

Improving Features Subset Selection Using Genetic Algorithms for Iris Recognition

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Abstract. In this paper, we propose an iris recognition method based on genetic algorithms (GA) to select the optimal features subset. The iris data usually contains huge number of textural features and a comparatively small number of samples per subject, which make the accurate iris patterns classification challenging. Feature selection scheme is used to identify the most important and irrelevant features from extracted features set of relatively high dimension based on some selection criterions. The traditional feature selection schemes require sufficient number of samples per subject to select the most representative features sequence; however, it is not always practical to accumulate a large number of samples due to some security issues. In this paper, we propose GA to improve the feature subset selection by combining valuable outcomes from multiple feature selection methods. The main objective of GA is to achieve a balance among the recognition rate, the false accept rate, the false reject rate and the selected features subset size. This paper also motivates and introduces the use of Gaussian Mixture Model for iris pattern classification. The proposed technique is computationally effective with the recognition rates of 97.81 % and 96.23% on the ICE (Iris Challenge Evaluation) and the WVU (West Virginia University) iris datasets respectively.

Keywords: Biometrics, Gaussian mixture model, genetic algorithms, collarete area localization.

1 Introduction

The popularity of the iris biometric has grown considerably over the past three to four years. The iris has been known as a biometric for some time [1, 5]. However, it has gained substantial attention to both the research community and governmental organizations recently. Five crucial factors that influenced the increased interest in the iris biometric are as follows: 1) unique structure of iris; 2) stability of iris pattern throughout the person's lifetime; 3) public acceptance; 4) new user-friendly capture devices with broad improved capabilities; and 5) a wide range of applications. As a result, a large number of new iris encoding and processing techniques have been developed over this short period of time [1]. Based on the technology developed by Daugman [2], iris scans have been used in several international airports for the rapid processing of passengers through the immigration who have pre-registered their iris

images. Iris technology has also been widely used in several countries for various security purposes (and also by the United Nations High Commission for refugees). A new technology development project for iris recognition namely, the *Iris Challenge Evaluation* (ICE) has been conducted by the National Institute of Standards and Technology (NIST) [10]. While most of the literatures are focused on preprocessing of iris images [1], recently, there have been important new directions identified in iris biometric research. These include optimal feature selection and iris pattern classification.

The optimal features set selection from a feature sequence with a relative high dimension has become an important factor in the field of iris recognition [3]. The conventional feature selection techniques (e.g., *Principal components analysis*, *Independent components analysis*, *Singular valued decomposition* etc.) require sufficient number of samples per subject to select the most representative features sequence. However, it is not realistic to accumulate a large number of samples due to some security issues. Moreover, different feature selection algorithm based on various theoretical arguments may produce different results on the same data set [15]. This makes selecting the optimal features subset for a data set difficult. In this paper, we emphasize on the utilization of the useful information from different feature selection methods to select the most important features subset and also to improve the classification accuracy. We propose Genetic algorithms (GA) to select the significant features subset by combining the multiple feature selection criteria. The proposed approach provides the convenient way of selecting a better feature subset based on the performance of the different feature selection schemes, and this approach is regarded as independent of the inductive learning algorithm used to build the classifier. To evaluate the proposed scheme, support vector machines (SVM)-recursive feature elimination (RFE), k-NN, T-statistics, and entropy-based methods are used to provide the candidate features for the selection of features subset using GA.

In this paper, we also introduce a new iris-subject model based on the Gaussian mixture model (GMM). GMM is used to take into account the interpersonal and intrapersonal variations due to occlusion occurred by the eyelids and the eyelashes and also due to changing light conditions, head tilt etc. The GMM is also applied to satisfy several security requirements with high matching accuracy based on the variation of the Gaussian mixture components.



Fig. 1. Samples of iris images form ICE and WVU datasets

2 Iris Image Preprocessing

The iris is surrounded by various non-relevant regions such as the pupil, the sclera, the eyelids, and also has some noise that include the eyelashes, the eyebrows, the reflections and the surrounding skin [5]. In order to isolate the iris, pupil, and

collarette boundaries from digital eye’s image, we use an efficient approach proposed in our previous work in [16]. Though collarette region is less affected by the eyelids and the eyelashes, there are few cases where this region is occluded by the eyelids and the eyelashes [16]. These noisy regions are required to be eliminated in order to improve the performance, and this approach is also illustrated in [16]. Fig. 2 shows the localized iris images. We use the rubber sheet model to normalize or unwrap the isolated collarette area [2]. Fig. 3 shows the unwrapping procedure. Since the normalized iris image has relatively low contrast and may have non-uniform intensity values due to the position of the light sources, a local intensity based histogram equalization technique is applied to enhance the contrast of the quality of the normalized iris image to improve the subsequent recognition accuracy. Fig. 3 also shows the effect of enhancement on the unwrapped iris image.

