

Towards an Evolution Strategy Approach in Binary Image Registration for Solving Digital Signature Recognition Tasks

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Abstract: This paper focuses on the development of an image registration methodology for digital signature recognition. We consider two perturbation models, namely the rigid transformation and a mixture of shear and rigid deformation. The proposed methodology involves three stages. In the first stage, both the acquired image and the stored one are binarized to reduce the computational effort. Then an evolution strategy (ES) is applied to register the obtained binary images. The quality of each chromosome belonging to a certain population is evaluated in terms of mutual information-based fitness function. In order to speed up the computation of fitness values, we propose a computation strategy based on the binary representation of images and the sparsity of the image matrices. Finally, we evaluate the registration capabilities of the proposed methodology by means of quantitative measures as well as qualitative indicators. The experimental results and some conclusions concerning the capabilities of various methods derived from the proposed methodology are reported in the final section of the paper.

1 INTRODUCTION

Digital image registration is one of the most important tasks in various systems which evaluate images, including sensed image recognition, global land monitoring in satellite images, aligning medical images. The main aim of any registration technique is to align images acquired at different times, using different sensors and from different viewpoints. In the following we adopt the assumption that the variations in the analysed images are due to the acquisition system and can be removed by applying various geometric transformations (Goshtasby, 2012; Modersitzki, 2004).

The most studied perturbation models involves spatial transformations of rigid, affine, projective, and respectively global polynomial type. In our work we consider two perturbation model, the rigid one and the affine transformation. The rigid transformation is described in terms of translation, rotation, and scale changes. The affine transformation is more general than the rigid one and is expressed as a mixture of rigid, shear and aspect ratio changes.

So far, various classes of registration techniques, mainly depending on the perturbation model, have

been presented in the literature (Goshtasby, 2012; Zhuang et al., 2016; Yang, Papa, 2017). One of the most popular classes of registration techniques is the optimization-based class that includes, besides direct optimization methods, evolutionary-based approaches (Zhang, Wu, 2012; Khader, Hamza, 2012; Mohamed, Hamza 2010; Singhai, Singhai, 2012). The evolutionary approaches of image registration are developed based on certain similarity measure corresponding to the fitness function. The methods involve heuristic search through the registration parameter values space to compute the variant maximizing the fitness function.

Our research work focuses on the development of an image registration methodology for digital signature recognition. More precisely, we address the problem of a particular component of banking security systems using the client's signature. In order to process payments, the system should recognize the client signature prior to finalizing the operation. The process mainly consists of the following steps: scan the payment order, identify the client's signature and compare it with its corresponding stored version. In most of the cases the sensed signature is different from the stored one from the geometrical point of view. We restrict the problem to two perturbation models, namely the

rigid transformation and a mixture of shear and rigid deformation. The second model is considered in order to suggest a viable methodology to register images disturbed by affine transformations. The proposed methodology involves three stages. To reduce the computational complexity, in the first stage, binary versions of both the acquired image and the stored one are computed. Then an evolution strategy (ES) is applied to register the obtained binary images. The quality of each chromosome belonging to a certain population is evaluated in terms of mutual information-based fitness function. The recombination schemes developed to compute offspring populations involve standard local or global convex and respectively discrete crossover procedures as well as new hybrid methods. The proposed hybrid approaches are set out taking into account the geometric relationship between the chromosome alleles. The mutation operator is of uncorrelated multistep sizes type. Also, we propose a computation strategy based on the binary representation of images and the sparsity of the image matrices to speed up the computation of fitness values. Finally, we evaluate the registration capabilities of the proposed methodology by means of quantitative measures as well as qualitative indicators.

Note that the proposed methodologies can be used to register any binary images represented by sparse matrices.

The rest of the paper is organized as follows: in Section 2 we briefly present the affine spatial transformations. The main characteristics of the evolution strategies (ES) based on uncorrelated multiple parameters mutation are provided in Section 3. The proposed registration methodology is described in the fourth section of the paper. The obtained results and some experimentally established conclusions are supplied in the final part of the paper.

2 AFFINE SPATIAL TRANSFORMATIONS

The rigid transformation is described in terms of translation, rotation, and scale changes. Its main property is that the objects in images hold their relative shape and dimensions.

