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Performance Analysis of Fingerprint and Iris Verification Based On ELM and Genetic Algorithm

Riya Mary Thomas[1], Linda Joseph[2]

[1] CSE,PG Scholar, Hindustan University, Chennai, Tamil Nadu, India

[2] CSE, Assistant Professor, Hindustan University, Chennai, Tamil Nadu, India

Abstract

In multimodal biometric system, the effective fusion method is necessary for combining information from various modality systems. In this study a new approach to overcome the limitations by using multiple pieces of evidence of the same identity: iris and fingerprint, by combining ELM and Genetic Algorithm. According to ELM theory: “The hidden node / neuron parameters are not only independent of the training data, but also of each other, standard feed forward neural networks with such hidden nodes have universal approximation capability and separation capability. Such hidden nodes and their related mappings are terms ELM random nodes, ELM random neurons or ELM random features.” Genetic algorithms (GAs) operates with a population formed by a set of individuals called chromosomes and every chromosome is constituted by a set of genes. ELM combined with Genetic Algorithm provides better performance as compare to the SVM. It improved the accuracy when compared to SVM.

Keywords: *Multimodal biometrics, Genetic algorithm, ELM, score level fusion, biometric system..*

1. Introduction

Information fusion utilizes a combination of different sources of information, either to generate one representational format, or to reach a decision. The motivations for using information fusion include: (1) Utilizing multi-sensor fusion to increase the estimation accuracy of target-tracking (2) Utilizing complementary information to reduce the measurement error (3) Utilizing multiple classifier fusion to increase the correct classification rates (4) Reducing the cost of implementation possibly by using several cheap sensors rather than one expensive sensor.

Establishing the identity of a person is a critical task in any identity management system. Surrogate representations of identity such as passwords and ill cards are not sufficient for reliable identity determination because they can be easily misplaced, shared, or stolen. Biometric recognition is the science of establishing the identity of a person using his/her anatomical and behavioral traits. Multi-modal biometric system is a relatively new application of information fusion while individual biometrics has been used for a fairly long time. For example, fingerprint has been widely used by police for person verification and identification. To increase the reliability, biometric fusion especially multi-modal biometric fusion has drawn a lot of attention recently. Common biometrics includes fingerprint, face, hand geometry, finger geometry, iris, retina, signature, voice, gait, smell, keystroke, ECG, etc. While unimodal biometrics uses the fusion of multiple measurements, it can be considered as the fusion of dependent sources. In the case of multi-modal biometric fusion such as fingerprint and face, the information fusion is performed over independent sources since the two sources hardly have any correlation in the statistical sense.

Unibiometric systems (based on single biometric trait) have several drawbacks like noisy sensor data, non-universality or lack of distinctiveness of the biometric trait, unacceptable error rates, and spoof attacks. Multimodal biometric systems, which combine multiple biometric samples, or characteristics derived from samples, have been developed in order to overcome those problems. Multibiometrics offers the following main advantages: 1) significantly improving the accuracy of the biometric identification or verification; 2) providing a certain degree of flexibility for some unusable biometric traits; and 3) resisting spoof attacks due to the difficulty in spoofing multiple biometric sources.

The key to multimodal biometric system is the fusion of various biometric modality data. In a multi modal biometric system that uses iris and fingerprint biometric traits, fusion can be done at different levels of information are: (a) feature extraction module, (b) matching module, and (c) decision making module .The paper is organized as follows. Section 2 present the over view of related work. Section 3 gives information about proposed techniques for multimodal biometric recognition system. Section 4 describes the experimental result multi modal biometric system. Finally some conclusions are reported in Section 5.

