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Off-line handwritten signature recognition based on genetic algorithm and Euclidean distance

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Article Info

ABSTRACT

Biometric authentication is a technology that has become significant in the high level of personal identity security. This paper provides a signature recognition system. This paper provides a static signature recognition system (SSRS). We have classified the signature in two ways. The first method uses the genetic algorithm (GA), considering that the signature is the chromosome with 35 genes, and each feature is a gene. With applying the processes of the GA between chromosomes and the formation of generations in sequence until we reach the optimal solution by finding the chromosome closest to the chromosome that enters the system. In the second method, we have classified the signature by calculating the Euclidean distance (ED) between the query signature and the signatures stored in the database. The signature closest to a confirmed threshold is considered the desired goal. The database uses 25 handwritten signatures (15 signatures for training and five original signatures, and five fake signatures written by other people for testing), so we have a database of 500 signatures. With a 94% discrimination rate, the genetic recognition system (GRS) was able to access the solutions, and with a (91% rate) the Euclidean recognition system (ERS) was done. The application uses MATLAB.

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1. INTRODUCTION

The difference between human and computer skills has been reduced because to artificial intelligence (AI). In order to bring about exceptional things in many disciplines, the researchers and enthusiasts are working really hard on a variety of facets of the field. One such area is the computer vision field. Various pattern recognition algorithms, such as Biometric systems, were created. Automatic recognition of an individual based on specific distinctive features or characteristics that an individual possesses is provided by a biometric system of identification and authentication. Pattren recognation (PR) provides a systematic way to describe and categorize objects by obtaining biometric data, extracting important features from them, and comparing those features with existing templates in a database [1]–[3]. In order to lessen security risks from military applications, government centers and airports, and criminal applications, biometric identification technology is crucial in security systems of many applications. Consequently, a secure, dependable, and practical identifying system is required [4]. Biometric techniques divide into two parts: physiological include fingerprints, iris, retina, Deoxyribonucleic acid (DNA), stroke and so on, and behaviors include signature, face, ear, walking, length [5]–[7].

Systems for securing information use knowledge-based, object-based, or biometric authentication. This study will help researchers better comprehend how artificial intelligence uses categorizes and verifies

handwritten signatures. A handwritten signature as a biometric authentication is a legal name or sign of a person's identity, carried out by hand and used for documentation [8], [9]. In general, to verify the authenticity of signatures, there are two types of systems, static systems that get signatures offline, the other type is dynamic systems that get signatures online. In static, we use a scanner that scans the signature drawn on the paper and stores it as an image on the computer. Usually used on bank checks and Signatures of documents [10], [11]. On the other hand, signature verification uses dynamic signature properties (signature path, pen pressure, pen drop, timestamp) taken through a tablet-based using the special pen. Anatomical and behavioral characteristics appear when a person signs their name or when writing any phrase. The shape of the signature can enable handwriting to be a reliable indicator of a person's [12]–[15]. The features extracted from the signature can be classified into three types, global features, local features, and geometric features. Global features the features extracted from the whole signature image, by typical of finding the height and width of the signature area, the ratio between height and width and calculating the core of the signature area. Local features are more accurate than global features in finding skew lines, sensitivity, local pixel density, and extracting from a small portion of a signature image. Geometric features are concerned with the distinctive geometric shape of the signature that preserves its global and local features [16]–[19].

Since there has been a greater need for surveillance applications, security and law enforcement, signature recognition has become a particularly active area of research. One of the more challenging research issues is signature recognition; there is currently no one solution that works for all signature recognition issues. But if a signature recognition system performs well in terms of discrimination, memory usage, computational complexity and a large number of data, then everyone will agree that it is good. Dimensionality reduction and feature extraction are crucial components of any signature recognition system. Despite the fact that signature images of modest sizes have big dimensions, this results in a tremendous increase in computing complexity, time, and memory usage. Any classifier's effectiveness is mostly determined by the strong discriminative characteristics of its images [20]. In this research, we have considered all these dimensions, and we have two types of static signature recognition systems (SSRS). First: Genetic recognition system (GRS), where we applied a genetic algorithm (GA) on handwritten signatures. We validated the signatures by adopting a database of 500 signature images and extracting 35 local and global features from each image. Each signature is a series of features (genes) that make up the individual (chromosome) in the community. The genetic processes (evaluation, selection, crossover and mutation) apply and repeat until the optimum solution is obtained. Second: The Euclidean recognition system (ERS), based on the same database, calculates the Euclidean distance (ED) between the features of query signature and the mean signature features of the original (training) signature images. The distance is compared with a value of threshold to select the closest solution, the matching signature. The remainder of the paper is organised into section 2, which briefly describes the previous studies. Section 3 presents a detailed explanation of the proposed work, then follows in section 4, the overall structure of the work, then follows it in section 5, a discussion and comparison of the results, and the conclusion is included in section 6.