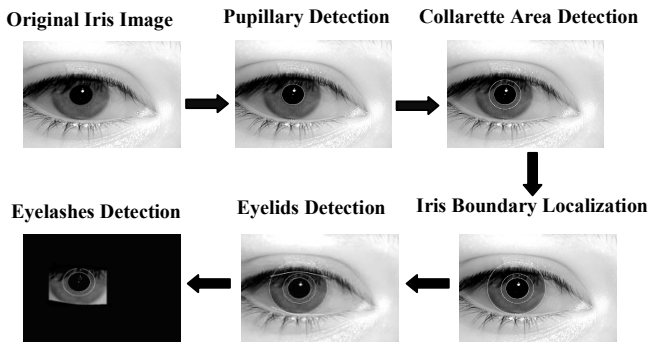


Fig. 2. Iris Image preprocessing on ICE dataset

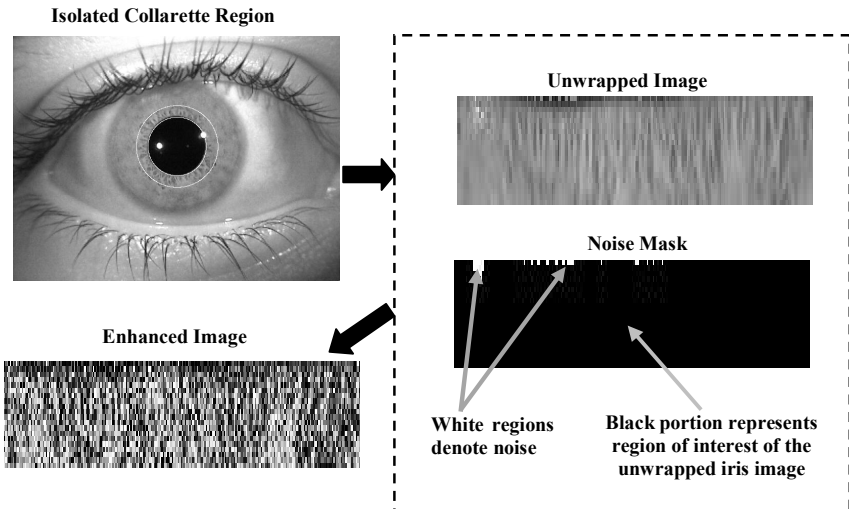


Fig. 3. Unwrapping and enhancement of an iris image on WVU dataset

3 Feature Extraction

Gabor filters based methods have been widely used as feature extractor in computer vision, especially for the texture analysis [2, 16, 17]. However, one weakness of the Gabor filter in which the even symmetric filter will have a DC component whenever the bandwidth is larger than one octave. To overcome this disadvantage, a type of Gabor filter known as log-Gabor filter, which is Gaussian on a logarithmic scale, can be used to produce zero DC components for any bandwidth. The log-Gabor function more closely reflects the frequency response for the task of analyzing natural images and is consistent with measurement of the mammalian visual system. The log-Gabor filters are obtained by multiplying the radial and the angular components together where each even and odd symmetric pair of log-Gabor filters comprises a complex log-Gabor filter at one scale. The frequency response of a log-Gabor filter is given as

$$G(f) = \exp\left(-\left(\log\left(\frac{f}{f_0}\right)\right)^2 / 2\left(\log\left(\frac{\sigma}{f_0}\right)\right)\right) \quad (1)$$

where f_0 is the centre frequency, and σ provides the bandwidth of the filter. In order to extract the discriminating features from the normalized collarette area, the normalized pattern is convolved with 1D log-Gabor filters [16].

