2014 14th International Conference on Frontiers in Handwriting Recognition

On-line Signature Verification by Multi-Domain Classification

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Abstract

In this paper a new on-line signature verification technique is proposed. Differently from previous works, this approach classifies a signature using a multi-domain strategy. In particular, based on the stability model of each signer, the signature is split into different segments and for each segment the most profitable domain of representation for verification purpose is detected. In the verification stage, Dynamic Time Warping (DTW) is used to evaluate the genuinity of each segment of the unknown signature, using the specific domain of representation. The experimental results, carried out on signatures of the SUSIG database, demonstrate the effectiveness of the proposed approach when compared to other approaches in literature.

1. Introduction

Biometry offers potentials for verifying the identity of a subject by the analysis of physical and behavioural characteristics. Physical characteristics can be obtained from finger-print, palm-print, face gestures, retina, or DNA. Behavioural characteristics can be obtained from key-stroke dynamics, speech, hand-written signature. Among others, hand-written signature is one of the most interesting means for automated personal verification. Signature is the customary way of identifying an individual in our society and it is well-accepted by every user for legal attestation and administrative certification [1, 2].

In addition, along with the growth of the internet, automatic signature verification is being considered with new interest. The creation of specific laws and regulations, which have been approved in many countries [3,4], and the attention that several national associations and international institutes have given to the standardization of signature data interchange formats [5,6] are evidence of the renewed attention in this field. The aim of these efforts is to facilitate the integration of signature verification technologies into other standard equipment to form complete solutions for a wide range of commercial applications such as banking, insurance, health care, ID-security, document management, e-commerce and retail point-of-sale (POS) [7].

Unfortunately, handwritten signatures are very complex biometric traits since they are the result of a complex process based on a sequence of predetermined actions, stored in the human brain, and realised by the writing systems of the signers (arms and hands) through ballistic-like movements. Therefore, also signatures written by the same person can be very different depending on the physical and psychological state of the writer. Thus, automatic signature verification involves aspects from a wide range of disciplines, as computer science, engineering, psychology, neuroscience, human anatomy and system science and several comprehensive survey papers reporting the development of the field have been published [8, 9, 10, 11]. In order to face with the enormous variability of signatures, multi-expert approach has been often considered and several systems have been proposed in the literature which combine verifiers based on different sets of features, using parallel [12], serial [13] or hybrid [14, 15] strategies.

This paper presents a new system for on-line dynamic signature verification. The technique uses a multi-domain approach that considers only the most profitable domain of representation for the verification of each segment of the signature. Precisely, the most profitable domain of representation of each segment is here considered as the domain in which the segment is most stable. For the verification of each segment of an unknown signature DTW was considered whereas a majority voting strategy is considered for combining local verification decisions, in order to obtain the verification decision for the entire signature. Signatures of the SUSIG database were considered for the experimental tests. The results demonstrate the superiority of the proposed approach with respect to other approaches in literature.

2. Multi-Domain Verification Technique

Let

$$S = \{S_1, S_2, \dots, S_n, \dots, S_N\} \tag{1}$$

be a set of N genuine signatures. In this paper each signature S_n is considered as a sequence of elements

$$S_n = (z^1_n, z^2_n, \dots, z^i_n, \dots, z^I_n) \tag{2}$$

where each element z^i_n is a 4-tuple

$$z^i_n = (x^i_n, y^i_n, t^i_n, p^i_n) \tag{3}$$

with:

- x^i_n and y^i_n : coordinates of the pen on the writing plane,
- t^i_n : the timestamp value
- p^i_n : the pressure value.

