Selection of Points for On-Line Signature Comparison

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Abstract

Authentication based on handwritten signature is the most accepted authentication system based on biometry because it is easy to use and because the use of signature is part of our habits. In the field of authentication by on-line signature, we present a method to reduce the amount of data to be stored for pattern comparison and that needs few processing. Many systems described in literature keep the whole signature's points even if it is not recommended, even advised against it, in order to avoid forgers to obtain a signature's pattern. The proposed method for data reduction was evaluated with respect to a method of curve comparison very often used for authentication by on-line handwritten signature: Dynamic Time Warping (DTW). After we have presented several reduction methods of signature data, we show the results obtained with each one. In order to evaluate their efficiency, the results were compared to those obtained with the whole coarse data points of the signature.

Keywords: Dynamic Time Warping, Signature, Vectorisation, selection of essential points.

1. Introduction

Few articles tackle the problem of points' selection to reduce the size of data to store and to analyse during the authentication phase of on-line signature. Usually the most interesting points are supposed to be those that realise signature segmentation and to study the different parts independently [6].

This work has two objectives. On the one hand, in order to reduce the amount of data to be stored and to minimize the duration of the whole processing during the authentication phase, it is interesting not to take into account all the points. On the other hand, the raw data is rather accurate and small warping could disturb the comparison process. Then a selection of points could allow to increase the system robustness. Moreover, taking into account the stability of signature's points allows to increase the efficiency of signature verification process [3].

We particularly insist on the optimisation of the choice of the best points implied in the comparison. This enables to make it as fast and as efficient as possible. In this context, after presenting the DTW algorithm, we present different methods to select characteristic points on which we apply the algorithm. In the last part, after presenting the base of signatures set up for the tests, we present and compare the results obtained by using DTW algorithm on the selected points given by the different selection methods.

2. Dynamic Time Warping

One of the most important difficulties in authentication using handwritten signatures is the choice of the comparison method. On-line signatures are given by a sequence of points sorted with respect to acquisition time. Since two signatures of the same person cannot be completely identical, we must make use of a measure that takes into account this variability. Indeed, two signatures cannot have exactly the same timing, besides these timing differences are not linear. Dynamic Time Warping is an interesting tool; it is a method that realises a point-to-point correspondence. It is insensitive to small differences in the timing.

Dynamic Time Warping is an application of the techniques of dynamic programming developed by Bellman in the Fifties [1]. It is particularly used in the domain of speech recognition. This method allows to find, for each element of one curve, the best corresponding element in the other curve according to some metric [5]. Here the metric used is the spatial Euclidean distance between the signature points. Once this matching is achieved, we compute the distance between the two curves by adding the distances between corresponding points. We have chosen to normalise the distance by dividing the sum result by the number of correspondences. The transformations allowed in the correspondence are stretching or compression along the temporal axis of a signal relatively in one or the other. The aim of these local adjustments is to minimize the difference between the two signals. We distinguish two approaches: asymmetrical and symmetrical. In the asymmetrical case, we seek to establish a correspondence between a sample and a pattern whereas, in the symmetrical case, the correspondence is sought in both senses sample-pattern and pattern-sample. This second criterion provides better results [4]. So we selected this method. This method to compare curves is the most used in the field of authentication by on-line handwritten signature. Calculating distances between signatures with DTW allows to achieve a verification system more flexible, more efficient and more adaptive than the systems based on neural networks or Hidden Markov Models, as the training phase can be incremental. This aspect is very important when we envisage to elaborate an authentication method that takes into account the evolution of the signature along the years.

3. Selection of representative points of the signature

Since we consider the coordinates of the signature points, before comparing the signatures, it is necessary to achieve a preprocessing in order to normalise the signatures. Indeed, a distance measurement is not invariant toward transformations such as rotation, translation and homothety, applied, with different parameters, on each of the elements we are comparing. The normalisation is performed in three stages. First of all, we determine the direction of the signature principal inertia axis, and then a rotation is carried out so that the inertia axis is horizontal. Then, a homothety is carried out so that all signatures are all contained in a surrounding rectangle with the same width. To finish, we position the signature so the coordinate of their gravity centre are at the origin of the coordinates.

