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Face recognition based on genetic algorithm ☆

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ABSTRACT

The development of computer technology has led to the development of face recognition technology. Nowadays, face recognition technology has been successfully applied in many fields with the help of computer technology and network technology. This paper establishes an effective face recognition model based on principal component analysis, genetic algorithm and support vector machine, in which principal component analysis is used to reduce feature dimension, genetic algorithm is used to optimize search strategy, and support vector machine is used to realize classification. Through the simulation experiment on the face database of the Institute of Technology of Chinese Academy of Sciences in 2003, the results show that the model can achieve face recognition with high efficiency, and the highest accuracy rate is 99%.

1. Introduction

With the rapid development of computer and network technology, information security shows unprecedented importance. Identity identification is a necessary prerequisite to ensure the security of the system. Accurate identification is needed in the fields of finance, national security, justice, e-commerce and so on. Biological characteristics are the intrinsic attributes of human beings. Their uniqueness and good characteristics, which are not easy to be duplicated, provide the necessary prerequisite for identification. Therefore, the personal identification system based on biometric recognition technology is getting more and more attention for its better security, reliability and validity, and has begun to enter into all areas of our lives. The commonly used biometric methods are fingerprint recognition [1,2], palmprint recognition [3,4], ECG recognition [5,6], iris recognition [7,8], DNA [9,10] recognition, etc.

Among many biometrics, face recognition has become the main research direction of biometrics because of its convenience in collecting face images, carrying a large number of personal information features, high recognition and uniqueness. Face recognition is an interdisciplinary subject involving image processing, computer technology, machine learning, biological science, neural network and other disciplines. In recent years, with the rapid development of various disciplines, face recognition technology has made tremendous progress, and its application field has gradually expanded. At this stage, it is mainly used in security system, public security system, payment system and so on.

The related research of face recognition began in the 1970s. Francis Galton [11] first proposed to use the geometric distance of the main organs of the face to represent the face, and expressed the distance as a vector. When recognizing the face, the Euclidean distance between each face vector is calculated separately. The nearest distance is considered to be the same person. Since then, many scholars have started the research of face recognition and proposed many classical face recognition algorithms. In 1987, the Massachusetts Institute of Technology put forward the famous "Eigenface" method. This method is easy to understand and has a good recognition effect. It was quickly popularized and applied, and became a classical algorithm in the field of face recognition. Face recognition is greatly influenced by background and expression. For this reason, Blanz and Vetter proposed a face recognition algorithm based on 3D deformable model [12]. The experiment on FERET multi-pose database achieved good recognition results. With the continuous development of the neural network, people use the powerful non-linear mapping ability of the neural network to carry out face recognition, and have achieved good recognition effect [13]. At present, face recognition using the neural network has become the main research method of face recognition.

In face recognition research based on neural network, the gray value of face image is usually input by neural network. Because the face images are generally large, the number of neurons in the input layer of the neural network is large, which makes the original complex neural network more complex, the calculation amount is

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further increased, and the convergence of the network is slow. Moreover, BP neural network needs a large number of samples for network training. The essence of training is to optimize network weights and optimize network performance. But because the steepest descent method is usually used in network training, when the network weight value is not appropriate, BP network is easy to fall into local optimum. Therefore, before using BP neural network for face recognition, dimensionality reduction of input features is needed to reduce the number of neurons. In dimensionality reduction research, principal component analysis is an effective method [14,15]. In face recognition research, principal component analysis is often used to extract facial features. For example, Nicholl, Paul [16] and others have proposed a face recognition system based on DWT/PCA, which automatically determines the most discriminative feature face by setting the standard deviation between and within the class of the weight vector of the feature face in the training set. Wang, Hong [17] and others proposed an improved PCA face recognition algorithm based on discrete wavelet transform and support vector machine. Face features are processed by two-dimensional discrete wavelet transform to extract low-frequency components to form low-frequency sub-images. Then the PCA method is used to obtain the features of these sub-images. Finally, the extracted feature vectors are put into the SVM classifier for training and recognition. With the deepening of face recognition research, more and more researchers realize the dimensionality reduction of PCA on face features, and also introduce PCA method into their own face recognition research [18,19].

Genetic algorithm is a computational model simulating the natural selection and genetic mechanism of Darwin's biological evolution theory. It is a method of searching the optimal solution by simulating the natural evolution process. Compared with the traditional gradient descent method in BP neural network, genetic algorithm is more efficient. Therefore, genetic algorithm is widely used in feature calculation and classification research. Samanta B [20] et al.'s genetic algorithm-based artificial neural network and support vector machine bearing fault detection; Yao H [21] et al.'s genetic algorithm-based selective principal component analysis (GA-SPCA) method for feature extraction of high-dimensional data; Kim SK [22] and others'research results of feature deletion in license plate recognition based on genetic algorithm are based on the dimensionality reduction characteristics of genetic algorithm.

