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Enhanced and Proficient Iris Recognition Through Weight Sampled Geodesic Active Contour and Convoluted Local Tetra Pattern

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Abstract

Iris recognition, a category of biometric identification based on noncontact imaging of the complex texture in an individual's iris, has been ostensible to be both speedy and precise. This makes the technology outstandingly valuable in areas such as information safekeeping, physical access fortification, ATMs and airport security. It is unruffled of iris image acquirement, image preprocessing, feature extraction and classifier design. In our work, we set into practice superior techniques. Iris segmentation is achieved using Weight Sampled Geodesic Active Contour method, which differs from traditional Geodesic Active Contour method. The features are extracted by means of Convoluted Local Tetra Pattern. Besides Fuzzy Bacterial Foraging algorithm is implemented for feature selection process, which will work in optimized result of feature values according to fitness value prescribed by Fuzzy rules. During classification stage, Relevance Vector Machine (RVM) classifier is employed. The simulation results on MATLAB with CASIA version3 iris dataset outperforms the existing methods with the parameters of recognition time taken, accuracy, sensitivity and specificity.

Keywords: Weight Sampled Geodesic Active Contour, Fuzzy Bacterial Foraging, Iris recognition, Iris segmentation, Relevance Vector Machine (RVM), Convoluted Local Tetra Pattern (CLTRP), Local Binary Pattern (LBP).

1. Introduction

The biometric information will facilitate in all fields to the identification process. A good biometric is characterized by uniqueness and its stability over ones’ life span.

Iris recognition is a biometric technology that relies on the uniqueness of the iris. The probability of finding two people with identical iris patterns is considered to be more or less 1 in 10^{52} (population of the earth is of the order 10^{10}). Not even one-egged twins or a future clone of a person will have the alike iris patterns. The iris comprise of variable sized hole called pupil. The average diameter of the iris is about 12 mm, while the pupil size varies from 10% to 80% of the iris diameter. The iris is a unique organ that is serene of pigmented vessels and arching ligaments, furrows, crypts, rings, corona, freckles and a zigzag collarette, slight ridges, grooves, vasculature and other analogous features and marks [1] as revealed in Fig.1.

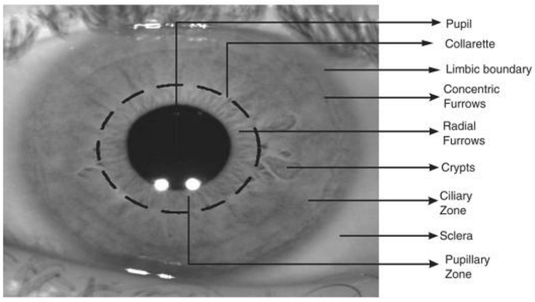


Fig.1. Iris structure [2].

Comparing additional features of the iris increases the probability of inimitability. Seeing as more features are being measured, it is less probable for two irises to match. An added advantage of using the iris is its stability. The iris relic is 'stable for ones' lifetime since it is not subjected to the milieu, as it is protected by the cornea and aqueous humor.

2. Traditional Iris Recognition Methods

The captured iris image is pre-processed as in Fig.2. During pre-processing unwanted parts like, eyelids, eyelashes areremoved. Since the proposed method emphasis only on software for performing recognition, image capturing methods are not discussed here. The diverse works carried out for iris recognition are enlisted here.