4 Feature Subset Selection Using Genetic Algorithms

In this paper, we propose GA to select the prominent features based on the outcomes of the four feature selection algorithms, namely: the Entropy-based approach, k-NN based method, T-statistics and the SVM-RFE approach. Usually, the feature selection algorithms can be divided into two categories: the filter approach and wrapper approach based on whether the selection method is performed independently of the learning algorithm used to construct the classifier. If the feature selection is done independently of the learning algorithm, the technique is referred as the filter approach. Otherwise, it is referred to as a wrapper approach [15]. Several feature selection schemes produce different results on the same data set because of the feature redundancy, interactions and correlations between features, and the biases in the selection or ranking criteria. In order to obtain the most significant feature subset from the different feature selection algorithms, we use a hybrid approach as shown in Fig. 4.

We adopt GA to combine multiple feature selection criteria to find the optimal subset of informative features. The GA searches the pool of hypotheses (denoted as population) consisting of complex interaction parts. Each hypothesis or individual of the current population is evaluated based on the specific fitness function. A new population is generated by applying genetic operations like selection, mutation and crossover. In this paper, we select sets of features by utilizing four feature selection algorithms instead of using all features set from the original extracted iris features sequence to form the collection of candidate features called the *feature pool*. The selection of features subset from these feature selection algorithm can be subjective to their performance. In order to choose the sets of feature selected by several feature

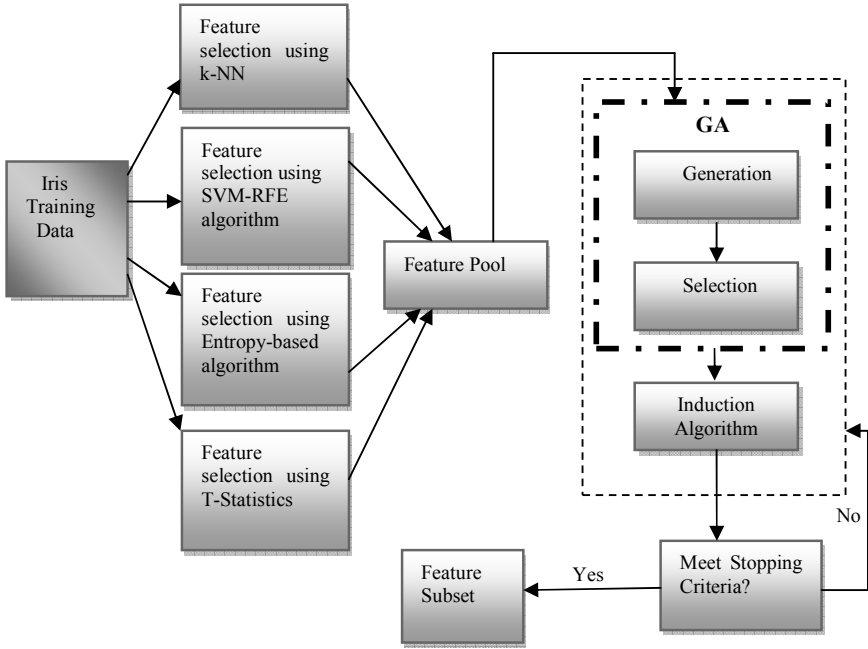


Fig. 4. Feature Selection Procedure using GA (Hybrid approach)

selection algorithms instead of using all the features from the original data set, we deploy four existing feature selection algorithms, two filters (entropy-based, T-statistics) approaches and two wrapper (SVM-RFE, k-NN) approaches to form the feature pool. We apply each algorithm to the extracted features sequence and generate a ranking of those features. Given a ranking of features, we pick a number of top ranked features from each algorithm and provide these top-ranked features into the feature pool. Here, we briefly describe four feature selection algorithms.

In entropy-based method, entropy is lower for orderly configurations and higher for disorderly configurations. Therefore, when an irrelevant feature is eliminated, the entropy is reduced more than that for a relevant feature. This algorithm ranks the features in descending order of the entropies after removing each feature one at a time. We can estimate the entropy measure of a data set of N instances as follows:

$$E = -\sum_{i=1}^N \sum_{j=1}^N (d_{ij} \times \log d_{ij} + (1 - d_{ij}) \times \log(1 - d_{ij})) \tag{2}$$

Where, $d_{ij} = \exp^{-\alpha \times ED_{ij}}$ and $\alpha = -\ln 0.5 / \overline{AD}$.

Here, d_{ij} denotes the similarity between two instances x_i and x_j , ED_{ij} is the Euclidean distance between the two, and \overline{AD} is the average distance among the instances. This approach is used for unsupervised data since no class information is required.