2167-6445/14 $31.00 © 2014 IEEE
DOI 10.1109/ICFHR.2014.19

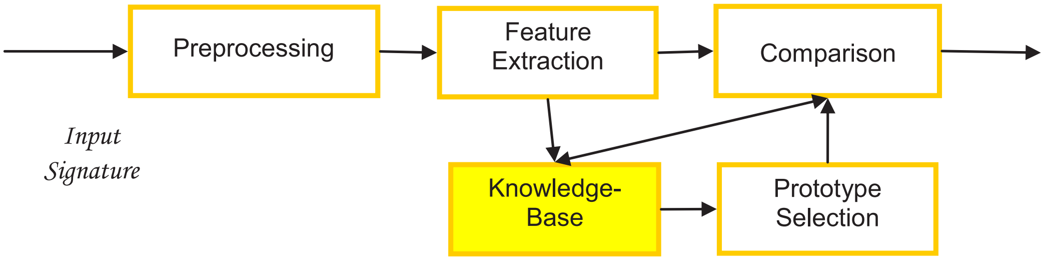

Figure 1. The Verification Technique

The multi-domain signature verification technique is based on the phases shown in Figure 1: prototype selection, preprocessing, prototype selection, feature extraction and classification. In the following, each phase is described in detail.

2.1 Prototype Selection

This phase has the aim to determine the prototype of the set of signatures of each signer. This is performed using Dynamic Time Warping (DTW). More precisely, for each signature S_n of the set S (see (1)) the following set of distances is computed:

$$\{\mathrm{DTW}(S_n, S_p) |\ p=1,2,...,N;\ n\neq p\}, \qquad (4)$$

where $d_{n,p}=\mathrm{DTW}(S_n, S_p)$ denotes the distance (computed by DTW) between the signatures S_n and S_p. The prototype signature is selected as the signature S_{n*} for which the average distance with respect to the other specimens is minimum, i.e.

$$S_{n^*} \rightarrow argmin_n \frac{\sum_{p=1,..,N;\ n\neq p} d_{n,p}}{N-1} \qquad (5)$$

2.2 Preprocessing

Preprocessing consists of two separate stages: value normalization and length normalization. Value normalization is performed according to a min-max linear normalization strategy [32], so that each values is reported in the range [0,1]. Similarly, Signature length normalization is performed using a linear interpolation algorithm [33] that transforms a signature with a variable number of points in a signature with a fixed number of points M, that is here fixed to M=256. Figure 2 shows three examples of preprocessed signatures.

2.3 Feature Extraction

In the feature extraction step, signature is converted into the four domains of representation we have considered in this work: displacement (s), velocity (v), acceleration (a) and pressure (p). For this purpose, the following equations were considered:

1) Displacement

- $s^i = \sqrt{(x^{i+1} - x^i)^2 + (y^{i+1} - y^i)^2}$, i=1,2,....,M-1
- $s^M = s^{M-1}$

2) Velocity

- $v^i = \frac{s^i}{(t^{i+1} - t^i)}$, i=1,2,....,M-1
- $v^M = v^{M-1}$

3) Acceleration

- $a^i = \frac{v^i}{(t^{i+1} - t^i)}$, i=1,2,....,M-1
- $a^M = a^{M-1}$

4) Pressure: no conversion was performed in the pressure domain (i.e. $p^i = p^i$, i=1,2,...M).

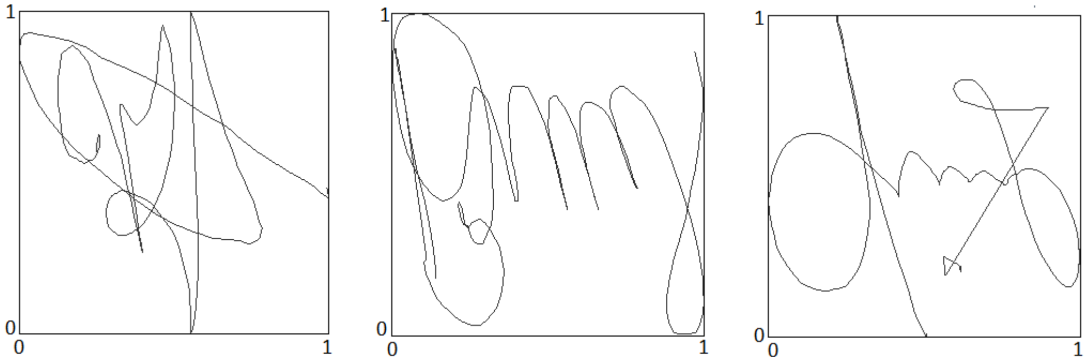

Figure 2. Examples of pre-processed signatures

Therefore, the feature extraction step allows the conversion of the signature representation domains from the space of the 4-tuples *(x,y,t,p)* to the space of the 4-tuples *(s,v,a,p)*:

$$(x,y,t,p) \rightarrow (s,v,a,p).$$

2.4 Classification

The classification step consists of two stages. The first stage concerns the training phase. The second stage concerns the test procedure.