In order to achieve fast and accurate face recognition, this paper uses PCA to extract features of gray-scale face, then uses GA to optimize the network weight of face features, and finally uses SVM to realize face recognition. The dimension of GA coding is reduced by improving the coding number of genetic algorithm, and the time and space complexity of GA coding is reduced without reducing the accuracy. All chromosomes with the highest fitness of each generation are saved during GA running, and the optimal results are screened according to various ways after the algorithm runs. By using SVM to classify the face database (cas-Peal) of Institute of Technology of Chinese Academy of Sciences in 2003, the simulation results show that this method can improve the classification speed without reducing the recognition accuracy.

2. Method

2.1. Principal component analysis

Principal Component Analysis (PCA) is a statistical method for dimensionality reduction. By means of an orthogonal transformation, the original random vectors of its components are transformed into new random vectors whose components are uncorrelated. In algebra, the covariance matrix of the original random vector is transformed into a diagonal matrix, and in geometry, the original coordinate system is transformed into a new orthogonal coordinate system, which points to the most open P orthogonal directions of the sample points. Then, the dimension reduction of the multidimensional variable system is processed to transform it into a low-dimensional variable system with a higher accuracy. Then, the low-dimensional system is further transformed into a one-dimensional system by constructing an appropriate value function.

Assuming that the sample set X containing n samples contains P features, the representation method of sample set X can transform the sample vector into the eigenvector representation by the following methods:

$$X = \begin{bmatrix} x_{11} & x_{12} & \dots & x_{1p} \\ x_{21} & x_{22} & \dots & x_{2p} \\ \dots & \dots & \dots & \dots \\ x_{n1} & x_{n2} & \dots & x_{np} \end{bmatrix} = [x_1, x_2, \dots, x_p] \quad (1)$$

The process of obtaining principal components can be achieved by:

The mean matrix and covariance matrix of X are respectively recorded as:

$$\mu = \mathrm{E(X)}, \mathrm{V} = \mathrm{D(x)}$$

For the transformation matrix W (2-8), set:$\mathrm{W} = [w_1, w_{2,\dots}, w_p]$

Among them,$w_i = (w_{1i}, w_{2i}, \cdots w_{pi)^T}, \mathrm{i} = 1, 2 \cdots, \mathrm{p}$

The formula (2–6) can be expressed as:

$$F_i = w_{1i}x_1 + w_{2i}x_2 + \cdots + w_{pi}x_p = w_i^T X, \quad i = 1, 2, \cdots, p$$

Through linear transformation, a group of new variables $F_1, F_2, \dots F_p$ are found which are not related to each other. The new variables can well reflect the information of the original variables and can be used to replace the original variables. The substitution are the following:

$$D(Fi) = w_i^T cov(X, X) w_j = w_i^T V w_j, \quad i, j = 1, 2, \dots p$$

According to the mutual correlation of the new variables, we can find let the variance $D(F_i)$ largest w_i, according to the definition of PCA.

According to the above analysis, the first major component is $F_1 = w_1^T X$, make $\mathrm{D}F_1 = W_1^T V w_1$ reach the maximum. The second principal component is the same $F_2 = w_2^T X$, and $\mathrm{cov}(F_2, F_2) = cov(w_2^T X,\ w_1^T X) = w_2^T V w_1 = 0$, make $\mathrm{D}(F_2) = w_2^T V w_2$ reach the next maximum. In general, the principal component of K is $F_K = w_k^T X$, and $\mathrm{cov}(F_k, F_1) = cov(w_k^T \mathrm{X}, w_1^T X) == w_k^T V w_i = 0, (l < k)$, make $\mathrm{D}(F_K) = w_k^T V w_k$ reach the k maximum values.

Finally, the principal components obtained by linear transformation can be expressed as follows:

$$\begin{cases} F_1 = w_1^T X \\ F_2 = w_2^T X \\ F_p = w_p^T X \end{cases}$$

The above w_k is the unit characteristic vector whose variance is the characteristic root of V.

3. Genetic algorithm

Genetic Algorithms [47] was put forward by Professor Holland in 1969. It is a kind of randomized search algorithm based on natural selection and genetic mechanism of organisms. By simulating the phenomena of reproduction, crossover and mutation in nature, a group of candidate solutions are retained in each iteration, and the better individuals are selected from the solution groups according to some index. The individuals are combined by genetic

operators to generate a new generation of candidate solutions, and the process is repeated until the convergence index is satisfied.

