=1}^{k_i} \boldsymbol{x}_{ij} = n_i\boldsymbol{\mu}_i \tag{11}$$

Therefore, if the dimension of the feature vector $\boldsymbol{x}_{ij}$ is p, the between-class scatter matrix $\boldsymbol{S}_{\mathrm{IX}} \in \mathbb{R}^{p\times p}$ of $\boldsymbol{X}$ is:

$$\boldsymbol{S}_{\mathrm{IX}} = \sum_{i=1}^{C} n_i(\boldsymbol{\mu}_i - \bar{\boldsymbol{\mu}})(\boldsymbol{\mu}_i - \bar{\boldsymbol{\mu}})^{\mathrm{T}} \tag{12}$$

3.1 Intra-class feature projecting

The first problem to be solved is that different classes in data $\boldsymbol{X}$ need to be separated, that is, the intra-class scatter matrix $\boldsymbol{S}_{\mathrm{IX}}$ need to project into a diagonal matrix. Due to the high dimension of $\boldsymbol{S}_{\mathrm{IX}}$, direct operation can result in low efficiency, so it is necessary to reduce the dimension according to Eq. (13):

$$\boldsymbol{Q}_{\mathrm{opt}} = [\boldsymbol{q}_1\ \boldsymbol{q}_2\ \cdots\ \boldsymbol{q}_r] \tag{13}$$

where $\boldsymbol{q}_r$ are the first r eigenvectors corresponding to the first r largest eigenvalues of p dimensional matrix $\boldsymbol{S}_{\mathrm{IX}}$, and $r \ll p$. projecting matrix after dimensionality reduction is Eq. (14):

$$\hat{\boldsymbol{S}}_{\mathrm{IX}_{r\times r}} = \boldsymbol{Q}_{\mathrm{opt}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{IX}}\boldsymbol{Q}_{\mathrm{opt}} \tag{14}$$

It is worth noting that, due to the maximum number of eigenvalues is $C-1$, therefore, the upper limit of r is also $C-1$ in the Eq. (13).

Let $\boldsymbol{W}_{\mathrm{IX}} \in \mathbb{R}^{p\times r}$ and $\boldsymbol{W}_{\mathrm{IX}_{p\times r}} = \boldsymbol{Q}_{\mathrm{opt}}\hat{\boldsymbol{S}}_{\mathrm{IX}}^{-(1/2)}$, then Eq. (14) can be transformed into Eq. (15):

$$\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{IX}}\boldsymbol{W}_{\mathrm{IX}} = \boldsymbol{I} \tag{15}$$

After projection operation, the biometric data set $\boldsymbol{X}$ is:

$$\boldsymbol{X}' = \boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{X} \tag{16}$$

The $\boldsymbol{W}_{\mathrm{IX}}$ project between-class scatter matrix $\boldsymbol{S}_{\mathrm{IX}}$ into $\boldsymbol{I}$ matrix means that all classes in biometric data set $\boldsymbol{X}$ is separated.

Similarly, different classes in biometric data set $\boldsymbol{Y}$ can be separated in the same way. After projection operation, the biometric data set $\boldsymbol{Y}$ is:

$$\boldsymbol{Y}' = \boldsymbol{W}_{\mathrm{IY}}^{\mathrm{T}}\boldsymbol{Y} \tag{17}$$

where $\boldsymbol{W}_{\mathrm{IY}}$ is the projection matrix, and $\boldsymbol{W}_{\mathrm{IY}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{IY}}\boldsymbol{W}_{\mathrm{IY}} = \boldsymbol{I}$.

Through the above steps, the between-class scatter $\boldsymbol{S}_{\mathrm{IX}}$ and $\boldsymbol{S}_{\mathrm{IY}}$ are projected into $\boldsymbol{I}$ matrix, therefore, all classes in $\boldsymbol{X}$ and $\boldsymbol{Y}$ are separated.

3.2 Between-class feature projecting

The second problem to be solved is that in order to ensure biometric data from $\boldsymbol{X}$ and $\boldsymbol{Y}$ have correlation only for a same user $\boldsymbol{\xi}$, it is necessary to project covariance matrix of dimension reduced $\boldsymbol{X}'$ and $\boldsymbol{Y}'$ into a diagonal matrix, that is, $\boldsymbol{S}'_{\mathrm{IXY}} = \boldsymbol{X}'\boldsymbol{Y}'^{\mathrm{T}}$ is a diagonal matrix and $S'_{\mathrm{IXY}} \in \mathbb{R}^{r\times r}$.

