Applying dynamic methods in off-line signature recognition

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ABSTRACT

In this paper we present the work developed on off-line signature verification using Hidden Markov Models[1] (HMM). HMM is a well-known technique used by other biometric features, for instance, in speaker recognition and dynamic or on-line signature verification. Our goal here is to extend Left-to-Right (LR)-HMM to the field of static or off-line signature processing using results provided by image connectivity analysis. The chain encoding of perimeter points for each blob obtained by this analysis is an ordered set of points in the space, clockwise around the perimeter of the blob. We discuss two different ways of generating the models depending on the way the blobs obtained from the connectivity analysis are ordered. In the first proposed method, blobs are ordered according to their perimeter length. In the second proposal, blobs are ordered in their natural reading order, i.e. from the top to the bottom and left to right. Finally, two LR-HMM models are trained using the parameters obtained by the mentioned techniques. Verification results of the two techniques are compared and some improvements are proposed.

Keywords: Off-line signature, LR-HMM, blob analysis.

1. INTRODUCTION

In any on-line signature process, parameters such as coordinates, pressure and pen tilt are acquired during the act of signing. In this way digitized points are ordered in time, meaning that we obtain those mentioned parameters as time functions. LR-HMM-s (those that allow forward transitions, but not backwards) have shown good performance while processing this kind of dynamic information[2,3]. Our goal here is to extend those LR-HMM models to the field of static or off-line signature processing using results provided by image connectivity analysis.

Connectivity analysis algorithm was designed at Stanford Research Institute and it determines which pixels in an image are interconnected and belong to the same object or region. This algorithm gives as a result a description of an image as a set of blobs that are hierarchically structured, providing father-child or sibling-sibling relationships. The processing of those results is known as blob analysis, a very useful tool in machine vision for image analysis of parts. For each blob a set of geometrical features are obtained such as its area, color, center of gravity or centroid, maximal and minimal coordinates or bounding box, moments of inertia or perimeter length. The most important feature for our purposes is the chain encoding of perimeter points for each blob, since it is an ordered set of points in the space, clockwise around the perimeter of the blob.

The next step is to generate the information to construct the LR-HMM for every signer in the database. Signatures are sets of strokes that are usually interlaced, so there is not a one-to-one relationship between strokes and blobs. As such, two strokes can be combined into a single blob, and a single stroke can have two or more blobs (for instance, the character 'o' has two blobs, the inner one and the outer one). It is clear that depending on how the order of blobs is chosen, the final sequence of perimeter points will be different and, as a consequence, final results can change dramatically.

We discuss two different ways of generating the models depending on the way the blobs obtained from the connectivity analysis are ordered. In the first proposed method, blobs whose father is the background (we will consider them as parts

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Biometric Technology for Human Identification, edited by Anil K. Jain, Nalini K. Ratha,
Proceedings of SPIE Vol. 5404 (SPIE, Bellingham, WA, 2004)
0277-786X/04/$15 · doi: 10.1117/12.540421

in the image) are ordered according to their perimeter length, from the longest one to the smallest one. Their children, if any, are inserted behind each father or part following the same criterion, i.e. form the longest one to the smallest one. The final sequence is the result of concatenating the perimeter of each blob as described.

In the second proposal, the main blobs or parts are ordered in their natural reading order, i.e. from the top to the bottom and left to right and their children are inserted behind each father following the same criterion.

For both cases the topology of the HMM has been chosen to optimize the results. In this way we studied the influence of the number of states of the model and well as the different possible normalizing values for the lengths of the perimeter's chain of points.

