

Finger Vein Recognition Based on 2DPCA and KMMC

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Abstract

A new finger vein recognition method based on two-dimensional principal component analysis (2DPCA) and kernel maximum between-class margin criterion (KMMC) is developed. The algorithm includes four stages. Firstly, perform preprocessing steps which include normalizing and mean-filtering on the finger vein images, secondly, employ the 2DPCA to condense the dimension of image vector, thirdly, apply the KMMC to reduce the dimension of training samples further, and finally, take the match and recognition step by computing the Euclidean distance between each sample. Our experimental results indicate that the new method has good recognition effect.

Keywords: PCA, MMC, KMMC, finger vein recognition

1. Introduction

Currently, finger vein recognition technology has become a very active research topic in the biometric recognition, and has a lot of applications in military, commercial and so on. How to extract the features of finger vein images effectively for better matching has become a hot issue in pattern recognition. With the characteristics of low computation time, facile realization, good performance on expression and separability, the feature extraction method based on subspace analysis has received wide attention [1-6] and become one of the mainstream methods for feature extraction and recognition of finger vein images.

The basic idea of the feature extraction method based on subspace analysis is to compress the high-dimensional finger vein images into a low-dimensional subspace to classify them by using linear or non-linear space transformation, which makes the subspace distribution more compact and also makes the computational complexity reduced greatly. Fisher Linear Discriminant (FLD) [2] is one of the most classic subspace analysis methods, and it is widely used in the vein recognition, but there is a small sample size problem in the process of feature extraction. In order to solve this problem, Liu et al. put forward a new method based on the maximum margin criterion (MMC) [7], which solved the small sample size problem existing in the method of FLD completely. The MMC algorithm is made up of the subtraction relationship of the between-class scatter and the within-class scatter. By minimizing the within-class scatter and maximizing the between-class scatter, this algorithm can obtain the maximum value of the MMC function, find the best projection direction and realize the optimal classification.

However, due to the impact of some external factors, such as light, temperature, humidity and horizontal displacement, the vein image has some degree of nonlinear distribution characteristic. In order to extract the nonlinear features of the vein image, Li et al. proposed the KMMC algorithm [8], which extended the MMC algorithm to the nonlinear situation, and its recognition effect was better than that of the MMC algorithm.

Whereas, during extracting the nonlinear features, the KMMC algorithm will also increase the amount of computation and the time for training sample greatly. In order to solve this problem, we put forward a new algorithm which combines the PCA algorithm

with KMMC algorithm. That is to say, we reduce its dimension by the 2DPCA algorithm before taking nonlinear mapping to the image data, and then take the KMMC algorithm on the data after dimension reduction. Finally, the simulation experiment results on the self-built vein library in the laboratory show that the time for training sample reduces a lot, but the recognition rate still keeps consistent.

2. KMMC Algorithm

The KMMC algorithm is a nonlinear extension of the maximum margin criterion (MMC). It makes the data in the original input space mapped into a high-dimensional even infinite dimensional feature space with a nonlinear mapping, and so the data can be divided in the feature space linearly, as shown in Figure 1, and then the MMC algorithm will be operated in this space.