The difficulty of the point selection comes from the definition of the criteria we want to respect. The points must be stable in some sense for a person and consequently the points must be located at remarkable points of the signature [8]. The principal method used in the field of authentication by on-line handwritten signature is based on a visual analysis of the signature and consists to segment at the points were speed is null or low as strong curvature points [2]. The point selection can be compared to polygonal approximation. Here, we consider what happens to be a polygonal approximation applied to a stroke line that should give a good compromise between accuracy and reduction of the volume data to be stored.

We are to evaluate the segmentation method based on the polygonal approximation proposed by Wall. For that purpose, comparisons with other methods are considered. The first one consists in choosing some points of the signature in a random way and the second one consists in using a genetic algorithm.

3.1. Random Selection

In order not to fix in an arbitrarily way the number of selected points *N*, this number is set to a quarter of the whole number of points of the first training signature with a maximum of 50 points. Since the signatures do not have the same number of points, the relative indexes of the points are considered and not the coordinates of points. So we choose randomly *N* relative indexes of the points in the signature. In figure 1, the selected points are figured by larger squares.

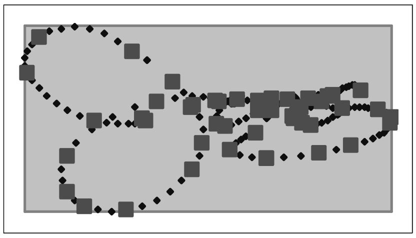

Fig. 1: Illustration of random selection.

This method is not an optimisation in the resolution of the problem, even if it allows to reduce the computing time during authentication. We detail then a method of point's selection based on a genetic algorithm.

3.2. Selection by genetic algorithm

Genetic algorithms are methods to optimise functions. Here, we want to select the most adapted points to the signatures authentication problem. Our objective is to determine stable points for a signer. So we use all the signatures in some one training set. The fitness function to minimize is the mean of the DTW distances between couples of signatures in the training set associated with a signer. As previously, since signatures do not have the same number of points, relative indexes and not point coordinates are used. So we seek the indexes that minimize the fitness. A chromosome represents the coding of a partial solution for the problem. Here, a chromosome corresponds to the indexes of the whole points of the signature and a gene corresponds to the index of a point of the signature. A gene takes value 1 if the point is retained and 0 in the other case. The number of points used in the comparison is found automatically and is limited by the size of the chromosome, which is fixed to 100. The size of the population is fixed to 100 chromosomes. As we could see on the figure 2, the mean of DTW distances between training signatures does not evolve any more after 100 generations. So we decide to generate 100 generations.

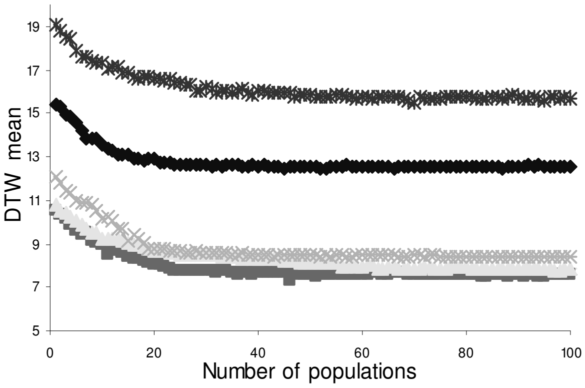

Fig. 2: Evolution of the means of inter-training DTW distances for five signers.

With this method, the choice of points to be preserved is not achieved according to the characteristics of the signature but in such a way that the distances between the training set signatures are minimized.

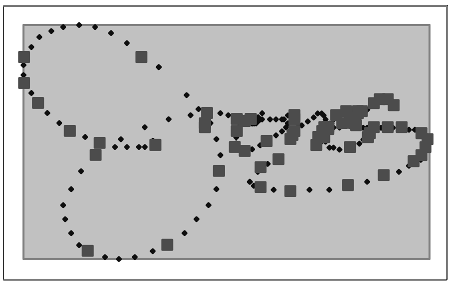

Fig. 3: Squares are figuring the points selected by genetic algorithm.

We note that the points selected by genetic algorithm are not exclusively the points of strong curvature contrary to vectorization methods. We observe the number of selected points is close to 50. An example of point selection is presented in figure 3.

3.3. Selection by polygonal approximation

Here, we select the vertices of a polygonal line that approximates the signature. We have chosen the polygonal approximation method proposed by Wall [7]. This approximation method introduces a new vertex when the error made by replacing the curve by a straight line segment becomes too important. The error is based on the calculation of an area and on some threshold. This threshold represents the cumulated error authorized by area unit, which is area between the curve and the approximating segment at each step of the trials.