2. SIGNATURES DATABASE

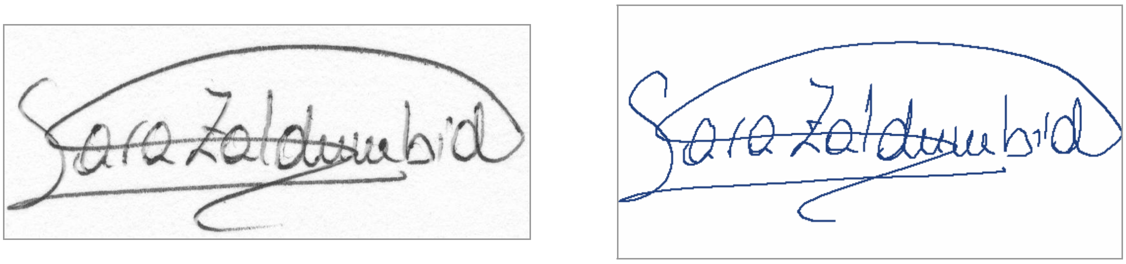
To perform the experiments, we have used a database containing a total amount of 3750 signatures corresponding to 75 individuals. Half of the signatures (25 for each signer), are true signatures. The rest are skilled forgeries, 25 for each signer done by 5 forgers. The forged signatures stored in the database are skilled forgeries, where every forger tries several times to forger the target signature. Only when he considers that his forgery is good enough the signature will be adquired and stored. All this process gives a high level of quality to the forgeries.
The database, called *MCYT baseline Corpus*[4], is a multimodal database that includes also fingerprints acquired by using both optical and capacitive sensors and voice of some signers. Figure 1 shows the original signature of an individual from the database together with his fingerprints, one captured with an optical device (DP) and the other one captured with a capacitive device (PB).

a) signature   b) fingerprint DP   c) fingerprint PB

Fig. 1 Original signature of an individual of the database, and his fingerprints captured with an optical sensor (b) and with a capacitive sensor (c). All of them are shown in real size.

All the signatures were acquired on-line using a graphic tablet with a spacial resolution of 100 points by millimeter and a sampling frequency of 100Hz to capture the x-y coordinates, the inking pen pressure on 1024 levels, its inclination and azimuth. Simultaneously the signatures are written on a paper with normal ink. After the acquisition phase the signatures were scanned to obtain 2D static images suitable for off-line processing. In this way, both on-line and off-line signature recognition can be accomplished for all of the signers in the database.

The signatures of this database have been obtained with black ink on whit sheets of paper, making it easier for the segmentation process. This is the reason why our work does not pay attention to the usual problem of signature extraction from a noisy background. The interest of our work lies on the study of the viability of using LR-HMM-s in the off-line signature verification problem, using and spatially ordered sequence of points. Figure 2 a) shows a scanned signature using 600 optical points per inch (without interpolation) and 256 grey levels. Part b) of figure 2 shows the same signature at 512x256 pixels obtained from the on-line signature, an eliminating any dynamic feature such as pressure level, inclination, azimuth and spatial or time sequence information.



a) b)

Fig. 2 a) Original signature of an individual of the database scanned at 600 ppi and b) his corresponding static image of 512 x 256 obtained by eliminating the dynamic information. Both images are enlarged to twice the real size.

The images extracted from the background are normalized to a maximum size of 512 pixels wide x 256 pixels high and they are centre justified to those dimensions. The signatures with horizontal trend will show empty rows (see Fig. 2 b) and those with vertical trend will show empty columns (see Fig. 3).Each image so generated keeps its conversion scale factor from pixels to millimeters inside the bmp file header. The aspect ratio is always 2:1 for all the images.

Fig. 3 The signature of this individual is justified to the 2:1 format, horizontally centered adding empty columns to the left and to the right. The image is enlarged by 2 relative to its natural size.

3. PREPROCESSING OF THE SIGNATURES

The preprocessing stage of the signatures consists on its segmentation from the background and on a specific normalization to avoid size fluctuations (every time we signed we get different dimensions for the signatures). Once the normalized binary image is obtained, the analysis is carried out in two steps. First a connectivity or blob analysis is performed. This can be done by using the static 512 x 256 pixels sized signatures. Secondly the perimeter points are extracted from the signature blobs, by analyzing the set of blob structures that constitute the binary image of the signature. This set of blobs is hierarchically structured, providing father-child or sibling-sibling relationships.

Fig. 4 shows in blue (dark) the part-blobs that are children of the image background and in red (gray) the child-blobs depending on them. In this example four part blobs can be seen: one main blob and three smaller, corresponding to the characters “b” and “i” that appear isolated in the image of the signature. Each child-blob can be identified by a number written slightly to the right and over the center of mass of the blob.