2.4.1 Training Phase

After preprocessing and feature extraction, each signature S_n of the set (1) is represented by a sequence of elements

$$S_n = (z^1_n, z^2_n, \dots, z^i_n, \dots, z^I_n) \qquad (6)$$

where each element z^i_n is a 4-tuple

$$(s^i_n, v^i_n, a^i_n, p^i_n) \qquad (7)$$

with:
- s^i_n : displacement
- v^i_n : velocity
- a^i_n : acceleration
- p^i_n : pressure.

Now, let be S_r, S_t two genuine signatures. A warping function between S_r and S_t is any sequence of couples of indexes identifying points of S_r and S_t to be joined [12]:

$$W(S_r, S_t) = c_1, c_2, \dots, c_K, \qquad (8)$$

where $c_k=(i_k,j_k)$ (k,i_k,j_k integers, $1 \le k \le K$, $1 \le i_k \le M$, $1 \le j_k \le M$). Now, if we consider a distance measure $d(c_k)=d(z^{i_k}_r, z^{j_k}_t)$ between points of S_r and S_t, we can associate to $W(S_r, S_t)$ the dissimilarity measure

$$D_{W(S_r,S_t)} = \sum_{k=1}^{K} d(c_k). \qquad (9)$$

The elastic matching procedure detects the warping function $W^*(S_r, S_t) = c^*_1, c^*_2, \dots, c^*_{K^*}$ which satisfies the monotonicity, continuity and boundary conditions, and for which it results [12]:

$$D_{W^*(S_r,S_t)} = \min_{W(S_r,S_t)} D_{W(S_r,S_t)}. \qquad (10)$$

From $W^*(S_r, S_t)$ we identify the *Direct Matching Points* (DMP) of S_r with respect to S_t [9]. A DMP of a signature S_r with respect to S_t is a point which has a one-to-one coupling with a point of S_t. In other words, let $z_r(p)$ be a point of S_r coupled with z^q_t of S_t; z^p_r is DMP of S_r with respect to S_t iff:

(a) $\forall\, \bar{p} = 1,..,M$, $\bar{p} \neq p$, it results that:

$z^{\bar{p}}_r$ is not coupled with z^q_t;

(b) $\forall\, \bar{q} = 1,..,M$, $\bar{q} \neq q$, it results that:

$z^{\bar{q}}_t$ is not coupled with $z^{\bar{p}}_r$.

Now, a DMP indicates the existence of a region of the r-th signature which is roughly similar to the corresponding region of the t-th signature (in the domain specified by the distance used for the elastic matching procedure). Therefore, for each point of S_r, a score is introduced according to its type of coupling with respect to the points of S_t [12]:

$$\text{Score}^t(z^p_r) = 1 \quad \text{if } z^p_r \text{ is a DMP, } 0 \text{ otherwise} \qquad (11)$$

The local stability function of S^r is defined as:

$$I(z^p_r) = \frac{1}{N-1} \sum_{\substack{t=1 \\ t \neq r}}^{N} \text{Score}^t(z^p_r). \qquad (12)$$

An example of computation of the stability index is reported in the following. Let $S=\{S_1,S_2,S_3,S_4\}$ be a set of four (pieces) of signatures of the same writer, Figure 3 shows the result of the elastic matching procedure between S_1 and S_2, S_1 and S_3, S_1 and S_4.