2. PREVIOUS WORK

The process of distinguishing handwritten signatures using computers has become very substantial in verifying identity, and a vast amount of studies and research have appeared to verify signatures and achieve reliability, for each of them has strengths and weaknesses. In [20], the recearchers introduced a framework based on robust and reliable fragmentation of images extracting many adjective image features to distinguish their performance when distinguishing between signature and non-signature images. They have demonstrated that the gradient-based and local ternary patterns (LTP) features, are more voracious in classifying signature segments in individual useses global features such as the energy, entropy, and aspect ratio of the candidate portions and can serve as profitable complementary characteristics. Once again in [9] the recearchers relied on a measure of similarity between the claimed signature and the template by ED, whereas signature features act as the template for verification against a claimed test signature. In [21], the recearchers introduced a handwritten signature authentication method using QR-codes and motion detection, taking into account the time dimension in the verification process as a grave factor to make the system more accurate by 10%, which gave the accuracy of its system up to 78.26%. In [22], the authors presented the literature review explaining how the problem had been dealt with in the past few decades, analyzing recent developments in the field and potential trends for future research. In [23], The researchers suggested an algorithm for a signature identification method based on a wavelet transform average frame entropy (AFE) and a probabilistic neural network (PNN). A wavelet packet entropy neural network system (WPENN) was used to test the system, and it was successful in achieving a threshold entropy of 92%. As recently as 2020 [24], the recearchers offered offline handwritten signature recognition relied on robust accelerated features, unchanged feature transfer features, and a supported vector machine. They experimented with 1,600 samples and reached a 95% identification success rate. At the same time [25], the researchers used a convolution neural network (CNN),

speeded up robust features (SURF), Harris corner detection (HAD) algorithm, and crest-trough (CT) method. They achieved an 89% in fraud detection and a signature verification rate of 94%.

3. THE PROPOSED SYSTEM

In this manuscript, a new workflow based on SSRS used a GA and ED. At first, images were simplified and unimportant parts were cut using digital image processing, to extract the good features significant in the classification process. The two classifiers (GA) and (EA) were used to classify the signatures and compare their results to obtain the best classification ratio.

3.1. Centroid distance function (CDF)

The signature can derive from the shape of the coordinate boundary. It is a one-dimensional function. There are many types of signature shapes such as tangent angle, area function, centroid distance function, complex coordinates, curvature function [26]. The centroid distance function r(n): is expressed by the limit distance points from the middle point of the shape .The g_x , g_y represent the coordinates of a pixel in the centre. The x(n), y(n) represented the coordinates of any other points within the shape, look at (1). After subtracting the "position of the shape" represented by the middle point from the coordinates of the boundary region, the point distance and the complex coordinates will be invariant when translated [27].

$$r(n) = \sqrt{((x(n) - g_x)^2 + (y(n) - g_y)^2)} \tag{1}$$

3.2. Genetic algorithm (GA)

It is one of the evolutionary optimization algorithms in computational mathematics and bioinformatics that established on the principle of applied inference, a series of dynamic processes such as convergence, experimentation, and selection that are performed iteratively by comparing different results until an accurate solution is found. The GA process depends on community members to find possible solutions to a specific problem. The main point is to address these solutions that are repeated with each generation. Accordingly, individuals are the solutions to the problem. And elementary solutions are randomly generated to be the first population group [28], [29]. In genetics, the formation of a new generation depends on selected individuals from the previous generation as workers in the current generation. After evaluation, the individuals selecting to see the extent of each individual's adaptation (one of the solutions) with the population. Assessment depends on the fitness function. Each new community is the entrance to the sequent community and the next step of the algorithm. One advantage of the GA is processing a large number of data (individuals) very efficiently [30], [31]. Here is a breakdown of the evaluation process steps in describing the structure of the GA:

- A chromosome: Each individual (chromosome) describes a possible solution to a problem. It is usually coded form as a series of strings. This string can be binary, integer, or decimal [32].
- A population: is the group of individuals who represent solutions to a problem (chromosomes).
- Fitness assessment: testing the degree of suitability of individuals, i.e. possible solutions (chromosomes) of the population.
- "Selection": the random selection of chromosomes. As the measure of the number of times "an individual" is chosen as the best of the population, it is called selective pressure, and the selection process aims to select the best solutions (the best individuals) and exclude the worst solutions in the future generations [33].
- "Genetic Operators": They are essential to diversify populations and maintain the adaptive characteristics of previous generations. The most commonly used genetic operators are mutation and crossover.
- The criterion to stop: the algorithm stops when it finds an optimal solution.

The following Figure 1 as shown in Appendix gives the general sequence of the simple GA.

3.3. Euclidean distance (ED)

ED is the most well-known unit of distance measurement. The classifier based on this distance measure is plain and straightforward. The ED rule uses the mean class values as class centres to determine pixel-centre distances. This approach is superior to the main level classification of a heterogeneous area. Its benefit stems from the fact that it requires the least amount of time to classify.

