



Optimized Framework for Signature Recognition Using Genetic Algorithm, Loci Method, and Fuzzy Classifier

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Abstract

The present research introduces an optimized framework for signature recognition. This framework incorporates three distinct methodologies: Loci method, Genetic Algorithm (GA), and Fuzzy Min Max Classifier (FMMC). The primary objective of this study is to achieve an enhanced recognition accuracy. The Loci method is a well-established approach used for pattern characterization, particularly suitable for patterns with strokes, especially in horizontal and vertical orientations, in this study, it is employed for signature recognition. However, a drawback of Loci method is its reliance on three critical hyperparameters: the degree of image division, the extent of zero padding and the restricted number of strokes. The choice of hyperparameters values significantly influences the efficiency of the recognition system. As a result, a GA is applied to ensure optimal hyperparameters values selection. This algorithm uses three phases with new strategies; selection, crossover, mutation; iteratively with the goal of maximizing the fitness function. The proposed fitness function is defined as the recognition rate calculated using FMMC. The effectiveness of the proposed methodology was tested and assessed through a comparative analysis with well-established models using an overly diversified signature database. The proposed model produced favorable outcomes compared to other approaches designed for the same task.

Keywords: Loci method; Fuzzy min max classifier; Genetic algorithm; Signature recognition; Hyperparameters selection.

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1. Introduction

Signature recognition stands as a pivotal technology with extensive implications, impacting sectors ranging from financial services and legal documentation to electoral processes, and identity verification.^[1]

Over the course of time, technological progress has led to the development of automated signature recognition systems. This evolution can manifest in various issues, encompassing feature extraction, classification, or even a combination of both.

Regarding the issue of feature extraction, a plethora of

methods can be developed to distill meaningful information from signature data. These methods encompass a wide array of techniques, including Histogram of Oriented Gradients (HOG),^[2,3] Profile Projection,^[2] Convolutional Neural Networks (CNN),^[4] Binarized Statistical Image Features (BSIF), Local Phase Quantization (LPQ) and Weber Local Descriptor (WLD),^[5] Scale-Invariant Feature Transform (SIFT).^[6] Each of these methods provides a distinct angle for capturing attributes present in signature images. However, they involve a complex algorithm and their effectiveness are significantly influenced by a range of parameters, which in turn can impact the accuracy of the recognition system.

In terms of classification, a diverse spectrum of techniques is put into action to effectively categorize and differentiate between patterns.^[6-8] The most used are: K-Nearest Neighbors (KNN),^[9,2] Neural Networks (NN),^[10] and Support Vector Machine (SVM),^[11] Fuzzy Min Max Classifier (FMMC).^[2,12] Each technique holds its own strengths and suitability for specific signature recognition scenarios.

The diversity and the complexity of features extraction and classification techniques gives rise to many stochastic optimization algorithms among them, genetic algorithms, genetic programming, differential evolution, evolution

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strategies, and evolutionary programming. Each method is suitable for the given problem.

Our study proposes an innovative approach to achieve the best accuracy for signature recognition. The proposed method involves implementing the Loci method for characterizing the images because of its simplicity and efficiency, it used particularly for patterns with strokes, especially in horizontal and vertical orientations. However, the drawback of this approach is its significant reliance on three hyperparameters: the degree of image division, the extent of zero padding and the restricted number of strokes. To overcome this constraint, a genetic algorithm^[12,13] is chosen as promoter model, it has been regarded as an effective way for tackling practical optimization challenges.^[14] It applied to select the most suitable hyperparameters values by exploring the search space. The AG maintain the diversity in population and avoid the solutions are being stuck in local optima while striving to maximize the fitness function. The effectiveness of genetic algorithm method is significantly impacted by the quality of the selected fitness function. As a result, the proposed fitness function is defined as the recognition rate, which is computed using the FMFC method. We used FMFC because of its computational efficiency and its robustness^[2] compared with other methods, such as KNN and NN.^[15] FMFC can handle noisy data and data with overlapping distributions efficiently, and can challenge both linear and non-linear classification problems.^[16] The functionality of the system is developed and executed within the MATLAB environment.

The present paper is planned as follows: section 2 describes a detailed explanation of the proposed methodology. The result of simulations and comparisons are presented and discussed in section 3. Conclusions are drawn in section 4.

2. Proposed methodology

The proposed structure for signature recognition uses four primary stages; preprocessing, features extraction, genetic algorithm and classification. Preprocessing is used to improve the image quality and decrease the processing time, then, Loci characteristics are used as features. The weakness of Loci is its high reliance on several parameters, the mediocre choice of these parameters values impairs the accuracy of recognition system. To select the suitable parameters values, a GA is employed with FMFC. The overall scheme of the proposed approach is exposed in Fig. 1.

2.1 Preprocessing

The preprocessing stage involves several steps. First, the input image of the signature, which is originally in color, is binarized.^[17] Next, the cropping step is performed, which aims to retain only the signature by removing any white space around it. The final step is normalization, where the size of the entire cropped signature image is adjusted to reduce the processing time.

2.2 Features extraction

A multitude of techniques have been employed and developed to capture distinct features present within the image to enhance the differentiation. These approaches encompass a wide spectrum of methodologies, ranging from traditional methods to more advanced techniques.