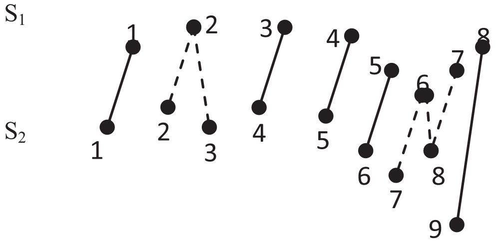

Figure 3a. W(S$_1$,S$_2$)

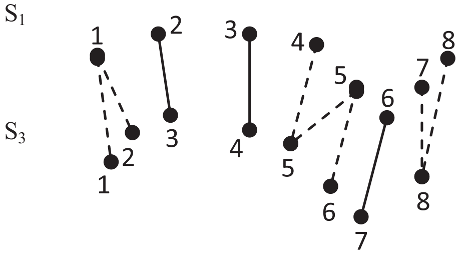

Figure 3b. W(S$_1$,S$_3$)

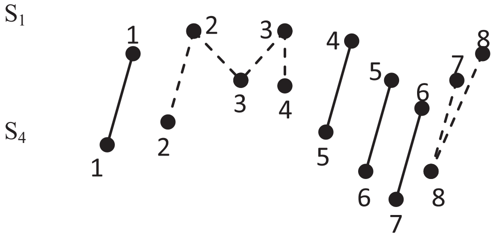

Figure 3c. W(S$_1$,S$_4$)

Figure 4. Examples of prototypes. Colours indicates the most stable domain of representation: Green - “displacement”, Red - “speed”, Yellow - “acceleration”, Blue - “pressure”.

Specifically, for S_1 and S_2 it results $W^*(S_1, S_2)$=(1,1), (2,2), (2,3), (3,4), (4,5), (5,6), (6,7), (6,8), (7,8), (8,9) (see Fig.3a).

For S_1 and S_3 it results $W^*(S_1, S_3)$= (1,1), (1,2), (2,3), (3,4), (4, 5), (5, 5), (5,6), (6,7), (7,8), (8, 8) (See Fig. 3b).

For S_1 and S_4 it results that $W^*(S_1, S_4)$= (1, 1), (2,2), (2, 3), (3, 3), (3, 4), (4, 5), (5, 6), (6, 7), (7, 8), (8, 8) (See Fig. 3c).

Concerning the DMP, from $W^*(S_1,S_2)$ it results that DMP for S_1 with respect to S_2 are the points $z_1(1)$, $z_1(3)$, $z_1(4)$, $z_1(5)$, $z_1(8)$.

From $W^*(S_1,S_3)$ it results that the DMP for S_1 with respect to S_3 are the points $z_1(2)$, $z_1(3)$, $z_1(4)$, $z_1(6)$.

From $W^*(S_1,S_4)$ it results that the DMP for S_1 with respect to S_4 are the points $z_1(1)$, $z_1(4)$, $z_1(5)$, $z_1(6)$.

Table 1 Local stability values for S_1.

	$Z_1(1)$	$Z_1(2)$	$Z_1(3)$	$Z_1(4)$	$Z_1(5)$	$Z_1(6)$	$Z_1(7)$	$Z_1(8)$
$Score^1(Z^1(p))$	1	0	1	1	1	0	0	1
$Score^2(Z^1(p))$	0	1	1	1	0	1	0	0
$Score^2(Z^1(p))$	1	0	0	1	1	1	0	0
$\mathbf{I(z^1(p))}$	**0.66**	**0.33**	**0.66**	**1**	**0.66**	**0.66**	**0**	**0.33**

The results are summarized in Table 1, that also reports the value of the similarity index. From this result it follows that the regions of high stability are close to the points $z^1(4)$, $z^1(7)$, $z^1(8)$; the regions of medium-high stability are close to the points $z^1(1)$, $z^1(3)$, $z^1(5)$, $z^1(6)$; the region of medium-low stability is the zone close to the point $z^1(2)$. Form the analysis it follows that there is no zone of very low stability.

According to this strategy, for each signer in the training phase the stability of each part of the prototype signature is estimated in the different domains of representation (displacement, velocity, acceleration, pressure) as shown in Table 2, and the most stable domain of representation is selected, as Figure 4 shows. In the test procedure the verification of an unknown test signature will be performed by considering only the most stable domain of representation of each part of the signature as shown in Table 3, that is expected to be more difficult to forger.