The general affine transformations consist of more general geometric distortions and they are linear in the sense that straight lines are mapped into straight lines. (Brown, 1992)

The 2D rigid transformation having as inputs the image I_1 and the parameters (a, b, s, θ) produces the output I_2 defined by

$$I_2(x, y) = I_1(x_1, y_1) \quad (1)$$

$$\begin{pmatrix} x_1 \\ y_1 \end{pmatrix} = \begin{pmatrix} a \\ b \end{pmatrix} + s \begin{pmatrix} \cos \theta & -\sin \theta \\ \sin \theta & \cos \theta \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} \quad (2)$$

where $\begin{pmatrix} a \\ b \end{pmatrix}$ defines the translation, s stands for the scale factor and $R = \begin{pmatrix} \cos \theta & -\sin \theta \\ \sin \theta & \cos \theta \end{pmatrix}$ is the rotation matrix.

A 2D affine transformation characterised by the parameters $A = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix}$ and $b = \begin{pmatrix} b_1 \\ b_2 \end{pmatrix}$ maps the input image I_1 into image I_2 such that

$$I_2(x, y) = I_1(x_1, y_1) \quad (3)$$

$$\begin{pmatrix} x_1 \\ y_1 \end{pmatrix} = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} b_1 \\ b_2 \end{pmatrix} \quad (4)$$

Besides the rigid spatial transformations, the affine transformations consist of shear effect acting along axes and changes in aspect ratio, as follows:

- shear along Ox and Oy respectively, defined by

$$F_x = \begin{pmatrix} 1 & d \\ 0 & 1 \end{pmatrix}, F_y = \begin{pmatrix} 1 & 0 \\ h & 1 \end{pmatrix} \quad (5)$$

- changes in aspect ratio, given by the matrix

$$S = \begin{pmatrix} s_x & 0 \\ 0 & s_y \end{pmatrix} \quad (6)$$

As we have mentioned before, the affine transformations are obtained by applying any sequence of rigid transformations, shears and changes in aspect ratio. (Brown, 1992)

3 EVOLUTION STRATEGIES

Evolution strategies belong to evolutionary algorithms class, being typically used for continuous parameter optimization problems (Eiben, Smith, 2003). One of the most important characteristics of ES is self-adaptability, a mechanism that adjusts the mutation strategy as the search is progressing by updating certain EA parameters during the evolution process (Edelkamp, Schrodler, 2012).

Self-adaptation involves the fact that some parameters are included in the chromosome representation, therefore the computation process updates them too. If the phenotype space is \mathbb{R}^n then in a typical ES the chromosome representation is

straightforward, each individual $x \in \mathbb{R}^n$ being given by its variables $x_1, \dots, x_n \in \mathbb{R}$. In case of self-adaptability, $x = (x_1, \dots, x_n)$ is only part of a genotype. If we consider the standard uncorrelated multistep mutation, each chromosome encoding a candidate solution $x = (x_1, \dots, x_n)$ is defined in terms of a solution part, c_{sol} , and a parameter part, c_{step_size} as follows (Eiben, Smith, 2003)

$$c = \left(\underbrace{x_1, \dots, x_n}_{c_{sol}}, \underbrace{\sigma_1, \dots, \sigma_n}_{c_{step_size}} \right) \quad (7)$$

ES methods usually use fixed size population model. In ES the whole population produces offspring. The offspring population should be significantly larger than the current multiset. The recommended size of offspring population is $\lambda \cong 7 \cdot \mu$, where μ denotes the population size. The recombination is either local or global. In case of local recombination each child is computed based on a single pair of parents. The global crossover involves more general computation scheme. Each allele of a child is calculated using pair of parents randomly drawn from the current population. The procedures that implements the computation of an allele is either discrete or convex with a certain random weight $\alpha \in (0,1)$. (Beyer, 2001; Eiben, Smith, 2003)