For this purpose, the Loci method is employed for its effectiveness and straightforwardness. It is a statistical approach involve examining the strokes, in horizontal and

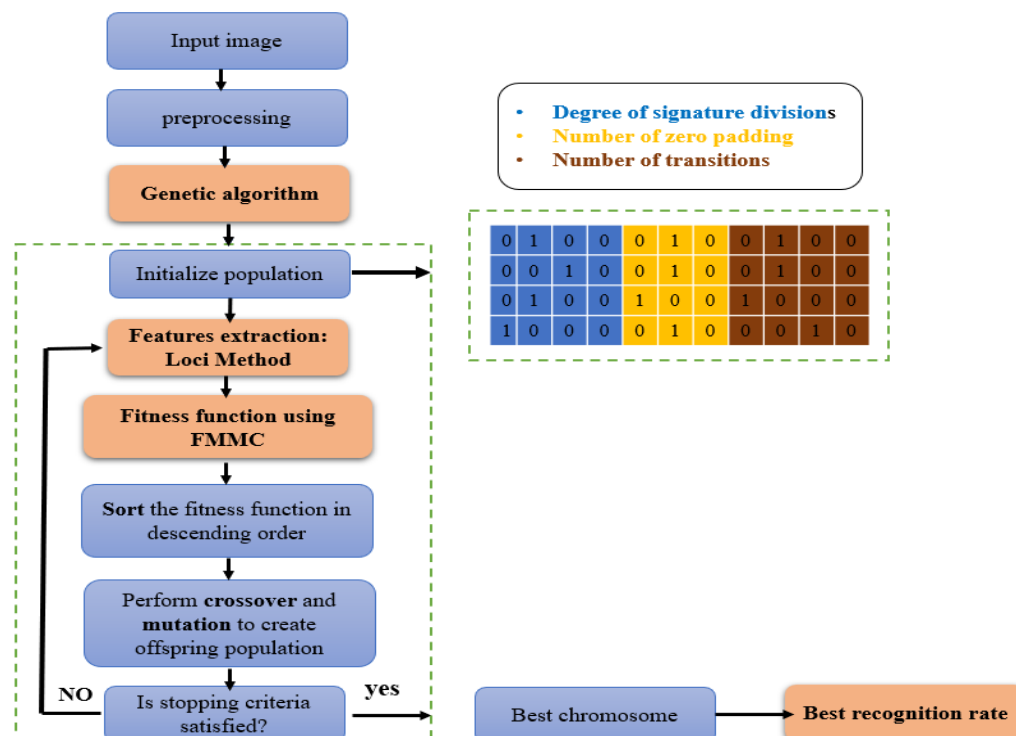


Fig. 1 Proposed structure for signature recognition.

vertical orientations relative to each background pixel. Each background pixel contributes to generating a Loci number, a four-digit numerical value, based on the transitions it encounters. An exploration of all the image background pixels is conducted, the total number of background pixels having the same Loci number constituted an element of an attribute vector.^[17] Fig. 2 presents an example of defining a Loci number of background pixel x for signature image.

The performance of the Loci method depends on three hyperparameters which are: the degree of image division, the extent of zero padding and the restraint number of strokes.

- The degree of image division determines how much an image is split. The final attribute vector is the combination of the attribute vector for each part of the image.
- The extent of zero padding involves creating a border of zeros around the image.
- The restraint number of strokes refers to a specific limitation on the number of transitions in various directions (up, left, down, and right).

Figure 3 presents the impact of each parameter on the image histogram.

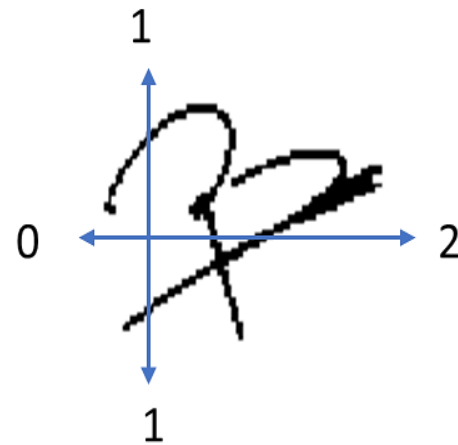


Fig. 2 The Loci number of background pixel x is (1,0,1,2).

