

Improved Critical Point Correspondence for On-line Signature Verification

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Abstract

This paper proposes an improved method to detect the critical points and obtain a matching path in 1 dimension (1D) for on-line signature verification. More critical points will be detected and the matching precision will be improved by the proposed method. We first detect critical points by searching 1D signature curves for extremum points. We then introduce an improved DTW algorithm, bidirectional backward-merging DTW (BBMDTW), for the flexible matching of two 1D signature curves. Finally, the critical points and their correspondences will be regressed to 2D signature curves, because the 2D signature curve has more physical appearances of a signer.

Keyword: Critical point correspondence, DTW, Backward-merging, 2D regression.

I. Introduction

The methods of on-line signature verification can be generally classified into two categories: function-based and parameter-based [1]. Critical point detection and correspondence are two stages of a parameter-based signature verification system. They are very important and difficult, because it is hardly achieved that we detect consistent critical points from each signature produced by a same signer. They are hot topics in the field of on-line signature verification that how to detect more critical points exactly and how to make correspondence of segments between two signatures more accurate. A signature is divided into segments in its 2D curve by detecting 2D critical points such as maximum curvature points[2,3] or local maximum points of 2D local velocity and angular velocity [4]. The classical DTW algorithm is used for the flexible matching of two signatures[5,7,8, 9] Using 2D detecting methods, the number of critical points that are detected is not sufficient. That is to say, there are a few complex segments which should be divided further. Furthermore, using classical DTW algorithm, incorrect segmentation cannot be overcome very well.

In this paper, we divide a signature into more and simpler segments by 1D detection. Only 5 novel features are defined for describing a 1D segment. An improved DTW algorithm, bidirectional

backward-merging DTW (BBMDTW for short), is introduced for 1D segments matching. This algorithm makes the flexible matching of two signatures more accurate. At last, two 1D matching paths which are produced by BBMDTW are regressed to 2D, because there are some redundant matching pairs that are produced in 1D segmenting and matching phases, and that the 2D signature curve has more physical appearances and can better represent the written action of a signer.

This paper consists of 5 sections. The critical point detection and the feature definition are introduced in section 2. In section 3, we describe the bidirectional backward-merging DTW algorithm and 2D regression of 1D corresponding paths in detail. The experiment results and comparisons are discussed in section 4. Finally, conclusions are given in section 5.

II. 1D Critical Point Detection and Feature Extraction

2D critical points are usually detected by searching for local maximum curvature or local minimum velocity points in a 2D signature curve. If a local part of a signature is not stably written by a signer, 2D critical points in this part can not be stably and accurately detected in each of his signatures. This will cause that some segments are divided incorrectly or some segments can not be divided at all. Furthermore, since critical points that are produced by 2D detection are not enough, fewer critical points will bring on that the shape of some 2D segments is complex and difficult to be described accurately.

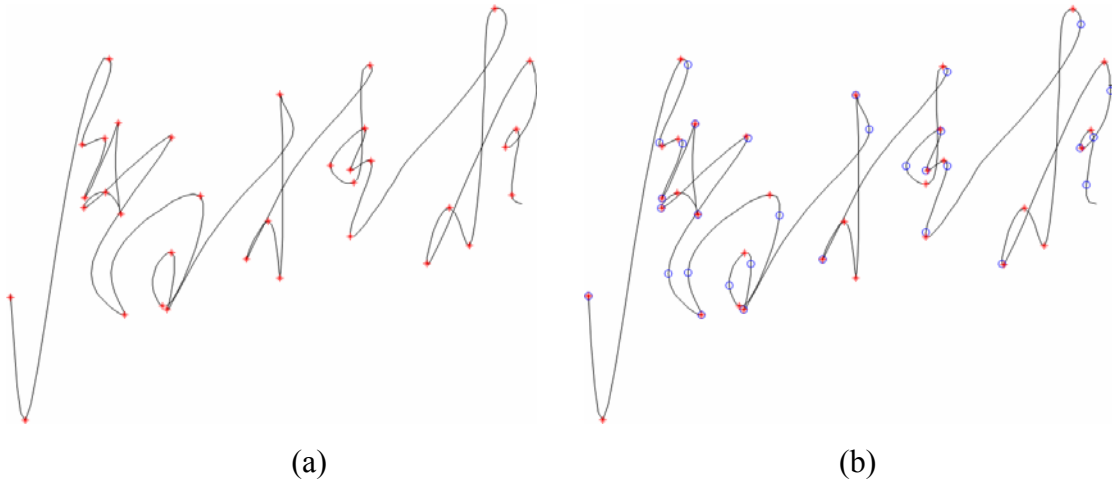


Fig. 1. The Comparison between the 2D detection and the 1D detection in a same signature. (a) Critical points detected by the 2D method. “*” denotes the 2D critical point. (b) Critical points detected by 1D method. “o” denotes the critical point in x-curve and “*” denotes the critical point in y-curve.