4. THE OVERALL STRUCTURE OF THE SYSTEM

Biometric authentication is a public security system. The importance of this technology has grown due to the high level of identity security for individuals. Physiographic characteristics and behavioural

characteristics are two types of verification. Signature recognition is one of the behavioural identifiers. Our system operates on these characteristics, and the system generally passes through several master stations, starting with initialization and ending with the recognition process.
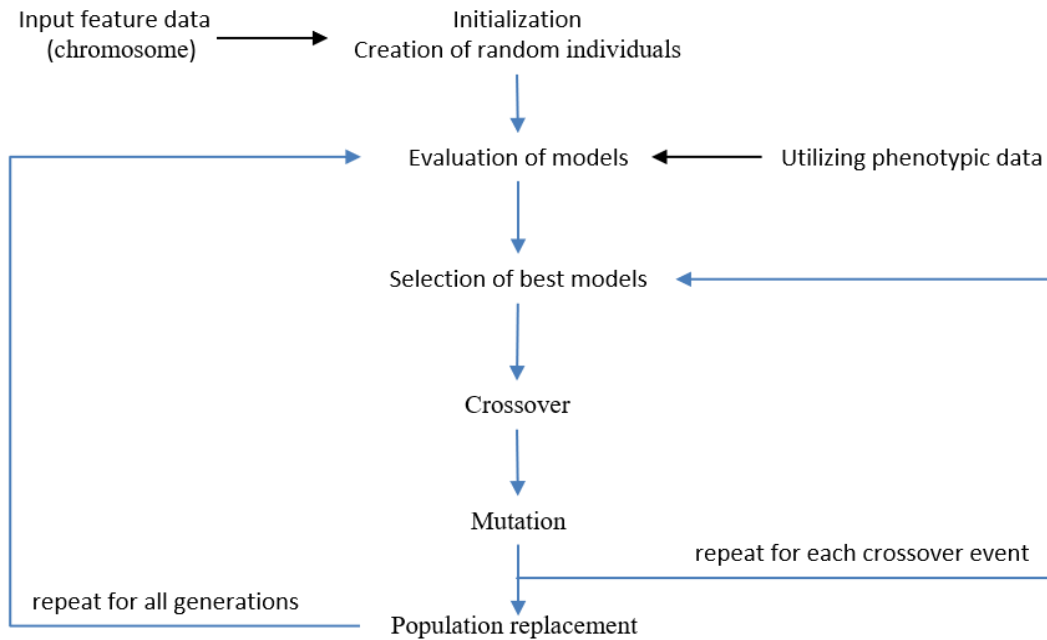

Figure 1. Basic steps in a GA

4.1. Initialization

The basis of our work here is the pictures of the signatures, so 500 signatures have been prepared by talking with 20 persons to present a report signed by them that includes 15 for training signatures and five original signatures and five fake signatures written by other people for testing. (This means there are 20 groups and each group contain 20 original signatures and 5 fake signatures specialized for one person). All the groups save on the computer by scanning the images with a resolution of 300 dpi. Figure 2 shows samples of the signatures database.

Figure 2. samples of the signatures database

4.2. Preprocessing

Start reading the signature image as a colour image. Preprocessing of the signature image is done through the following five main sequential steps,
a.   Read the colour image.
b.   Convert the image to a gray image. Thus, the image matrix becomes two-dimensional instead of three.
c.   Carry out optimization operations that include noise removal, area clipping, resampling, and downsampling to ensure the quality of the extracted features later.
d.   Convert the image to a binary image by decomposing the threshold.
e.   Bounding box by subtracting the signature portion from the background by deleting the white lines and white columns surrounding the signature.
f.   Replace white points with black points and vice versa so that the pixel carried a "1" becomes "0", While

the pixel with a "0" is converted to "1". Figure 3 shows an example of the preprocessing steps on one of the signature images forms.

Figure 3. Preprocessing

4.3. Acquiring features

The main tasks that strongly influence the success of any subsequent differentiation process. In our approach, we extracted the local and global features from the signature image. We have done this according to the signature's format derived from "CDF" and the "35 features" we extracted from the signature image. The signature features represent the template for the verification of the test signature. The features such as energy, occupancy rate, critical points, density rate, the centre of gravity, aspect ratio, entropy and other features are called global features. These features describe the whole of the signature. As for the local features, extract from the signature parts after dividing the signature in different ways into several parts or cells. The centre of the cells and slope of the centre of gravity of the cell is examples of local features.

4.4. Recognition system

Signature recognition systems try to identify whether a biometric sample belongs to the individual in question. It means they are used to validate the legitimacy of query signatures. The substantial intra-class variability is one of the most severe aspects of the signature verification task. Handwritten signatures from the same user often exhibit a lot of variation between samples, especially when compared to physical biometric features like fingerprints or iris. This issue is drawn in Figure 4. When we discuss the forgery of experts with the intent of stealing from a particular person, this problem exacerbates by the lack of diversity between classes, calculation of the average signature for each group's signatures and is a convenient solution to this problem. The quality of the extracted features is measured to estimate recognition accuracy. The measurement is done once by the GA and again by ED.