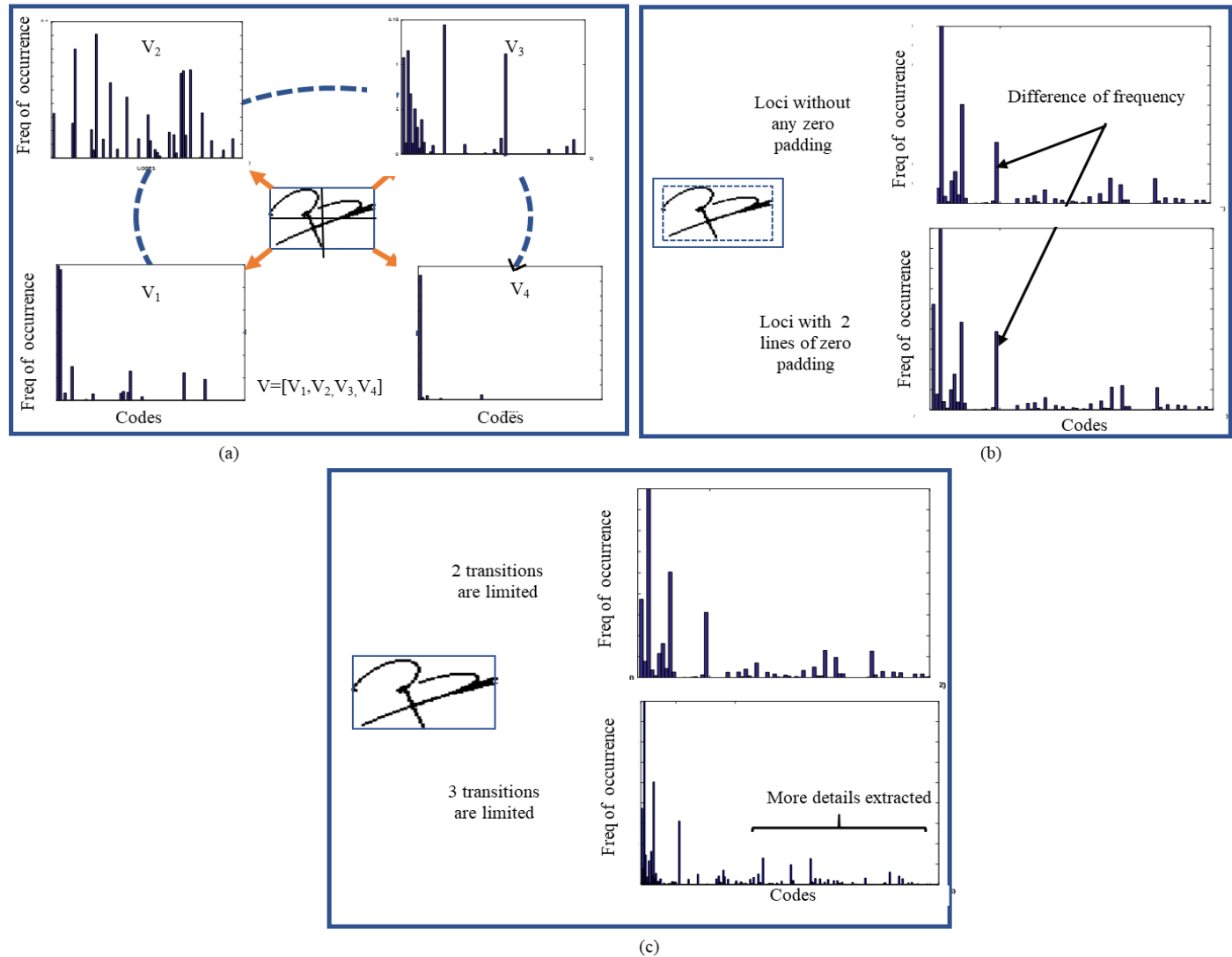


Fig. 3 (a): The histograms of each part of the divided image, (b): The difference of histogram between an image without any zero padding lines and the image with two zero padding lines, (c): The difference of histogram between an image with a limited number of transitions of 2 and the image with a limited number of transitions of 3.

The hyperparameters values notably impact the Loci method, thus directly affecting the outcome of the recognition process. As a result, it may require careful selection to achieve optimal results. For this purpose, a GA is used to explore different parts of the solution space.^[18]

2.3 Hyperparameters selection by a genetic algorithm

In recent years a rapid growth of work using GA is observed, because of its efficiency.^[18] The algorithm starts with a set of population which is randomly generated called as chromosomes. The chromosomes are associated a criterion function to be optimized,^[19,20] called fitness function. In a GA, a population of chromosomes undergoes in iterative process to evolve towards better solutions. Each chromosome represents a probable solution to the problem.^[21] The algorithm works by applying genetic operators; selection, crossover, and mutation to create new generations of solutions. The different steps of GA are shown in algorithm 1.

Algorithm 1^[13,14]: GA

- 1: Initialize: size of population, crossover and mutation probabilities.
 - 2: Assign number of iteration t to 0.
 - 3: Generate an initial population of chromosomes $P(t)$.
 - 4: Compute the fitness function of each chromosome in the population $P(t)$.
 - 5: **While** the stop criterion is not satisfied **do**
 - 6: $t=t+1$
 - 7: Sort the fitness function.
 - 8: Select individuals for reproduction to $P(t)$ from $P(t-1)$
 - 9: Create a new population through crossover and mutation.
 - 10: Calculate fitness in population $P(t)$.
 - 11: **End while**
 - 12: Return the best chromosome.
-

2.3.1 Generate an initial population of chromosomes:

Proposed coding

First of all, a population of chromosomes, with a maximum size of $maxpop$, is generated, and it comprises the variables to be optimized. The objective is to explore within this population of potential candidate solutions to uncover the global solution.