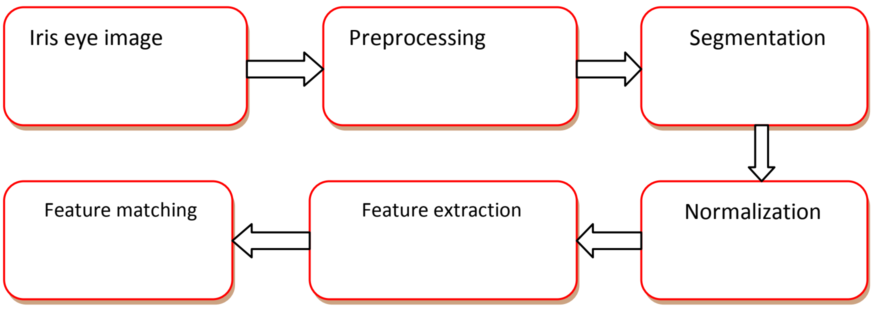


Fig.2. Iris recognition system

An automatic segmentation algorithm based on the circular Hough transform is employed by Wildes et al [3] and Ma et al [5]. By calculating the first derivatives of intensity values in an eye image, edge map is generated and then thresholding the result. But, Hough transform suffers from limitations like, i) requiring threshold values to be chosen for edge detection, which may result in critical edge points being removed, resulting in failure to detect circles/arcs. ii) computationally intensive due to its 'brute-force' approach, and consequently may not be proper for real time applications.

During segmentation phase, the inner papillary boundary and outer Limbic boundary are detected by approximated circles. The noise akin to eyelids and eyelashes, which occlude the iris image are isolated from iris image. Daugman [6] proposed integro-differential operator to detect the centre and diameter of the iris and used the differential operators to identify the pupil in order to maximize,

$$| G_\sigma(\mathrm{r}) * \frac{\partial}{\partial r} \oint_{r,x_0,y_0} \frac{I(x,y)}{2\pi r} \mathrm{ds} | \qquad (1)$$

where, *I(x,y)* is the intensity of the eye image at position *(x,y)*, r is the radius to search for, $G_\sigma(\mathrm{r})$ is a Gaussian smoothing function, s is the contour of the circle given by $r, x_{0,} y_0$. Wildes [3] used the first derivative of image intensity to find the location of edges corresponding to the borders of the iris. This approach explicitly models the upper and lower eyelids with parabolic arcs, whereas Daugman [6] excludes the upper and lower portion of the image in its modal. In view of the fact that it works with raw derivative information, it does not endure from the thresholding problems of the Hough transform. On the other hand, the algorithm can be unsuccessful where there is noise in the eye image, such as from reflections, since it works only on a local scale.

Samir Shah et al. [2] put together active contour models for localizing the pupil in eye images. Active contours respond to pre-set internal and external forces by deforming internally or moving across an image until equilibrium is reached.

The segmented iris image is transformed from polar coordinates system into rectangular region (normalization process). The Cartesian to polar transform of the iris region as shown in Fig. 4, is based on the Daugman's Rubber Sheet model shown in Fig. 3. The rubber sheet model takes into account pupil dilation and size dimensions. Daugman remap each point within the iris region to a pair of polar coordinates (r, θ) where r is on the interval [0, 1] and θ is angle [0, 2π]. The remapping of the iris region is modeled as,

$$I(x(r,\theta), y(r,\theta)) \rightarrow I(r,\theta) \qquad (2)$$

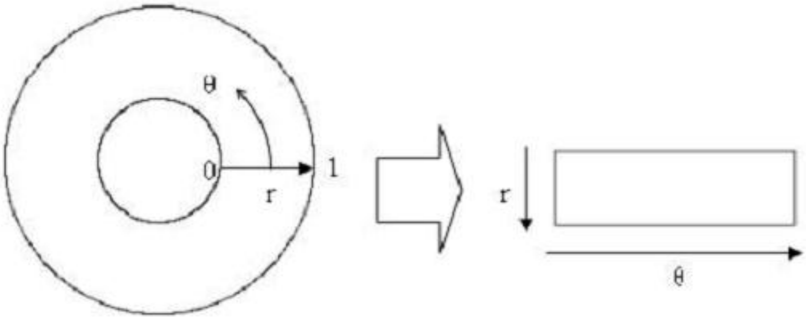
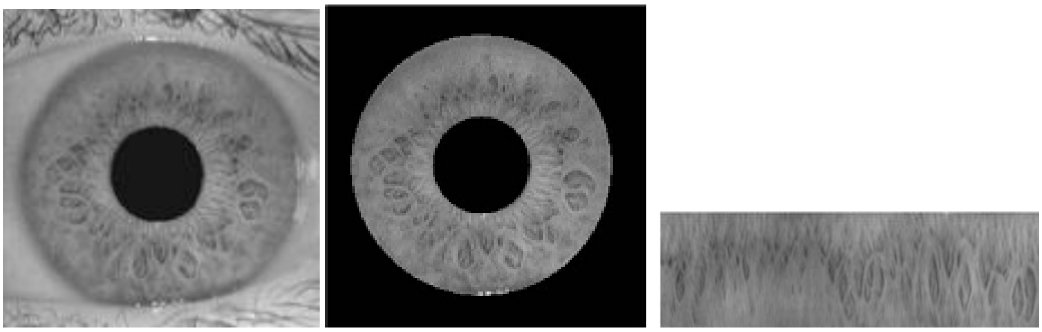