Figure 4. Variation between samples of one person

4.4.1. Genetic recognition system (GRS)

Twenty signature patterns were identified using the GA and depending on the trait vector. Each feature represents the value of a gene in the chromosome (this is the input to the genetic identification algorithm). GA calculations continue to identify spurious or original signatures by comparing the feature vector extracted from the signature image with the vectors stored in the database. determing the owner of the handwritten signature. That is, each chromosome (signature) contains 35 genes (features) and represents the input of the GRS. Figure 5 shows an example of the signature form that represents the input of the GRS.
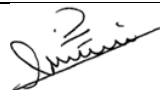

	Gene1	Gene2	Gene3	Gene4	…	…	Gene35
	Feature1	Feature2	Feature3	Feature4	…	…	Feature35

Figure 5. Signature's chromosome form

Here are the sequential steps of the GRS,

a. Choose features for signature images that you will be rely upon in the composition of chromosomes (individuals).

b. Let the first generation be the features of the first signature file, and the second generation be the features of the second signature, and so on for all twenty signature forms.

c. Calculate the minimum ED between the new image and the image of the first signature and store the value of the fitness function in a distinctive vector and name its Fitness 1.

d. Depending on the fitness of each individual, the current generation ranked in descending order from best to worst fitness.

e. Determining the replacement and retention ratio, to designate individuals in the current generation whose genes (vector values of signature characteristics) will be copied to the new generation, in order to preserve the best features of signatures and the type of signatures that form the basis of recognition.

f. Copy a specified number of signatures (parents) from the beginning of the parent generation signatures to the first signature based on the replacement and survival ratio, and store them in a new array we call (strongest parent 1), and store the fitness values of these parents in fitness vectors.

g. Examine the retention and substitution ratio, delete the worst original generation signatures (the array) from the beginning of the first sign to the end, and delete the fitness values for these signatures.

h. Rely on the latest generation of the first generation (Signature 1). Generate a new generation using two of the fittest chromosomes, excluding the previously identified chromosomes.

i. Create new (sub) signatures by cross-computing the correct values.

j. After calculating the ED, you can select new signature (children) based on the least distances and identify the unknown chromosome, store the fitness value in (fitness 2) and represent the new generation fitness (first-order signatures).

k. Implement the RAND function to generate random values representing the probability of a mutation occurring on the current chromosome. The chance of applying the sub mutation increases if the random value is less than 0.001.

l. Create a vector from new signatures (children) representing the new generation of signatures (first generation).

m. After crossover between signature chromosomes, the chromosomes (along with their fitness vector, fitness 2) are used in the current generation detection to avoid duplication and revert the process to the rest of the signature chromosomes.

n. Steps (8) through (13) reapplied to the remaining signature chromosomes from the previous generation.

o. Include the resulting generation (first generation) with the best and strongest signatures (parents-1) taken from the previous generation with their fitness values (Ideal Fitness-1) into the fitness values of the new generation (Fitness-2), thus obtaining the same number of signatures from the original-generation. For the resulting generation while preserving the best signature's genes that might lead to a better solution.

p. After completing the formation of the new signature generation, this generation store in a class (signature-1) within the current generation (current matrix) and, their fitness values convert from fitness 2 (matrix 2) to fitness 1 (matrix 1).

q. Saving the best (lowest) fitness value of the new signature generation as (best-1), which represents a vector with the best possible values (optimal solution) taken from the whole generation.

r. This process is repeated to generate up to 100 new-generations. Step-3 to step-17 and is repeating one hundred times.

s. The process of generating 100 new generations is repeating as long as the fitness function is constantly changing and, when the fitness function becomes fixed for three successive generations, then it will stop.

t. The same for signature -2 and all 20 signature styles. Noting that the best fitness values is stored for each signature.

u. After applying the algorithm to 20 signatures and obtaining the highest fitness for each generation, the unknown or fake signatures will be those with the lowest fitness value.

v. Print the result of recognition for the unknown signature type.

w. Repeat steps (3) through (22) to read the features of the remaining signature image and check each type up to the last vector in the array. Initiate gene approach by obtaining each unknown chromosome from the original generations of the 20 signature patterns.

x. End of the GRS.

4.4.2. Euclidean recognition system (ERS)

Depending on the pre-configured database, pre-processing steps are applied to images of signatures and extract important features. Then the dataset is generated by finding the modified signature for each group by averaging the signature features values for each group. The minimum and maximum values within the features of the average signature are determined to determine the acceptable range of the group. Then the ED