The proposed coding for each chromosome is:

$$chr = (g_i)_{1 \leq i \leq s} = (D \ P \ T) \text{ Where } D = (x_1 \dots x_n), P = (y_1 \dots y_m) \text{ and } T = (z_1 \dots z_k)$$

chr is a binary line matrix of s dimension. Each g_i gene codes the degree of signature division or the number of zero padding or the restraint number of transitions.

$D = (x_i, 1 \leq i \leq n)$ is the first part of chromosome chr , each gene x_i codes the degree of signature division. If $x_i=1$, the image is split into i equal parts vertically and horizontally.

$P = (y_i, 1 \leq i \leq m)$ is the second part of chromosome chr , each gene y_i codes the number of zero padding or the number of lines of background pixels. If $y_i=1$, the signature image is encountered by $i-1$ lines of background pixels.

$T = (z_i, 1 \leq i \leq k)$ is the last part of chromosome chr , each gene z_i codes the restraint number of black white transitions. If $z_i=1$, the number of black white transitions is limited to $i+1$.

chr may not be a possible solution unless if it satisfies the following condition:

$$\sum_1^n x_i = 1, \sum_1^m y_i = 1 \text{ and } \sum_1^k z_i = 1 \tag{1}$$

If the chromosome fails to satisfy the specified condition, it is discarded and regenerated iteratively until the condition is met. The structure of chromosome is illustrated in Fig. 4.

Subsequently, we create an initial population of chromosomes with a size of $maxpop$ employing the encoding method mentioned earlier, ensuring that the generated population satisfies the equation (1). For this purpose, we predefined the length of chromosome by establishing three specific factors:

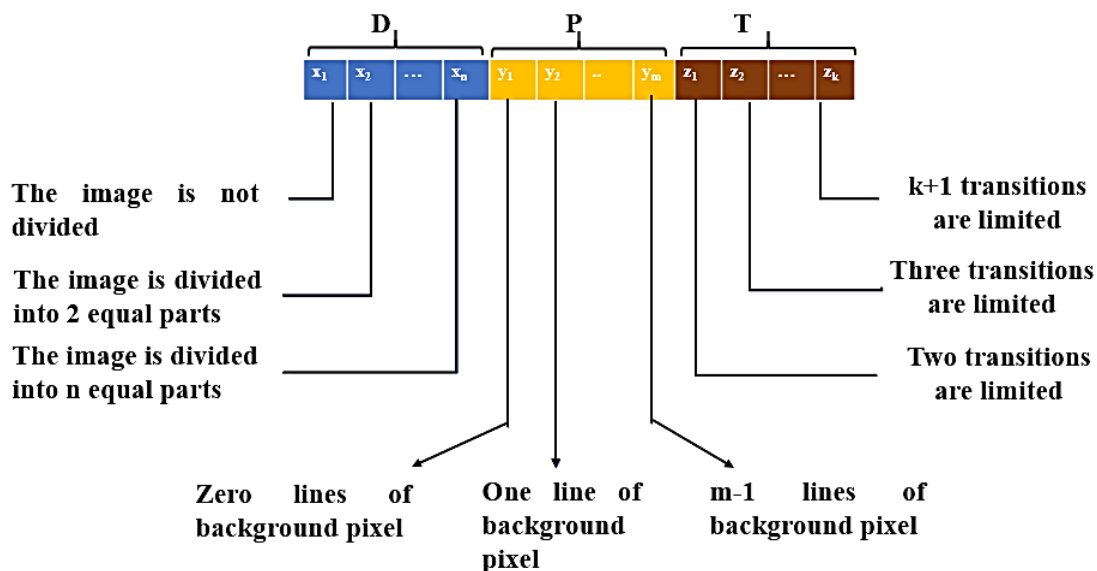


Fig. 4 Chromosome structure.

- The maximum degree of signature divisions which is intended to be set at 4, so the size of the first part of chromosome $\text{dim}(D)$ is 4. $D = (x_i, 1 \leq i \leq 4)$, this implies that the signature image can't be divided if $x_1=1$, or into two equal parts vertically or horizontally if $x_2=1$, or into three equal parts if $x_3=1$, or into four equal parts if $x_4=1$.

- The maximum number of zero padding, it is set to 2, so the size of the second part of chromosome $\text{Dim}(P)$ is 3. $P = (y_i, 1 \leq i \leq 3)$, the signature image is encountered by 0 lines of background pixels if $y_1=1$ or one line if $y_2=1$ or two lines if $y_3=1$.

- The maximum limited number of transitions, which is intended to be set at 5, then the size of the third part of chromosome is $\text{Dim}(T) = 4$. $T = (z_i, 1 \leq i \leq 4)$, the restraint number of transitions for each background pixel is limited to 2 if $z_1=1$ or 3 if $z_2=1$ or 4 if $z_3=1$ or 5 if $z_4=1$.

The chromosome chr should satisfy the following condition:

$$\sum_1^4 x_i = 1, \sum_1^3 y_i = 1 \text{ and } \sum_1^4 z_i = 1$$

As a result, the chromosome's dimension is $4 + 3 + 4 = 11$.

The chromosome $\text{chr} = 0010\ 010\ 0010$ implies that the image is divided into 3 equal parts vertically and horizontally, each part is cropped with one line of background pixels in the border and for each background pixel 4 transitions are limited. The Loci characteristics are then calculated for each part of the image and combined to form features vector.