Fig.3. Daugman's Rubber Sheet model [23].

In order to recognize the individuals accurately, the most discriminating features that are present in the region must be extracted (feature extraction phase). Only the significant features of the iris must be encoded. There are a range of algorithm that are presented for feature extraction such as Wavelet encoding [7], Gabor filters [6], Log-Gabor filter [20], Zero-crossings of the 1D wavelet [24], Haar Wavelet [8], Haarlet Pyramid [21] and Laplacian of Gaussian filters [3].

To verify a person's identity, the extracted iris template needs to be matched with the stored template. Matching algorithm that normally used are Hamming Distance, Weighted Euclidean Distance, Normalized Correlation and Gamma correction with histogram thresholding [19]. The Table 1 depicts the comparison of existing Iris recognition algorithms and their pitfalls.



(a)Original Image (b) Localized Image (c) Normalized Image

Fig.4. Iris image normalised into polar co-ordinates [5].

Table 1: Assessment of Available Iris Recognition Algorithms[9].

Author	Quality Evaluation Methods	Segmentation	Image Enhancement	Feature Extraction and Matching	Comments
Daugman [25], [6], [4]	Frequency approach	Integro-differential operator	--	Neural network + 2D Gabor transform + Hamming Distance	First Iris recognition algorithm. Computation time is high
Wildes [3]	Using high contrast edges	Image intensity gradient and Hough transform	--	Laplacian of Gaussian filters + normalized correlation	Does not provide interest to reflections
Ma [5]	Frequency based SVM classification	Gray-level information and canny edge detection	Background subtraction	Multichannel spatial filter + fisher-linear discriminant classification	Does not work with occluded images
Vatsa [9]	--	Intensity based detection	--	1D log polar Gabor and Euler number + Hamming distance and L1 distance	Rule based decision strategy is used to improve accuracy
Monro [17]	--	Heuristic gray level edge feature	Background subtraction	1D DCT + Hamming distance	Fast feature extraction + matching
Boles and Boashash [24]	--	Edge Detection	--	Wavelet transform Zero crossing + dissimilarity function	Does not perform for non-ideal iris images
Daugman [4]	--	Active contours and generalized coordinates	--	Iris Code	Gaze deviation correction, Low time complexity

3. DESIGN AND IMPLEMENTATION OF THE PROPOSED IRIS IMAGE RECOGNITION ALGORITHMS

In this proposed technique, (as shown in Fig.5) the human authentication system is provided for unimodal-biometric based recognition system for input images of Iris. In the initial stage, preprocessing is implemented as image filtering by using Adaptive Median filter and contrast enhancement is provided to view the input image in noise free and enhanced state. In Iris image processing, iris image segmentation is implemented by using weight sampled geodesic active contour method to find iris structure from the given eye image, since active contours [2] can: 1) presume any silhouette and 2) segment multiple objects concurrently, they mitigate some of the concerns associated with the traditional iris segmentation models. The texture patterns are extracted by using convoluted local tetra pattern, which will extract more numbers of patterns than in LBP [26]. From that texture pattern extraction, feature extraction is employed and histogram values are obtained as feature vector for that given image. Then from database, the training data is collected and feature selection operation is provided by using Fuzzy Bacterial Foraging algorithm to form optimized feature particles and fitness values of it are extracted and selected feature column is collected. From this result, the selected index value is given for testing feature vector and reduced training and testing features are formed.