The formula used to compute the error is: $Error = Error + \left\| \vec{U} \wedge \vec{V} \right\|$. A new vertex is introduced when:

$Error > Lg \times Epsilon$ where Lg denotes the segment length and Epsilon is a constant.

Thus we determine the vertices of the polygonal line.

Here is an iterative process and consequently it presents two advantages. On the one hand, it is not necessary to store all the points of the curve and, on the other hand the points of polygonal approximation are extracted in the order of appearance in the signature.

Nevertheless, this algorithm requires choosing one parameter linked to the quality of the obtained approximation. We have considered two methods to choose the value of this parameter: first, a fixed threshold, valid for all the signatures independently to the signer, and second, a threshold that is optimised in an automatic way according to the author of the signature.

3.3.1. Fixed threshold

The value of the threshold corresponds to a precision level for the signature representation. We make a compromise between quality of representation and data volume. The threshold should allow to smooth the signature to reduce the noise while preserving sufficient information for characterizing the signature in an efficient way. Moreover, a single threshold seems to be reasonable enough as we have normalised the signatures. The figure 4 gives an example of result provided by the use of a fixed threshold on a signature.

The segmentation takes into account as single parameter the degree of accuracy wished. To evaluate the influence of this parameter, we can seek the best approximation threshold for each person, according to two criteria.

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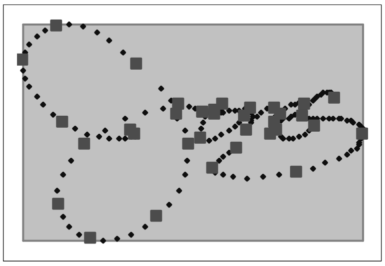

Fig. 4: Illustration of the points selected by the polygonal approximation.

3.3.2. Individualized Threshold

The aim is to find the threshold that gives the most stable correspondence for each signer. We tested two different criteria.

First we consider the number of segments defined on the signatures of the training set. The criterion expresses a low difference between these numbers by minimising their variances. Second criterion is to minimize the mean of the DTW distances between training signatures. To do that, we make the value of the threshold vary and we evaluate the parameters involved in both criteria. So we determine, for each criterion, the best threshold for each signer.

The mean of the DTW distances between training signatures evolves in an irregular way according to the selected threshold. However, the best threshold is generally superior to the threshold associated with all the points. Figure 5 shows an example of selected points using individual thresholds.

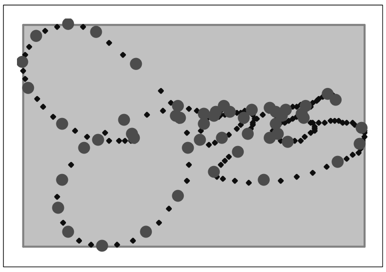

Fig. 5: Circles indicate the points selected by polygonal approximation with an individualized threshold by minimizing the mean of the DTW distances.

4. Evaluation method

The term "authentication" covers in fact two different problems: identification and verification. Here, we are interested in the problem of verification. Moreover, the errors of authentication can be classified in two categories; False Reject Rate (FRR) indicates the rate of genuine signatures rejected and False Acceptance Rate (FAR) indicates the rate of accepted forgeries. The Equal Error Rate (EER) corresponds to the error value for which FAR is equal to FRR. These rates determine the quality of an authentication system, but the acceptable values depend on the level of security desired for a specific application.

To evaluate the different methods of representative points selection we have presented before, we made use of a base of 800 signatures realised by 40 writers. Among the 20 genuine signatures of each signer, 5 are used to elaborate the patterns of the signature and the others are used to achieve the tests. To model each signer we have chosen to consider the 5 patterns: one for each training signature. No process is performed to build single model from the training signatures.