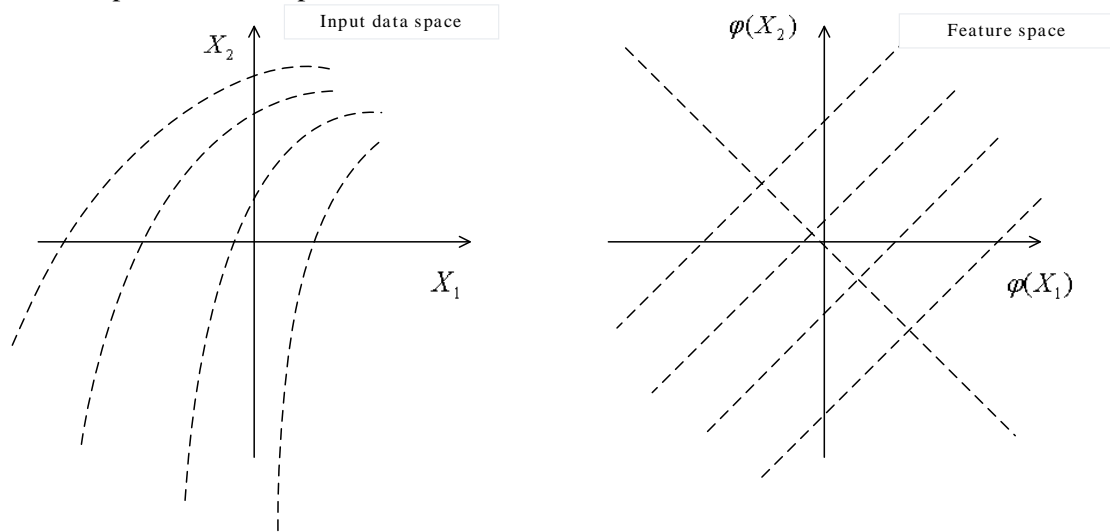


Figure 1. KMMC projection schematic

Suppose that there are c model classes, M is the total number of the training samples, M_i is the number of the training samples of class i , $X_k \in R^n$ is the k -th training sample in the original input space, $X_j^i \in R^n$ is the j -th training sample of class i , and they are $m \times n$ image data matrix, where $k = 1, 2, \dots, M$, $i = 1, 2, \dots, c$, $j = 1, 2, \dots, M_i$. Making the data of X_j^i mapped into a high-dimensional feature space F using a nonlinear mapping function φ , that is,

$$\begin{aligned} \varphi: R^n &\rightarrow F \\ X_j^i &\mapsto \varphi(X_j^i) \end{aligned} \quad (1)$$

For the training samples in high dimensional feature space, the between-class scatter matrix H_b^φ and the within-class scatter matrix H_w^φ can be written as:

$$H_b^\varphi = \sum_{i=1}^c \frac{M_i}{M} (\mu_i^\varphi - \mu^\varphi)(\mu_i^\varphi - \mu^\varphi)^T \quad (2)$$

$$H_w^\varphi = \frac{1}{M} \sum_{i=1}^c \sum_{j=1}^{M_i} (\varphi(X_j^i) - \mu_i^\varphi)(\varphi(X_j^i) - \mu_i^\varphi)^T \quad (3)$$

where $\mu^\varphi = \frac{1}{M} \sum_{i=1}^c \sum_{j=1}^{M_i} \varphi(X_j^i)$, $\mu_i^\varphi = \frac{1}{M_i} \sum_{j=1}^{M_i} \varphi(X_j^i)$.

Here, we define the KMMC function in the feature space F as $\max J^{KMMC}(V)$, that is,

$$\max J^{KMMC}(V) = \sum_{j=1}^d v_j^T (H_b^\varphi - H_w^\varphi) v_j \quad (4)$$

where $V = [v_1, v_2, \dots, v_d] \in R^{L \times d}$, $v_i \in R^L$ is a nonzero vector in the feature space F .

According to the reproducing kernel theory, the solution vector v of Eq. (4) must exist in the space produced by the M vectors $\varphi(X_1), \varphi(X_2), \dots, \varphi(X_M)$, hence v can be represented by their linear combination, as follows,

$$v = \sum_{i=1}^M a_i \varphi(X_i) = \varphi \alpha \quad (5)$$

where $\varphi = [\varphi(X_1), \varphi(X_2), \dots, \varphi(X_M)]$, $\alpha = [a_1, a_2, \dots, a_M]^T \in R^M$.