is calculated between the query signature features and the average signature of the groups. If the ED is less than a certain threshold, the query signature confirms as genuine otherwise, it is fake. Figure 6 as shows in Appendix the sequential steps of the ERS system. Three different percentages have been used to measure the performance of the system. These are false rejection rate (FRR), false acceptance rate (FAR), and accuracy. The FRR is the percentage of original signatures that are misclassified. FAR is the percentage of forgeries that are classified incorrectly. The percentage of signatures that are correctly classified is referred to as accuracy. The threshold must be chosen in such a way that the trade-off between FAR and FRR is acceptable FRR. Choosing a high threshold value increases FAR, while selecting a low threshold value increases FRR. According to our features the value 2.5 has been chosen as a threshold for the purposes of this work.
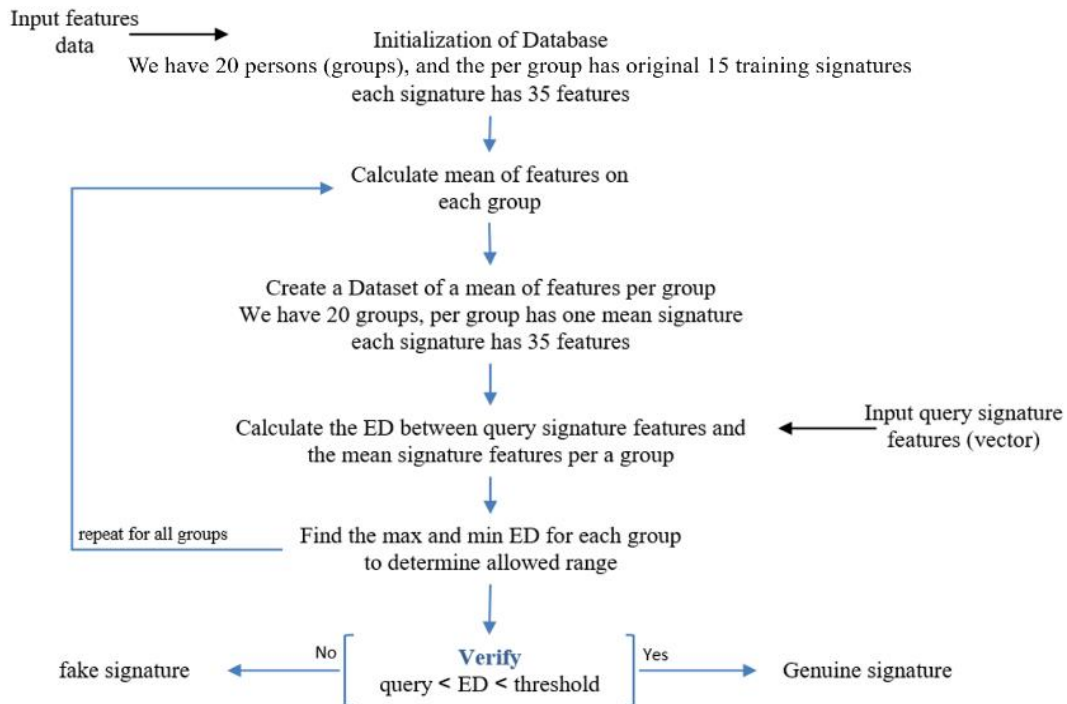

Figure 6. The sequential steps of the ERS

5. RESULTS AND DISCUSSIONS

We assess the behaviour of both the evolutionary and Euclidean systems in this section. Examines and contrasts the classification ratios of the two. The total recognition ratio, error rate (ER) and the true rate (TR) was estimated.

a. 20 different signature types are identified. Image features are extracted from the signature images after completing the pre-processing. The signature person identified using one of two systems: The first one GRS using the GA. The second is the ERS using the minmum distance ED.

b. The signature images for each category dividing into two groups, the first being the training group, consisting of 15-images, and the second being the examination group, consisting of 5-originals images and 5-forgeries images.

In the experimental outcomes of the ERS model. FAR, FRR, and Accuracy were tested with various threshold values, and the results are tabulated in Table 1. The training signature sample's maximum and minimum Euclidian distance values are utilized to determine the acceptance range. The query signature is verified as valid if the ED between it and the mean signature image is within the acceptable range, else a forgery is identified. Figure 7 Impact of threshold function change on the accuracy FRR, and FAR, (a) The threshold=2.3 (A low threshold value increases FRR). (b) The threshold=2.5 (The threshold limit is selected to determine the best results.). (c) The threshold=2.7 (A high threshold value increases FAR) and Figure 8 shows a relationship between the accuracy, FRR, and FAR at various threshold levels. (a) Accuracy rates at the 2.3, 2.5, and 2.7 threshold levels. (b) FAR rates at the 2.3, 2.5, and 2.7 threshold levels. (c) FRR rates at the 2.3, 2.5, and 2.7 threshold levels.

Table 1. Comparison of results from experiments on the ERS model, data base (DB) original signatures=15, test original signatures=5, test forgeries signatures=5, with various threshold

| DB groups	Th=2.3			Th=2.5			Th=2.7		
	FRR %	FAR%	Accuracy %	FRR %	FAR %	Accuracy %	FRR %	FAR %	Accuracy %
P1	80	0	60	60	60	40	0	80	60
P2	60	20	40	60	60	40	40	60	50
P3	40	0	20	0	0	100	20	80	50
P4	60	20	40	0	0	100	20	80	50
P5	80	0	60	0	0	100	40	60	50
P6	80	0	60	0	0	100	40	60	50
P7	80	0	60	0	0	100	40	60	50
P8	60	20	40	0	0	100	0	80	60
P9	60	20	40	0	0	100	20	80	50
P10	60	20	40	0	0	100	0	80	60
P11	40	0	20	0	0	100	40	60	50
P12	40	0	20	0	0	100	40	60	50
P13	40	0	20	0	0	100	20	80	50
P14	80	0	60	0	0	100	0	80	60
P15	60	20	40	0	0	100	20	80	50
P16	60	20	40	0	0	100	40	60	50
P17	80	0	60	0	0	100	40	60	50
P18	40	0	20	0	0	100	0	80	60
P19	40	0	20	0	0	100	0	80	60
P20	80	0	60	60	60	40	0	80	60