The chain of (x, y) points of the blobs perimeters, both for part blobs and their children are the biometric information relevant to the work here presented. In each blob, this chain of (x, y) points is covered clockwise starting with the most up righted point in the blob.

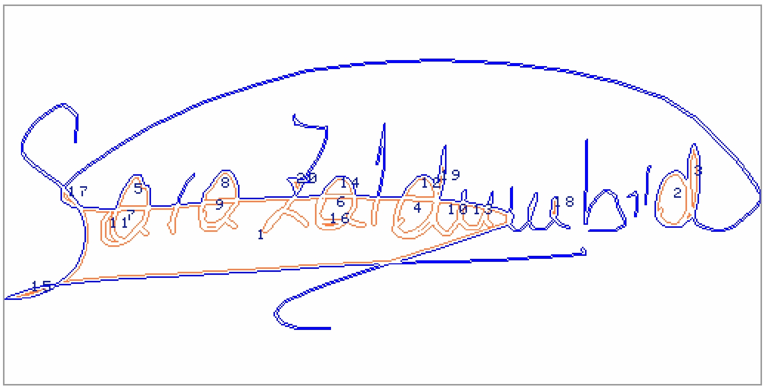


Fig. 4 Blobs corresponding to the signature of Fig. 2. The final image has been enlarged 3 times to allow the reading of the child blobs identification numbers.

As can be observed in Fig. 4, signatures are sets of strokes that are usually interlaced, so there is not a one-to-one relationship between strokes and blobs. As such, two or more strokes can be combined into a single blob ('S', 'a', 'r', 'a') and a single stroke can have two or more blobs ('d' and the flourish). So depending on how the order of blobs is chosen, the final sequence of perimeter points will be different and, as a consequence, final results can change dramatically. For this reason, two ways of sorting the blobs of the signatures are proposed in the next section.

4. TRAINING OF THE MODELS

We discuss two different ways of generating the models depending on the way the blobs obtained from the connectivity analysis are ordered. In the first proposal, blobs whose father is the background are ordered according to their perimeter length (LEN), from the longest one to the smallest one. Their children, if any, are inserted behind each father or part following the same criterion, i.e. form the longest one to the smallest one. The final sequence is the result of concatenating the perimeter of each blob as described. In the second proposal, parts are ordered in their natural reading order (NAT), i.e. from the top to the bottom and left to right and their children are inserted behind each father following the same criterion. It can be thought a priori that the NAT order is more adequate to the Latin writing in which the signatures have been captured.

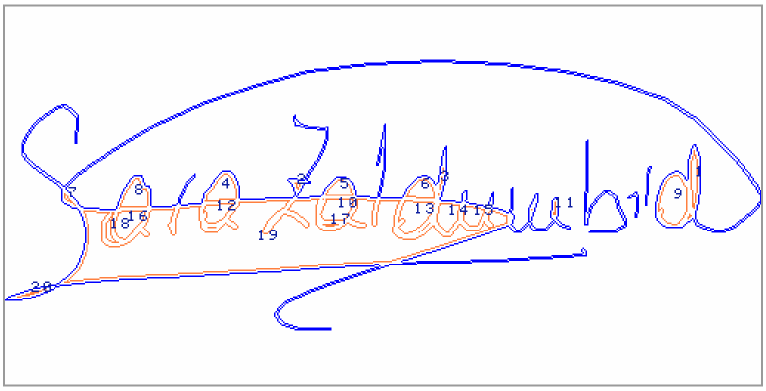


Fig. 5 Blobs of the image from the signature of Fig. 2 ordered according to the NAT criterion. The final image has been enlarged 3 times to allow the reading of the child blobs identification numbers.

For every criterion we will generate one HMM representing the signatures of one user. One image will always give the same blob structure, so the difference in the modeling will be given by the different criteria used in the sorting of the blob perimeter points. Fig. 4 shows the LEN criterion applied over the same image as Fig. 5, where the NAT criterion was applied. Both pictures include a increasing numbering of the child-blobs according to the used criterion.

