



## IRIS-FACE FUSION AND SECURITY ANALYSIS BASED ON FISHER DISCRIMINANT

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*Abstract- With the development of society and science technology, the information security becomes more and more important for people and nation. In this paper, we focus on the technology of iris-face fusion in multi-mode sense in order to find an algorithm to get a better recognition performance. Firstly, we introduce the feature extraction of iris and face, and fusion the features using different algorithms. By simulation, we find out the recognition performance with different fusion methods, which provide some new conclusions. In order to improve the performance of recognition system, we classify these features with fisher discriminant analysis again. Then we analyze the security of recognition system from the aspect of influence of leak in biology features. Finally, experiments were designed to demonstrate the effectiveness of the proposed algorithms.*

**Index terms:** iris feature; face feature; fisher discriminant analysis; fusion.

## I. INTRODUCTION

With the development of science and the digitization of people's life, the requirement of authentication is increasing, which becomes a common problem that every people, every society, and every nation need to face. The traditional identification methods are usually based on id, magnetic CARDS, passwords, and certificates, etc., which needs people to carry and remember the card number and password. So the main drawback of traditional identification method is that the certificates and magnetic card are easily lost and forged. Fortunately, the biology identification technology uses the people's biology features, such as fingerprint, iris, voice, signature, etc., and recognizes automatically with computer or in other ways. It overcomes the drawback of the traditional identification method and has its own unique advantages, which makes a continuous development. Especially after the 9.11 terrorist attacks on the United States, people's identity and the information security have attracted more and attention [1-3].

Through the recognition with biology feature, we can build some rules for identity, rather than using the ID cards, or the passwords. In fact, in 19 century, the criminal department in pair's prison provided and realized the ideal that identified the criminals with biology features. Later, this ideal was used widely in legal department, even in many other applications. Which biology features can be used for recognition, which is the main question need to be answered at first. Generally, the physiological feature or behavior characteristics can be used for recognition must satisfy the conditions of universality, discrimination, permanency, and collect-ability. There are several commonly used single mode biology recognition methods: voice recognition [4], fingerprint recognition [5-7], faces recognition [8-10], iris recognition [11-13, 25-26], and signature recognition and so on. Voice feature is a coalition of physiological and behavior characteristics. The voice of people depends on physical structures, such as the characteristic of vocal cords, mouth, nose cavity, which are used to compound voice with differences for each one. The main disadvantage of voice recognition is that, it is sensitive for some factors, such as noises, and is easily forged with recording. Moreover, as the discrimination of voice is not very obvious, it can not be used in large recognition system. The recognition rate of fingerprint is satisfying, which had been used long ago. The fingerprint is composed by valley line and regression line, which are formed in seven month old fetus. Even for twins the fingerprints are not the same. The accuracy of modern fingerprint recognition system can be satisfied the certification system with

of medium-sized scale. Several fingerprint of a person can meet the requirement of system with large-size scale. However, there is a big problem in fingerprint recognition system that it need large amount of samples for testing. Due to some factors, such as the genetic, age, environment, and professional, the fingerprint of some people can not be used for identity. Face is the mostly used method in biology recognition. Face recognition has the following advantages, the most of which is that it collects face images with non invasive. And it is intuitive, convenient, of a lower cost. In actual applications, multiple face recognition can be simultaneously made. Of course, there are still some problems in face recognition system. The face features are easily influenced by the external environment; It is difficult to identify the faces of twins; The varieties of face makes it difficult to recognize. Iris is the annular section between the pupil and sclera. The texture information of iris is formed during the embryonic and becomes stable in two years. The texture of iris is very complex, which carries lots of different information that can be used for identity recognition. Each iris is different, even for the twins, and it is difficult to change by operation. These characteristics provide a great application prospect of iris recognition system. In the early iris recognition system, it requires a lot of users participation and the cost is much high, but now, it becomes more friendly cost and more reasonable.

From the overall view of biology recognition system based on single mode, the applicability of a specific biology recognition technology depends on the demand of corresponding application, no one of which is superior to the others. Each of the above biology characteristics has its own advantage, but is not the best features for recognition. Fortunately, the multiple mode biology technology can solve this problem, for it has the following several advantages of accuracy, security, and applicability. In recent years, multiple mode biology recognition system has attracted more and more attention. Early in [14], the ideal of identifying people by fusing the biology characteristic was put forward by Bmnnelli et al. The conception of multiple modes was firstly proposed in 1997, it realized the authentication by fusing voice and face based on the theory of supervised learning and Bayes, which achieved a high accuracy. In [15], the face and fingerprint are combined for personal identification. The geometrical characteristic of hands and palm print are used in authentication system. BioD developed a recognition system of three types of biology features, i.e., human face, lips, and voice, called Dialog Communication System.