In order to detect more and reliable critical points and make the detection accurate, in the proposed method, we detect the critical point by searching for the local maximum and minimum point in the x-curve and the y-curve of a signature. A comparison of 2D detection and 1D detection in a same signature is shown in Fig. 2. We can see that the segments detected by 1D detection are so simple that the shape of segments is simpler, even some of these segments can be taken as linear segments. Whereas, there are also many redundant critical points to be detected, such as critical points which

are very close or even overlapping in 2D signature curve. These redundant points will be filtered by 2D regression in section 3.2.

After the detection of critical points, a 1D curve is divided into several 1D segments by these critical points. The information of a 1D segment can be classified into two parts: the information of its start and end critical points, and the information of the curve between this pair of neighboring critical points. Now, we give definitions of critical point features and curve features as following:

Let the point (c_i, t_i) denote the critical point i .

(1) Critical point features:

- The position of the critical point i :

$$p_i = \frac{t_i}{T}, \tag{1}$$

where T is the length of the whole 1D curve.

- The attribute of critical point i :

$$a_i = \begin{cases} crest \\ trough \end{cases}. \tag{2}$$

(2) Curve features:

- The distance between two neighboring critical points i and $i+1$:

$$l_i = \|((c_{i+1}, t_{i+1}) - (c_i, t_i))\|. \tag{3}$$

- The horizontal obliquity of the line connected critical points i and $i+1$:

$$\theta_i = \tan^{-1} \frac{c_{i+1} - c_i}{t_{i+1} - t_i}. \tag{4}$$

- The area enveloped by the straight line $l(t_i)$ and the curve $c(t_i)$ which connect critical points i and $i+1$:

$$s_i = \int_{t_i}^{t_{i+1}} \|c(t) - l(t)\| dt. \tag{5}$$

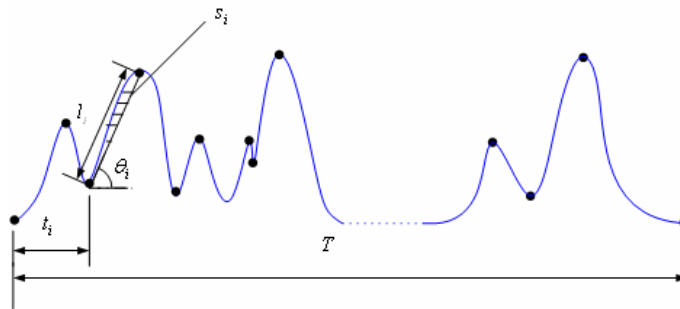


Fig. 2. Feature description of a 1D segment. “●” denotes the 1D critical point.

Fig. 2 shows the feature description of a 1D segment. We define a quintuple $h_i = (p_i, l_i, \theta_i, s_i, a_i)$ of these 5 features to describe the segment i .

III. Bidirectional Backward-Merging DTW and 2D Regression

When we get two sequences of quintuples, x-sequence and y-sequence, to describe the x-curve and the y-curve of a signature, it is necessary to introduce an algorithm of flexible matching to find the

optimum matching path between two different length sequences. DTW is just an effective algorithm for the flexible matching between two different length sequences.

Using the classical DTW algorithm, each segment is isolated during we calculate the distance between each pair of segments. If a segment is missed in the searching result, this segment will be regarded as a noise and thrown away. Actually, most of this kind of segment is not a noise but a part of an available segment. This segment is usually produced by incorrect segmentation. For example, in Fig. 3(a), segment 2 in curve B corresponds to segment 4 in curve A by the classical DTW, actually, segment 2 in curve B should correspond to both segments 2, 3 and 4 in curve A.