The uncorrelated mutation with multiple step sizes is developed such that the dimensions are treated differently. In other words, different solution alleles are affected by different white noises. The mutated version of a chromosome $c = (x_1, \dots, x_n, \sigma_1, \dots, \sigma_n)$ is the genotype $c' = (x'_1, \dots, x'_n, \sigma'_1, \dots, \sigma'_n)$ computed as follows. First, mutate the parameter variables of c based on the relation

$$\sigma'_i = \sigma \cdot \exp\{r_{\tau,i} + r_{\tau'}\} \quad (8)$$

where $r_{\tau'}$ denotes a draw from the distribution $N(0, \tau')$, $r_{\tau,i}$ is a distinct draw from the distribution $N(0, \tau)$ for each $1 \leq i \leq n$. The most commonly used settings of the parameters τ and τ' are

$$\tau \propto \frac{1}{\sqrt{2 \cdot \sqrt{n}}} \quad (9)$$

$$\tau' \propto \frac{1}{\sqrt{2 \cdot n}} \quad (10)$$

Next update the solution alleles of c using the relation

$$x'_i = x_i + f_{x_i} \quad (11)$$

where f_{x_i} is a separate draw from $N(0, \sigma'_i)$ for each $1 \leq i \leq n$. Finally, one can apply the rule

$$\text{if } \sigma'_i < \varepsilon_\sigma \text{ then } \sigma'_i \leftarrow \varepsilon_\sigma$$

to avoid the use of very small step sizes.

The survivor selection is deterministic, the most commonly used schemes being (μ, λ) and $(\mu + \lambda)$ (Eiben, Smith, 2003).

4 THE PROPOSED ES REGISTRATION METHODOLOGY

Taking into account the characteristics of the processed images, i.e. digital signatures, the proposed methodology is developed using binary images. Let I be a $M \times N$ gray scale image. The binary variant of I , BI , is computed using a threshold function as follows

$$BI(x,y) = \begin{cases} 1, & I(x,y) > 127 \\ 0, & \text{otherwise} \end{cases} \quad (12)$$

We consider that the pixel (x,y) is of background type if $BI(x,y)=1$, otherwise it belongs to one of the objects represented in image I .

The following ES-based method solves the alignment problem of two binary images, the target T and the sensed image I .

Two different perturbation models are addressed in our approach. The first degradation model is defined in terms of rigid transformation only. Thus the observed image I is given by

$$I(x,y) = T \left(\left(f_0(x,y) \right)^T \right) \quad (13)$$

where for each $1 \leq x \leq M$ and $1 \leq y \leq N$

$$f_0(x,y) = \begin{pmatrix} a \\ b \end{pmatrix} + s \cdot \begin{pmatrix} \cos\theta & -\sin\theta \\ \sin\theta & \cos\theta \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} \quad (14)$$

The second perturbation model is a sequence of a shear transformation, acting along the x axis, and respectively a rigid function. We consider this second model to explain how the registration methodology in case of rigid perturbation can be extended to the more general case of affine transformation. Note that the affine degradation is a mixture of rigid, shear and aspect ratio changes, each one of these being added to the first model accordingly.

The function that expresses the above mentioned degradation process is defined by

$$f_1(x,y) = \begin{pmatrix} 1 & d \\ 0 & 1 \end{pmatrix} \cdot f_0(x,y) \tag{15}$$

and the sensed image I is computed as

$$I(x,y) = T \left(\left(f_1(x,y) \right)^T \right) \tag{16}$$

In order to solve the registration problem, one has to compute a function $f(x,y)$ such that $I \left(\left(f(x,y) \right)^T \right) = T(x,y)$. Note that $R^{-1} = R^T$, i.e. the rotation matrix is orthogonal. In case of rigid transformation the function f is defined in terms of parameters (a,b,s,θ) by

$$f_{a,b,s,\theta}(x,y) = \frac{1}{s} \cdot R^T \cdot \left[\begin{pmatrix} x \\ y \end{pmatrix} - \begin{pmatrix} a \\ b \end{pmatrix} \right] \tag{17}$$

If we consider the second model, the function f is expressed using the parameters (d,a,b,s,θ) by

$$f_{d,a,b,s,\theta}(x,y) = \frac{1}{s} \cdot R^T \cdot \left[\begin{pmatrix} 1 & -d \\ 0 & 1 \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} - \begin{pmatrix} a \\ b \end{pmatrix} \right] \tag{18}$$

Based on the uncorrelated multistep sizes mutation idea, we design an evolution strategy in which the solution sequence of an individual is either $c_{sol} = (a_c, b_c, s_c, \theta_c)$ or $c_{sol} = (d_c, a_c, b_c, s_c, \theta_c)$.