Assume that the rank of $\boldsymbol{S}'_{\mathrm{IXY}}$ is r, by using singular value decomposition (SVD) method, because $\boldsymbol{S}'_{\mathrm{IXY}} = \boldsymbol{U}\boldsymbol{\Sigma}_{\mathrm{XY}}\boldsymbol{V}^{\mathrm{T}}$, therefore $\boldsymbol{U}^{\mathrm{T}}\boldsymbol{S}'_{\mathrm{IXY}}\boldsymbol{V} = \boldsymbol{\Sigma}_{\mathrm{XY}}$. The $\boldsymbol{\Sigma}_{\mathrm{XY}}$ is a diagonal matrix whose only main diagonal elements are non-zero, $\boldsymbol{U}$ and $\boldsymbol{V}$ are orthogonal matrices. Let $\boldsymbol{W}_{\mathrm{CX}} = \boldsymbol{U}\boldsymbol{\Sigma}_{\mathrm{XY}}^{-\frac{1}{2}}$ and $\boldsymbol{W}_{\mathrm{CY}} = \boldsymbol{V}\boldsymbol{\Sigma}_{\mathrm{XY}}^{-\frac{1}{2}}$, then:

$$(\boldsymbol{U}\boldsymbol{\Sigma}_{\mathrm{XY}}^{-\frac{1}{2}})\boldsymbol{S}'_{\mathrm{IXY}}(\boldsymbol{V}\boldsymbol{\Sigma}_{\mathrm{XY}}^{-\frac{1}{2}}) = \boldsymbol{W}_{\mathrm{CY}}^{\mathrm{T}}\boldsymbol{S}'_{\mathrm{IXY}}\boldsymbol{W}_{\mathrm{CX}} = \boldsymbol{I} \tag{18}$$

Therefore, the final projection of biometric feature set $\boldsymbol{X}$ and $\boldsymbol{Y}$ are as follow:

$$\tilde{\boldsymbol{X}} = \boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{X}' = \boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{X} = \boldsymbol{W}_{\mathrm{X}}\boldsymbol{X} \tag{19}$$

$$\tilde{\boldsymbol{Y}} = \boldsymbol{W}_{\mathrm{CY}}^{\mathrm{T}}\boldsymbol{Y}' = \boldsymbol{W}_{\mathrm{CY}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IY}}^{\mathrm{T}}\boldsymbol{Y} = \boldsymbol{W}_{\mathrm{Y}}\boldsymbol{Y} \tag{20}$$

It is worth noting that, according to the above method, the between-class scatter matrix is still a diagonal matrix. Take $\tilde{\boldsymbol{X}}$ as an example:

$$\hat{\boldsymbol{S}}_{\mathrm{IX}} = \tilde{\boldsymbol{X}}\tilde{\boldsymbol{X}}^{\mathrm{T}} = (\boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{X})(\boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{X})^{\mathrm{T}} = \boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{X}\boldsymbol{X}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IX}}\boldsymbol{W}_{\mathrm{CX}} = \boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{IX}}\boldsymbol{W}_{\mathrm{IX}}\boldsymbol{W}_{\mathrm{CX}} \tag{21}$$

Eq. (15) shows that $\boldsymbol{W}_{\mathrm{IX}}^{\mathrm{T}}\boldsymbol{S}_{\mathrm{IX}}\boldsymbol{W}_{\mathrm{IX}} = \boldsymbol{I}$, therefore,

$$\tilde{\boldsymbol{S}}_{\mathrm{IX}} = \boldsymbol{W}_{\mathrm{CX}}^{\mathrm{T}}\boldsymbol{W}_{\mathrm{CX}} = (\boldsymbol{U}\boldsymbol{\Sigma}_{\mathrm{XY}}^{-\frac{1}{2}})^{\mathrm{T}}(\boldsymbol{U}\boldsymbol{\Sigma}_{\mathrm{XY}}^{-\frac{1}{2}}) = \boldsymbol{\Sigma}_{\mathrm{XY}}^{-1} \tag{22}$$

The $\tilde{\boldsymbol{S}}_{\mathrm{IX}}$ equals a diagonal matrix means that all classes in data $\boldsymbol{X}$ has been separated. Similarly, all classes in data $\boldsymbol{Y}$ can be separated in the same way.