As was mentioned previously in section 2, a total of 25 signatures by user are available. The signatures are numbered from 00 to 24 according to the time they were acquired. The first five signatures (00 to 04) are used for the initial training of the HMM. Additionally, four more signatures (05, 10, 15 and 20) are chosen to re-estimate the initial model. In this way 16 original signatures and 25 forgeries are finally available for training and testing.

An important point to consider when training an HMM is the topology selection and the length of the sequences used to generated them. In this way, two topologies have been tested, with different number of states and different kind of state transitions. The ergodic topologies have been rejected (those that allow both forward and backward transitions) in favor of LR, which have given clearly better results. Also, the models have been trained with free length of samples versus using different normalized lengths. In particular the values of 750, 1000, 1500 and 2000 normalizing values have been used. The normalization has been applied to the sequences of points obtained from the connectivity analysis and the NAT and LEN sorting.

The influence of the normalizing length was first studied. LR-HMM with 6 states (4 intermediate states plus initial and final states) were trained with the four above mentioned values both for NAT and LEN sorting criteria. The 6 state topology was chosen based on the values obtained for on-line[2,3] signature. Table 1 shows the EER values obtained for the experiments, and the results can be compared to the values obtained without using any normalization.

Table 1 EER rates obtained for the four normalizing values in the training of the 6 states LR-HMMs and later verification tests.

Number of samples.	**EER NAT**	**EER LEN**
Free	30,413	32,925
750	30,242	32,473
1000	29,514	33,054
1500	29,632	31,591
2000	29,730	31,968

As can be seen in table 1, the best results are obtained when a normalizing value of 1000 is used under the NAT criterion, but a 1500 value produces better results for the LEN criterion.

Next we studied the influence of the number of states of the HMMs. Models with 5, 6, 7 and 8 states were tried, using a value of 1500 to normalize the sequences length. Table 2 shows the EER values obtained in the experiments.

Table 2 EER values obtained varying the number of states using a normalizing value of 1500 for the sequences length.

Number of states	**EER NAT**	**EER LEN**
5	32.323	34,590
6	29,632	31,591
7	**27,577**	30.367
8	31.523	32,940

In can be seen that the NAT criterion produces better results than the LEN criterion in all the experiments, independently of the number of states of the models and the value of the normalizing length. The models obtained using the LEN criterion never give EER values better than 30%, while the models obtained using the NAT criterion give better results with 6 and 7 states, reaching the best rates for 7 states and using 1500 normalized samples.

Considering that when 6 states are used, the results are slightly better for 1000 normalized samples than for 1500 for the case of NAT criterion, the experiments were repeated with a normalizing value of 1000. As can be seen in Table 3, the best results are obtained with the 1500 normalizing length.

Table 3 Values of EER obtained for a 7 states LR-HMM

7 states	EER NAT	EER LEN
1000 samples	28.347	31,670
1500 samples	27,577	30.367

5. CONCLUSIONS

An off-line signature verification system has been developed based on LR-HMM that has been tested over a skilled forgeries database. The points of the perimeters of the blobs of the signature have been used as the input of the models, and two criteria on sorting them, the so-called NAT and LEN criteria have been tested.

The best results are obtained when the NAT criterion is used in all the performed experiments. The best results are obtained for a 7 state LR-HMM and using 1500 normalized samples, giving an EER of 27,5%.

Adding additional geometrical parameters such as linear and circular segments length, curvature radii, etc.[7] calculated from the perimeter points and sorted according to any of the two criteria would result in a large EER improvement of the system, so improving the security level.

Multimodal fusion of several biometric methods (fingerprints, voice, signature, etc.) is another way to improve the efficiency of the verification. In the same way, we could talk about intramodal fusion, combining several verification methods based on the same biometric feature. Fusion of on-line and off-line signature methods can make the system more robust and efficient.

ACKNOWLEDGEMENTS

This work is supported by the "Ministerio de Ciencia y Tecnología" of the Spanish Government under project MCYT TIC2000-1669-C04-03 called *Aplicación de la Identificación de Personas mediante Multimodalidad Biométrica en Entornos de Seguridad y Acceso Natural a Servicios de Información* [6]. We also want to thank the students Amalur Colau and Jon Escolar for the data collecting work.

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