(a)

(b)

(c)
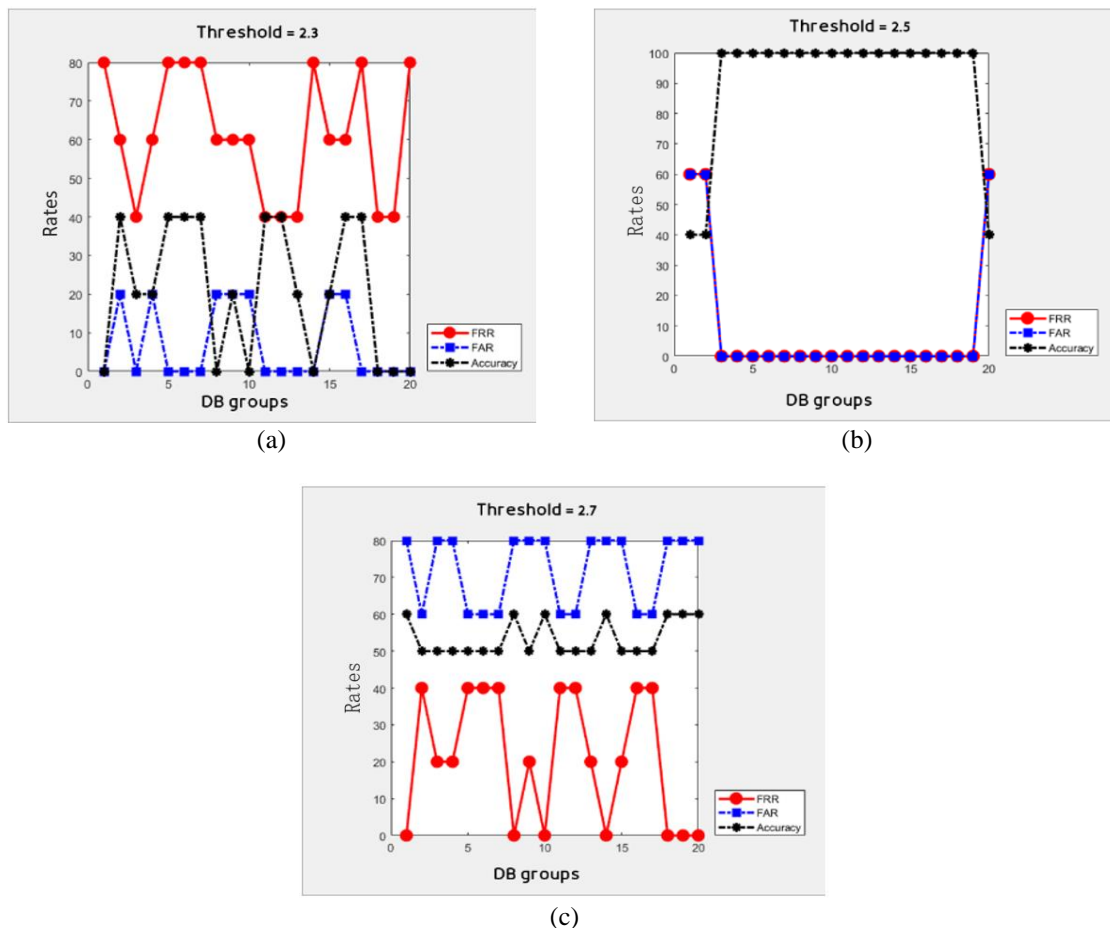
Figure 7. Impact of threshold function change on the accuracy, FRR, and FAR, (a) The threshold=2.3, (b) The threshold=2.5 and (c) The threshold=2.7

c. The proposed method gives an excellent discrimination rate. The main advantage of this method is its ability to intelligently process and reduce computational requirements depending on the quality of features extracted from signature images to explore a combination of linear chromosomes and trees. Repeated application of mutation, crossover, inversion and selection identifies regions where optimal solutions are