Let $\varphi(X_k^i)$, the class mean vector μ_i^φ and the population mean vector μ^φ be projected respectively onto v , then,

$$\begin{aligned} v^T \varphi(X_k^i) &= \alpha^T \varphi^T \varphi(X_k^i) = \alpha^T [\varphi(X_1)^T \varphi(X_k^i), \dots, \varphi(X_M)^T \varphi(X_k^i)] \\ &= \alpha^T [k(X_1, X_k^i), \dots, k(X_M, X_k^i)] = \alpha^T \lambda_k^i \end{aligned} \quad (6)$$

$$v^T \mu_i^\varphi = \alpha^T \frac{1}{M} \sum_{j=1}^{M_i} [k(X_i, X_j^i), \dots, k(X_M, X_j^i)] = \alpha^T \beta_i \quad (7)$$

$$v^T \mu^\varphi = \alpha^T \frac{1}{M} \sum_{j=1}^c \sum_{i=1}^{M_i} [k(X_i, X_j^i), \dots, k(X_M, X_j^i)] = \alpha^T \beta \quad (8)$$

where $\lambda_k^i = [k(X_1, X_k^i), \dots, k(X_M, X_k^i)]$, $\beta_i = \frac{1}{M} \sum_{j=1}^{M_i} \lambda_k^i$, $\beta = \frac{1}{M} \sum_{i=1}^c \sum_{j=1}^{M_i} \lambda_k^i$.

By applying Eq. (6), Eq. (7) and Eq. (8) on Eq. (4), we can get the KMMC function as the following:

$$\max J^{KMMC}(v) = \sum_{j=1}^d v_j^T (H_b^\varphi - H_w^\varphi) v_j = \sum_{j=1}^d \alpha_j^T (K_b - K_w) \alpha_j \quad (9)$$

where $K_b = \sum_{i=1}^c \frac{M_i}{M} (\beta_i - \beta)(\beta_i - \beta)^T$, $K_w = \frac{1}{M} \sum_{i=1}^c \sum_{j=1}^{M_i} (\lambda_j^i - \mu_i^\varphi)(\lambda_j^i - \mu_i^\varphi)^T$.

Define the Lagrange function as follows,

$$L(\alpha, t) = \alpha^T (K_b - K_w) \alpha - t(\alpha^T \alpha - I) \quad (10)$$

Take its partial derivatives to α ,

$$\frac{\partial L(\alpha, t)}{\partial \alpha} = 2(K_b - K_w) \alpha - 2t \alpha \quad (11)$$

Make the partial derivative be zero,

$$2(K_b - K_w) \alpha^* - 2t \alpha^* = 0 \quad (12)$$

Thus, we have

$$(K_b - K_w) \alpha^* = t \alpha^* \quad (13)$$

where α^* is the extreme solutions of $J_{KMMC}(v)$. Solving α^* is equivalent to solving the eigenvectors of $K_b - K_w$. Thus, the orthogonal eigenvectors corresponding to the first d largest eigenvalues of $K_b - K_w$, $\alpha_1, \alpha_2, \dots, \alpha_d$, make up the optimal projection of the projection matrix, that is,

$$\alpha = [\alpha_1, \alpha_2, \dots, \alpha_d] \quad (14)$$

3. Our Algorithm

The KMMC algorithm, a kind of nonlinear feature extraction methods, overcomes the shortcoming of the linear analysis which fails to use the high order statistics of image. However, it will make the dimensionality unusually large and pose a challenge to

computer and memory space when it converts the image to a one-dimensional vector. In order to solve this problem, this paper proposes a new vein recognition algorithm. Firstly, it reduces the dimensionality of the original image data by the 2DPCA algorithm. After that, it compresses the matrix after dimension reduction and extracts the features by KMMC algorithm. Finally, it improves the operation speed of the KMMC algorithm effectively, and keeps the recognition rate consistent.

Principal component analysis (PCA, also called K-L transform) is a very classic finger vein recognition algorithm. It is widely used as it can extract the linear feature of image and data. PCA algorithm is used to search for the optimal unit orthogonal eigenvalues and reconstruct the original image with their linear combination. When the original image and the reconstructed image have the minimum mean square error, the PCA algorithm will achieve the best compression effect [9].

After the 2DPCA transformation, the image is compressed in the horizontal direction, and the classification information is compressed to a small amount of columns. Then, the classification information is compressed further in the vertical direction by the KMMC transformation, and is compressed to a small amount of rows. In the end, the whole image information is compressed to the upper left corner of the image, as shown in Figure 2.