Although, the multiple mode biology recognition system is the new development direction of the future biology technology, there still requires a lot of works, such as a unified standard for

fusion, how to determine the used characteristic to get a best performance, how to evaluate the performance of recognition fusion system. In order to improve the performance of multiple mode recognition system, in this paper, we will research the problem of recognition and security in fusion system with the features of face and iris.

## II. OVERVIEW OF RECOGNITION WITH MULTIPLE MODE

### A. Iris Recognition Based on Texture

Iris recognition is a kind of biology technology. It was firstly proposed in 1949 by James in a textbook, which recorded the shape of iris to identify people. However, it did not obtain the development until two ophthalmologists put forward a similar ideal in 1989. Later in 1994, John Daugman proposed a practical iris recognition algorithm, and applied for a patent, which became the basis of modern iris recognition algorithm and the corresponding products. Thus, the experts in iris have long been interested in this problem.

In general, any a biology recognition system can be divided into two phases: authentication phase (training phase) and testing phase, as shown in figure 1.

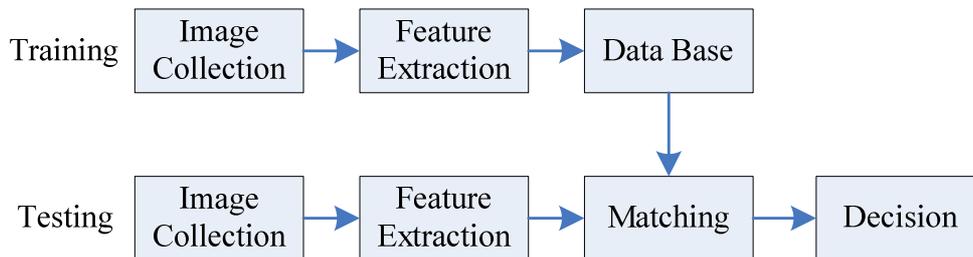


Figure 1. The basic conception of biology recognition

Similarly, iris recognition can also be divided the above two stages. In training phase, the preprocessing of the original image in database, including iris location, image enhancement, normalized processing, as a preparation for the next step. And then extract the feature of the located iris and save it into data base as template. In the recognition phase, the operation on iris is the same as in training phase, which is mainly to compare the texture characteristic of the iris in data base.

#### ✧ Iris Location

Generally, an eye image not only includes the iris itself, also includes the other parts that have nothing to do with the feature extraction, such as eyelash, eyelid, and pupil. In fact, the only area that we need is the part between pupil and sclera. So the accuracy of iris location will influence the later steps, such as the feature extraction and matching. As a result, the accuracy of iris

location before feature extraction is important, in which the inner and outer boundary are determined. The inner edge of iris usually refers to the edge of pupil and iris intersects, in which the center and radius of pupil are determined firstly. Usually, the gray change among pupil, iris, and sclera is obvious, in which the pupil can be roughly separated from them by binary methods [16 - 18]. In the histogram of pupil, there usually exists a peak and a valley value, the peak one represents the grayscale of pupil, and the valley one stands for the gray between the pupil and iris.

After the above separation operation, the projection method can be used to determine the center and radius of the pupil. Then do the projection operation of the processed image in the direction of horizontal and vertical. As the pixels with lower gray are much more in the direction of horizontal and vertical of pupil center, the value is the smallest. Thus, the projection values in these two directions are shown as:

$$\begin{cases} x_i = \arg \min \left( \sum_{y=1}^m I(x, y) \right) \\ y_i = \arg \min \left( \sum_{x=1}^m I(x, y) \right) \end{cases} \quad (1)$$

In (1),  $x_i$  and  $y_i$  stand for the ordinate, and  $I$  is the original image. A sample of location of pupil is shown in figure 2.

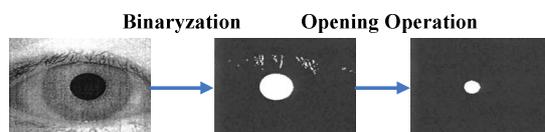


Figure 2. The preprocessing of iris image

The inner and outer edges can be approximately regarded as round, usually as concentric circles. The radius of pupil is usually 0.1 to 0.8 times of that of iris. John had proposed a very effective algorithm based on calculus operator to get the three main parameters of the iris [19, 20], the basic idea of which is that when the radius of original image increases along the radial direction of the radius, the gray of circumference and the differential to radius is larger, where the corresponding circle at this time is the outer edge of this iris, as shown in the next formula.

$$\begin{cases} \max_{(r, x_0, y_0)} \left| G_s(r) * \frac{\partial}{\partial r} \int_{(r, x_0, y_0)} \frac{I(x, y)}{2\pi r} ds \right| \\ G_s(r) = \left( 1/\sqrt{2ps} \exp\left(\frac{(r-r_0)^2}{2s^2}\right) \right) \end{cases} \quad (2)$$

In (2), \* represents convolution,  $G_s(r)$  is a smooth function,  $I(x, y)$  stands for the original image,  $ds$  is the circulation integral.