The main components of genetic algorithm are [48]: coding mechanism, fitness function, genetic operators (selection, crossover and variation) and control parameters. When genetic algorithm is used to solve the problem, the possible solutions of the problem will be coded into chromosomes, i.e. individuals. Several individuals form an initial solution group. After calculating the fitness function, the individuals satisfying the termination conditions can be output, and the algorithm ends. Otherwise, individuals will cross, mutate and recombine to form the next generation of new population. The new population inherits the good characteristics of the previous generation and is superior to the previous generation, so that it can gradually evolve towards a better solution.

Through the introduction above, it can be seen that genetic algorithm provides a general framework for solving complex system optimization problems, which does not depend on the domain and type of problems. The genetic algorithm is based on fitness function. By applying genetic operation to individuals in the population, the iterative process of individual structure reorganization in the population is realized. Simple genetic algorithm models can be described in the following ways:

$$\mathrm{SGA} = (\mathrm{C}, \mathrm{E}, P_0, N, \Phi, \Gamma, \psi, T)$$

In formula: C------- Individual coding method
E------ Evaluation function of individual fitness
P_0-----Initial population
N---- Population size
Φ---- Selection operator
Γ---- Crossover operator
ψ---- Mutation operator
T---- Termination condition of genetic operation

The steps of genetic algorithm can be described as follows:

1. Coding and generating initial population

Select the corresponding coding method according to the problem. And randomly generate an initial population composed of N chromosomes of definite length.

$$pop_i(t), t = 1, i = 1, 2, \ldots N$$

2. Calculating fitness value

The fitness of each chromosome tpop (t) in population pop (t) is calculated.

$$f_i = fitness(pop_i(t))$$

3. Judge whether the convergence criterion is satisfied. If the output search results are satisfied, the following steps will continue.
4. Select operation

The probability of selection is calculated according to the fitness of each individual.

$$P_i = \frac{f_i}{\sum_{i=1}^{N} f_i}, i = 1, 2, 3, \ldots N$$

The above probability distribution is randomly selected from the current generation population TPOP (t) to form a new population in the next generation population.

$$newpop(t+1) = \{pop_j(t) | j = 1, 2, \ldots, N\}$$

5. Cross operation

A group of N chromosomes tcrosspop (t + 1) was obtained by mating with probability P_c.

6. Mutation operation

Use a smaller probability P_m to make chromosomal genes mutate. A new population t mutpop (t + 1) is formed. The new population is named pop (t) = mutpop (t + 1) for the offspring after a genetic operation. At the same time, it acts as the father of the next genetic operation and returns to 2.

4. Support vector machine

Because of the breakthrough of computer development, people find that the identification problem of model has the characteristics of "unstability" through a large number of simulation calculations. Traditional statistical learning theory is often very difficult to solve higher-dimensional problems, and it is extremely prone to "dimension disaster". In order to solve this problem, Vapnik proposed support vector machines theory (SVMs Theory) based on the optimal classification surface, using the theory of traditional neural network learning methods. Through support vector machine, people can construct better prediction and classification mechanism in higher dimensional space. SVMs is a self-correcting learning algorithm based on statistical learning theory. Compared with artificial neural network, it has better minimization of structural risk, avoids the unavoidable transition fitting problem in artificial neural network, and has better generalization ability. Its characteristics are universality, robustness, effectiveness, simpler calculation and more perfect theory.

The classification process of SVM can be expressed in the following formula, assuming that there is a hyperplane $\omega^T \mathrm{x} + \mathrm{b} = 0$ let the sample set $\{(x_i, y_i), i = 1, K, N\}$ separating correctly, that is to say,

$$\varpi^T x_i + b \geqslant 1, \quad when\ y_i = +1$$

$$\varpi^T x_i + b \leqslant -1, \quad when\ y_i = -1$$

The "margin" of the separated hyperplane is defined as:

$$margin = d_+ + d_-$$

Among them,

$$d_+ = \min_{i:y_i=1} \{(\varpi^T x_i + b)/||\varpi||\}$$

$$d_- = \min_{i:y_i=-1} \{(\varpi^T x_i + b)/||\varpi||\}$$

Intuitively, the "margin" defined in this paper is the sum of the shortest distances from two different types of sample points to the hyperplane. It can be seen from the definition that the larger the "margin" of the separated hyperplane, the stronger the classification ability of the sample. SVM is the requirement for optimal separation of hyperplanes, that is, to seek $\varpi^T x + b = 0$, among them ϖ is the following convex two step solutions:

$$(P1) \begin{cases} \min \frac{1}{2} \varpi^T \varpi \\ y_l(\varpi^T x_l + b) \geqslant 1, \quad i = 1, k, N \end{cases}$$