4.1. Strategy of Authentication

When a signature obviously differs from those it has to be compared to, there is no need to apply time consuming processing, like the computation of DTW. Then, we have organised the all process as a "coarse to fine" approach. Thus the first step only aims at detecting the obvious forgeries with constraints relative to speed and simplicity. After eliminating these false candidates only forgeries and genuine signatures have to be processed by use of elaborated models. The principal constraint of the first stage is to not reject genuine signatures. As the characteristics used must be relatively stable, we chose global characteristics: length and duration of the signature. Let Lt and Dt denote respectively the length and the duration of the tested signature, and Li and Di respectively the length and the duration of the i^{th} training signature. The decision rule is:

If $Lt > 1.4 \times \max_{i=1 to n}(Li) \; or \; Lt < 0.6 \times \min_{i=1 to n}(Li)$, Then the signature is considered as a forgery, otherwise we enter the second stage. We apply the same principle with the duration of the signature. This first stage allows to detect 58% of forgeries and to accept 99,8% of genuine signatures.

4.2. Comparison by DTW

The aim of the next stage is to detect the forgeries that are not detected during the first stage. Let St be the tested signature and Si the i^{th} training signature. The decision rule is: If $\min_{i=1 to n}(DTW(St, Si)) < \alpha$, then the signature is considered as genuine else the signature is rejected. We chose to make alpha evolve in order to define different systems of authentication more or less tolerant. The value of alpha is independent from the signer. The quality of these systems can be represented in a two dimensions space indicating FAR and FRR values.

5. Results

To evaluate the methods of point selection and their impact on authentication process, the results obtained with DTW carried out on the selected points are compared with those obtained considering all the points of the signature.

5.1. Points obtained in a random way

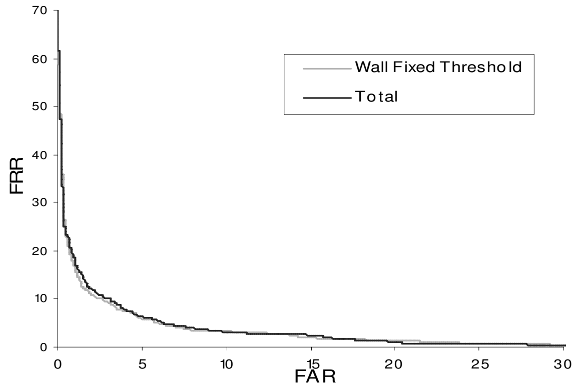

Fig. 6: FAR vs FRR in case of random selection

As we could expect it, recognition rates are worse with random points than those obtained with all the points of the signature.

5.2. Points obtained by genetic algorithm

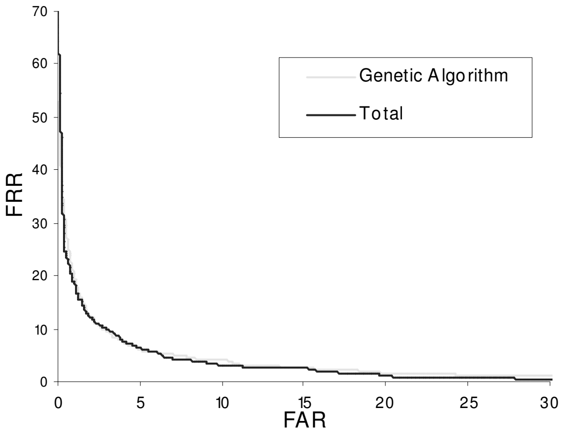

Fig. 7: FAR vs FRR in case of GA selection

Results obtained with genetic algorithm are worse than those obtained with all the points of the signature. This is due to the fact that the training is not a good quality training. The two small training set lead to a training by heart. Indeed, we can note that the obtained mean of distances intra-signers is very low but the inconvenient is that the distances to the other genuine signatures are more important and more variable. The method requires having more signatures for training purpose (see figure 10).

5.3. Points obtained by polygonal approximation

When the threshold was fixed in an empirical way, the mean number of points retained is 30. The reduction of the number of points is all the more large, as the straight is rectilinear.