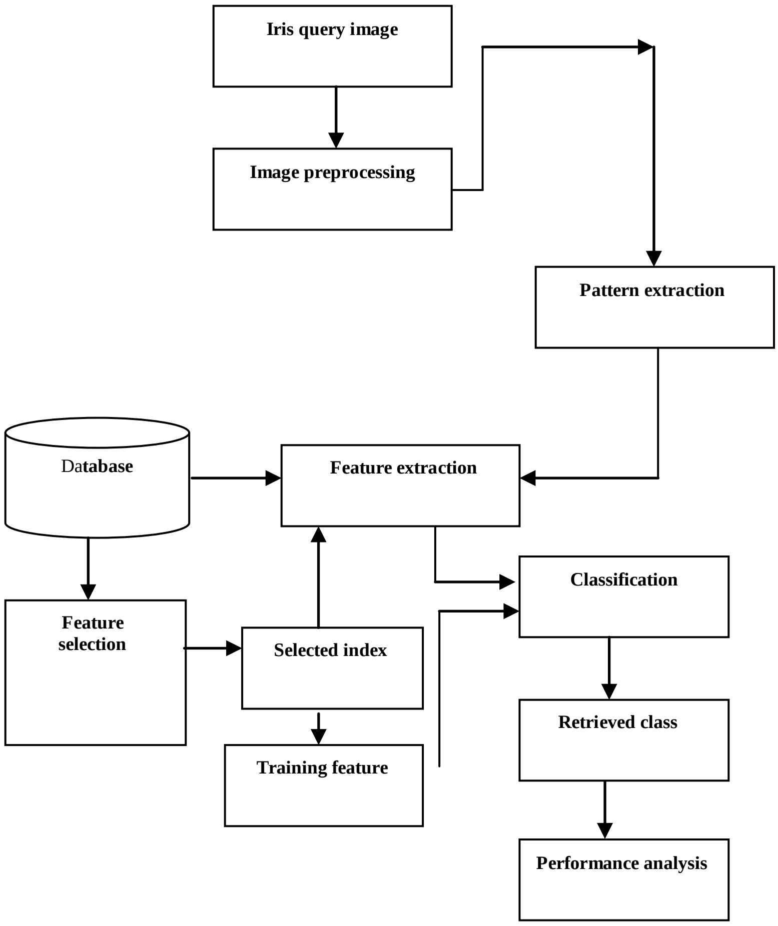


Fig.5 Block Diagram of the proposed methodology for iris recognition

These features are given to classification stage to recognize human identification class. During classification stage, RVM classifier is applied to get better classification performance than SVM, Neural network and HMM classifiers.

3.1 CLTRP Feature Extraction Algorithm:

The idea of local patterns (the LBP, the LDP, and the LTP) proposed in various practices has been adopted to define Local Tetra Patterns (LTrP) [10], [11], [12], [13]. The LTrP describes the spatial structure of the local texture using the direction of the center gray pixel gc. The proposed CLTrP algorithm extracts more numbers of patterns than in LBP.

3.1.1 Advantages of the LTrP over Other Patterns

The advantages of the LTrP over the LBP, the LDP and the LTP can be justified with the help of three points:

i) The LBP, the LDP and the LTP are able to encode images with only two (either “0” or “1”) and three distinct values, respectively. However, the LTrP is able to encode images with four distinct values as it is able to extract more detailed information.

ii) The LBP and the LTP encode the relationship between the gray value of the center pixel and its neighbors, whereas the LTrP encodes the relationship between the center pixel and its neighbors based on directions that are calculated with the help of $(n-1)^{th}$ order derivatives.

iii) The LDP encodes the relationship between the $(n-1)^{th}$ order derivatives of the center pixel and its neighbors in 0^0, 45^0, 90^0 and 135^0 directions separately, whereas the LTrP encodes the relationship based on the direction of the center pixel and its neighbors, which are calculated by combining $(n-1)^{th}$ order derivatives of the 0^0 and 90^0 directions.