5. Experiment

CAS-PEAL Face Database is a large facial database for Chinese people established by the Chinese National Academy of Sciences. The face database is a personal face database built on the basis of the national "863" project. CAS-PEAL face database began to collect face images from the database in August 2002, and established a

face database in April 2003. A total of 1040 Chinese volunteers from CAS-PEAL face database participated in the collection, including 595 males, 445 females and a total of 99,450 images. The face images collected from CAS-PEAL face database can better reflect the changes under complex conditions. There are seven kinds of changes, namely, illumination change, posture change, expression change, occlusion and decoration change, background change, distance change and time span change. Among the seven changes, four subsets are the most concentrated, namely Lighting, Pose, Expression and Accessory. These four parts are the origin of PEAL naming in CAS-PEAL face database. The following is a partial face image sample of some CAS- PEAL face database.

Genetic algorithm parameters

(1) Coding. Since the gray value of the image is between 0 and 255, each chromosome is coded as a bit binary code, and each chromosome represents a segmentation value, that is, an 8-bit binary code between 00000000 and 11111111 is used to represent the segmentation value.
(2) Population. If the population size is too large, the number of fitness evaluation increases, the amount of calculation increases, and the population size is too small, which may lead to immature convergence. Therefore, the scale of population should be set reasonably. Here, the population size is 20 and the maximum reproductive algebra is 50.
(3) Decoding. The binary chromosome array is decoded to a value between 0 and 255, so as to get its fitness value.
(4) Fitness function

$$\varphi(t) = H_o(t) + H_B(t) = \lg\frac{P_t}{(1-P_t)} + \frac{H_t}{p_t} + \frac{H_L - H_t}{1-P_t}$$

Among them,

$$H_t = -\sum_{i=0}^{t} p_i \lg p_i$$

$$H_L = -\sum_{i=0}^{L-1} p_i \lg p_i$$

(5) Choice. This genetic algorithm is selected by elite selection method. First, roulette method is used to select, then paired crossover, mutation and other genetic operators are used to generate the next generation of individuals, and then the best individuals of the previous generation are copied by the best individual preservation method. In order to maintain the size of the group, we should eliminate the worst individuals from this new group. Obviously, the selection strategy can increase the competition pressure appropriately and accelerate the convergence of genetic algorithm.
(6) Crossover. Cross-swapping can produce offspring different from the parent. The greater the probability of cross-over, the greater the possibility of cross-operation. If the probability of cross-over is too low, the convergence rate may be reduced. The genetic algorithm adopts crossover between father and son. The principle of father-son competition mechanism comes from the survival of the fittest in biological evolution. Two new individuals are generated by the crossover of the father-generation individuals. When there are individuals with greater fitness than the maximum fitness of the father-generation individuals in the newly-generated offspring, the offspring are considered superior to the father-generation and the offspring are substituted for the father-generation. Otherwise, keep the parent and let it enter the next round of evolution. In this way, it can be avoided that, as long as the crossover operation is carried out, the son must replace the father, but choose the best individual from the father and son to enter the next generation. In general, the offspring are superior to the parent, and the evolution process is always in the best direction. The probability of crossover and crossover is set.
(7) Variation. Using the basic mutation operator, the mutation probability is 0.02.
(8) The termination criterion stipulates that when the maximum algebraic termination condition of the algorithm or the stability condition of the maximum fitness of the population has not changed after generational evolution, the algorithm stops running and the individual with the highest fitness value is the segmentation value.

6. Results and analysis

Results 1 face image segmentation based on genetic algorithm.

Through the analysis of face, we can know that the layout of face is similar in a certain set relation. This similarity reflects that each face has a similar layout of eyes, nose and mouth, so we can find out the geometric relationship between them to define a face template. That is, the eyes, nose and mouth can be seen as distributed in a rectangular area, the width and height ratio of the rectangular area is about 0.75–0.92, as shown in Fig. 1. As can be seen from Fig. 2, the rectangular area can include the main parts of the face, eyes, nose, mouth and eyebrows. Because of the symmetry of the face, the rectangular area can be divided into three areas on average: eyebrow area, nose area and mouth area, and eyebrow area can be divided into two equal-sized left and right areas. Based on the above location, the facial feature can be located.

Face localization using genetic algorithm is as follows:

1. Fitness function

$$E_{temp} = 0.3E_{l-e} + 0.3E_{r-e} + 0.2E_n + 0.2E_m$$

2. Coding

Each chromosome is binary coded, including the upper left coordinate (ULx, ULy) and the lower right coordinate (BRx) with a chromosome length of 3*m, where m is each variable coding digit.

3. Selection

Assuming that the population size is N, after crossing and mutation operations, N sub generation individuals are generated. Sort the 2 N groups made by the parent parent, and take the preceding N/2 individual into the matching pool. Then randomly select N/2 from the N individuals in the back into the matching pool. In this way, we can not only guarantee the convergence of the population to the optimal solution, but also make the population diversity less rapidly.