In [15], the SVM-RFE has been used for selecting the genes that are relevant for cancer classification problem. Here, we adopt this approach to find top ranked iris features from the extracted features sequence. The idea is to eliminate one worst feature (i.e., the one that modified the objective function Obj least after being eliminated) at one time. This method is based on backward sequential selection.

$$Obj = \|w\|^2 / 2 \tag{3}$$

$$w = \sum_{i=1}^{N_s} \alpha_i y_i x_i \tag{4}$$

Where N_s denotes the number of support vectors that are defined to be the training samples with $0 < \alpha_i \leq C$. C is the penalty parameter for the error term. x_i and y_j are the data instance and its class label respectively. The modification of Obj is approximated by *Optimal Brain Damage* (OBD) algorithm so that

$$\Delta Obj(i) = (\Delta w_i)^2 \tag{5}$$

w_i^2 is considered as the ranking criteria. The iterative procedure of RFE is as follows:

- The SVM is trained with training data.
- The ranking criterion is measured for all features.
- Then the feature with smallest ranking criterion is eliminated.
- The procedure is stopped when all the features are ranked.

In T-statistics based feature selection approach, each sample is labeled with $\{1, -1\}$. The mean, $\mu_i^1(\mu_i^{-1})$ and the standard deviation, $\delta_i^1(\delta_i^{-1})$ are calculated for the samples labeled as 1 (-1) or each feature, f_i . Then a score $T(f_i)$ is obtained as follows

$$T(f_i) = \frac{|\mu_i^1 - \mu_i^{-1}|}{\sqrt{\frac{(\delta_i^1)^2}{n_1} + \frac{(\delta_i^{-1})^2}{n_{-1}}}} \tag{6}$$

where $n_1(n_{-1})$ denotes the number of samples labeled as 1 (-1). In order to make decision, the features with highest scores are considered as the most distinctive features.

In k-NN based feature selection, a direct method based on nonparametric feature subset selection evaluation is applied. The evaluation technique denoted as ‘leave-one-out (LOO)’ method has been used. The main idea of LOO method is as follows:

- Design the decision rule using N-1 samples of the total N samples.
- Apply decision rule to the one remaining sample.

- This process is repeated for all partitions of size N-1 for the design sample set and size one for the test
- Estimate the probability of error by the ratio of the test samples incorrectly classified to the total number of samples classified.

The k-nearest neighbour (k-NN) has been used as non parametric classification technique in the evaluation procedure. Overall the feature selection procedure is given as below:

1. Apply k-NN as the classifier.
2. Use the LOO test for recognition rate estimation.
3. Select the first feature that has the highest LOO recognition rate among all features.
4. Select the feature, among all unselected features, together with the selected features that gives the highest recognition rate.
5. Repeat the previous process until enough number of features has been selected, or until the recognition rate is good enough.

Each individual represents a feature subset. In this subsection, we present the choice of a representation for encoding the candidate solutions to be manipulated by the genetic algorithms, and each individual in the population represents a candidate solution to the feature subset selection problem. If n be the total number of features available to represent the patterns to be classified, the individual (chromosome) is represented by a binary vector of dimension, n . If a bit is a 1, it means that the corresponding feature is selected; otherwise the feature is not selected. This is the simplest and most straightforward representation scheme [3]. In this paper, we propose the following fitness function based on the nature of our problem:

$$Fitness = W_1 \cdot (1 - RR) + W_2 \cdot FAR + W_3 \cdot FRR + W_4 \cdot \left(\frac{FeatureSize}{TotalNumberOfFeatures} \right) \quad (7)$$

Where W_1, W_2, W_3 and W_4 are constant weighting parameters which reflect the relative importance between *Recognition Rate* (RR), *False Accept Rate* (FAR), *False Reject Rate* (FRR) and *Feature Size*. The genetic algorithm is independent of the inductive learning algorithm used by the classifier. In this paper, we use asymmetrical SVM classifier as an induction algorithm in the experiments to separate the cases of false accepts and false reject [12]. We use Roulette wheel selection to probabilistically select individuals from a population for latter breeding. The probability of selecting an individual ind_{ij} is estimated as;

$$p(ind_i) = \frac{F(ind_i)}{\sum_{i=1}^p F(ind_i)} \quad (8)$$

The probability that an individual will be selected is proportional to its own fitness and is inversely proportional to the fitness of the other competing hypothesis in the current population. Here, we use single point crossover, and each individual has a probability, P_n to mutate. The number of n bits is randomly selected to be flipped in every mutation stage.