4 Fusion strategy of MGCDP

Based on the MGCDP method mentioned above, we propose S-MGCDP and P-MGCDP strategy, which can fuse more than two kinds of biometric information, so as to achieve better identification effect.

Let $\boldsymbol{X}_{\mathrm{L1}}^1$, $\boldsymbol{X}_{\mathrm{L1}}^2$, and $\boldsymbol{X}_{\mathrm{L1}}^3$ denote three kinds of biometric information to be fused, the Figs. 1 and 2 show the S-MGCDP and P-MGCDP strategy, respectively.

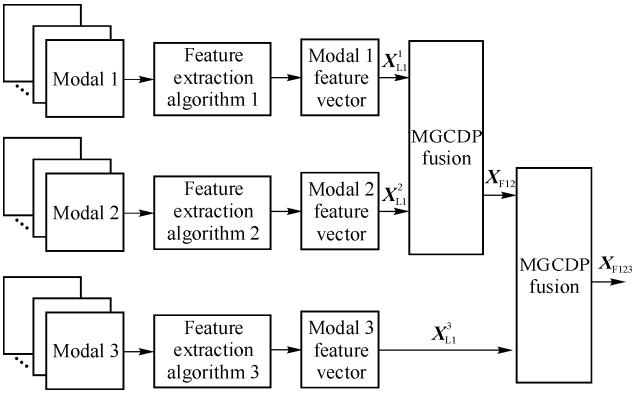

Fig. 1 S-MGCDP fusion strategy

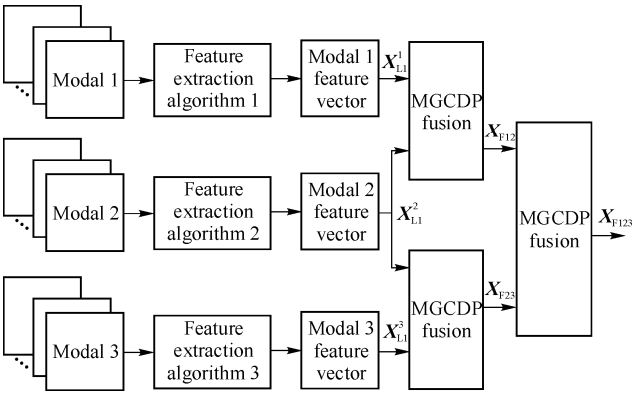

Fig. 2 P-MGCDP fusion strategy

In the S-MGCDP strategy, $\boldsymbol{X}_{\mathrm{L1}}^{1}$ and $\boldsymbol{X}_{\mathrm{L1}}^{2}$ are fused firstly, and the fused feature $\boldsymbol{X}_{\mathrm{F12}}$ can be expressed as:

$$\boldsymbol{X}_{\mathrm{F12}}=\begin{pmatrix} w_{\mathrm{L1}}\boldsymbol{W}_{\mathrm{X1}}\boldsymbol{X}_{\mathrm{L1}}^{1} \\ w_{\mathrm{L2}}\boldsymbol{W}_{\mathrm{X2}}\boldsymbol{X}_{\mathrm{L1}}^{2} \end{pmatrix} \tag{23}$$

where $\boldsymbol{W}_{\mathrm{X1}}$ and $\boldsymbol{W}_{\mathrm{X2}}$ are projection matrix of $\boldsymbol{X}_{\mathrm{L1}}^{1}$ and $\boldsymbol{X}_{\mathrm{L1}}^{2}$ by using MGCDP method, the w_{L1} and w_{L2} are weights ranging from 0 to 1, and subject to $w_{\mathrm{L1}}+w_{\mathrm{L2}}=1$. Next, continue to fuse $\boldsymbol{X}_{\mathrm{F12}}$ and $\boldsymbol{X}_{\mathrm{L1}}^{3}$ by using MGCDP method:

$$\boldsymbol{X}_{\mathrm{F123}}=\begin{pmatrix} w_{\mathrm{F12}}\boldsymbol{W}_{\mathrm{F12}}\boldsymbol{X}_{\mathrm{F12}} \\ w_{\mathrm{L3}}\boldsymbol{W}_{\mathrm{X3}}\boldsymbol{X}_{\mathrm{L1}}^{3} \end{pmatrix} \tag{24}$$

where the w_{F12} and w_{L3} are also weights ranging from 0 to 1, and subject to $w_{\mathrm{F12}}+w_{\mathrm{L3}}=1$.