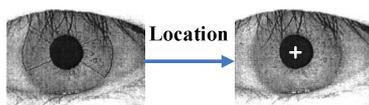


Figure 3. Location of the outer edge of iris

According to this method, it needs to search the entire eye image, which will consume much time and slow down the efficiency of the system. Furthermore, this algorithm is sensitive to noises. In order to solve this problem, in this paper, we suppose that the centers of iris and pupil are the same, only use a part of image, and delimit the scope of parameters to ensure narrowing the search scope.

#### ✧ Iris Feature Extraction and Matching

If classified according to feature extraction, the current used methods mainly have three classes, i.e., phase analysis based, zero description based, and texture analysis based. From the view of biological, iris is composed of very complex fibrous tissue that contains many details features, such as spots, filaments, striped pits, etc., which presents a kind of radial structure from the inside. At present, the structure and details of iris feature are seemed as a kind of texture information. Adopt the texture based method to extract the iris feature is popular, which can achieve an ideal extraction performance. The information of the iris feature can be represented by the frequency, the direction, and the position iris texture, the specific frequency and direction information of which can be extracted by filter. In 1980, Daugman had proposed a 2-D Gabor filter based on physiological. At present, Gabor based filter has been widely used in machine vision, especially in analysis of texture feature.

As the differences of focal length and capture speed, the rotation of the eyeball, the pupil contraction, and open and close of eyes, the collected iris image will have big differences, which will influence the accuracy of the iris in extracted in the next step. This will finally affect the recognition performance. For a biology recognition system that needs a high request of security, this must be avoided. Thus, before feature extraction, normalization processing is needed for the iris that has been located, which will make the feature extraction in a unified size and location environment. The details of normalization processing are shown as follows:

1) Take a line in the direction of radius of iris, and form it into a vector in accordance with the column scanning, as the first column of the rectangle:

$$\begin{cases} x = a - R \sin \theta - k \sin \theta \\ y = b + R \cos \theta + k \cos \theta \end{cases} \quad (3)$$

In (3),  $a$  and  $b$  represent the centers of inner edge and outer edge of iris,  $R$  is the distance from the center to any point in the area of iris,  $k$  stands for the step size in radial direction, and  $p$  is the angle between the radial line and the abscissa.

2) Take the center of pupil as the center of the iris, and increase the angle. For each line in the radial direction of each value of angle, make it as a vector according to the column scanning, as a column vector of the rectangular.

3) Do the above operation on the left and right fan, and combine them into a normalized rectangle.

As the texture feature of iris changes along the direction of radius, i.e., the vertical direction in the normalized rectangle, thus the normalized iris can be divided into several regions along the direction of vertical. In each region, the change of texture feature is small. As a result, the filter for feature extraction with the same frequency can be used. Usually, the following formula can be used for extraction the frequency and direction information of the normalized iris:

$$F_i(x, y) = \iint G_i(x - \tau_1, y - \tau_2) I_i(\tau_1, \tau_2) d\tau_1 d\tau_2 \quad (4)$$

By this formula, for a image  $I_i$ , the frequency and direction information of filter  $G_i$  can be extracted, where  $I_i$  stands for the characteristic of the  $i$ -th region of iris,  $G_i$  represents the filter used for the  $i$ -th region of iris, and  $F_i$  stands for the image after filtering. In this paper, we will divide the image after filtering into  $8 \times 8$  small pieces. For each piece of image, encode it according to the following formula, which can be used to represent the extraction feature:

$$\begin{cases} \sigma = \frac{1}{N} (\sum_w |F_i(x, y) - m|) \\ m = \frac{1}{N} \sum_w |F_i(x, y)| \end{cases} \quad (5)$$

In (5),  $\sigma$  is the mean absolute distance in each image, which also represents the feature of each image,  $m$  stands for the mean value of image after filtering, and  $N$  represents the number of pixels in the image. Finally, form all the  $\sigma$  as a vector  $V = [\sigma_1, \sigma_2, \sigma_3, \dots, \sigma_n]$ , which can be regarded as the feature of an iris.