5 Iris Pattern Classification Using Multi-class Gaussian Mixture Model

In this paper, we propose Gaussian mixture model (GMM) to accurately classify the iris pattern. We apply GMM to address the following two important issues. First issue is the significant inter and intra personal variation and second issue is to obtain the required *false accept* and *false reject* rates with a high recognition accuracy to meet several security demands by changing the number of Gaussian mixtures. In the following subsections, we briefly discuss the form of GMM. A detailed discussion on GMM can be found at [14].

5.1 Model Description

A Gaussian mixture model is s weighted sum of M component densities and can be described by the following equation

$$p(\bar{x} | \lambda) = \sum_{i=1}^M p_i b_i(\bar{x}) \tag{9}$$

Where, \bar{x} denotes the D -dimensional random vector, $b_i(\bar{x}), i = 1, 2, \dots, M$, are the component densities and $p_i, i = 1, \dots, M$, are the mixture weights. Each component density is a D-variate Gaussian function of the following form [14]

$$b_i(\bar{x}) = \frac{1}{(2\pi)^{D/2} |\sum_i|^{1/2}} \exp \left\{ -\frac{1}{2} (\bar{x} - \bar{\mu}_i)^T \sum_i^{-1} (\bar{x} - \bar{\mu}_i) \right\} \tag{10}$$

Here, $\bar{\mu}_i$ is the mean vector and \sum_i is the covariance matrix. The mixture weight satisfies the constraint $\sum_{i=1}^M p_i = 1$. Therefore, the Gaussian mixture density is parameterized by the mean vectors, covariance matrix and mixture weights from all the component weights. The parameters can be represented by the following equation [14]

$$\lambda = \{p_i, \mu_i, \sum_i\} i = 1, 2, \dots, M \tag{11}$$

For iris recognition, each subject is represented by a GMM and is denoted by the model, λ .

5.2 Estimation of Maximum Likelihood Parameters

Given a training sample from a subject, the main objective of the person model training is to estimate the parameters of the GMM, λ , that best matches the distribution of the training feature vectors. The popular maximum likelihood estimation (ML) is used to estimate the parameters of a GMM. The idea is to find the model parameters that maximize the likelihood of the GMM provided the training

data is given. If T denotes the sequence of training vectors $\mathbf{X} = \{\vec{x}_1, \dots, \vec{x}_T\}$, the GMM likelihood can be defined as

$$p(X | \lambda) = \prod_{t=1}^T p(\vec{x}_t | \lambda) \tag{12}$$

However, this expression is a non linear function of the parameters λ and direct maximization is not possible. Therefore, ML parameters estimation can be obtained iteratively by using a special case of the expectation-maximization algorithm [14]. The basic idea of the EM algorithm is to begin with an initial model λ , then a new model $\bar{\lambda}$ is estimated from the initial model such that $p(X | \bar{\lambda}) > p(X | \lambda)$. The new model becomes the initial model for the next iteration and the process is repeated until some convergence threshold is reached.

5.3 Subject Identification

For iris recognition, a group of *subjects*, $S = \{ 1, 2, \dots, S \}$ represented by GMM’s $\lambda_1, \lambda_2, \dots, \lambda_s$. The objective is to find the person model which has the maximum a posteriori probability for a given observation sequence.

Formally,

$$\hat{S} = \arg \max_{1 \leq k \leq S} P_r(\lambda_k | X) = \arg \max_{1 \leq k \leq S} \frac{p(X | \lambda_k) P_r(\lambda_k)}{p(X)} \tag{13}$$

Let us consider the equally likely subjects (i. e., $P_r(\lambda_k) = 1/S$) and, it is also assumed that $P(X)$ is the same for all subjects, the classification simplifies to

$$\hat{S} = \arg \max_{1 \leq k \leq S} P_r(\lambda_k | X) \tag{14}$$

By using independence between observations, the iris recognition system computes

$$\hat{S} = \arg \max_{1 \leq k \leq S} \sum \log p(\vec{x}_t | \lambda_k) \tag{15}$$

Where, $p(\vec{x}_t | \lambda_k) = \sum_i^M p_i b_i(\vec{x})$, the Gaussian mixture density which is weighted sum of M components as given in (9).