The genotype space consists of vectors c described by

$$c = \left(\underbrace{a_c, b_c, s_c, \theta_c}_{c_{sol}}, \underbrace{\sigma_{a_c}, \sigma_{b_c}, \sigma_{s_c}, \sigma_{\theta_c}}_{c_{step_size}} \right) \tag{19}$$

in case of model (14) and respectively by

$$c = \left(\underbrace{d_c, a_c, b_c, s_c, \theta_c}_{c_{sol}}, \underbrace{\sigma_{d_c}, \sigma_{a_c}, \sigma_{b_c}, \sigma_{s_c}, \sigma_{\theta_c}}_{c_{step_size}} \right) \tag{20}$$

in case of the degradation model (15). The parameters $\sigma_{d_c}, \sigma_{a_c}, \sigma_{b_c}, \sigma_{s_c}, \sigma_{\theta_c}$ stand for the step sizes corresponding to the solution alleles. We adopt the fixed size population model and we denote by μ the population size.

One of the most important components of an ES is represented by the fitness function. From the evolutionary computing point of view, the role of the fitness function corresponds to the requirements each genotype should adapt to. From the mathematical point of view, the fitness function is an objective function to be maximized. In our work the fitness value of each chromosome c representing the similarity between the target image T and the computed variant $I_c = I \left(f_{d_c, a_c, b_c, s_c, \theta_c} \right)$ is expressed in terms of MI (Mutual Information) measure.

In the following we denote by \mathcal{J} the space of images having the same sizes N and M , and L gray levels. Let $I_1, I_2 \in \mathcal{J}$. The mutual information $MI(I_1, I_2)$ is defined in terms of Shannon entropy $H(\cdot)$ and joint entropy $H(\cdot, \cdot)$ by (Cover, Thomas, 2006)

$$MI(I_1, I_2) = H(I_1) + H(I_2) - H(I_1, I_2) \tag{21}$$

where

$$H(I) = - \sum_{i=1}^L p_i \cdot \log(p_i) \tag{22}$$

$$H(I_1, I_2) = - \sum_{1 \leq i,j \leq L} p(i,j) \cdot \log(p(i,j)) \tag{23}$$

Obviously,

$$\max_{J \in \mathcal{J}} MI(I, J) = MI(I, I) = H(I) \tag{24}$$

The fitness function of a chromosome c is given by

$$\text{fitness}(c) = \frac{MI(T, I_c)}{MI(T, T)} = \frac{MI(T, I_c)}{H(T)} \tag{25}$$

Using (24) and (25) we get that the maximum fitness value is 1 and it can be obtained when $I_c = T$.

The recombination procedure enables self-adaptability of the resulted ES method. Let us denote by \mathcal{P}_t the current population and let k be a constant, $k > 1$. The offspring population \mathcal{O}_t having $\lambda = k \cdot \mu$ individuals is computed using either local or global procedures described in Section 3, or hybrid crossover mechanisms. The standard crossover is usually used when $k \leq 1$, for example by genetic algorithms. Typically, ES uses global recombination strategies, but in case of very complex problems these approaches could lead to intractable algorithms. Thus we propose various hybrid recombination methods to find a trade-off between the quality of the results and the computational complexity.

The proposed hybrid approaches are set out taking into account the geometric relationship between the chromosome alleles.

In case of the degradation model (14), two hybrid recombination strategies can be considered. The parameters are divided:

- into two groups: the translation variables set and the rotation and scale factors – strategy RHYB1;
- into three classes: translation variables, scale factor and rotation angle – procedure RHYB2;

In case of the degradation model (15), the most natural ways to divide parameters are:

- into two classes, each group corresponding to one of the perturbation transformations, share and rigid respectively – strategy SRHYB1;
- into three classes: share factor, translation variables, and rotation and scale factors– strategy SRHYB2;
- into four groups: share factor, translation variables, rotation angle and scale factor– strategy SRHYB3.