likely to be found and identifies the target accurately. We had a 94% recognition success rate for GRS. ERS gave an overall rating rate of 91%. See Figure 9 and Table 2. Figure 10 explains the results of untrained images on the GRS Figure 11 explains the results on the ERS.
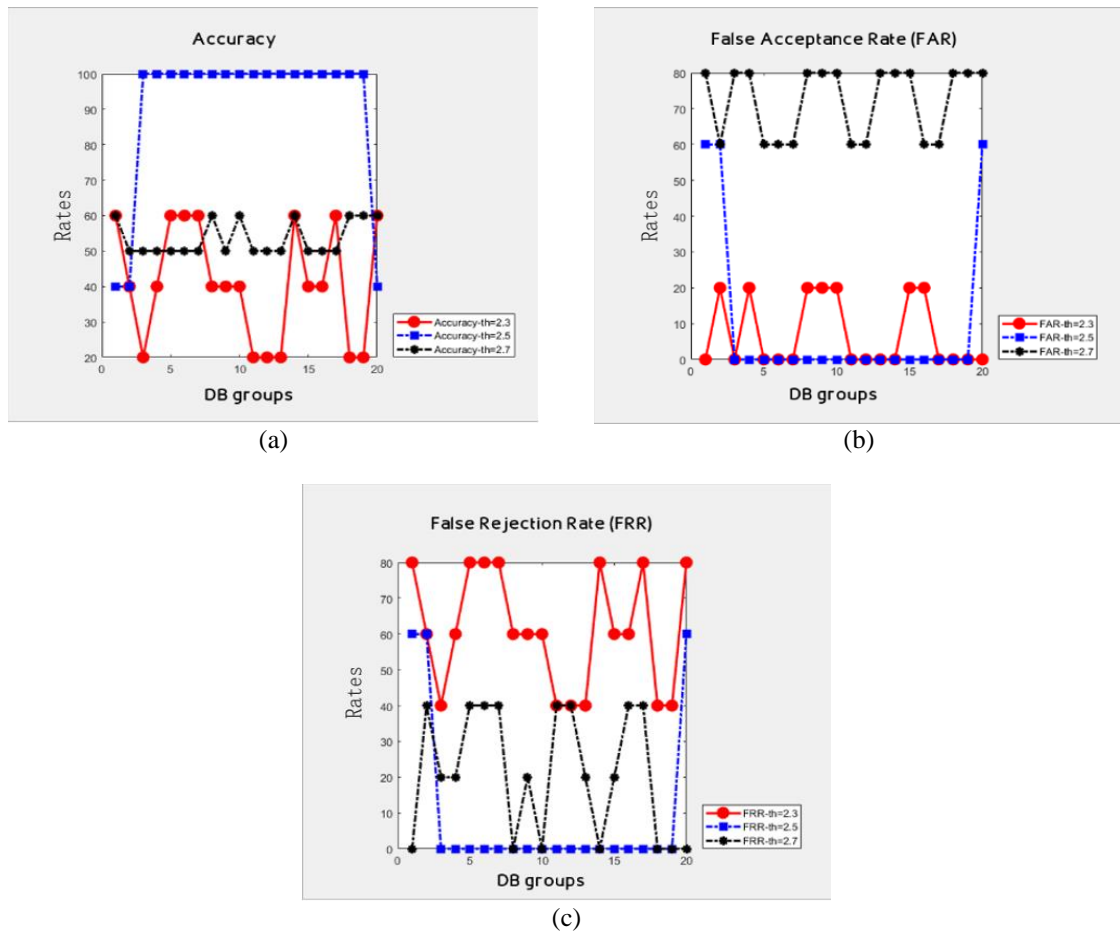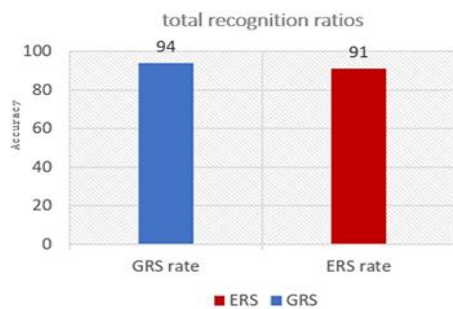

(a)

(b)

(c)

Figure 8. Relationship between the accuracy, FRR, and FAR at various threshold levels, (a) Accuracy rates at the 2.3, 2.5, and 2.7 threshold levels, (b) FAR rates at the 2.3, 2.5, and 2.7 threshold levels, (c) FRR rates at the 2.3, 2.5, and 2.7 threshold levels

Figure 9. The total recognition ratios of the two system
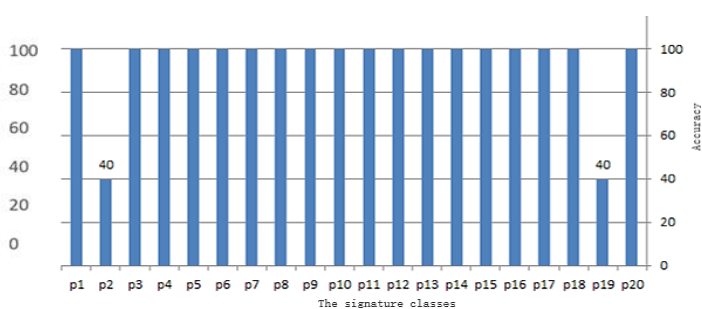
Figure 10. The GRS results

d. The results of the two systems show that the genetic system can identify the new signatures and distinguish them well. This indicates the appropriateness of the GA in raising the rate of recognition of signatures. From the results of the two systems, we found that the GRS succeeded in identifying the signature patterns of person2 (p2) and person19 (p19) by 40% only, and the ERS identifies three types of signatures p1, p2,

and p19 by 40% only. That indicates the difficulty, similarity, complexity, and there is typically a lot of variation between samples of these types of signatures. We used two quality measured performance of our systems. The first measure the correct value. The second measures the error value, as shown by formulas (2) and (3), respectively [34]. See Figure 12 compares the results of GRS-TR and ERS-TR for persons p1, p2, p19 and p20.