3.2 FUZZY – Bacterial Foraging Algorithm

Here, Bacterial Foraging algorithm is implemented for the feature selection process which works in optimized result of feature values according to fitness value controlled by Fuzzy rules.

Bacterial Foraging is developed based on the Darwin’s theory of ‘The Survival of the fittest in natural selection’. Foraging behaviors of foraging animals all the time changes depending on its own physiology and environment.

Animals with meager foraging strategies are either eliminated after generations or formed into superior ones. E.coli bacteria’s foraging behavior which is present in human guts is cautiously noticed and utilized in developing the optimization algorithm. The bacteria ensue through four foraging states, i.e., chemotaxis, swarming, reproduction and elimination-dispersal [14]. All these states are briefly explained below:

(i) Chemotaxis: The two types of movements observed in E.Coli bacteria are viz., tumble (rotation with respect to an axis) using its flagella and swim. In order to find food E.Coli bacteria always attempt to scale up the nutrient concentration and trace the more neutral regions.

Assume θ as the position of the bacteria in p dimensional space $\theta \in R^p$ and $J(\theta)$ is the cost function to be minimized. $J(\theta) \leq 0$ is nutrient rich $J(\theta)$=0 is neutral and $J(\theta)$>0 is venomous environment. If $\emptyset(J)$ is a unit vector in random direction to describe tumble, then, for the *i*th bacteria, the position after *j*th chemotactic step is given by:

$$\theta(i, j+1, k, l) = \theta(i, j, k, l) + C(i, k)\emptyset(j) \qquad (3)$$

where $\theta(i, j, k, l)$represents *i*th bacterium at *j*th chemotactic, *k*th reproductive and *l*th elimination dispersal step. $C(i, k)$is the size of the step taken in the random direction specified by the tumble.

(ii) Swarming: E.coli and other bacteria show the property of attracting and repelling group behavior when placed at the center of a semisolid medium with a single nutrient chemo effecter. They try to step forward out from the center in traveling ring of cells by moving up the nutrient gradient created by consumption of the nutrient by the group [15]. Simultaneously, there conceivably occurs a repelling action between cells. This happens by consuming nearby nutrients. Mathematically swarming can be represented as:

$$Jcc(\theta, P(j,k,l)) = \sum_{i=1}^{s} Jcc\left(\theta, \theta^i(j,k,l)\right) = \sum_{i=1}^{s}[-d_{\text{attractant}} \exp(-w_{\text{attractant}} \sum_{m=1}^{p} (\theta_m - \theta_m{}^i)^2)] + \sum_{i=1}^{s}[-h_{\text{repellant}} \exp(-w_{\text{repellant}} \sum_{m=1}^{p} (\theta_m - \theta_m{}^i)^2)] \ldots\ldots \qquad (4)$$

where, $Jcc(\theta, P(j,k,l)$indicates the objective function value to be added to the actual objective function to present a time varying objective function, p represents number of variables to be optimized, S is the number of bacteria, $d_{attractant}$, $w_{attractant}$, $h_{repellent}$, $w_{repellent}$ *and* $\theta = [\theta_1, \theta_2, \ldots \theta_p]^T$is the point in the p-dimensional space domain.

(iii) Reproduction: After the completion of the Chemotaxis, reproduction state starts. The least healthy bacteria Sr sooner or later depart this life while each of the healthier bacteria asexually splits into two bacteria without mutation, which in turn keeps the swarm size constant. In case, the specified reproduction steps found to be less, then next generation of bacteria will instigate chemotaxis process.

$$Sr = \frac{Sr}{2} \qquad (5)$$

(iv) Elimination and Dispersal: Existence of bacteria possibly will alter subsequent to steady conservation of food or nutrient.

Consequently, due to other mysterious reasons the bacteria might diffuse into the other part of environment with probability p_{ed}. This destroys the previous chemotactic processes.