The corresponding crossover procedure SRHYB1 is presented below.

SRHYB 1

for $i=1 \dots \lambda$ c results as follows

- randomly select $p1, q1 \in \mathcal{P}_T$ and compute

$$(d_c, \sigma_{d_c}) \leftarrow \text{crossover between } (d_{p1}, \sigma_{d_{p1}}) \text{ and } (d_{q1}, \sigma_{d_{q1}})$$

- randomly select $p2, q2 \in \mathcal{P}_T$ and compute

$$(a_c, b_c, s_c, \theta_c, \sigma_{a_c}, \sigma_{b_c}, \sigma_{s_c}, \sigma_{\theta_c}) \leftarrow \text{crossover between } (a_{p2}, b_{p2}, s_{p2}, \theta_{p2}, \sigma_{a_{p2}}, \sigma_{b_{p2}}, \sigma_{s_{p2}}, \sigma_{\theta_{p2}}) \text{ and } (a_{q2}, b_{q2}, s_{q2}, \theta_{q2}, \sigma_{a_{q2}}, \sigma_{b_{q2}}, \sigma_{s_{q2}}, \sigma_{\theta_{q2}})$$

- $c = (d_c, a_c, b_c, s_c, \theta_c, \sigma_{d_c}, \sigma_{a_c}, \sigma_{b_c}, \sigma_{s_c}, \sigma_{\theta_c})$

The proposed hybridization techniques perform the recombination taking into account the grouping strategy, similarly to procedure SRHYB1. The survivor selection mechanism is applied in a deterministic manner to obtain the next generation, \mathcal{P}_{t+1} .

In the following we consider only the degradation model (15), because of its generality. From the implementation point of view, in case of fitness function defined by (25), each chromosome $c = (d_c, a_c, b_c, s_c, \theta_c, \sigma_{d_c}, \sigma_{a_c}, \sigma_{b_c}, \sigma_{s_c}, \sigma_{\theta_c})$ is evaluated based on the procedure FITNESS as follows.

FITNESS(c)

$$F = \frac{1}{s_c} \cdot R_c^T$$

$$A = F \cdot \begin{pmatrix} 1 & -d_c \\ 0 & 1 \end{pmatrix}; B = -F \cdot \begin{pmatrix} a_c \\ b_c \end{pmatrix}$$

for $i=1 \dots M$

for $j=1 \dots N$

$$\begin{pmatrix} x \\ y \end{pmatrix} = A \cdot \begin{pmatrix} i \\ j \end{pmatrix} + B$$

$$I_c(i, j) = T(x, y)$$

$$\text{Compute } \frac{MI(T, I_c)}{H(T)}$$

Next we intend to speed up the computation of FITNESS(c) by proposing an alternative procedure based on the binary representation of images and the sparsity of the image matrices. For a given chromosome c we compute a new image I_c^{new} by

$$I_c^{new}(x, y) = T\left(\left(f_1(x, y)\right)^T\right) = T(x_T, y_T) \quad (26)$$

where

$$\begin{pmatrix} x_T \\ y_T \end{pmatrix} = \begin{pmatrix} 1 & d_c \\ 0 & 1 \end{pmatrix} \cdot \left[\begin{pmatrix} a_c \\ b_c \end{pmatrix} + s_c \cdot R_c \begin{pmatrix} x \\ y \end{pmatrix} \right] \quad (27)$$

Obviously, $MI(I_c^{new}, I) = 1$ if $I = I_c^{new}$. Let $\mathcal{O}(T)$ be the set of object pixels belonging to T . We get that $|\mathcal{O}(T)| \ll N \cdot M$. The image corresponding to c is computed using the following procedure.