In the P-MGCDP strategy, $\boldsymbol{X}_{\mathrm{L1}}^{2}$ is fused with $\boldsymbol{X}_{\mathrm{L1}}^{1}$ and $\boldsymbol{X}_{\mathrm{L1}}^{3}$ by using MGCDP method, respectively:

$$\boldsymbol{X}_{\mathrm{F12}}=\begin{pmatrix} w_{\mathrm{L1}}\boldsymbol{W}_{\mathrm{X1}}\boldsymbol{X}_{\mathrm{L1}}^{1} \\ w_{\mathrm{L2}}\boldsymbol{W}_{\mathrm{X2}}\boldsymbol{X}_{\mathrm{L1}}^{2} \end{pmatrix} \tag{25}$$

$$\boldsymbol{X}_{\mathrm{F23}}=\begin{pmatrix} w_{\mathrm{L2}}\boldsymbol{W}_{\mathrm{X2}}\boldsymbol{X}_{\mathrm{L1}}^{2} \\ w_{\mathrm{L3}}\boldsymbol{W}_{\mathrm{X3}}\boldsymbol{X}_{\mathrm{L1}}^{3} \end{pmatrix} \tag{26}$$

and then, fuse the $\boldsymbol{X}_{\mathrm{F12}}$ and $\boldsymbol{X}_{\mathrm{F23}}$:

$$\boldsymbol{X}_{\mathrm{F123}}=\begin{pmatrix} w_{\mathrm{F12}}\boldsymbol{W}_{\mathrm{F12}}\boldsymbol{X}_{\mathrm{F12}} \\ w_{\mathrm{F23}}\boldsymbol{W}_{\mathrm{F23}}\boldsymbol{X}_{\mathrm{F23}} \end{pmatrix} \tag{27}$$

where w_{L1}, w_{L2}, w_{L3}, w_{f12} and w_{F23} are weights ranging from 0 to 1, subject to $w_{\mathrm{L1}}+w_{\mathrm{L2}}=1$, $w_{\mathrm{L2}}+w_{\mathrm{L3}}=1$ and $w_{\mathrm{F12}}+w_{\mathrm{F23}}=1$.

For both S-MGCDP and P-MGCDP strategy, the maximum length of fused feature vector is $\min\{C-1, \operatorname{rank}\boldsymbol{X}_{\mathrm{L1}}^{i}\}$, $i=1,2,\ldots,k$. In order to keep the length of the fused vector as maximum as possible, in each step, the two feature sets with the highest ranks should be fused together. Therefore, all biometric modals should be sorted according to the rank of each matrix, thus $\operatorname{rank}\boldsymbol{X}_{\mathrm{L1}}^{1}\geqslant\operatorname{rank}\boldsymbol{X}_{\mathrm{L1}}^{2}\geqslant\operatorname{rank}\boldsymbol{X}_{\mathrm{L1}}^{3}$.

5 Experimental results

5.1 Database

The multimodal biometric experimental database consists of three modes: palm vein, human face and fingerprint. These basic data are from CASIA-MS-PalmprintV1 [10], PolyU multispectral palm print Database [11], CASIA-FaceV5 [12] and CASIA-FingerprintV5 [13].

The experimental database contains 700 users (N=700), each user contains 5 samples (C=5), and each sample consists of palm vein, human face and fingerprint data. If the number of users in the database is N and the number of sample is C, then the number of intra-class matches will be $NC!/(2(C-2)!)=7\,000$ and the number of between-class matches will be $C^2N(N-1)/2=6\,116\,250$. Therefore, in this experimental database, the number of intra-class and between-class matches was 7 000 and 6 116 250 respectively. Samples of experimental database are shown in Fig. 3.

Fig. 3 Samples of experimental database

5.2 Unimodal biometric fusion

To evaluate the effect of MGCDP method on fusing different algorithm feature from unimodal biometric data set, we use all 700 palm vein samples in experimental database, and three palm vein feature extraction algorithms are implemented: mutual foreground LBP (MF-LBP) [14], local invariant feature (LIF) [15] and adaptive Gabor filter (AGF) [16]. All users in this database contain 5 palm vein samples, we randomly select 3 samples for training, and the remaining 2 samples for testing.