4. Hybrids

In this algorithm, m hybridization sites are randomly selected from 1 to 3 m loci by multi-point hybridization. Thus, individual chromosomes are divided into M-1 gene segments. The odd segments of the two chromosomes remain unchanged, and even segments of genes are exchanged.

5. Variation

The method used in this paper is that when two chromosomes are identical or operated on, if the alleles at the same locus of two chromosomes are identical, the mutated chromosome will take 1

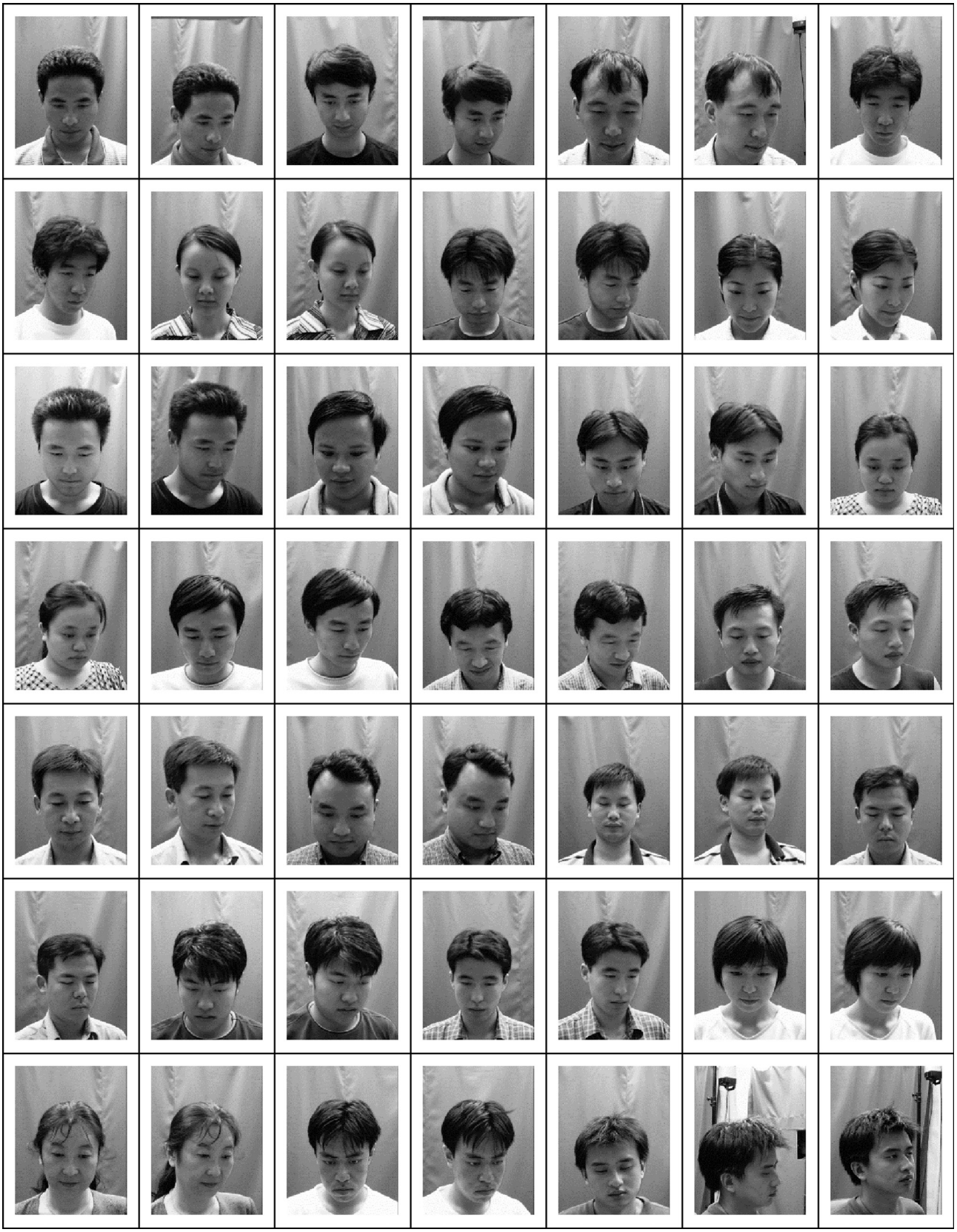

Fig. 1. Face sample library.

locus or 0 locus. For the XOR operator, it is just opposite to the same or operator. If the alleles of two chromosomes are identical at the same locus, the mutated chromosome will take 0 or 1.

After completing face localization, the existence of face has been determined from a given image and the most dominant face has been found.