The mode matching is used to determine the similarity of a certain biological characteristic between that in the testing phase and training phase, i.e., to determine whether the two biological features belong to a same person. The feature vector obtained after the feature extraction of biological samples can be regarded as a point in the feature space. Determining whether two features belong to the same person by the distance of two points is a commonly used matching

method, in which, the shorter distance represents the more similar. In mode recognition, the widely used matching algorithms based on distance have Euclidean Distance and Cosine Distance [21 - 23]. Euclidean Distance is the distance between two points, such as in n dimensions space:

$$d = \left( \sum_{i=1}^n (x_i - y_i)^2 \right)^{1/2} \quad (6)$$

Any kind of biological feature in a same mode can not be the same, even for the same person, the feature in each collection can not be completely the same. Thus, for the same biological recognition system or algorithm, a given threshold value is needed, to determine the similarity of two biological features. When the distance of two biological features after matched is larger than the given threshold, it can be seemed as a successful matching, or else, as a fail.

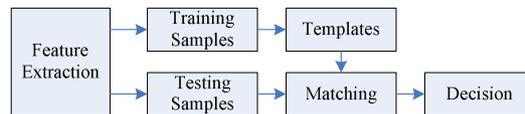


Figure 4. The basic model of face recognition

#### B. Face Recognition Based on Principal Component Analysis

Most of the early visual functions only need to establish a retinal visual model. Different from it, face recognition is a high-level task. For the early face recognition method based on computer, it was only limited in neural activity. So the researchers start to pay more attention onto the mode recognition, so as to develop a rapid, simple, and correct recognition mode, as shown in figure 4.

With the development of face recognition technology, a lot of algorithms have been proposed; mainly have Geometry method [24], Elastic Graph Matching, Principal Component Analysis, Liner Discriminant Analysis, and so on.

Principal Component Analysis is a kind of space projection technology, widely used in data compression and dimension reduction. The basic idea of it is though solving the eigenvalue problem of the training sample scattering matrix, to give a group of orthogonal basis that far fewer than the dimension of training samples, which are used to represent the subspace of the training samples. This group of orthogonal basis is called as the principal component, which compress the original signal to the space with lower dimension to make the data distribution in subspace more compact. Moreover, it keeps the main information while reducing the dimension.

The core of the principal component analysis is  $K$  conversion, a kind of orthogonal transformation, the detailed knowledge of which can be found in [21].  $K$ - $L$  transform was firstly

proposed by Kirby and Sirovich, and firstly used for face recognition by Turk, as the conception of feature face. Face recognition with principal component analysis is to do the principal component operation to the samples of human face. The obtained orthogonal vector in space of human face called feature face. The feature of face is the projection vector of the human face on the feature face.

Suppose the size of each is  $N \times N$ , link them together according to the column, an  $N \times N$  dimension vector can be obtained, as shown in (7).

$$X = (x_{11}, x_{21}, \dots, x_{n1}, x_{22}, \dots, x_{n2}, \dots, x_{m1}, \dots, x_{nm})^T \quad (7)$$

In the practical application, the number of human face is huge, and the dimension is high. In a large dimension space, the distribution of points is scattered, which is bad for human face classification and characteristics expression. Thus, through  $K-L$  transform, it can map the human face to a lower dimension subspace, i.e., description the image use a subspace with low dimension, and keep the main information at the same time.

The main steps of face recognition are shown as follows:

1) Scan the human face image in training data base to a vector according to the column. And then form all the vectors into a matrix, denoted as:

$$X = (X_1, X_2, \dots, X_M)^T \quad (8)$$

2) Produce the matrix with the overall spread in the training sample set:

$$\Sigma = \frac{1}{M} \sum_{i=0}^{M-1} (X - \mu)(X - \mu) \quad (9)$$

3) Calculate the eigenvalue and eigenvector of  $\Sigma$ .

4) Get the projection matrix by composing numbers of  $M$  eigenvector according to the  $M$  larger eigenvalue of covariance matrix  $\Sigma$ .

5) Project every human face images in the training set to the subspace expanded by the above  $M$  eigenvector. The obtained vectors represent the position in the subspace, which can be treated as the basis of human face recognition.

6) Repeat the step from 1 to 5 above of the human face images that need testing, to get the feature vector of human face.

7) Match the faces in the training and testing sets by the method of Euclidean Distance.

8) Make the recognition decision.

### C. Biological Feature Fusion based on Multiple Modes

Fusion can connect different kinds of information, which will improve the performance of recognition system. It plays an important role in detection, identification authentication, tracking, and decision, and is widely used in medicine, robot, space, defense and other fields.