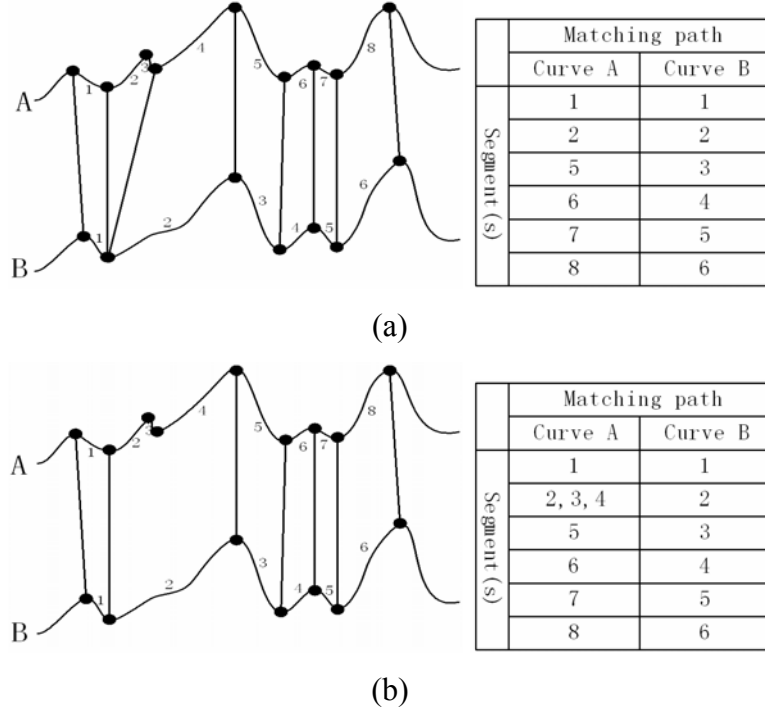


Fig. 3. Comparison of the classical DTW and the backward-merging DTW. (a). Correspondence of segments in two curves by the classical DTW, and the list of the matching path. (b) Correspondence of segments in two curves by the backward-merging DTW, and the list of the matching path.

A. Bidirectional Backward-Merging DTW

In order to overcome the shortage of incorrect segmentation, we design an improved DTW algorithm, bidirectional backward-merging DTW (BBMDTW) algorithm. By the definitions of 5 features defined in section 2, it is very easy to merge two or more neighboring segments into one segment. If we want to merge two neighboring segments, A and B, into a new segment C, critical point features of the new segment C are directly replaced by those of the fore segment A, and curve features of the new segment C need to be re-calculated by Eq. (3-5).

We define a matrix $D(I, J)$ to add up the distances between corresponding segments of two curves. The backward-merging DTW algorithm is given by:

$$D_{i,j} = \min \begin{pmatrix} D_{i,j-1} + d_{i,j} \\ D_{i-1,j} + d_{i,j} \\ D_{i-1,j-1} + d_{i,j} + p_1 \\ D_{i-1,j-3} + d_{i,merge(j-2,j)} + p_2 \\ D_{i-3,j-1} + d_{merge(i-2,i),j} + p_3 \end{pmatrix}, |i-j| \leq Tw, \quad (6)$$

where $d_{i,j}$ is the distance between element r_i and element t_j which belong to two different sequences respectively, and $D_{i,j}$ is the sum of the distances, and p_1 is the jump-punishment and p_2, p_3 are the merge-punishments. Tw is the maximum width of searching window. $merge(i-2,i)$ is a backward-merging function to merge the segment r_{i-2} and r_i which have same attribute (crest or trough).

Thinking about the instability of the merge, we only introduce one step merge of segments in Eq. (6). From the definition of BMDTW, we can see that both the noise segment and the incorrect segmentation are all taken into account. At the same time, a few instable parts also appear in the matching path. Namely, the matching paths that are produced by the forward BMDTW and the backward BMDTW are not identical entirely (different regions in Fig. 4 (a) and (b)). Therefore the Bidirectional BMDTW (BBMDTW) is introduced for eliminating the unstable parts of the matching path and adjusts the local matching paths to be more accurate.