The next step is to evaluate each chromosome by calculating the fitness function which corresponds to a recognition rate, using the FMMC.

2.3.2 Fitness evaluation: Proposed fitness function.

For each chromosome the fitness function is calculated which measures how well the individual solves the problem. The fitness function used in this approach is the recognition rate based on fuzzy min max classifier (FMMC). FMMC^[2,16] is a type of pattern recognition algorithm that belongs to the family of fuzzy logic-based classifiers. It has been utilized in various fields, including machine learning, data mining, and image processing. FMMC consists of generating and adjusting hyperboxes to accommodate patterns.^[16] When a new pattern is encountered, the classifier computes the fuzzy hyperbox membership function to evaluate if the pattern falls within an existing hyperbox or if a new hyperbox needs to be created to encompass the pattern.

The fuzzy hyperbox membership function of h^{th} object O_h = $(a_{h1}, a_{h2}, \dots, a_{hN})$ to a hyperbox b_j is defined as follows:

$$f_j(O_h) = \frac{1}{2N} \sum_{n=1}^N \left[\max \left(0, 1 - \max \left(0, \gamma \min(1, a_{hn} - w_{jn}) \right) \right) + \max \left(0, 1 - \max \left(0, \gamma \min(1, v_{jn} - a_{hn}) \right) \right) \right] \quad (2)$$

N is the dimension of the attribute vector.

$V_j = (v_{jn})_{1 \leq n \leq N}$, $W_j = (w_{jn})_{1 \leq n \leq N}$ are the min point and the max point of a hyperbox b_j .

γ is the sensitivity parameter that regulates how fast the

membership value decreases.^[2]

Hyperboxes generation occurs in an iterative manner using; expansion, overlapping, contraction; until their stability is achieved. The mechanism of FMMC is shown in algorithm 2.

Algorithm 2^[2]: FMMC

- 1: Initialize Sensitivity parameter γ , Vigilance parameter θ .
 - 2: Create the first prototype, $b_1(V_1, W_1)$, where $V_1=W_1=O_1(a_{11}, \dots, a_{1N})$.
 - 3: **While** the hyperboxes are not stabilized **do**
 - 4: Select a new object (O_h, C_h) from the training samples. C_h is the class assigned to O_h .
 - 5: Find the hyperbox that shares the same class as object O_h with the highest $f_j(O_h)$.
 - 6: **If** such a hyperbox is not found, a new hyperbox is added to the neural network.
 - 7: **ELSE**, continue as follows:
 - 8: Expand the prototype b_j to b_j^* where $v_{jn}^* = \min(v_{jn}, a_{hn})$, $w_{jn}^* = \max(w_{jn}, a_{hn})$ $1 \leq n \leq N$.
 - 9: Compute the hyperbox size $T(b_j^*)$, $T(b_j^*) = \frac{1}{N} \left(\sum_{n=1}^N (w_{jn}^* - v_{jn}^*) \right)$
 - 10: Test for hyperbox overlap :
 - 11: **If** $T > \theta$, a new hyperbox is produced.
 - 12: **ELSE** retain the hyperbox b_j^* and check for any overlap with hyperboxes of different classes.
 - 13: Contract b_j^* if an overlap is detected between b_j^* and an hyperbox of different class.
 - 14: **End While**
 - 15: **Return** Hyperboxes classes C .
-

In the testing phase, the fuzzy hyperbox membership function for an unknown object is computed using all the generated hyperboxes. The object class is then assigned based on the hyperbox with the highest membership function. Then the recognition rate (RR) is calculated as follows:

$$RR = \frac{\text{the correctly classified images}}{\text{All templets in Database}} * 100 \quad (3)$$

Once the fitness function is calculated for all chromosomes, these fitness values are sorted in descending order, then the genetic operators are systematically applied iteratively with specific probabilities until the stopped criterium is satisfied.

2.3.3 Genetic operators

At each iteration, a new population of chromosomes is generated using genetic operators, selection, crossover and mutation.

Selection: The chromosomes are selected from the present population to serve as parents for the next generation. Selection is often based on chromosome recognition rate, giving higher recognition rate individuals a higher chance of being selected.^[11] In this study, the utilization of the elitist