An effective fusion method usually has the advantages of improving the accuracy of decision, improving the performance while suffering from interference, and improving the performance in bad environment. Any biological recognition system may include four modules, i.e., the image collection module, feature extraction module, feature matching module, and decision module. Image collection is used to capture the information of biological. For example, fingerprint acquisition module is to obtain the direction and location information of ridge line and valley line of user's finger. The feature extraction module is used to obtain the significant or difference features. Matching module is to match the features of human face in training and testing sets. Decision module is used to save the biological features of users'.

The four modules above reflect a processing of biometric identification system. Any variety of information fusion of biological feature can occur in any stage in the process of the above four. The biological feature information fusion can be divided into the following kinds, according to the different stages that fusion occurs.

1) Sensor Fusion. Also known as data fusion, in which the original image data are fused to produce a set of more abundant information, before it is processed. Then, do the operation of feature extraction and matching. This kind of fusion is the lowest level of integration, the advantage of which is that it can keep more original information. However, it cost much more time according to the large amount of data.

2) Feature Fusion. In this fusion level, the features from different biological characteristic are connected into a feature vector, and then matched with the templates. Its advantage is that it needs only less computation time.

3) Matching Fusion. In this way, each feature of each kind of single mode biological characteristic is extracted separately.

4) Decision Fusion. Different kinds of biological features make decision respectively, and use this result to fuse a final fusion result. It can be regarded as the highest level of fusion, in which more original information may lose but has a good real-time performance and is more robust.

For a biometric recognition system, information fusion in early stage can produce a better recognition performance than that in later stages, as in the early stage, more original information can be kept. And because the data in feature level include more information than that in matching and decision stage, feature fusion is regarded as a better method for biometric recognition, which has been researched widely. Thus, in this paper, we will use the feature fusion for iris and face recognition.

### III. IRIS-FACE FEATURE FUSION BASED ON FISHER DISCRIMINANT AND SECURITY ANALYSIS

#### A. Feature Fusion of Iris and Face

##### ✧ Fusion Rule

As stated above, we will use the feature fusion method for iris and face recognition. There are several algorithms for feature fusion, such as serial rule, sum rule, and weighted sum rule.

Serial Rule: as shown in (10), connect two vectors to form a long vector:

$$\left. \begin{array}{l} X = (x_1, x_2, \dots, x_d) \\ Y = (y_1, y_2, \dots, y_d) \end{array} \right\} \Rightarrow Z = (x_1, x_2, \dots, x_d, y_1, y_2, \dots, y_d) \quad (10)$$

In (10),  $X = (x_1, x_2, \dots, x_d)$  and  $Y = (y_1, y_2, \dots, y_d)$  are two different vector sets of modes, and the samples include  $d$  pieces of images. The vector sets  $Z$  represents the feature vector set by serial fusion.

Sum Rule: add the different vectors of modes with the corresponding position, i.e.:

$$\left. \begin{array}{l} X = (x_1, x_2, \dots, x_d) \\ Y = (y_1, y_2, \dots, y_d) \end{array} \right\} \Rightarrow Z = (x_1 + x_2, \dots, x_d + y_d) \quad (11)$$

Weighted Sum Rule: add with weight coefficient  $\theta$ .

$$\left. \begin{array}{l} X = (x_1, x_2, \dots, x_d) \\ Y = (y_1, y_2, \dots, y_d) \end{array} \right\} \Rightarrow Z = (x_1 + \theta x_2, \dots, x_d + \theta y_d) \quad (12)$$

In this paper, we will use the serial rule for feature fusion.

##### ✧ Normalized Processing

Because of the differences of biology mode and feature extraction method, the feature vector and region of iris and face feature are different. In order to eliminate this case and get a better performance, the feature need to be normalized. In this paper, we will use Z-Score algorithm.

Let  $a^j$  is the  $j$ th iris with  $d$  dimensions of class  $i$  in training samples, by which the iris set can be expressed as  $P$ , where  $P = (a_1^1, \dots, a_m^1, a_1^2, \dots, a_m^n)$ . And  $b_i^j$  is the  $j$ th iris with  $d$  dimensions of

class  $i$  in testing samples, by which the iris set can be expressed as  $Q$ , where  $Q = (b_1^1, \dots, b_m^1, b_1^2, \dots, b_m^2)$ .

Take the iris normalized for example. The process of Z-Score algorithm is shown as follows.