Step1. $I_c^{new}(x, y) \leftarrow -1, 1 \leq x \leq M, 1 \leq y \leq N$

Step 2. $I_c^{new}(x, y) \leftarrow 0$ for all (x, y) such that $(x_T, y_T) \in \mathcal{O}(T)$

where

$$\begin{pmatrix} x_T \\ y_T \end{pmatrix} = \begin{pmatrix} 1 & d_c \\ 0 & 1 \end{pmatrix} \cdot \left[\begin{pmatrix} a_c \\ b_c \end{pmatrix} + s_c \cdot R_c \begin{pmatrix} x \\ y \end{pmatrix} \right] \quad (28)$$

Consequently,

$$\begin{pmatrix} x \\ y \end{pmatrix} = \frac{1}{s_c} \cdot R_c^T \cdot \left[\begin{pmatrix} 1 & -d_c \\ 0 & 1 \end{pmatrix} \cdot \begin{pmatrix} x_T \\ y_T \end{pmatrix} - \begin{pmatrix} a_c \\ b_c \end{pmatrix} \right] \quad (29)$$

The algorithm FITNESS can be replaced by FITNESS1 described below.

FITNESS1(c)

$I_c^{new}(x, y) \leftarrow -1, 1 \leq x \leq M, 1 \leq y \leq N$

$$F = \frac{1}{s_c} \cdot R_c^T$$

$$A = F \cdot \begin{pmatrix} 1 & -d_c \\ 0 & 1 \end{pmatrix}; B = -F \cdot \begin{pmatrix} a_c \\ b_c \end{pmatrix}$$

for all $(x_T, y_T) \in \mathcal{O}(T)$

$$\begin{pmatrix} x \\ y \end{pmatrix} = A \cdot \begin{pmatrix} x_T \\ y_T \end{pmatrix} + B$$

$$I_c^{new}(x, y) \leftarrow 0$$

Compute $MI(I_c^{new}, I)$

It is worth to mention that the image I_c^{new} computed by FITNESS1(c) should be close to I from the similarity measure $MI(I_c^{new}, I)$ point of view. The algorithm first computes the best individual of the current population, $best$, then computes I_{best} and finally applies the transform $FITNESS(best)$ to compute the fitness function $\frac{MI(T, I_{best})}{H(T)}$. Note that, in case of sparse matrices, the computation scheme FITNESS1 is significantly faster than the procedure FITNESS.

5 EXPERIMENTAL RESULTS

We have performed an extensive testing work to evaluate the performances of the proposed methodology. In our work, the ES parameters are: σ_{ini} the initial values of σ -parameter, ϵ_{σ} , the minimum value of each step size, $NMax$, the maximum number of generations, and τ , a threshold parameter controlling the best fitness value, $\tau \in (0,1)$.

The quality of each resulted algorithm from the accuracy point of view has been measured in terms of success rates. We denote by NR the number of algorithm executions and let NS be the number of successful runs. An algorithm run is successful if the fitness of the final best individual exceeds 0.9. The success rate of a certain algorithm, SR , is given by

$$SR = \frac{NS}{NR} \cdot 100\% \tag{30}$$

We also used the SNR quantitative similarity measure to evaluate the registration quality. Let S and T be $M \times N$ images. Then

$$SNR(S, T) = 10 \cdot \log_{10} \left[\frac{\sum_{x=1}^M \sum_{y=1}^N (S(x,y))^2}{\sum_{x=1}^M \sum_{y=1}^N (T(x,y) - S(x,y))^2} \right] \tag{31}$$

A. In case of rigid transformation, we used the following setting of the parameters: $\mu=30$, $\lambda=200$, $NMax=100$, $\tau=0.925$. The initial step sizes were established taking into account the genotype space. The corresponding translation step sizes were set to 1, while the step sizes associated to scale factor and rotation angle respectively were set in $[0.01,0.25]$. The minimum value of each step size was set to 0.005. The value of NR was set to 300. Each time the convex recombination scheme is applied the value of α is randomly drawn in the interval $(0, 1)$.

The results of applying the proposed methodology on a large set of digital signature images are displayed in Table 1. The tests pointed out that the best success rate and SNR values were obtained in case of using the proposed RHYB1 procedure, where only convex recombination scheme was considered. Also, the survivor selection mechanism should be $(\mu + \lambda)$.

An instance of a digital signature representing the target image is displayed in Figure 1 while its corresponding sensed image is presented in Figure 2. One of the results obtained when the proposed RHYB 1 procedure is used together with the convex

recombination operator, and the survivor selection scheme is $(\mu + \lambda)$, is supplied in Figure 3.

The experiments pointed out that the best SNR value is around 29, while $SNR(I, T) = 10.9698$



Figure 1: Target image.