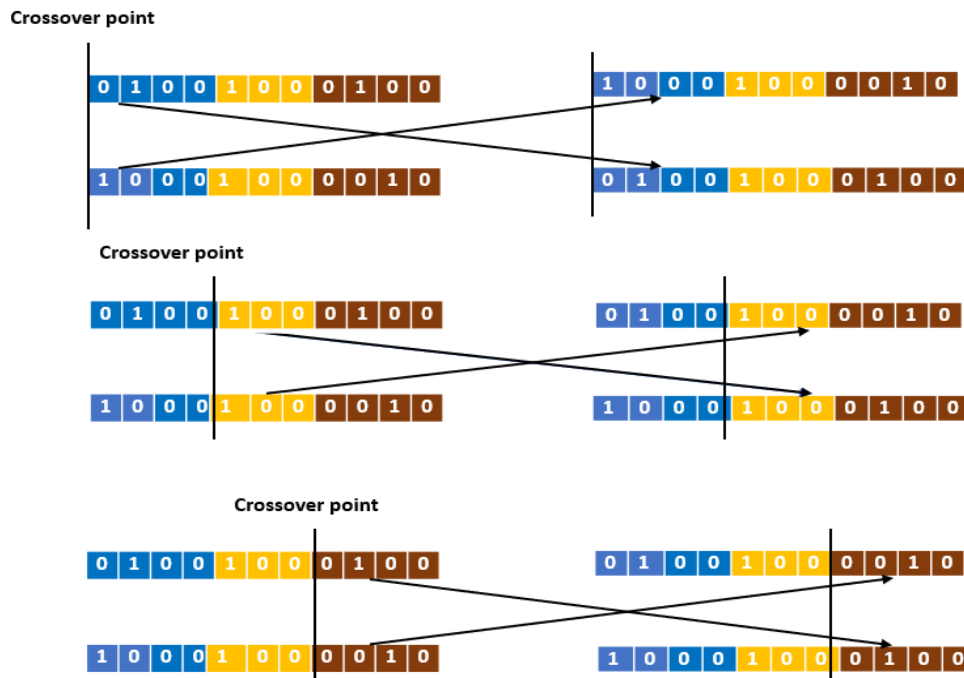


Fig. 5 Crossover operator.

strategy has proven to be highly effective in discovering global optimum solutions.^[18] The selection strategy adopted in our system consists of retaining the initial maxpop-2 individuals for use in the upcoming generation.

Crossover: It applied with a certain probability; it consists of interchanging distinct portions of chromosome between parent individuals, resulting two offspring. The proposed crossover consists of replacing the last two chromosomes in the population with the first two chromosomes of the population after crossover.

The single point crossover, must be chosen either from the first gene of the first part of the chromosome, or from the first gene of the second part of the chromosome, or from the first gene of the last part of the chromosome, this choice is necessary to satisfy the previous condition mentioned in equation (1). The strategy of crossover operator is shown in Fig. 5.

Mutation: It introduces minor random variations to the genetic information of the offspring. This adds diversity to the population and helps explore different parts of the solution space that might not be immediately apparent. In this paper, the proposed mutation strategy consists of choosing randomly one gene within an individual's chromosome with a specified probability and assigning it a value of 1. If the chosen gene resides in the initial part of the chromosome, the corresponding genes within that same part must be set to a value of 0 to adhere to the previous condition. The probability of mutation is a vital parameter to consider. If the mutation probability is too low, there might not be enough exploration, and the algorithm might converge quickly. Conversely, if the mutation probability is too high, there's a risk of losing good solutions that have already been found. The Fig. 6 presents the strategy of mutation operator.

Figure 7 presents the process of creating the current

population.

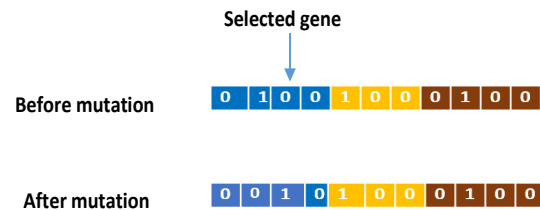


Fig. 6 Mutation operator.

3. Results and discussions

3.1 Experimental results

The proposed methodology utilized a database provided by our laboratory because with this type of data, no international database is offered due to the privacy problems. The data base comprises 240 signatures.^[2] These signatures were amassed from a collective of 12 individuals, with each person contributing 20 signatures. For system training, a subset of 120 signatures was chosen, leaving the remaining signatures for testing purposes.

Table 1 defines the initial predefined parameters; population size, chromosome dimension, maximum number of iterations, crossover probability, mutation probability.

Table 1. The predefined parameters for genetic algorithm.

Parameters	Values
Population size	4
Chromosome dimension	11
Number of iterations	4
Crossover probability	0.9
Mutation probability	0.4