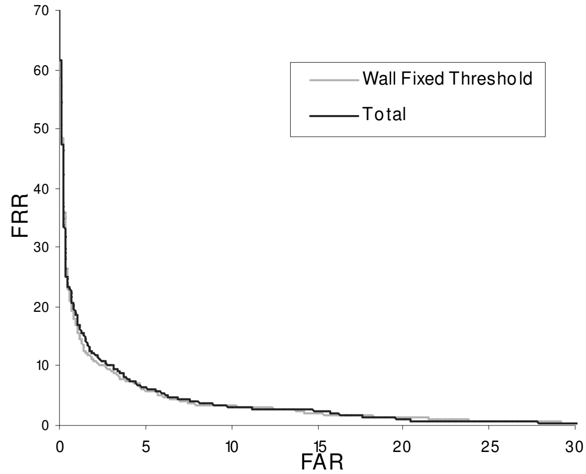

Fig. 8: FAR vs FRR in case of polygonalisation

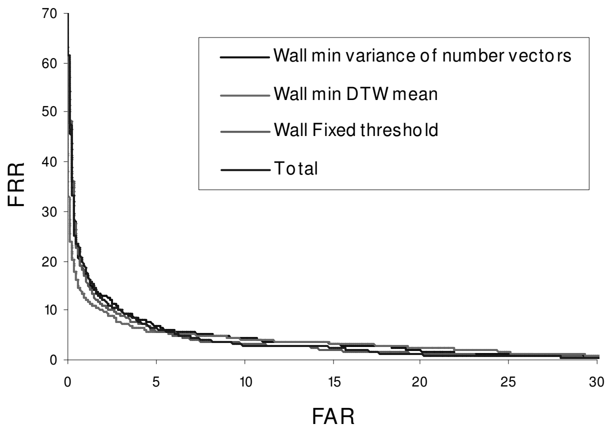

Fig. 9: FAR vs FRR.

Moreover, with a fixed threshold, we observe a considerable reduction of FRR.

Concerning the first search criterion with an individualized threshold (stability of the number of selected points) the results obtained are worse than those obtained with a fixed threshold. We note that the value of EER is increased by 36% compared to that obtained with a fixed threshold.

Concerning the second criterion, minimization of the mean of the intra-signer distances, the results obtained are better than those obtained with a fixed threshold. We note that the value of EER is reduced by 3,6% compared to that obtained with a fixed threshold. This improvement is relatively small compared to the processing necessary to find this threshold. So we note that the individualized threshold used for the point selection can be independent from the signer.

	Total	Random	Genetic Algorithm	Wall fixed threshold	Wall min Variance of numbers of vectors	Wall min DTW mean
EER	5.90%	7.10%	7.70%	5.70%	6.10%	5.70%

Table 1. EER results according to the different presented method

The method using Wall algorithm with fixed threshold for computing distance between signatures gives the best result. So the selection of points based on the Wall algorithm allows to reduce, by an important way, the number of points without decreasing authentication performances.

5.4. Improvements

Here we are studying how important is the influence of the number of signatures in the training set.

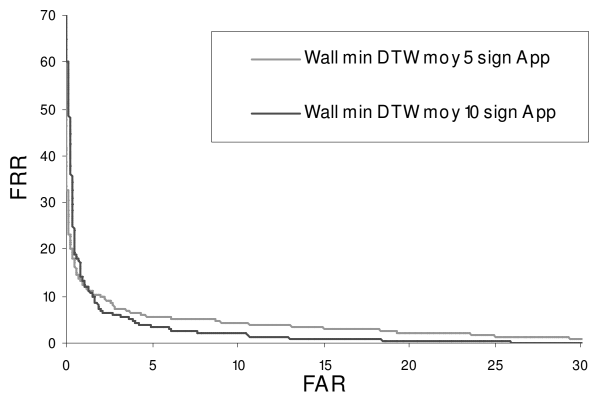

Fig. 10: FAR vs FRR according to the training set

We have tested the best method presented previously, i.e. the approximation polygonal method with an individualized threshold obtained by minimization of the mean of the distances between training signatures. 10 signatures have been considered for training instead of 5. We obtain thus a reduction of 25% of EER, i.e. a value of EER of 4,2%. The number of training signatures has a strong influence on the resulting authentication system quality.

6. Conclusion

Our study shows that the presented method for selecting representative points allows to smooth the initial data and thus to eliminate the noise contained in the signatures before comparing them, which makes it possible to improve the results of the authentication system. Moreover, the results obtained illustrate the fact that among all the methods suggested to select the best representative points, polygonal approximation with a threshold adapted to the user is the best. Indeed the points retained by the Wall algorithm allow to have better results than the best obtained by genetic algorithm. Moreover not preserving all the points of the signature allows to have a more stable representation.

One of the principal prospects is to take into account the signature dynamic in the computation of DTW and to study the impact of the reduction of data on this characteristic. Another improvement point consists in using a decision threshold adapted to the variability of the signatures of a person. Another approach to be explored is to change the metric and to use the Mahalanobis distance during DTW.

7. References

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