Figs. 4–7 show the fusion effect of different algorithm feature from unimodal biometric set, and Table 1 shows the equal error rate (EER) for different palm vein feature extraction algorithm in unimodal environment. In Table 1, A, B and C represent MFLBP, LIF and AGF respectively.

The experimental results show that the use of MGCDP for fusion different algorithms can significantly improve the system recognition rate and reduce the EER, thus improving the performance of biometric recognition system.

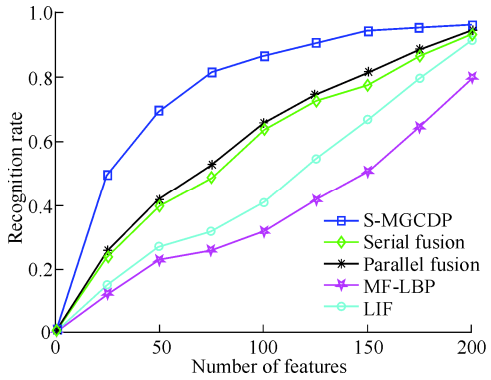

Fig. 4 Unimodal recognition rate curve of fusion of MF-LBP and LIF

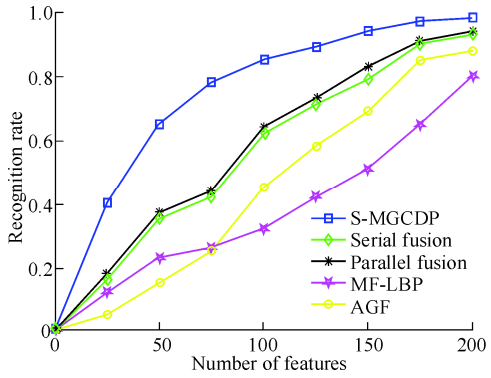

Fig. 5 Unimodal recognition rate curve of fusion of MF-LBP and AGF

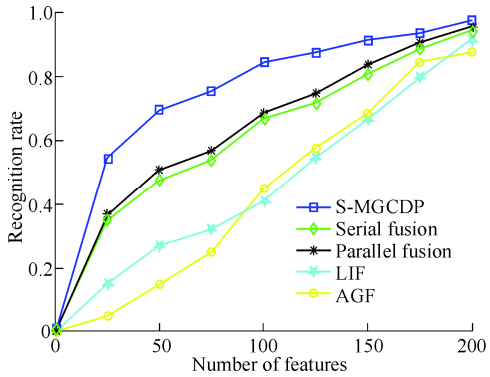

Fig. 6 Unimodal recognition rate curve of fusion of LIF and AGF

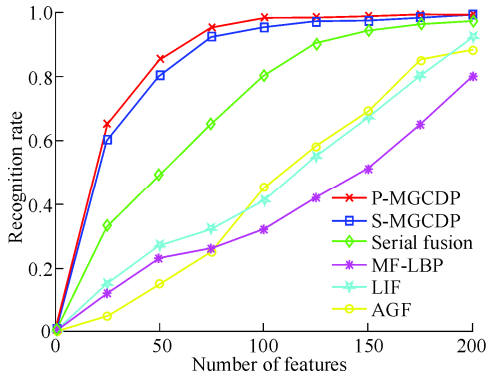

Fig. 7 Unimodal recognition rate curve of fusion of MF-LBP, LIF and AGF

Table 1 EER for different palm vein feature extraction algorithm

Method	EER/(%)						
	A	B	C	A+B	A+C	B+C	A+B+C
Serial	2.00	0.99	0.86	0.52	0.59	0.66	0.18
Parallel	2.00	0.99	0.86	0.49	0.54	0.41	-
KCCA	2.00	0.99	0.86	0.67	0.78	0.92	-
DCCA	2.00	0.99	0.86	0.55	0.41	0.47	-
GCCA	2.00	0.99	0.86	0.59	0.44	0.52	-
S-MGCDP	2.00	0.99	0.86	0.22	0.36	0.30	0.15
M-MGCDP	2.00	0.99	0.86	0.22	0.36	0.30	0.11

The experimental results are consistent with the expectation that the fusion of a variety of relevant biometric information can improve the class discriminative degree, thereby improving system performance without additional original biometric information.