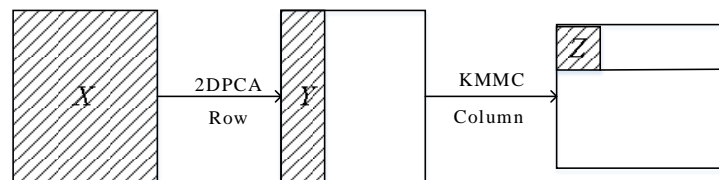


Figure 2. Our Algorithm

Suppose that X_i is any image of the training set. First of all, we apply the 2DPCA transformation on X_i in the horizontal direction to get the projection matrix Y_i , and then use the transformed matrix Y_i as a new training set. Finally, we apply the KMMC transformation on it.

Below is a detailed description of our algorithm.

Suppose that there are c model classes (that is, there are c different fingers), M is the total number of training samples, M_i is the number of the training samples of class i (that is, the i -th finger has M_i images), X_j^i is the j -th training samples of class i , X_k is the k -th training sample of the overall training samples, \bar{X}^i is the mean of the training samples of class i , and \bar{X} is the mean of the overall training samples, that is,

$$\bar{X} = \frac{1}{M} \sum_{i=1}^c X_i \quad (15)$$

Suppose that X is a $m \times n$ random image matrix. Projecting X to a $n \times d$ matrix W , the 2DPCA algorithm will generate a $m \times d$ matrix Z with $d \ll n$.

Where the covariance matrix of the original image is,

$$S_i = E[(Y^T - EY^T)(Y^T - EY^T)^T] = \frac{1}{M} \sum_{k=1}^M ((Y^T)_k - \bar{Y}^T)^T ((Y^T)_k - \bar{Y}^T) \quad (16)$$

According to the rule of 2DPCA [10], the orthogonal eigenvectors corresponding to the first d largest eigenvalues of S_i , w_1, w_2, \dots, w_d , make up the optimal projection of the projection matrix, that is,

$$W = [w_1, w_2, \dots, w_d] \quad (17)$$

By solving the matrix W and take the 2DPCA transformation with it on the training image data, we can get the projection matrix Y and then perform the KMMC transformation on Y . Finally, we can get the mage matrix by two transformations, that is,

$$Z = Y^T W \quad (18)$$

4. Experimental Analysis

To verify the validity of the algorithm, this experiment is divided into three steps, that is, preprocessing the vein images, comparing the recognition rate of the KMMC algorithm with that of our algorithm and also comparing their operation time.

1) Preprocessing the vein images

To verify the validity of our finger vein recognition algorithm based on 2DPCA and KMMC, our laboratory has established a finger vein image database. It is composed of the finger vein images captured from 70 different fingers, and each finger has eight images collected in different time, which have illuminations and position changes from each other. That is, there are 560 images in all. Figure 3(a) is four different images from the same finger. Figure 3(b) is four different images from four different fingers.

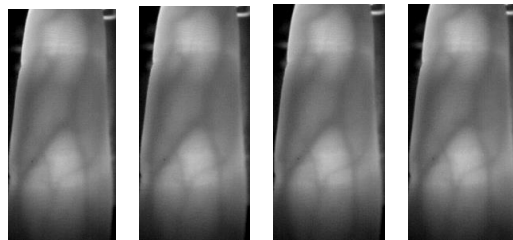


Figure 3(a).

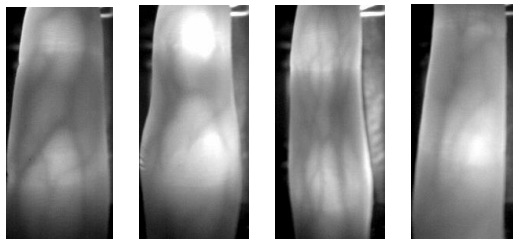


Figure 3(b).

In order to reduce the noise influence and improve the operation speed, we normalize the size and gray level of the original vein images which size is 300×140 , and then take the mean filter on it. At last, we get the vein images size of 90×40 , as shown in Figure 4.