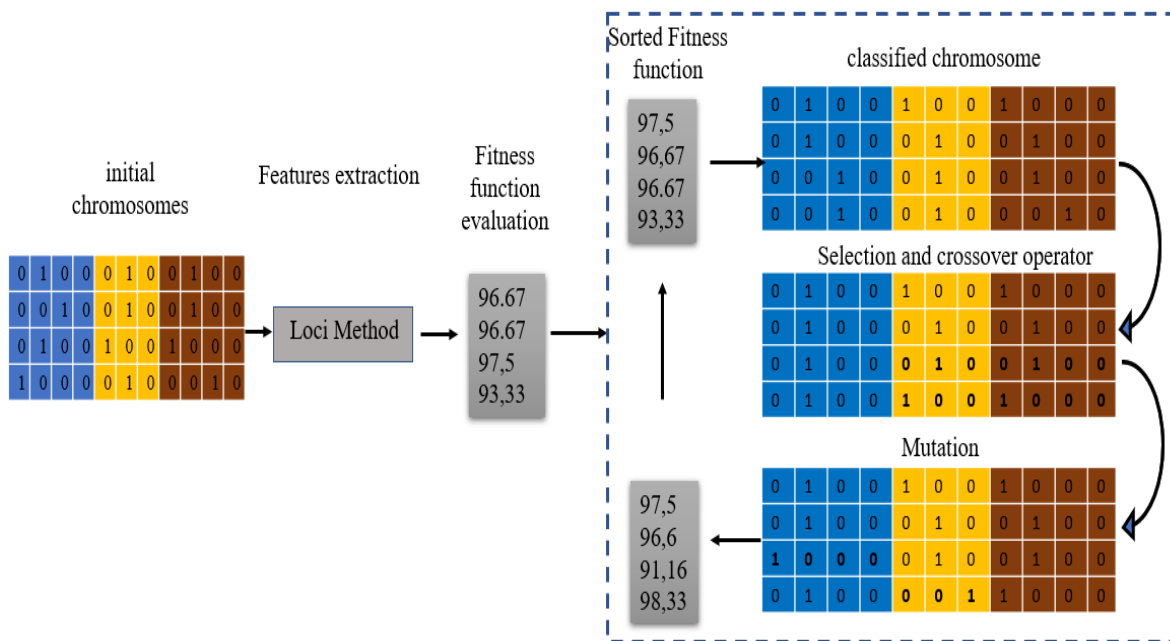


Fig. 7 The process of creating the current population.

Several experimentations are provided using different normalization sizes, Fig. 8 illustrates the evolution of the fitness function or recognition rate of the best chromosome of the current population, obtained by the genetic algorithm across multiple iterations.

From Fig. 8 it demonstrates that with fewer iterations and small population size, the value of the fitness function stabilizes. The optimal recognition rate is achieved by the best chromosome, denoted as 0100 010 0010. This implies that a favorable outcome is reached when the image is partitioned into 2 parts vertically and horizontally, with a single line of zero pixels encircling the edge of each part of the image and a maximum of four transitions is allowed for each background pixel.

Table 2 presents the fitness function values obtained by the best chromosome with the respect of normalization size.

Table 2. Fitness function with the respect of normalization size.

Normalization size	Fitness function
40*40	97.5%
40*60	97.5%
100*60	97.5%
100*80	98.33%
100*100	99.16%
.....
100*160	99.16%
100*180	99.16%
200*200	99.16%

From Table 2, we notice as the image dimensions increase from 40x40 to 200x200, the recognition accuracy of the system consistently improves, reaching a peak accuracy of 99.16%. This can be attributed to the fact that larger image sizes offer more information and detail, which makes it easier

for the system to accurately identify person signatures. Conversely, when the image size is reduced, it undergoes a process of compression, which results in a loss of detail and quality. This degradation in image quality can have an effect on recognition system.

3.2 Comparative study

To compare the results of the proposed algorithm with existing signature recognition techniques, Table 3 displays the outcomes achieved by the proposed model with state-of-the-art methods. From Table 3, the proposed system outperforms all described systems.

Table 3. Recognition and error rates of signature images using different systems.

Signature recognition systems	Recognition rate	Error rate
Features type	Classifier	
HOG ^[2]	FMMC	96%
	KNN	95%
Profile	FMMC	78.5%
	KNN	79%
Projection ^[2]	MLP	78%
	FMMC	78%
CNN	FMMC	96.6%
	KNN	96.6%
Traditional Loci	FMMC	93%
	KNN	88%
Proposed system		99.16%
		0.84%

The HOG model involves dividing the image into small cells and computing the gradient magnitude and orientation for each pixel in an image and then normalizing these histograms to create a robust feature descriptor for object