e. The comparison was made with previous studies over several years, as shown in Table 3.

$$TR_v = \frac{AV_i}{EV_i} * 100 \% \tag{2}$$

$$ER_v = (100 - TR_v) * 100 \% \tag{3}$$

AV is the correctly classified images; EV is all templets in DB.

Table 2. Comparison of results from experiments on the proposed systems

PERSON'S SIG.	GRS-TR %	GRS-ER %	ERS-TR %	ERS-ER %
P1	100	0	40	60
P2	40	60	40	60
P3	100	0	100	0
P4	100	0	100	0
P5	100	0	100	0
P6	100	0	100	0
P7	100	0	100	0
P8	100	0	100	0
P9	100	0	100	0
P10	100	0	100	0
P11	100	0	100	0
P12	100	0	100	0
P13	100	0	100	0
P14	100	0	100	0
P15	100	0	100	0
P16	100	0	100	0
P17	100	0	100	0
P18	100	0	100	0
P19	40	60	40	60
P20	100	0	100	0

Table 3. Comparison of our study with previous relevant studies regarding signature recognition

| The classifier	Reference	Extracted features	Dataset	Ratio%
SVM	[20], 2014	LTP + global features	755 samples	92.9
SVM	[20], 2014	LTP + global features	4082 samples	57.3
SVM	[24], 2020	SIFT and SURF	1600 samples	95
CNN	[26], 2020	biometric features	1320 samples	90-94
DWT	[35], 2022	uniform local binary pattern (ULBP) features	400 samples	85
DWT	[35], 2022	histogram of oriented gradient (HOG) features	400 samples	91
GA	This work,	local and global features from CDF	500 samples	94
ED	This work,	local and global features from CDF	500 samples	92
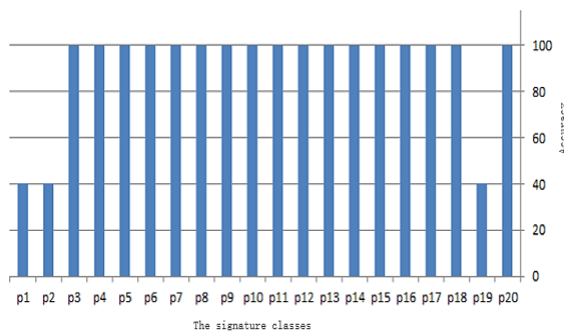
Figure 11. ERS results
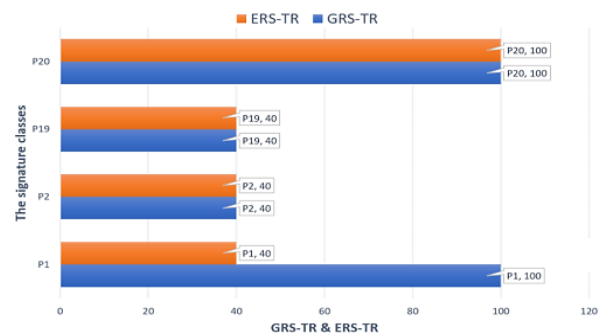
Figure 12. Comparison of GRS-TR and ERS-TR results

6. CONCLUSION

Two techniques are used in this study to identify handwritten signature patterns. The "Genetic recognition system (GRS)" is the first system. GA is used to investigate the signature structure by using specimen spatial data in the primary community formation, Genetic data is generated frequently until the best individual is the query signature image and the genetic system had a success rate of 94%. The second is the "Euclidean recognition system (ERS)," which finds a maximum and minimum Euclidian Distance values of the training signature sample are used to set the acceptance range. The Euclidian distance between the claimed signature and the template in the feature space serves as a measure of similarity between the two. If the distance between the test signature and the original signature is smaller than a pre-determined threshold, the test signature is verified to be the genuine signature, otherwise, the forgery is identified. The Euclidean system had a success rate of 91% in recognizing signature patterns. Thus, the GA-based approach of distinguishing signatures proved to be effective and successful. To successfully handle the searching system strategy GA employs selection, crossover, and mutation operators. Natural selection and genetics principles are used to create this method. GA is an intelligent application of random search supported by historical data to contribute to the search in a coverage framework with a better output. According to experiments, combining feature extraction methodologies with the diversity of features can improve verification ratios. The local features extracted from signatures such as aspect ratio, energy, entropy and the global features that describe the whole of the signature help a lot in verifying query signatures and other features may be tried in the future. The proposed work applied on verifying the handwritten signatures in an offline form, and the work could be applied online in the future.

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