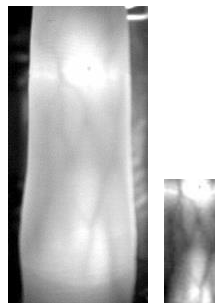


Figure 4.

2) Comparing the recognition rates

Considering the complexity of calculation, the experimental data is based on that the kernel function which is chosen as a polynomial of degree d , as show in Eq. (19), and the Euclidean distance is used as the identification scale.

$$K(x_i, x_j) = (x_i, x_j)^d \quad (19)$$

This experiment tests the recognition rates of the MMC algorithm, the KMMC algorithm and our algorithm with the number of training samples being chosen as 1 to 7. The experimental results are shown in Figure 5.

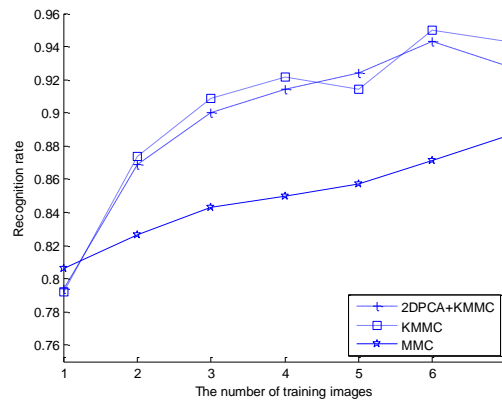


Figure 5. The Recognition Rate Curves of Different Algorithms

From the recognition rate curves of different algorithms in Figure 5, we can see that the recognition rates of the KMMC algorithm and our algorithm are nearly equal, and they are higher than the recognition rate of the MMC algorithm. In addition, the recognition rate of our algorithm increases gradually with the increasing of the number of the training samples.

3) Comparing operation time

This experiment is operated in the Matlab R2011b platform of a small server computer, which CPU is E5-2603 1.80GHz and ram is 8 GB. Table 1 is the statistic data of the operation time of the KMMC algorithm and the 2DPCA+KMMC algorithm for different numbers of the training samples.

Table 1. The Operation Time of KMMC and Our Algorithm

| Number of training samples | KMMC | | | Our algorithm | | |
|----------------------------|-----------------|--------------------|--------------|-----------------|--------------------|--------------|
| | training time/s | recognition time/s | total time/s | training time/s | recognition time/s | total time/s |
| 1 | 41.68 | 20.24 | 61.92 | 3.81 | 15.4 | 19.21 |
| 2 | 187.26 | 15.7 | 202.96 | 12.49 | 14.18 | 26.67 |
| 3 | 553.18 | 14.22 | 567.4 | 28.98 | 11.36 | 40.34 |
| 4 | 1254.49 | 12.98 | 1267.47 | 60.16 | 9.27 | 69.43 |
| 5 | 3460.87 | 9.5 | 3470.37 | 109.61 | 7.85 | 117.46 |
| 6 | 8848.22 | 6.63 | 8854.85 | 183.27 | 4.99 | 188.26 |
| 7 | 28435.32 | 4.17 | 28439.49 | 281.67 | 2.66 | 284.33 |

From Table 1, we know that the time for training sample and the recognition time of our algorithm are less than those of the KMMC algorithm, and its training time is shortened more than 90%. With the increasing of the number of training samples, the effect of shortening the training time is more obvious.

5. Conclusion

This paper puts forward a new kind of effective finger vein image recognition algorithm—a novel finger vein recognition algorithm based on 2DPCA and KMMC. By combining the 2DPCA algorithm with the KMMC algorithm, our algorithm reduces the time for training sample effectively and keeps the recognition rate consistent. In addition, its recognition effect is better.

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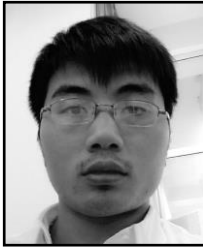
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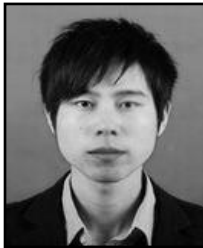
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