The momentous steps involved in the algorithm are furnished below:

Step 1: Defining the optimization problem, and initializing the optimization parameters.

p: dimension of the search space

S: the number of bacteria in the population iterated by the counter i

N_C: the number of chemotactic steps iterated by the counter j

Ns: the number of swims after tumble, iterated by the counter m

N_{re}: the number of reproduction state, iterated by the counter k

N_{ed}: the number of elimination-dispersal events iterated by the counter ell

p_{ed}: elimination-dispersal with probability

$C_{(i,k)}$: the size of the step taken in the random direction specified by the tumble.

Step 2: Iterative algorithm for optimization. In this step, the bacterial population, chemotaxis loop, reproduction loop, and elimination and dispersal operations loop are performed.

Step 3: If $j<Nc$, continue chemotaxis process, since the life of the bacteria is not over.

Step 4: Reproduction according to Fuzzy Rule.

Step 5: If $k<N_{re}$, go to reproduction process.

Step 6: Elimination-dispersal.

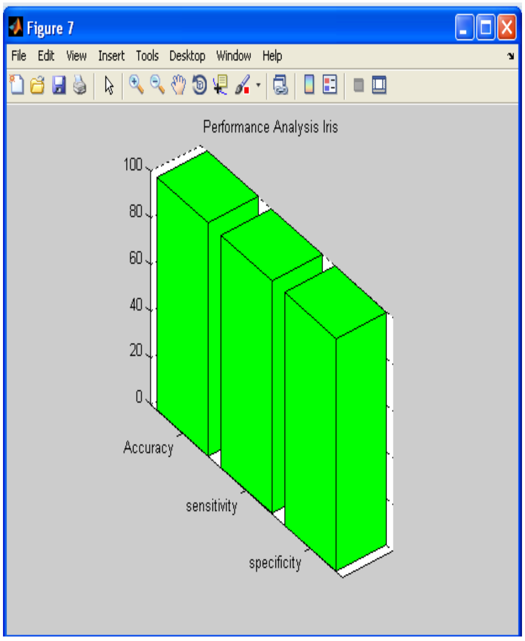
Step 7: If $l<N_{ed}$, then go to elimination-dispersal process; otherwise end.

4. EXPERIMENTAL RESULTS

The simulation is carried out in the MATLAB version R2010a (***mat***rix ***lab***oratory), a multi-paradigm numerical computing environment and fourth-generation programming language. Images from CASIA version 3 have been used for testing purpose. The CASIA database consists of large number of iris images. The size of each and every one image is 320 X 280 pixels as shown in Fig. 6. CASIA version3 (CASIAV3) is acquired in an indoor environment. Most of the images have been captured in two sessions with an interval of at least one month. The database comprises 249 subjects with total of 2655 images from left and right eyes. CASIAV3 is a superset of CASIAV1.

Fig.6. Sample CASIA version3 Iris Images

The tests results in comparison with other existing algorithms are enlisted in the Table 2. The proposed method provide evidence to be better compared with existing methods like, Gabor filter, 2D wavelet [16], DCT based approach [17], SVM and by using LBP with the parameters of Recognition Time taken, Accuracy, Sensitivity and Specificity with CASIA Ver. 3 [18] iris image datasets. The performance analysis of the proposed method is shown in Fig. 7 and Fig. 8. The Table 3 depicts the time taken for each phase of Iris recognition using the proposed methodology. The total time taken for the complete recognition process is approximately 15 seconds.



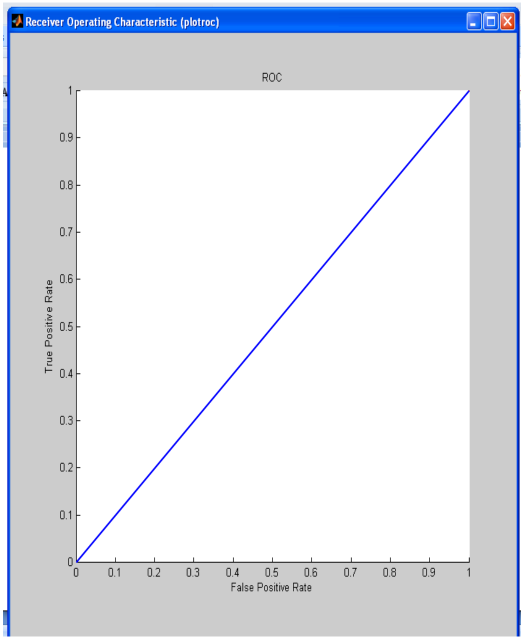


Fig.7 Performance Analysis of Iris Using Proposed MethodFig.8 ROC Analysis of Iris Using Proposed Method