5.3 Multimodal biometric fusion

Next, we evaluate the effect of MGCDP method on fusing multimodal biometric data set. Three training samples were randomly selected from the experimental database, and the rest were used for testing, and the classification method is k-nearest neighbor (kNN). Biometric feature were extract by AGF [16], histogram of Gabor phase patterns (HGPP) [17], and latent fingerprint

matching (LFM) [18] methods from palm vein, human face and fingerprint data sets, respectively. The EER of these methods were evaluated after PCA and LDA dimension reduction step.

Tables 2 and 3 shows the EER of recognition system under unimodal and multimodal, respectively. Experimental result shows that the MGCDP method is superior to the traditional fusion methods. In Table 3, A, B and C represent palm vein, human face and fingerprint respectively.

Table 2 EER of unimodal biometric feature

Unimodal feature	EER/(%)
Palm vein	2.80
Human face	1.71
Fingerprint	3.03

Table 3 EER of multimodal biometric feature

Method	EER/(%)			
	A+B	A+C	B+C	A+B+C
PCA + KCCA	0.75	0.74	0.61	0.44
LDA + KCCA	0.82	0.71	0.63	0.52
PCA + DCCA	0.69	0.64	0.71	0.55
LDA + DCCA	0.89	0.81	0.83	0.67
PCA + GCCA	0.51	0.65	0.59	0.40
LDA + GCCA	0.67	0.86	0.72	0.63
PCA + S-GCDP	0.39	0.29	0.32	0.16
LDA + S-GCDP	0.33	0.27	0.29	0.13
PCA + P-GCDP	0.30	0.17	0.24	0.10
LDA + P-GCDP	0.27	0.19	0.25	0.12

5.4 Generalization ability of MGCDP method

In this experiment, the generalization ability of the MGCDP method is evaluated by identifying the new user data that is not appear in the training stage. All experimental data are divided into two parts: M_{training} and M_{test}, which contain m and remaining $700-m$ groups user data, respectively. First, the MGCDP projecting matrix is calculated by using all the multimodal biometric samples from M_{training} part, and then project all biometric feature in M_{test} part with this projecting matrix. Finally, randomly select h groups multimodal biometric data as gallery set, and the remaining $5-h$ groups data as probe set. The effect of different number of user in M_{training} and M_{test} on identification were evaluated. It is worth noting that when the parameter m in the M_{training} is selected, in order to avoid the number of features that exceed the number of classes, the number of features is limited to $m-1$. Table 4 shows the recognition rate under different m and x conditions.

Table 4 Recognition rate under different m and h conditions

Data set	Recognition rate/(%)		
	Training m=50	Training m=100	Training m=150
Gallery h=1	86.57	89.74	87.93
Gallery h=2	94.50	97.52	96.54
Gallery h=3	95.49	96.94	97.11

Fig. 8 shows the influence of feature dimension on system recognition rate when selecting different m values and fixing parameter $h=2$.

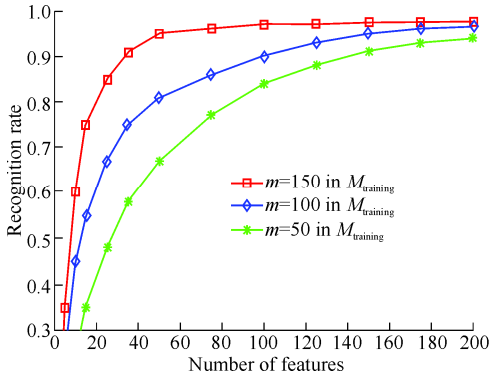

Fig. 8 Generalization of MGCDP under different training samples

The experimental results show that with the increase of number of training data, the generalization ability of the MGCDP projecting matrix is enhanced, and the recognition accuracy of the system is improved. When m=100 and h=2, that is M_{training} and M_{test} contains 100 and 2 groups of data, the overall recognition rate of the system reaches the maximum. The results show that the MGCDP method has a good ability to identify new user samples.

6 Conclusions

In this paper, we presented a feature fusion technique based on correlation analysis method. Our proposed method, called MGCDP, uses the class associations of the samples in the analysis. This method is aim to maximize the correlation of the intra-class features while minimize the correlation of the between-class. The MGDCP method can be used in biometric identification applications for fusing the features extracted from multiple modalities or combining different feature vectors extracted from a single modality. Extensive experiments on various multimodal biometric databases demonstrated that MGCDP method outperforms the other state-of-the-art feature-level information fusion approaches.

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