2. Related Work

A variety of articles can be found which propose different approaches for unimodal and multimodal biometric systems. Traditional unimodal biometric systems have many limitations. Fierrez-Aguilar et al.[1] the authors perform a decision level fusion based on Sum, Support Vector Machine and Dempster-Shafer theory on multiple fingerprint matching algorithms submitted to FVC 2004 competition with a view to evaluate which biometrics to fuse and which technique to use for fusion. Ajay kumar and sumit shekhar[2] developed a biometric system of palm print recognition using rank level fusion. The recognition rate of the proposed system is 98.75%. Yas Abbas Alsultanny et al[3] proposed genetic algorithm implemented with neural network to determine automatically the suitable network architecture and the set of parameters from a restricted region of space. In this algorithm, the result showed good optimization, by reducing the number of hidden nodes required to train the neural network (epoch's reduced to less than 50%). One of the important results of the implemented algorithm is the reduction in the time required to train the neural network. K.C. Chan et al[4] proposed a fast fingerprint matching methodology based on localizing the matching regions in captured fingerprint images. The relationship between authentication reliability and region size is studied experimentally. Results show that accurate enough fingerprint matching can be achieved using very small bitmaps, making it possible to implement very fast fingerprint authentication systems using the relatively slow embedding processors. Anil Jain et al proposed[5] Fingerprint verification is one of the most reliable personal identification methods. it describes the design and implementation of an on-line fingerprint verification system which operates in two stages: minutia extraction and minutia matching.The system has been tested on two sets of fingerprint images captured with inkless scanners. The verification accuracy is found to be acceptable. Typically, a complete fingerprint verification procedure takes, on an average, about eight seconds on a SPARC 20 workstation. The experimental results show that our system meets the response time requirements of on-line verification with high accuracy. YunhongWang et al[6] proposed Face and iris identification have been employed in various biometric applications. Besides improving verification performance, the fusion of these two biometrics has several other advantages. Two different strategies for fusing iris and face classifiers. The first strategy is to compute either an unweighted or weighted sum and to compare the result to a threshold. The second strategy is to treat the matching distances of face and iris classifiers as a two-dimensional feature vector and to use a classifier such as Fisher's discriminant analysis and a neural network with radial basis function (RBFNN) to classify the vector as being genuine or an impostor. It compare the results of the combined classifier with the results of the individual face and iris classifiers. Fierrez-Aguilar et al. [7] the authors perform a decision level fusion based on Sum, Support Vector Machine and Dempster-Shafer theory on mUltiple fingerprint matching algorithms submitted to FVC 2004 competition with a view to evaluate which biometrics to fuse and which technique to use for fusion.

3. Proposed System

Multimodal biometric offers many advantages like 1)Significantly improving the accuracy and performance of the biometric identification / verification system.2)Providing a certain degree of flexibility for some unusable biometric traits. 3)Resisting spoof attacks due to the difficulty in spoofing multiple biometric sources.

A.Preprocessing

Iris preprocessing: includes edge detection using Canny and noise removal using Hough Transform.
Fingerprint preprocessing: includes binarization and thinning.

B. Feature Extraction

Fingerprint: The aggregate characteristics of ridges, and minutia points, form the unique features for fingerprint. The three basic patterns of fingerprint ridges are the arch, loop, and whorl:

arch: The ridges enter from one side of the finger, rise in the center forming an arc, and then exit the other side of the finger.

loop: The ridges enter from one side of a finger, form a curve, and then exit on that same side.

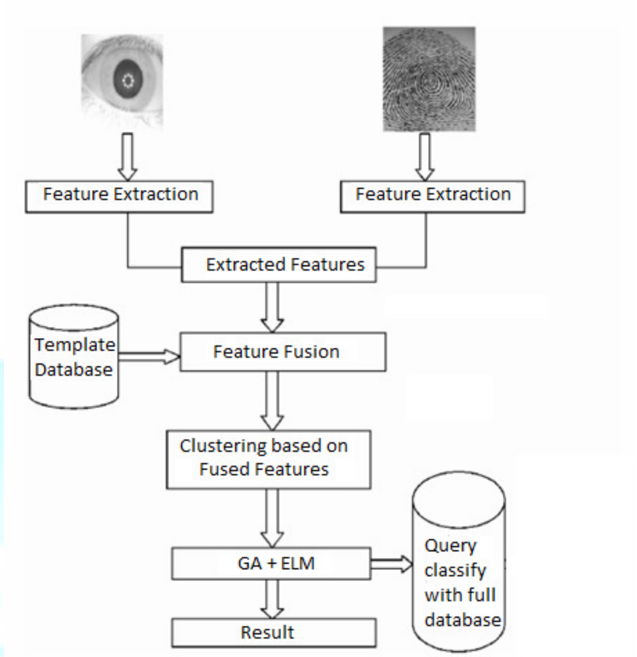
whorl: Ridges form circularly around a central point on the finger.