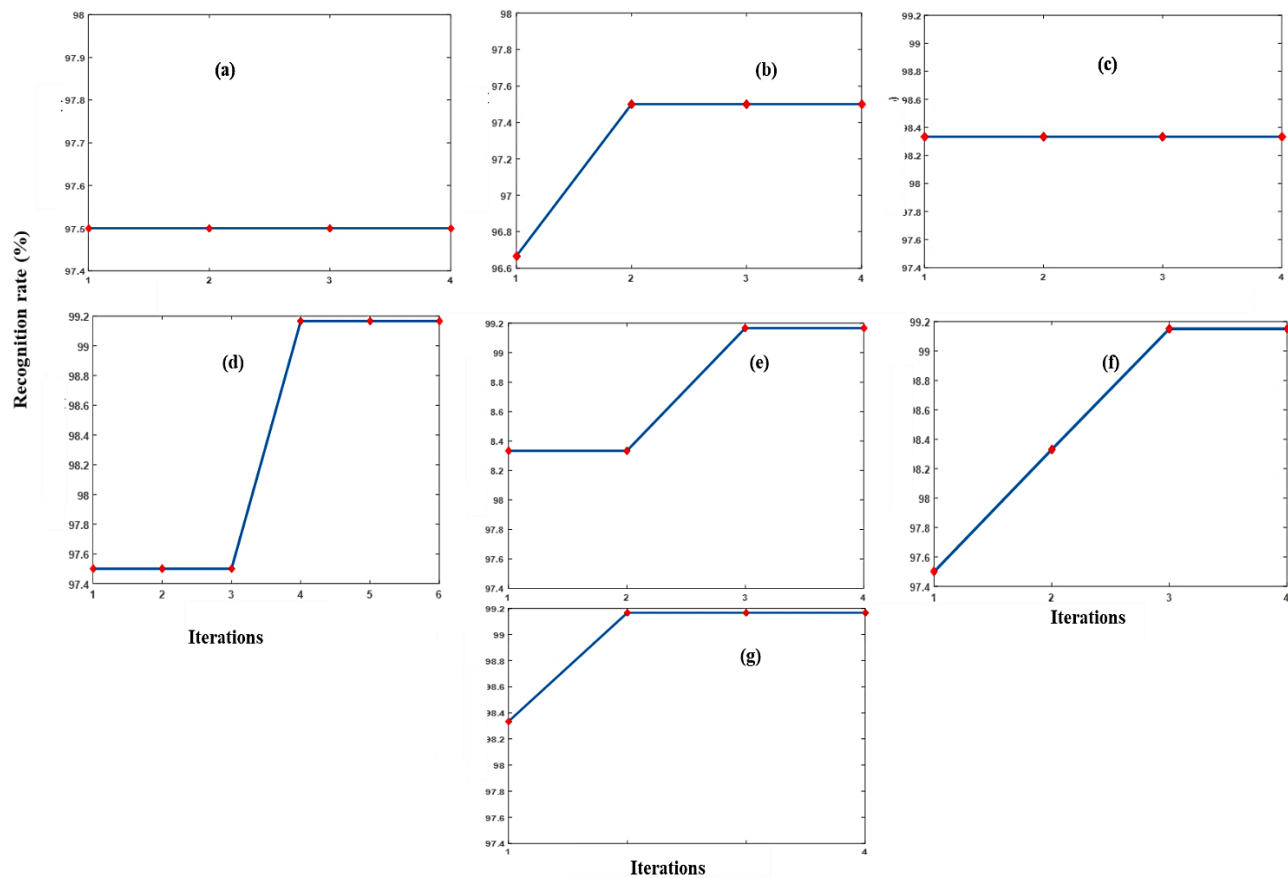


Fig. 8 The evolution of the fitness function with the respect of iterations for different normalization sizes. (a):40*40, (b):100*60, (c):100*80, (d):100*100, (e): 100*160, (f): 100*180, (g): 200*200.

detection and recognition tasks. The HOG approach heavily depends on several parameter settings,^[22] optimizing these parameters for achieving good accuracy 96% or 95%, requires numerous experiments, which can be time-consuming.

The profile projection method involves scanning along a specific direction or axis in an image, calculating the sum of background pixels until the first foreground pixel is encountered. The profile projection yielded a lower level of accuracy compared to other methods. This outcome may be attributed to potential limitations in the feature extraction process, which might have led to the omission of essential information.

The CNN uses convolutional layers to automatically learn and extract hierarchical features from visual data. Through a hierarchical arrangement of layers, they progressively capture more complex patterns, making them highly effective for image recognition. The CNN attained also a lower recognition rate, it is equal 78%, which can be attributed to the use of a multilayer perceptron (MLP) as classifier. The MLP could have had a significant impact on the CNN performance, due to its reliance on predetermined parameters, including; random weight initialization, learning rate, learning algorithm, and the number of hidden layer neuron. When MLP is replaced by FMMC and KNN the CNN performance increase but, it is still complicated by the large number of hyperparameters, and requires significant effort, expertise and time consuming.^[23,24]

The traditional Loci method combined with FMMC achieved a recognition rate of 93%. This outcome highlights that when extracting Loci characteristics from images without including any additional background pixels and imposing a maximum limit of two transitions, the method efficiency declines especially when it is combined with KNN.

The proposed system achieved an impressive accuracy of 99.16%, and an error rate 0.84%, it outperformed the other methods. The system demonstrates the potential of GA to refine the Loci method performance by fine-tuning hyperparameters for optimal results. Furthermore, it underscores the effectiveness of integrating fuzzy logic^[25] as classifier method to compute the fitness function.

4. Conclusion

The current paper has introduced an innovative approach for enhancing signature recognition accuracy by combining the Loci method, Fuzzy min max classifier (FMMC), and Genetic algorithm (GA). Additionally, it successfully addressed the prevalent issue of hyperparameter tuning, which is a common challenge in many machine learning applications.

The Loci method is used for signature characterization, to capture strokes in both horizontal and vertical orientation. However, the notable challenge of this technique is its significant reliance on multiple hyperparameters, including the degree of image division, the extent of zero padding, and

the restraint number of transitions. To overcome this challenge, a GA is implemented using diverse operators with distinct strategies. It applied to select the most suitable hyperparameters values by exploring the search space, while striving to maximize the fitness function. The proposed fitness function is defined as the recognition rate, computed using the FMCC method.

Our proposed system is compared with different efficient systems, and it performed an impressive accuracy of 99.16%. This outcome highlights the effectiveness of both the feature extraction process of Loci method and the learning mechanism of the FMCC. Moreover, it emphasizes the crucial role of optimal parameter tuning using the GA in achieving this high recognition rate.

Conflict of Interest

There is no conflict of interest.

Supporting Information

Not applicable.

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