Figure 2: Sensed image.



Figure 3: The result of the proposed alignment methodology.

Table 1: The mean success rates for different ES implementations.

Crossover Procedure Solution part/ Parameter part	Success rate Survivor Selection ($\mu + \lambda$)	Success rate Survivor selection (μ, λ)
Local Convex/Local Convex	97%	90%
Local Convex/Local Discrete	91.33%	48.33%
Local Discrete/Local Convex	92.33%	87%
Global Convex/Global Convex	97%	91%
Global Convex/Global Discrete	90.33%	32.33%
Global Discrete/Global Convex	94%	87.67%
RHYB1 Convex/ RHYB1 1 Convex	98.67%	91%
RHYB1 Convex/ RHYB1 Discrete	93%	29.33%
RHYB1 Discrete/ RHYB1 Convex	95.33%	89.33%
RHYB 2 Convex/ RHYB 2 Convex	94.33%	87%
RHYB 2 Convex/ RHYB 2 Discrete	89.67%	30.33%
RHYB 2 Discrete/ RHYB 2 Convex	95.33%	90%

B. If we consider the perturbation model (15), the parameter settings are: $\mu=30$, $\lambda=200$, $NMax=120$, $\tau=0.9$. The dispersions of the translation parameters were set to 1, while the step sizes associated to scale factor, rotation angle and shear factor respectively were set in the range $[0.01, 0.05]$. The minimum value of each step size was 0.005. The value of NR was set to 200. The parameter α defining the convex crossover is randomly drawn in $(0, 1)$ each time a new allele is computed. In this case the procedure SRHYB3 implemented based only the convex crossover proved to be the most successful strategy from both points of view of mutual information ratio and SNR measure respectively. Note that similar results are obtaining when a common global strategy is applied, but with higher computational effort as compared to the above mentioned procedure. The results are provided in Table 2.

An instance of a digital signature representing the target image is displayed in Figure 4 while its corresponding sensed image is presented in Figure 5. One of the results obtained when the proposed SRHYB3 procedure is used together with the convex recombination operator, and the survivor selection scheme is $(\mu + \lambda)$, is supplied in Figure 6.

The experiments pointed out that the best SNR value is around 26, while the SNR value between the sensed image and the target one is 10.7737.



Figure 4: Target image.



Figure 5: Sensed image.



Figure 6: The result of the proposed alignment methodology.

Table 2: The mean success rates for different ES implementations.

Crossover Procedure Solution part/ Parameter part	Success rate Survivor Selection ($\mu + \lambda$)	Success rate Survivor selection (μ, λ)
Local Convex/Local Convex	92%	59%
Local Convex/Local Discrete	79%	44.5%
Local Discrete/Local Convex	91%	81.5%
Global Convex/Global Convex	98%	83.5%
Global Convex/Global Discrete	85.5%	21%
Global Discrete/Global Convex	98.5%	93%
SRHYB1 Convex/ SRHYB1 1 Convex	95%	86%
SRHYB1 Convex/ SRHYB1 Discrete	78%	49.5%
SRHYB1 Discrete/ SRHYB1 Convex	85.5%	87.5%
SRHYB 2 Convex/ SRHYB 2 Convex	97.5%	87.5%
SRHYB 2 Convex/ SRHYB 2 Discrete	79.5%	28.5%
SRHYB 2 Discrete/ SRHYB 2 Convex	89.5%	89.5%
SRHYB3 Convex/ SRHYB3 Convex	98.5%	90%
SRHYB 3 Convex/ SRHYB 3 Discrete	85%	29%
SRHYB 3 Discrete/ SRHYB 3 Convex	92.5%	92%

6 CONCLUSIONS

We have performed an extensive testing work to evaluate the performances of the proposed methodology. The effectiveness of our ES-based strategies has been established by implementing it using various crossover procedures as well as different selection techniques to compute the next generation.

The tests pointed out that the best success rate and SNR values were obtained in case of using the proposed hybrid procedures together with the survivor selection scheme $(\mu + \lambda)$.

Taking into account the quality of the experimental results, we conclude that more

effective registration methods could be derived by extending the proposed approach to other complex degradation models.

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