Table-2:Comparative Performance Analysis of Different Iris Recognition Techniques

Method	Accuracy (%)	Sensitivity (%)	Specificity (%)
2D Wavelet	93.85	92	94
DCT based	90.2370	89	93
LBP	94.32	93	94
Gabor	93.2931	94	95
SVM	95.0704	100	100
Proposed	100	100	100

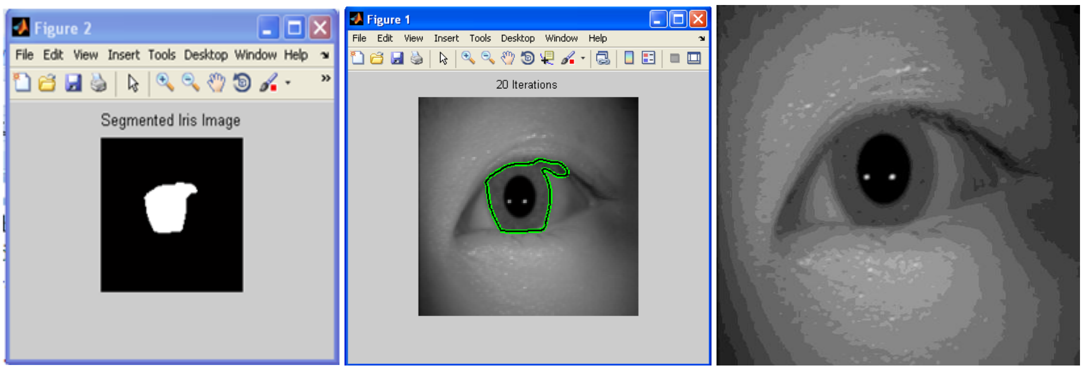
The time taken for different phases of the iris recognition is calculated and is furnished in the Table 3.

Table-3: Time taken for different phases of Iris Recognition process using proposed methodology

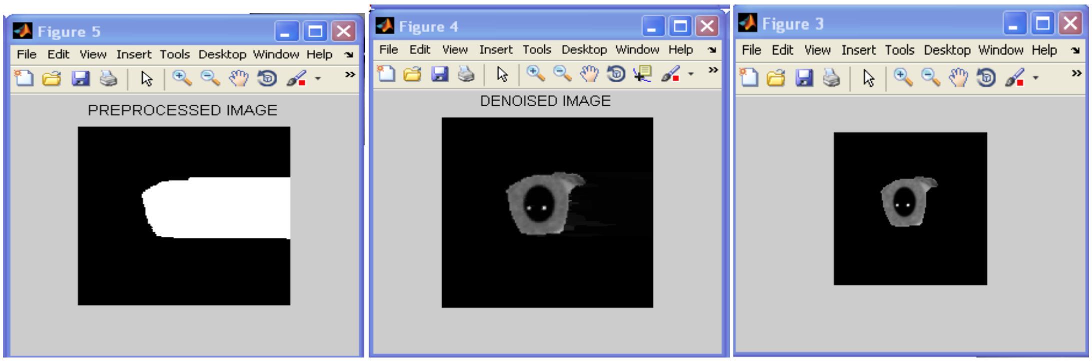
Method Used	**Time Taken (in Sec)**
Iris Segmentation Using Weight Sampled Geodesic Active Contour	1.2716
Iris Pre-processing Using Adaptive Median Filter	0.5789
Iris Feature Extraction Using Convoluted Local Tetra Pattern	11.7486
Iris Feature Selection Using Fuzzy Bacterial Foraging algorithm	0.1951
Iris Classification Using RVM classifier	0.2619