6 Experimental Results

We conduct the experimentation on two iris data sets namely, the ICE (Iris Challenge Evaluation) dataset created by the University of Notre Dame, USA, [10] and the WVU (West Virginia University) dataset [11]. The ICE database consists of left and right iris images for experimentation. We consider only the left iris images in our experiments. There are 1528 left iris images corresponding to the 120 subjects in our

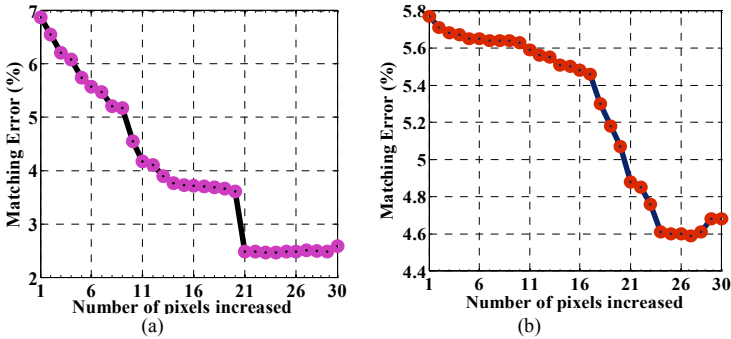


Fig. 5. Matching error vs. number of pixels increased on (a) ICE and (b) WVU datasets

experiments. We also evaluated the performance of the proposed iris recognition scheme on the WVU dataset [11]. The WVU iris dataset has a total of 1852 iris images from 380 different persons. The number of iris images for each person ranges from 3-6 in this database. Since the number of samples from most iris research is limited, cross-validation procedure is commonly used to evaluate the performance of a classifier. In k -fold cross validation, the data is divided into k subsets of (approximately) equal size. We train the classifier k times, each time leaving out one of the subsets from training, but using only the omitted subset to compute the classification accuracy. LOO cross-validation (LOOCV) is a special case of k -fold cross-validation where k equals the sample size. LOOCV is used for ICE dataset, and for WVU dataset, we use 3-fold cross-validation to obtain the training accuracy for GA. We evaluate the success rate for the proposed method on the ICE and WVU datasets by detecting the pupil boundary and the collarette area. The obtained success rates are 98.80% and 97.95% for the ICE and WVU data sets respectively. From the experimental results, it is found that a reasonable recognition accuracy is achieved when the collarette area is isolated by increasing the previously detected radius value of the pupil up to a certain number of pixels. A rapid drop of matching error from 3.61% to 2.48% is observed in Fig.5 (a) for the case of ICE data set when the pixel value is increased from 20 to 21. Therefore, we choose to increase the pupil radius up to 23 pixels because a stable matching accuracy of 97.54% is achieved in this case. From Fig. 5(b) it is found that if we increase the pixel values up to 26 we obtain the highest matching accuracy of 95.53% for WVU data set. Fig. 6 shows the accuracy of the feature subsets with a different number of top-ranked features from the four feature selection algorithms on two data sets. Fig.6 (a) shows that SVM-RFE achieves the better accuracy than the other feature selection methods used in this paper with a subset of 600 top-ranked features. In Fig. 6(b), we can see that SVM-RFE also find the better accuracy among the four algorithms with the 800-top ranked features. Therefore, after obtaining the top-ranked features subset from the SVM-RFE algorithm on both of the two data sets, we input them to the feature pool used by the GA. In order to select the optimum features for the improvement of the matching accuracy, GA involves running the genetic process for several generations. We