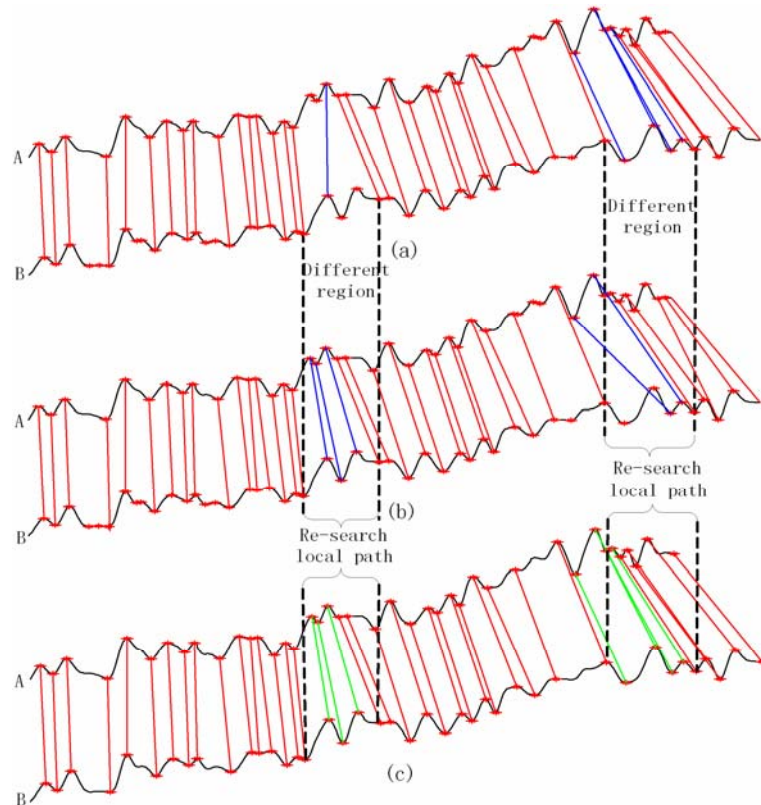


Fig.4. Matching paths produced by forward BMDTW, backward BMDTW and BBMDTW. (a) Matching path produced by forward BMDTW, (b) Matching path produced by backward BMDTW, (c) Matching path produced by BBMDTW.

We search for the optimal matching path based on BMDTW in two directions, forward and backward. For those local unstable parts, a quadratic searching is carried out. Fig. 4 shows the process that a matching path between two 1D signature curves is achieved by the BBMDTW. The BBMDTW algorithm is further described as following:

We define a structure to record the matching path

$$path = \{pair_i\}, pair_i = (tt_i^0, tt_i^1, rt_i^0, rt_i^1, d_i), 1 \leq i \leq P, \quad (7)$$

where P is the length of $path$. tt_i^0, tt_i^1 is the start and the end of the segment(or continuous segments) in one curve, and rt_i^0, rt_i^1 is the start and the end of the segment(or continuous segments) in the other curve. d_i is the distance between these two corresponding segments.

Two matching paths $path^F$ and $path^B$ are produced by the forward and backward BMDTW. In order to obtain a final optimal path, we search $path^F$ and $path^B$ as following steps:

Let $path^F$ and $path^B$ be two matching paths produced by the forward and backward BMDTW respectively.

$$\begin{cases} path^F = \{pair_i^F\} & pair_i^F = (tt_i^{F0}, tt_i^{F1}, rt_i^{F0}, rt_i^{F1}, d_i^F) \quad 1 \leq i \leq P \\ path^B = \{pair_j^B\} & pair_j^B = (tt_j^{B0}, tt_j^{B1}, rt_j^{B0}, rt_j^{B1}, d_j^B) \quad 1 \leq j \leq Q \end{cases} \quad (8)$$

(1) Record the segment pair as a stable matching pair which is under the following conditions

$$\begin{cases} tt_i^{F0} = tt_j^{B0}, & rt_i^{F0} = rt_j^{B0} \\ tt_i^{F1} = tt_j^{B1}, & rt_i^{F1} = rt_j^{B1} \end{cases}, \quad (9)$$

and then take them out of $path^F$ and $path^B$.

Do (1) until reach the end of $path^F$ or $path^B$.

(2) For the rest pairs in $path^F$ and $path^B$, search each group of pairs which is under the following conditions:

$$\begin{cases} tt_i^{F0} = tt_j^{B0}, & rt_i^{F0} = rt_j^{B0} \\ tt_{i'}^{F1} = tt_{j'}^{B1}, & rt_{i'}^{F1} = rt_{j'}^{B1} \end{cases}, \quad (i'-i) > 1, (j'-j) > 1, \quad (10)$$

and decide which is the local-optimal path by

$$\begin{cases} \{pair_m^F\}, i \leq m \leq i', & \text{if } \frac{\sum_i d_m^F}{(i'-i)} \leq \frac{\sum_j d_n^B}{(j'-j)}, \\ \{pair_n^B\}, j \leq n \leq j', & \text{else} \end{cases} \quad (11)$$

and record this local path.