Denote  $P_k$  as the  $k$ th row vector in iris set  $P$ :

$$C_k = \frac{P_k - \bar{P}_k}{\sigma_k} \quad (13)$$

In (13),  $\bar{P}_k$  represents the average of  $P_k$ , and  $\sigma_k$  is the variance of  $P_k$ . The normalized operation is defined in (14):

$$X_k = \frac{C_k - C_{\min}}{C_{\max}} \quad (14)$$

#### ✧ Fusion Algorithm

In this paper, we fuse the face feature and iris feature with serial method, which mainly contains two stages, as registration and certification.

The flowchart of our algorithm is shown in figure 5.

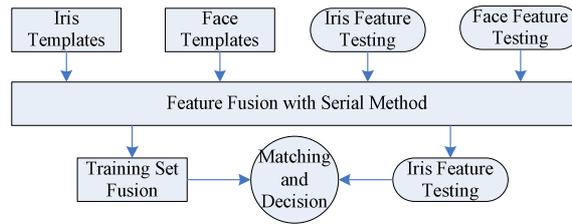


Figure 5. The feature fusion of iris and face

#### B. Fisher Discriminant Function and Solution

As an important component of biological recognition system, classifier is used for classification of the extraction feature again, which will influence the final recognition decision. In this paper, we propose a classification method based on fisher discriminant analysis.

#### ✧ Fisher Discriminant Function

Fisher discriminant, also called linear discriminant, is proposed by R.A. Fisher in 1936, the idea of which is shown as in figure 6.

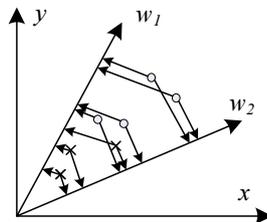


Figure 6. The theory of fisher discriminant analysis

In figure 6, circle represents the same kind of samples, and the fork stands for another kind of samples. When project all the samples onto  $w_1$ , the different kinds of samples can be successfully divided, but false while projecting onto  $w_2$ .The basic idea of fisher discriminant analysis is to find a best projection direction, in which the different kinds of samples can be divided. Furthermore, it projects the samples onto a line with lower dimensions.

Let  $X = (x_1, x_2, \dots, x_N)$  represent a set with  $N$  samples. If there are  $N_1$  numbers of samples belonging to  $w_1$ , marked by set  $X_1$ , and there are  $N_2$  numbers of samples belonging to  $w_2$ , marked by set  $X_2$ . The projection of samples  $X_N$  onto vector  $W$  is defined as:

$$Y_N = W^T X_N \tag{15}$$

In the geometry sense, if  $\|W\|=1$ , then  $Y_N$  is the projection of  $X_N$  in the direction of line  $W$ . In this paper, we do not care the magnitude of  $\|W\|$ , and we only focus on the direction of it, which is better for classification. So we define a Fisher function  $J(W)$  to determine what the condition it should satisfy for classification. First, we give some variables for Fisher function.

1) The average of all samples:

$$m = \frac{1}{N} \sum_{x \in X} x \tag{16}$$

2) The average of samples:

$$m_i = \frac{1}{N} \sum_{x \in X_i} x, i = 1, 2, \dots, N \tag{17}$$

3) The scatter matrix of the  $i$ th sample set:

$$S_i = \sum_{x \in X_i} (x - m_i)(x - m_i)^T, i = 1, 2, \dots, N \tag{18}$$

4) The scatter matrix between samples:

$$S_B = \sum_{i=1}^N (m - m_i)(m - m_i)^T \tag{19}$$

5) The total scatter matrix:

$$S_T = S_1 + S_2 + \dots + S_N \tag{20}$$

In above formulas,  $N$  is the number of sample kinds, and  $M_i$  is the number of samples in kind  $i$ . Then, Fisher function can be defined as:

$$J_{FLD}(W_{opt}) = \arg \max_W \frac{|W^T S_B W|}{|W^T S_T W|} \tag{21}$$

Our goal is to minimize scatter between the samples in subspace, and maximize the scatter if of inner samples, where the direction of  $W$  is optimal.

✧ Solution of Fisher Discriminant Function

The solution of fisher discriminant function can be obtained by Lagrange multiplier method.

Let the denominator of (21) be a non-zero constant, i.e.,  $W^T S_T W = C \neq 0$ , to form a Lagrange function with the Lagrange multiplier  $\lambda$  :

$$L(W, \lambda) = W^T S_B W + \lambda (C - W^T S_T W) \quad (22)$$

The maximum condition is:

$$\begin{aligned} \frac{\partial L(W, \lambda)}{\partial W} &= 2S_B W - 2\lambda S_T W = 0 \\ \Leftrightarrow S_B W &= \lambda S_T W \end{aligned} \quad (23)$$

Thus, we can get the steps of solving the function above:

- 1) Expand the human face image by column scanning, denoted by  $A$  ;
- 2) Calculate the average of all the samples vectors, as  $m$  ;
- 3) Calculate the average of the  $i$ th kind of samples, as  $m_i$  ;
- 4) Calculate the scatter matrix  $S_T$  ;
- 5) Calculate  $S_B$  ;
- 6) Calculate the eigenvalue and eigenvector of  $S_T^{-1} S_B$  ;
- 7) Calculate the projection according to (15).