The major minutia features of fingerprint ridges are ridge ending, bifurcation, and short ridge (or dot). The ridge ending is the point at which a ridge terminates. Bifurcations are points at which a single ridge splits into two ridges. Short ridges (or dots) are ridges which are significantly shorter than the average ridge length on the fingerprint. Minutiae and patterns are very important in the analysis of fingerprints since no two fingers have been shown to be identical

Iris: A set of Gabor filters with different frequencies and orientations is used for extracting features from iris. Gabor wavelets (filters or functions) are based on physiological studies of simple cells in the human visual cortex. The cells are selectively tuned to orientation as well as spatial frequency, and their response can be accurately enough approximated by 2D Gabor filters. Thus, the increased popularity of this approach is biologically well justified. A set of Gabor filters is applied with specific parameters such as frequency, sharpness of Gaussian envelope and different rotation angles. The object image undergoes convolution with these Gabor filters to produce Gabor jets. These Gabor gets are processed in various ways to form the feature vectors.

(c)Feature Fusion

Feature fusion is commonly preferred in multimodal biometric systems because matching contain sufficient information to make genuine and impostor case distinguishable and they are relatively easy to obtain. Given a number of biometric systems, matching scores for a pre-specified number of users can be generated even with no knowledge of the underlying feature extraction and matching algorithms of each system. Therefore, combining information obtained from individual modalities using score level fusion seems both feasible and practical. Since the scores generated by a biometric system can be either similarity scores or distance scores, one needs to convert these scores into a same nature. The common practice, which is followed paper, is to convert all the scores into similarity scores. In general, score level fusion techniques can be divided into three categories as follows (a) transformation-based score level fusion (e.g., sum-rule based fusion preceded by min-max normalization), (b) classifier based score level fusion (e.g., SVM- based fusion), and (c) density-based score level fusion (e.g., likelihood ratio test with Gaussian Mixture Model). We adopt transformation-based score level fusion.



(D)K-means Clustering

k-means clustering is a method of vector quantization, that is popular for cluster analysis. This iterative partitioning minimizes the sum, over all clusters, of the within-cluster sums of point-to-cluster-centroid distances. Rows of X correspond to points, columns correspond to variables. kmeans returns an n-by-1 vector IDX containing the cluster indices of each point. By default, kmeans uses squared Euclidean distances. When X is a vector, kmeans treats it as an n-by-1 data matrix, regardless of its orientation.

The objective function,

$$J = \sum_{j=1}^{n} \sum_{i=1}^{n} | x_i^{(j)} - c_j |^2$$

Where,
$\left| x_i^{(j)} - c_j \right|^2$ is a chosen distance measure between a data point and
$x_i^{(j)}$ the cluster centre c_j, is an indicator of the distance of the n data points from their respective cluster centers. The algorithm is composed of the following steps:

1. Place K points into the space represented by the objects that are being clustered. These points represent initial group centroids.
2. Assign each object to the group that has the closest centroid.
3. When all objects have been assigned, recalculate the positions of the K centroids.

4. Repeat Steps 2 and 3 until the centroids no longer move. This produces a separation of the objects into groups from which the metric to be minimized can be calculated.

(E)GA and ELM Learning

(a) Genetic Algorithm**:** In a genetic algorithm, a population of candidate solutions (called individuals, creatures, or phenotypes) to an optimization problem is evolved toward better solutions. Each candidate solution has a set of properties (its chromosomes or genotype) which can be mutated and altered; traditionally, solutions are represented in binary as strings of 0s and 1s, but other encodings are also possible.

The evolution usually starts from a population of randomly generated individuals, and is an iterative process, with the population in each iteration called a generation. In each generation, the fitness of every individual in the population is evaluated; the fitness is usually the value of the objective function in the optimization problem being solved. The more fit individuals are stochastically selected from the current population, and each individual's genome is modified (recombined and possibly randomly mutated) to form a new generation. The new generation of candidate solutions is then used in the next iteration of the algorithm. Commonly, the algorithm terminates when either a maximum number of generations has been produced, or a satisfactory fitness level has been reached for the population. A typical genetic algorithm requires:

a genetic representation of the solution domain,
a fitness function to evaluate the solution domain.

A standard representation of each candidate solution is as an array of bits. Arrays of other types and structures can be used in essentially the same way. The main property that makes these genetic representations convenient is that their parts are easily aligned due to their fixed size, which facilitates simple crossover operations. Variable length representations may also be used, but crossover implementation is more complex in this case. Tree-like representations are explored in genetic programming and graph-form representations are explored in evolutionary programming; a mix of both linear chromosomes and trees is explored in gene expression programming. Once the genetic representation and the fitness function are defined, a GA proceeds to initialize a population of solutions and then to improve it through repetitive application of the mutation, crossover, inversion and selection operators.