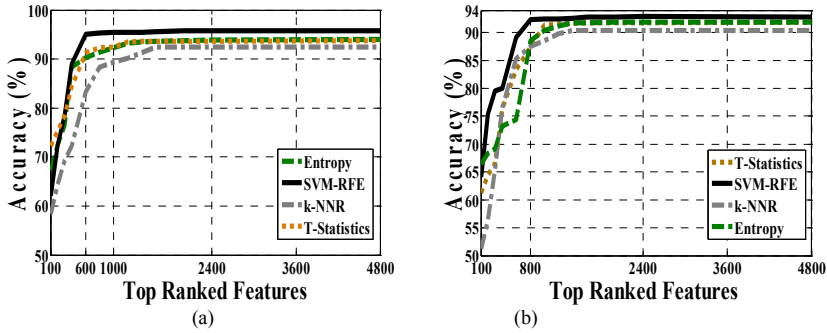


Fig. 6. Accuracy vs. top ranked features on (a) ICE (b) WVU datasets

Table 1. The Selected Values of the Arguments of GA for ICE and WVU Datasets

Parameters	ICE Dataset	WVU dataset
Population Size	120 (the scale of iris sample)	380 (the scale of iris sample)
Length of chromosome code	600 (selected dimensionality of top ranked feature sequence)	800 (selected dimensionality of top-ranked feature sequence)
Crossover probability	0.40	0.89
Mutation probability	0.008	0.007
Number of generation	130	80
Weighting Parameters	$W_1=2000, W_2=150$ $W_3=10, W_4=1000$	$W_1=3500, W_2=100$ $W_3=10, W_4=2000$

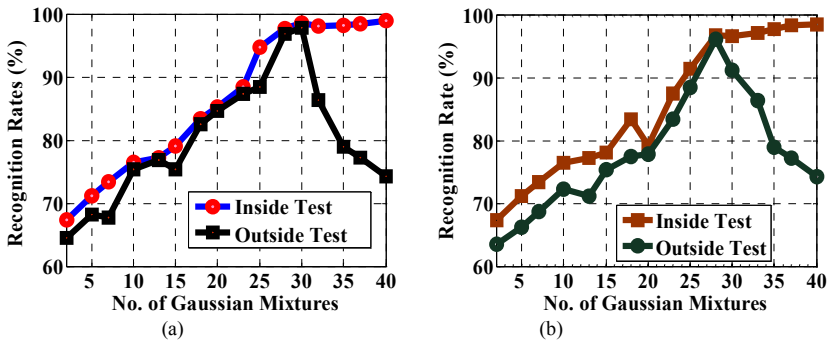


Fig. 7. Recognition accuracy vs. No. of Gaussian mixtures for (a) ICE and (b) (WVU) data sets

conduct several experimentations, and the arguments of the GA are set as shown in Table 1. From experimentation, we find that the proposed GA scheme achieves the highest accuracy of 97.60% at the generation 90 with reduced features subset of 520 for the ICE dataset. Based on the experimentation, we also find that at the generation

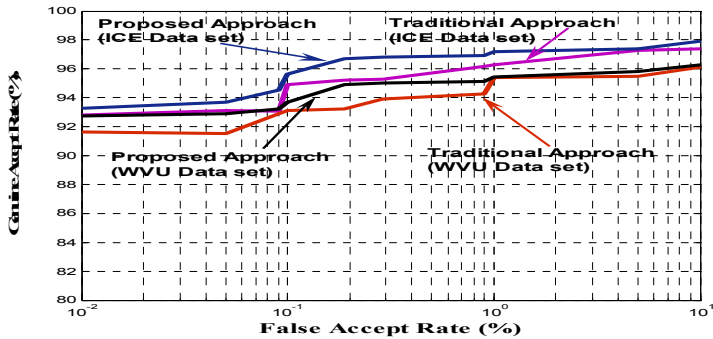


Fig. 8. ROC curve shows the comparison between GAR (%) and FAR (%) for the traditional approach with the complete iris information and proposed approach with collarette information

of 60, the highest accuracy of 95.95% is obtained with the reduced features subset of 680 on the WVU data set. Fig 7 shows the classification accuracy vs. number of Gaussian mixture components. From this figure, we can see that highest accuracy of 97.80% is achieved when the number of Gaussian components is 32 on the ICE data set. For WVU data set, highest recognition accuracy of 96.20% is found at 28 mixture components. In Fig. 8, ROC curve shows how the Genuine Accept Rate (GAR) changes with the False Accept Rate (FAR). It is found from this figure that the proposed approach performs better than the traditional approach with the complete iris information for both of the data sets.

7 Conclusions

In this paper, we mainly focus on the feature subset selection of iris data based on GA. The proposed GA incorporates four feature selection criteria, namely: the SVM-RFE, the k-NN, the T-statistics, and the entropy-based methods to find the subset of informative texture features that can improve the analysis of iris data. The experimental results show that the proposed method is capable of finding feature subsets with a better classification accuracy and/or smaller size than each single individual feature selection algorithm does. This paper also introduces the use of GMM as an iris patterns classifier. The experimental results indicate that the proposed iris recognition scheme with GMM approach can be applied to a wide range of security-related application fields with encouraging recognition rates.

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