4.1 Snapshot of different phases of iris recognition using proposed methodology

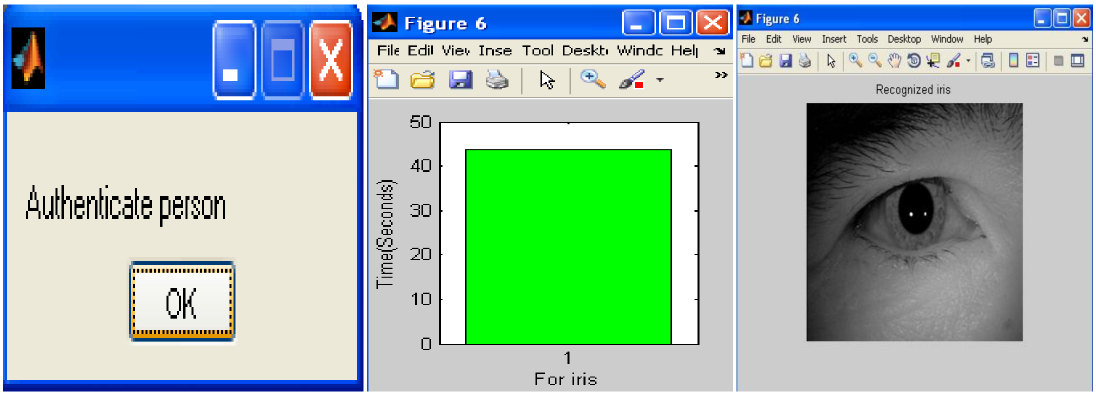
Fig. 9 shows the snapshot of different phases of iris recognition using proposed methodology. Fig. 9(a) shows the query iris image used as one of the input image used. Fig. 9(b) shows the preprocessed output after 20 iterations. Fig. 9(c) shows the segmented binary iris image obtained after the segmentation phase. Fig. 9(d) shows the segmented iris image obtained after the segmentation phase. Fig. 9(e) shows the deniosed iris image obtained after the noised removal phase. Fig. 9(f) shows the preprocessed iris image. Fig. 9(g) shows the recognized iris image obtained after the noised removal phase. Fig. 9(h) shows the total time plot for recognition. Fig. 9(i) shows final result of authentication phase.



(a) Query Iris Image (b) Preprocessing (c) Segmentation Process



(d) Segmented Image (e) Denoised Iris Image (f)Preprocessed Image



(g)Recognized Iris Image (h) Total Time Plot for Recognition of Authentication phase (i)Final Result

Fig. 9. Snapshot of different phases of iris recognition using proposed methodology

5. CONCLUSIONS

In our recognition process, secured authentication using unimodal iris biometric is proposed. The new methodology provides better performance rate. According to the market survey [22], only 16% of the global market is utilized by the iris biometric applications. At present biometric is playing a key role in numerous application areas like forensic, military, access controls, etc. Although Iris biometric suffers from pitfalls like, requirement of expensive scanners and co-operation from user, still iris biometric is considered to be more precise technique.

In this proposed method, iris segmentation is performed by finding the contour for binary extracted output of round area using weight updated contour method, which differs from traditional Geodesic Active Contour. In texture feature extraction method, other than LBP, CLTRP gets more number of patterns to extract image feature at different angles. In the classification process, to get better performance rate, feature size is reduced. To accomplish this, Fuzzy controlled Bacterial foraging optimization algorithm is used, which will include enhanced objective function to generate fitness values for feature selection. The optimization is done with the help of Fuzzy rules combined with Bacterial Foraging Algorithm. Then in recognition system, Relevance Vector Machine is employed to classify image representation so as to get efficient result in the classification of the output. The time taken by the algorithm is also estimated at each phase of iris recognition. The parameters like time taken for recognition, accuracy, sensitivity and specificity are compared with the existing methods, viz., Gabor filter, 2D wavelet, DCT based approach, SVM and by using LBP. The performance evaluation carried out with CASIA version3 iris image datasets proves the proposed methodology outperforms the classical methods.

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