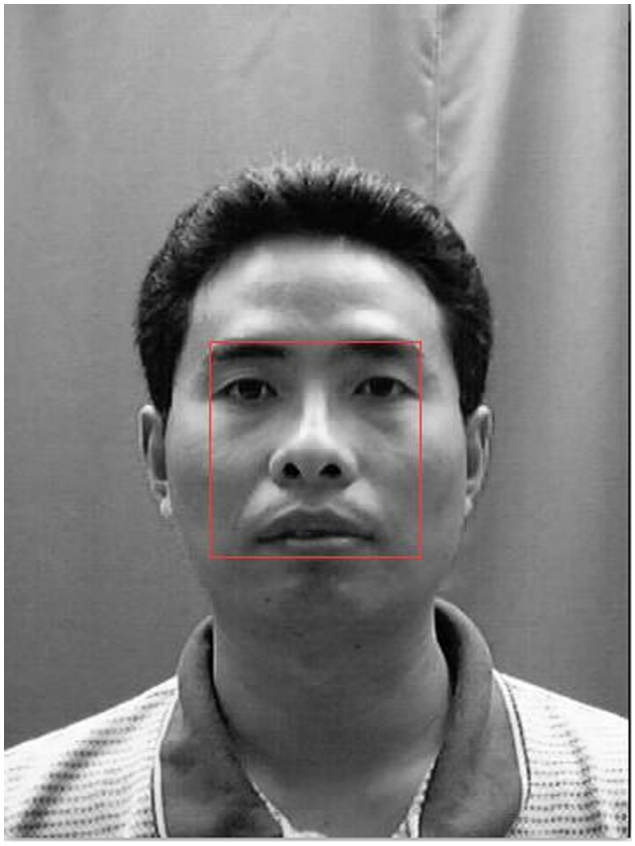

Fig. 2. Face feature rectangle box.

The most suitable rectangular image region for eyes, nose and mouth is segmented from the original image and matched with the face image in the face database. Because the size of the rectangular area segmented from the original image is uncertain, it must be enlarged or reduced to the same size as the face in the standard face database. Usually, the size of the face image in the face database and the most suitable rectangular image area including the eyes, nose and mouth are also determined.

The result of face segmentation is shown in Fig. 3.

From Fig. 3, it can be seen that the general watershed method has obvious over-fitting in face feature recognition. The reason is that the face features are distributed in small intervals, and the gradient and noise between them lead to over-fitting in segmentation. However, this method avoids over-fitting phenomenon and achieves a good segmentation effect.

Results the relationship between 2 characteristic number and recognition rate.

In this paper, we simulate the relationship between recognition rate and feature number of face in database. Face features are derived from different posture features collected by subjects in normal light. These features in normal light are taken as learning samples, and the face features collected in abnormal light are fitted by learning samples. The relationship between the final recognition rate and the number of features is shown in Fig. 4. Training sample Y = 40, Chromosome length L = Y−1 = 39, number of chromosomes per generation R = 40, mutation probability V = 0.01, crossover probability RE = 0.7.

Fig. 4 shows the relationship between the accuracy and the number of features. From the result of Fig. 4, it can be seen that the recognition rate increases slowly with the increase of the number of features. The main reason is that the number of features is too small to accurately describe the features of a face. Therefore, with the increase of the number of features, the description of face features becomes more and more fine. As a result, the recognition rate increases, but when the number of features reaches 35, Fig. 4 shows the highest accuracy rate, 92.38%, followed by a downward trend in accuracy. This shows that although the increase of the number of features will improve the accuracy, the accuracy will not increase with the increase of the number of features when it exceeds a certain threshold, on the contrary, there will be redundant features, which will have a negative impact on the accuracy.

Conclusion 3 the influence of iterations on recognition rate.

The number of iterations of genetic algorithm directly affects the efficiency of recognition. In order to improve the efficiency of recognition, it is very important to find the optimal number of iterations. Fig. 5 shows the relationship between the number of iterations and the number of identification error samples. For comparative analysis, 300 photos were selected as the test samples.

From the results of Fig. 5, we can see that with the increase of the number of iterations, the number of false samples is getting lower and lower. Although the number of iterations does not decrease monotonously from 1 to 20, on the whole, the larger the number of iterations, the less the number of false samples identified. 16 errors occurred when iterating 1, and the number of errors dropped to 3 when iterating 20 times.