### C. Security Analysis of Recognition System

Compared with the traditional identification technology, biometric identification has its own advantages, which has attracted more and more attention in recent years, and is widely used in various fields.

Widely use makes people, at the same time, pay more attention on the security of biometric identification. Whether it is superior to the traditional identification system in security has attracted more and more researchers to study. In the real application, attackers more hope to get the biological samples. For single-mode biological identification system, once the samples leak means the security of entire system is lost, in which attacker can forge the user access security systems or very easy to steal the user's information, which will cause big damage to the nation society, and people. In multimode biometric identification system, samples partial reveal means that a variety of modes of biological samples or multiple mode of sample is leakage. In the case of partial samples leak, multimode biometric identification system will be equivalent to a single mode biometric system, where the attacker can forge the other mode samples and attack the fusion system. Even if some samples reveal, it may become a single-mode recognition system, also lost the role of multimode recognition system, which will inevitably affect the security of the system.

Therefore, how to evaluate the influence on security while parts of samples leaked is an important problem that should be considered.

The important indexes for evaluating the performance of system are False Acceptance Rate (FAR) and False Rejection Rate (FRR). If the FAR in partial leakage and normal situation are same or adjacent, then the security of system can be regarded as good. So, we should take FAR as the index of system security. Next, we will define the security threaten coefficient, and then based on this definition, give out the measurement criterion, so as to evaluate the performance changes after the samples partial leakage.

Define the security threaten coefficient as:

$$D = \int_{\Omega} f(t) dt \quad (24)$$

It represents the integration of FAR in  $\Omega$ . It expands the FAR in discrete domain to that of all the possible value for matching, which can reflect the performance of algorithm in the round. In (24),  $t$  is the possible threshold, and  $\Omega$  is the threshold region that may occur in matching processing. The discrete of (24) with  $\Omega$  in the forms of  $x_0, x_1, \dots, x_n$  can be expressed as:

$$D = \lim_{n \rightarrow \infty} \sum_{i=1}^n f(x_i)(x_i - x_{i-1}) \quad (25)$$

However, the above algorithm only can reflect the performance in partial leakage or normal case. In this paper, we only focus on the performance change while partial leakage, so based on (25), we define the difference criterion for multiple mode biological recognition system:

$$R = |D_n - D_l| = \lim_{x \rightarrow \infty} \sum_{i=1}^n f_n(t_i) - f_l(t_i)(x_i - x_{i-1}) \quad (26)$$

In (26),  $D_n$  and  $f_n$  represent the security threaten parameters and FAR curve respectively. Also,  $D_l$  and  $f_l$  represent the security threaten parameters and FAR curve respectively while samples leakage.

In this model,  $R$  stands for the degree of security changes when the samples partial leakage, the smaller value means the FAR under normal and partial leakage situation is adjacent, i.e., recognition system with a good performance of security, the ideal case of which is that the value equals to zero. In practical application, we hope that the value changes smaller while samples leaking, in which the system security can hold when suffers from the attractors.

#### IV. EXPERIMENT TEST AND VALIDATION

##### A. Compare the Iris and Face Feature Fusion Based on Fisher Discriminant Analysis with Single Mode

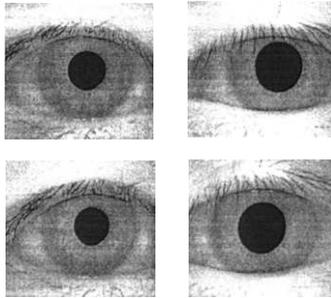


Figure 7. Iris images in CASIA database



Figure 8. Human face images in ORL database



Figure 9. Human face images in Yale database

In this section, we use the iris images in database CASIA, human face images in database ORL, and human face images in database Yale. In experiment 1, the images in CASIA and ORL are used to test the performance of algorithms. In experiment 2, the images in CASIA and Yale are adopted.