2.4.2 Testing Stage

The testing stage concerns the comparison between the unknown test signature and the author prototype. The matching is computed only considering the most stable domain of representation for each part of the signature as shown in Table 3. More specifically, let us consider the i-th part of the signature (i.e. the region of the signature related to the i-th point) the following verification rule is used:

$$|p-k| \quad < \alpha\ avg \rightarrow i\text{-}th \text{ part is genuine}$$

Table 2 Stability values of Author 1 prototype in each part for all domains

	Domains			
Parts	Displ.	Pressure	Speed	Acceleration
1	0.75	0.0	0.0	0.0
2	1.0	0.25	0.0	0.0
3	1.0	0.5	0.0	0.0
…	…	…	…	…
32	0.0	0.25	1.0	0.5
33	0.0	0.25	1.0	0.5
34	0.25	0.0	0.5	0.25
35	0.25	0.25	0.75	0.75
…	…	…	…	…
254	0.75	0.5	0.5	0.5
255	0.75	0.75	1.0	0.5
256	0.25	0.75	0.25	0.75

Table 3 Author 1 prototype with the most stable domains in each part

	Multidomain author prototype	
Parts	Domain	Stability
1	Displ.	0.75
2	Displ.	1.0
3	Displ.	1.0
...	...	...
32	Speed	1.0
33	Speed	1.0
34	Speed	0.5
35	Acceleration	0.75
...	...	...
254	Displ.	0.75
255	Speed	1.0
256	Acceleration	0.75

$$|p - k| \geq \alpha\ avg \rightarrow \textit{i-th} \text{ part is a forgery}$$

being:

- *p* the value of the best domain of representation (d^*) for the *i*-th part of the test signature;
- *k* the value of the selected domain of representation (d^*) for the *i*-th part of the prototype signature;
- *avg* is the average value of the selected domain of representation (d^*) (the average values is computed considering the entire prototype signature);
- α value is a weight used to balance False Rejection Rate (FRR) and False Acceptance rate (FAR). In this work, the value is set to make FRR and FAR as balanced as possible. In a supposed real use of this technique, the FAR can be further reduced adjusting this value, according to the requirements of applications.

Finally, the test signature is considered genuine if the number of positive parts exceeds the number of parts considered as forgeries.

3. Experimental Results

For testing the system, the SUSIG database - Visual Subcorpus was used. The Visual subcorpus contains 20 genuine and 10 skilled forgeries of 100 authors. For the experimental tests, 10 genuine signatures were used for training the system and 10 genuine and 10 forgeries for the test.

Table 4 reports system performance in terms of FRR and FAR. In particular the verification results of the multi-domain system are FRR=1.76% and FAR=1.1%. In addition, Table 4 also reports the performance of other systems in the literature, evaluated on the same database. The results demonstrate the effectiveness of the proposed multi-domain strategy when compared to traditional approaches.

Table 4 Signature verification results on SUSIG Database

	FRR(%)	FAR(%)
C. Yuen et. al. [36] (Prob. Model)	14.8	2.64
B.Yanikoglu et al. [37] (Fourier descr.)	3.03	3.03
S. Rashidi et. al [38] (Pole-zero Models)	2.09	2.09
A.Kholmatov et. al [34] (Bayes Classif.)	3.60	3.52
A.Kholmatov et. al [34] (SVM Classif.)	1.64	3.85
A.Kholmatov et. al [34] (Linear Classif.)	1.64	1.28
Multidomain technique (this work)	**1.76**	**1.1**

4. Conclusion

A new multi-domain system for dynamic signature verification is presented in this paper. The technique uses the stability analysis to determine, for each part of a signature, the most suitable domain of representation for verification aims. In this way we perform the matching for signature verification only using the most relevant domain of representation for each part of the signature, avoiding waste of time and increasing system performance.

The experimental results demonstrate the effectiveness of the proposed technique and lead to investigate more accurately on the potential of a multi-domain approach for dynamic signature verification.

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