Although the higher the number of iterations is, the higher the recognition rate is, the number of iterations directly affects the efficiency of the algorithm. The main running time of the genetic

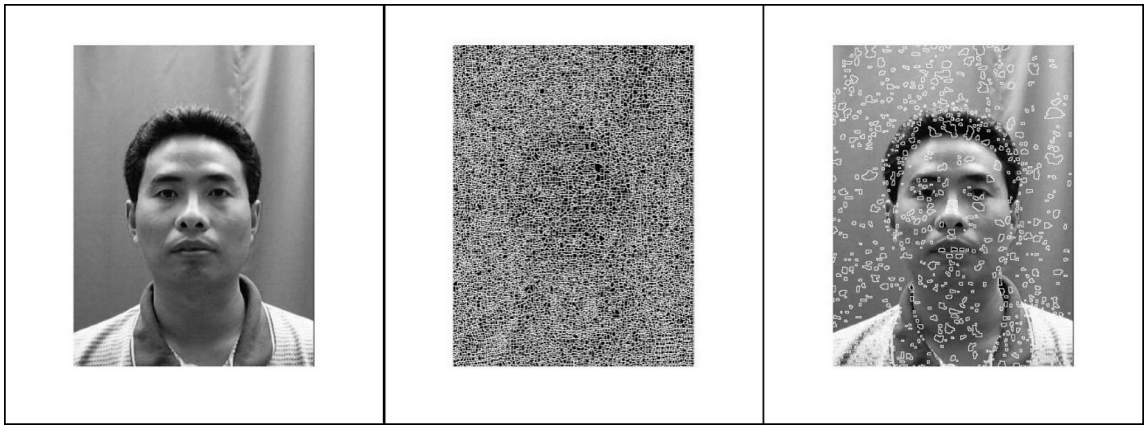

Fig. 3. Face segmentation based on watershed transform (left is original image, middle is watershed transform, right is this method).

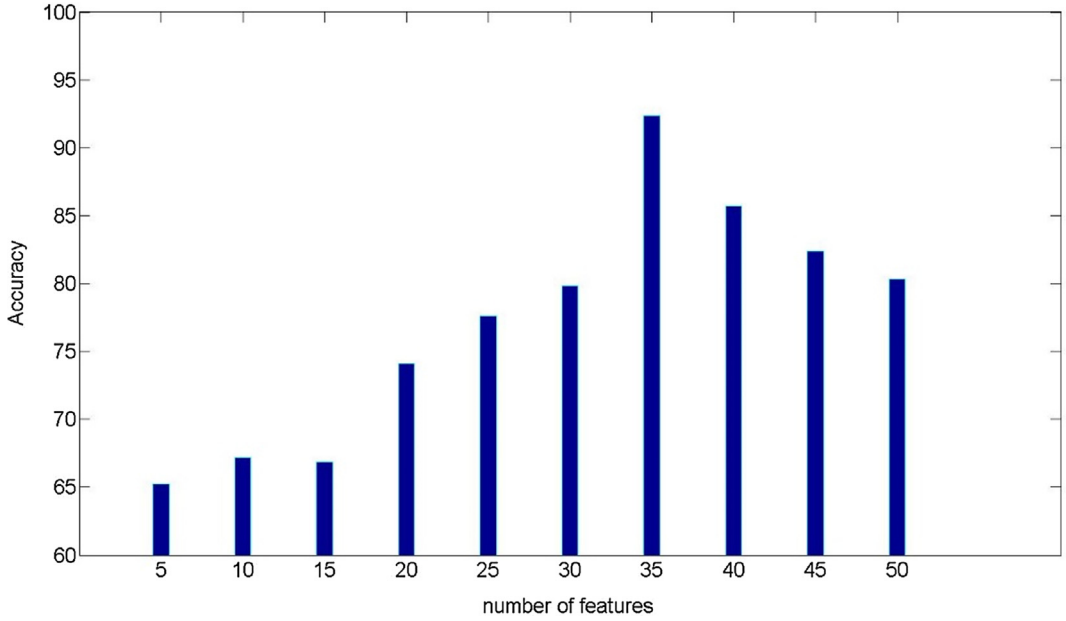

Fig. 4. Relationship between recognition rate and characteristic number.