In a problem of optimization by the genetic algorithms, the first step is to initialize the population randomly or with existing solutions. The second step involves a cost for each individual via a fitness function respecting the principle that the individuals survive well-adaptably. The third step is the reproduction: parents are selected by a method that favors the best of them; a crossover will give (new individuals) inheriting some of the characters of their parents. Finally, a mutation changes the value of some genes to prevent the establishment of a similar population unable to evolve.

(b) Extreme Learning Machine: ELM was originally proposed for standard single hidden layer feedforward neural networks (with random hidden nodes (random hidden neurons, random features)), and has recently been extended to kernel learning as well. ELM provides a unified learning platform with widespread type of feature mappings and can be applied in regression and multi-class classification applications directly. ELM can approximate any target continuous function and classify any disjoint regions. ELM is efficient in: Batch learning, Sequential learning and Incremental learning. According to ELM theory:

The hidden node / neuron parameters are not only independent of the training data but also of each other, standard feedforward neural networks with such hidden nodes have universial approximation capability and separation capability. Such hidden nodes and their related mappings are terms ELM random nodes, ELM random neurons or ELM random features.

Unlike conventional learning methods which MUST see the training data before generating the hidden node / neuron parameters, ELM could randomly generate the hidden node / neuron parameters before seeing the training data.

Extreme learning machine (ELM) was proposed in Huang. Suppose training SLFNs with K hidden neurons and activation function $g\ (x)$ to learn N distinct samples (x_i, t_i), where $x_i = [x_{i1,}\ x_{i2\ldots}\ x_{in}]\ T \in R_n$ and $t_i = [t_{il},\ t_{i2}\ \ldots\ t_{im}]\ T \in R_{m.}$ In ELM, the input weights and hidden biases are randomly generated instead of tuned. By doing so, the nonlinear system has been converted to a linear system:

$$H\beta = T$$

Where $H = \{h_{ij}\}$ ($i = 1 \ldots N$ and $j = 1 \ldots K$) is the hidden layer output matrix, $h_{ij} = g\ (w_j .\ x_i + b_j)$ denotes the output of j^{th} hidden neuron with respect to $x_{i;}$ $w_j = [w_{j1,}\ w_{j2\ldots}\ w_{jn}]^T$ is the weight vector connecting j^{th} hidden neuron and input neurons, and b_j denotes the bias of j^{th} hidden neuron; $w_j .\ x_i$ denotes the inner product of w_j and x_i; $\beta = [\beta_{1,}\ \beta_{2\ldots}\ \beta_k]^T$ is the matrix of output weights and $\beta_j = [\beta_{j1,}\ \beta_{j2\ldots}\ \beta_{jm}]^T$ ($j= 1. . . K$) denotes the weight vector connecting the j^{th} hidden neuron and output neurons; $T = [t_1,\ t_2\ \ldots\ t_N]^T$ is the matrix of targets (desired output). Thus, the determination of the output weights (linking the hidden layer to the output layer) is as simple as finding the least-square solution to the given linear system. The minimum norm Least-Square (LS) solution to the linear system is,

$$\beta^{\wedge} = H^{\dagger}\ T$$

Where $H^{\dagger}$ is the MP generalized in verse of matrix H. The minimum norm LS solution is unique and has the smallest norm among all the LS solutions. As analyzed by Huang, ELM using such MP inverse method tends to obtain good generalization performance with dramatically increased learning speed.

4. RESULT AND ANALYSIS

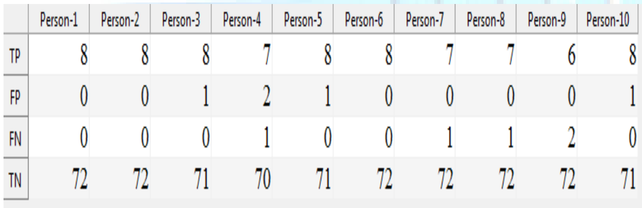
The proposed system can only generate four possible recognition results: correctly matching (true positive: TP), correctly not matching (true negative: TN), incorrectly matching (false positive: FP), and incorrectly not matching (false negative: FN). The False Accept Rate (FAR), False Reject Rate (FRR), and Genuine Acceptance Rate (GAR) are calculated by