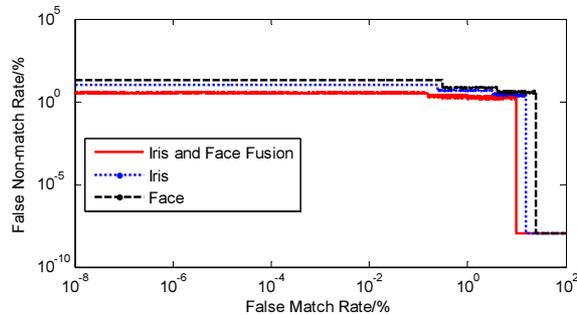


Figure 10. The DET curve of recognition results for experiment 1

First, based on fisher discriminant analysis, compare the recognition performance of multiple mode, as iris and face, with single mode. In order to evaluate the performance of recognition system, the False Match Rate (FMR) and False Non-Match Rate (FNMR) are used in this section. The curves of FMR and FNMR must have a crossing point when plot them in a same coordinate system. The Detection Error Tradeoff (DET) is the curve with FMR as  $x$  axis and FNMR as  $y$  axis. The closer to  $x$  axis of DET means the better performance. The experiment results are shown in figure 10 and figure 11.

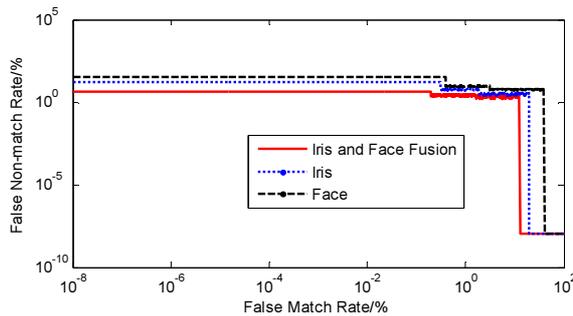


Figure 11. The DET curve of recognition results ffor experiment 2

From the experiment results, it concludes that multiple mode features recognition has a better performance than that of single mode.

B. Security Analysis for Iris an face Recognition System

In this part, first, we will use three fusion rules in section III, i.e., serial rule (SR), sum rule (UR) and weigthed sum rule (WR) ro produce the recognition resluts respectively. Then use fisher clasification method to classfy again, and evaluate the security of the coressponding fusion system by the algorithm indicadated in section III part C. The used experiment data set is same as that in section A.

The results are shown as in table 1 and table 2.

Table 1. Security analysis for experiment data 1

Rule	Threshold	0.5	0.6	0.7	0.8	$R$
	Condition					
Serial Rule	normal	3.31	9.2	17.2	26.7	7.1
	leakage	7.52	14.	21.2	33.2	
Sum Rule	normal	11.5	19.	28.7	38.1	8.9
	leakage	17.2	26.	36.5	46.3	

			4			
Weighted Sum Rule	normal	9.89	18.	29.2	37.5	9.3
	leakage	17.9	25.	37.3	47.2	
			2			
			6			

Table 2. Security analysis for experiment data 2

Rule	Threshold	0.5	0.6	0.7	0.8	<i>R</i>
	Condition					
Serial Rule	normal	4.16	10.3	18.3	27.3	5.6
	leakage	8.12	15.1	23.2	33.6	
Sum Rule	normal	13.2	21.2	31.2	41.2	11.2
	leakage	23.2	33.1	43.5	53.7	
Weighted Sum Rule	normal	20.1	29.7	40.2	49.9	8.3
	leakage	28.6	38.7	47.1	58.7	

From the experiment results above, we can see the influence of different fusion rules on the security of system, and the difference value with serial fusion rule is fewer than that of the others’.

## V. CONCLUSION

With the development of society and technology, security information has attracted more and more attention. For security of traditional recognition cannot satisfy the increasing requirements, researchers pay more attentions on biological recognition technology. As the single mode based biological recognition is easily suffered from attacks, in this paper, we studied the multiple modes fusion/recognition, i.e., iris and face, based on fisher discriminant analysis, and further investigate the security of the fusion systems.

First, we studied the iris and face fusion with different fusion rules. The experiment results show that the multiple modes with serial fusion rule plays a better performance than that of single mode based algorithms. And then, we classify the fused features with fisher linear again, rather than matching immediately. After it, do the matching and recognition according to the commonly used way. The experiment results illustrate that the proposed algorithm can improve the recognition performance.

Furthermore, we considered the problem that what the influence will take place on the fusion system when a part of the samples leaks. We compare the results of our algorithm with the commonly used method by experiment, which also show the prior of our algorithm in security scene in the case of samples partial leakage.

However, there is still not a uniformed algorithm and evaluation criterion for biological recognition technology. For example, in this paper, when samples leaking, how to evaluate the influence on the recognition performance and the security of fusion system in the round, which still needing more and more further research.

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