Do (2) until reach the end of $path^F$ or $path^B$.

So a new optimal matching path is obtained by combining the new local-optimal matching paths and the stable matching pairs. Fig. 4 (c) shows a final optimal path produced by BBMDTW.

B. 2D Regression of 1D Critical Points and Their Correspondences

The matching path of two 1D signature curves can be directly used for verification [10]. Since it is a 2D written process that a signer writes his signature on the paper or tablet, and a signature is generally identified by eyes in 2D, 2D features are very important for verifying an on-line signature. In order to provide for 2D feature extraction and verification, 1D critical points and their correspondence in the matching path should be regressed into 2D signature curves.

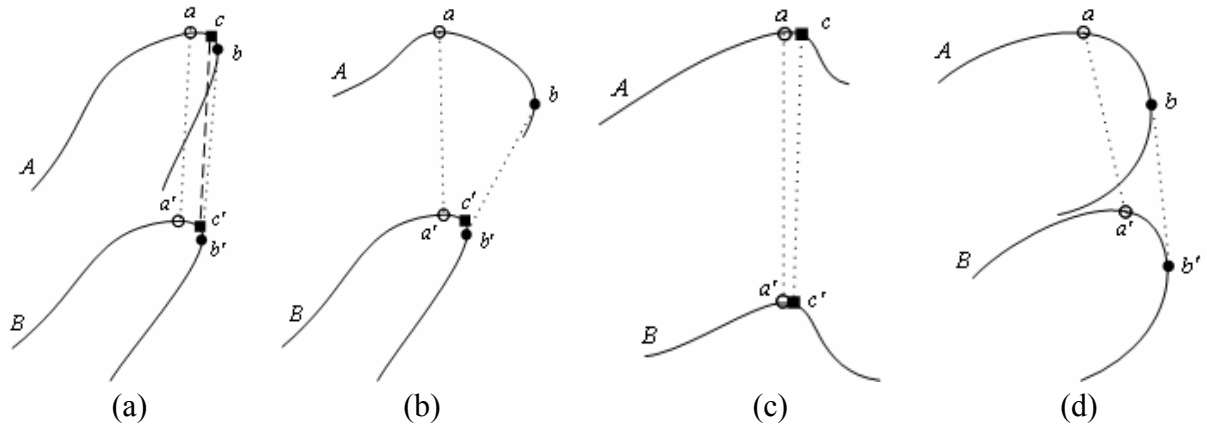


Fig. 5. Several instances of 2D regression of 1D corresponding pairs.

We generalize all kinds of 2D regression of 1D corresponding critical points into the following three instances:

- (1) A critical point a (Fig. 5 (a)) in the x -curve *and* its neighboring critical point b in the y -curve are very close or even overlapping in the 2D signature curve A . They are usually close to a 2D critical point c in the 2D signature curve. If their corresponding points a' and b' in the other signature curve B are also very close to a 2D critical point c' , these two pairs of 1D points can be replaced by their closest 2D critical points, and these two 2D points is recorded as a 2D matching pair. Otherwise, these 1D corresponding pairs will be thrown away (Fig. 5 (b)).
- (2) A critical point a (Fig. 5 (c)) in the x -curve *or* the y -curve is very close to a 2D critical point c . The 1D critical point a is replaced by the 2D critical point c . In the other signature curve B , if the corresponding critical point a' is also very close to a 2D critical point c' , it is replaced by this 2D point. Otherwise, it is replaced by a maximum curvature point in a predefining neighboring field.
- (3) If the distance between a 1D critical point a (Fig. 5 (d)) and its neighboring critical point b is not close (out of a predefining field) in the 2D signature curve A , and the 1D critical point a is also not close to any 2D critical point, we call the point a as an isolated point. This type of point is replaced by a maximum curvature point in a predefining field of the curve A . In the other signature curve B , the corresponding critical point a' is also replaced by a maximum curvature point in a predefining field of the curve B .