$$FAR = \frac{FP}{TN + FP} X100\%$$

$$FRR = \frac{FN}{TP + FN} X100\%$$

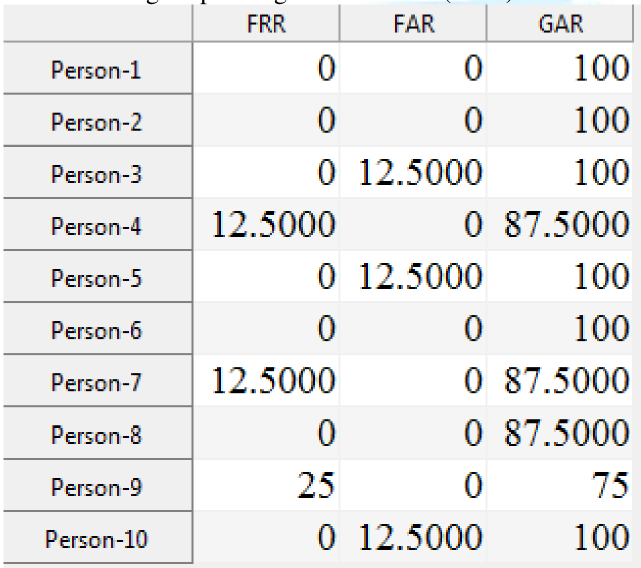
$$GAR = 1 - FAR$$

The receiver operating characteristic (ROC), a balanced plot of FAR and GAR, which illustrates the performance of the proposed system.



	Person-1	Person-2	Person-3	Person-4	Person-5	Person-6	Person-7	Person-8	Person-9	Person-10
TP	8	8	8	7	8	8	7	7	6	8
FP	0	0	1	2	1	0	0	0	0	1
FN	0	0	0	1	0	0	1	1	2	0
TN	72	72	71	70	71	72	72	72	72	71

Fig2: operating characteristic (ROC)



	FRR	FAR	GAR
Person-1	0	0	100
Person-2	0	0	100
Person-3	0	12.5000	100
Person-4	12.5000	0	87.5000
Person-5	0	12.5000	100
Person-6	0	0	100
Person-7	12.5000	0	87.5000
Person-8	0	0	87.5000
Person-9	25	0	75
Person-10	0	12.5000	100

Fig3: a balanced plot of FAR and GAR

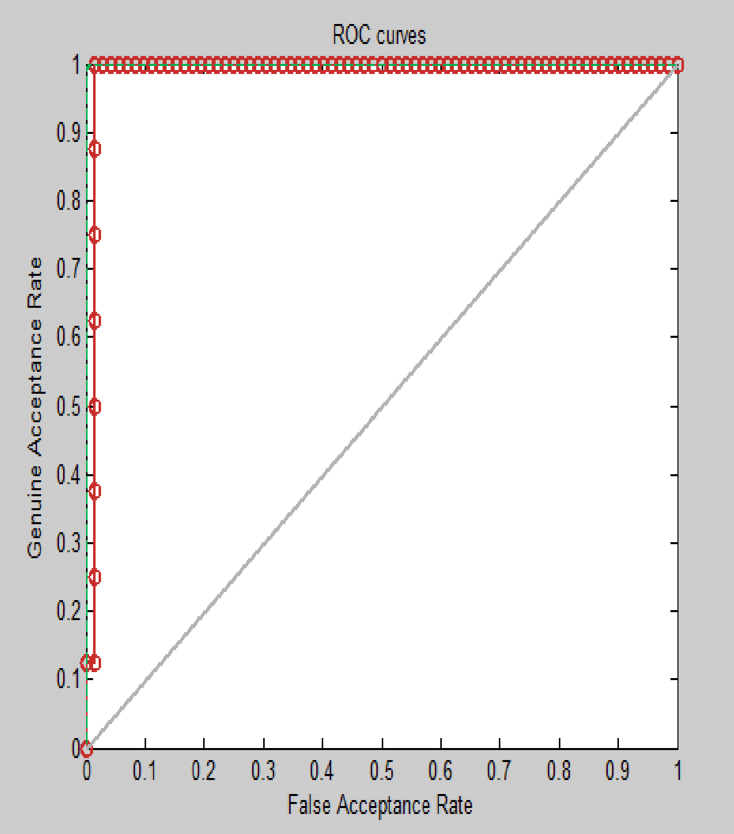


Fig4: performance of the proposed system.

5. CONCLUSION

Biometric systems offer several advantages over traditional based methods. This work focuses on using the multimodal biometrics. A New framework for fingerprint and iris recognition using Extreme learning machine and Genetic Algorithm based score level fusion. The individual scores of two traits, iris and fingerprint are combined at the matching score level to develop a multimodal biometric authentication system. The proposed multimodal biometric systems offer several advantages over traditional single based methods. The experimental results show that comparing Genetic Algorithm and ELM with K-mean cluster methods provide clustering score based on similarity done and improve accuracy.

Acknowledgments

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