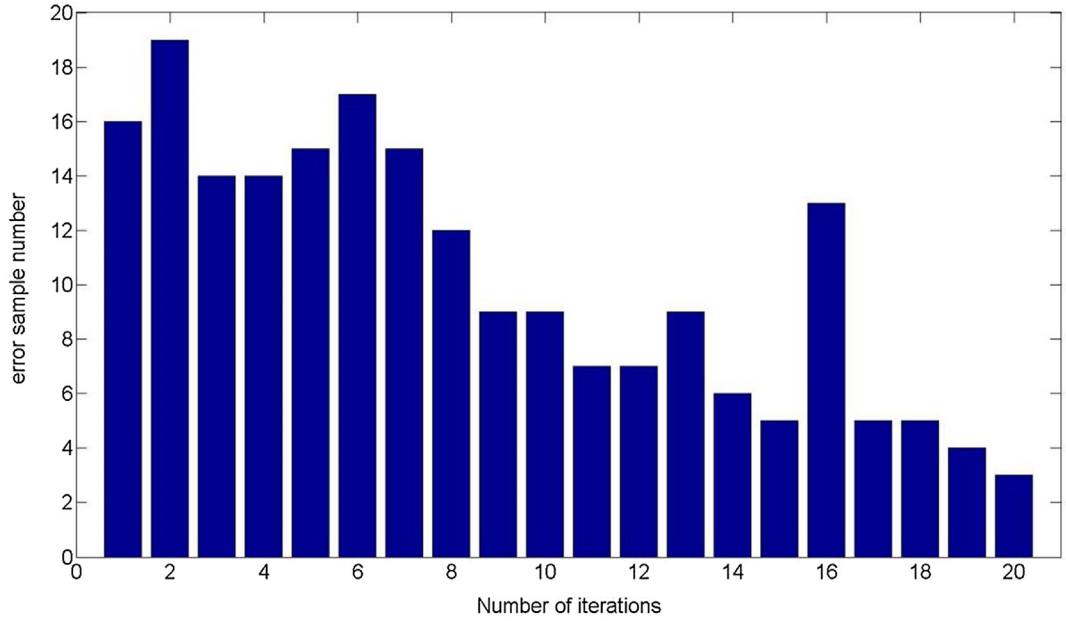

Fig. 5. Relationship between iterations and erroneous samples.

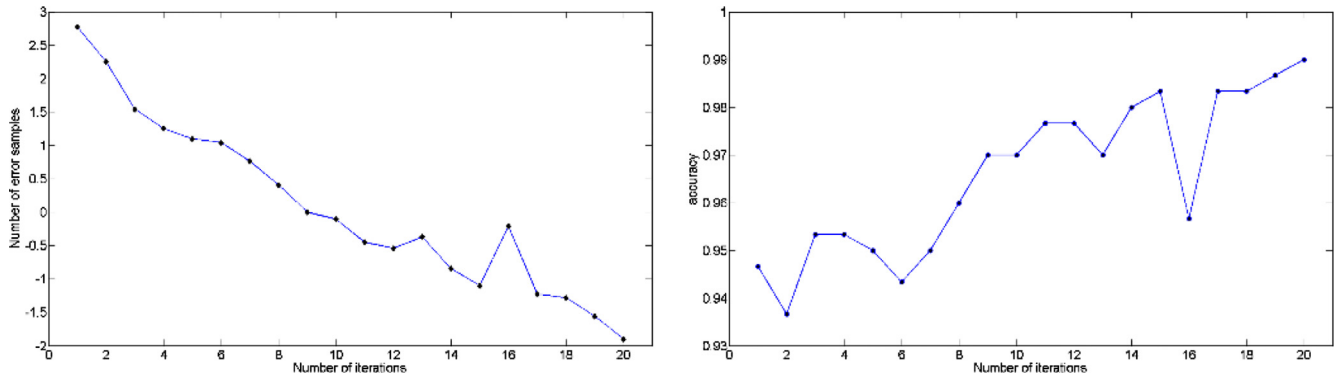

Fig. 6. Relationship between iteration number and error sample.

algorithm is spent on iterations, so the large number of iterations directly affects the high running time. Therefore, there is a contradiction between accuracy and efficiency. How to find the best one? Fig. 4 shows the relationship between iteration number, calculation efficiency and accuracy. The left side is the relationship between iteration number and calculation efficiency. The calculation method of calculation efficiency is defined as:

$$F = \log\left(\frac{E_n}{I_n}\right)$$

Among them E_n is the wrong sample number, I_n is the number of iterations.

Fig. 6 is on the right side of the relationship between the number of iterations and the accuracy.

As can be seen from Fig. 6, the influence factors of iteration times on efficiency are significantly higher than the number of error samples, because the total number of error samples is large, but from the accuracy of the right side of Fig. 6, it can be seen that the number of iterations is low, although the efficiency is high. But the accuracy is obviously too low, so compared with Fig. 6, we can see that the accuracy and efficiency can be balanced when the number of iterations is 10.

7. Conclusion

With the development of information technology, more and more occasions need personal identity authentication. Face recognition is widely used in these authentication methods for convenience and accuracy. Many researchers are also using many methods to study face recognition, trying to improve the practicability of face recognition.

This paper establishes a face recognition model based on genetic algorithm. PCA is used to reduce the dimension of features, genetic algorithm is used to optimize the process of feature search, and SVM is used to realize classification. The final results show that the proposed model can achieve personal identity authentication very well.

Conflicts of interest

There is no conflict of interest.

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