After two 1D matching paths of critical points are regressed to a new matching path of two 2D signature curves, not only some incorrect matching pairs are thrown away, but some redundant critical points which were mentioned in section 2 are filtered. In this matching path, more segment matching pairs are produced, and the critical points can be matched more accurately.

IV. Experimental Results

The proposed method has been evaluated with 800 genuine signatures from 200 Chinese writers. 400 pairs of genuine signatures (two pairs of signatures for each writer) are used for evaluation. We compare the proposed method (1D-BBMDTW for short) with the method which based on 2D critical point detection and classical DTW matching (2D-DTW for short).

We respectively count the correct and total matching segment pairs in all 400 testing samples. The total rate of correct matching pairs is increased from 93.35% of 2D-DTW to 97.23% of 1D-BBMDTW. In order to make a more detailed comparison, for each pair of testing signatures, a rate is defined to measure that the number of correct matching pairs based on 1D-BBMDTW method is more than, or equal to, or less than that based on 2D-DTW method. This rate can be calculated as following:

$$R^i = \frac{N_1^i - N_2^i}{N_2^i} \quad (12)$$

where N_1^i is the number of correct matching segment pairs in the testing sample i based on 1D-BBMDTW method, and N_2^i is the number of correct matching segment pairs of the testing sample i based on 2D-DTW method.

Table 1. Comparison of the number of testing samples which correct matching pairs based on 1D-BBMDTW are more than, equal to or less than those based on 2D-DTW.

Correct matching pairs of 1D-BBMDTW are	More than those of 2D-DTW	Equal to those of 2D-DTW	Less than those of 2D-DTW
Number of testing samples (total number is 400)	364	17	19
Rate (%)	91	4.25	4.75

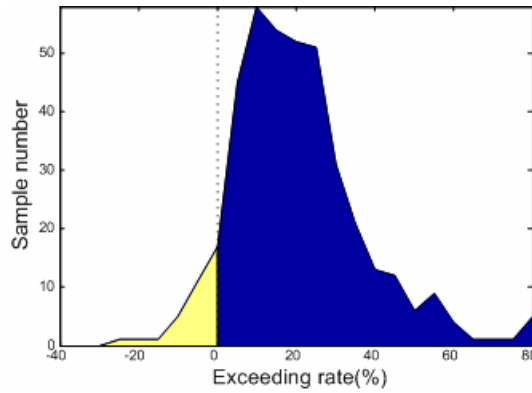


Fig. 6. The histogram of the rate that the correct matching pairs based on the proposed method exceed to those based on 2D-DTW method.

Table 1 shows the comparisons of the rate R . In total 400 testing samples, 91% (364 of 400) are that correct segment matching pairs based on 1D-BBMDTW method are more than those based on 2D-DTW method, 4.25% (17 of 400) are that correct segment matching pairs based on 1D-BBMDTW method are equal to those based on 2D-DTW method, and only 4.75% (19 of 400) are that correct segment matching pairs based on 1D-BBMDTW method are less than those based on 2D-DTW method. Fig. 8 shows a histogram of this experiment. The blue area denotes that the results of 1D-BBMDTW are better than those of 2D-DTW. The yellow area denotes that the results of 1D-BBMDTW are worse than those of 2D-DTW. We can observe that 1D-BBMDTW method can obtain more correct matching pairs in most of the testing samples (91%), and the exceeding rate R is mainly concentrated in about 20%.

We also give the detailed comparison between these two methods according to the complexity of Chinese signatures. Chinese character is a structural character that is composed by some simple natural-strokes. The complexity of a Chinese signature can be ordinarily represented by the number of its natural-strokes which are written by KaiShu type. In the further experiment, the testing set is divided into 5 subsets according to the natural-stroke number of each signature, and we test these two methods in these 5 subsets. The results are shown in Table 2. This table includes two parts: the comparison of the correct matching numbers in each testing sample between the proposed method and 2D-DTW method (row 3~5); the comparison of the correct matching rates in each testing sample between our method and 2D-DTW method (row 6~7).

Table.2. The comparison of matching results in the subsets of different complexity of signatures.

Number of natural strokes	< 15	≥ 15 < 20	≥ 20 < 25	≥ 25 < 30	≥ 30
Number of testing samples	36	114	142	84	24
Correct matching pairs of the proposed method are <i>more than</i> those of 2D method	88.89%	89.47%	88.73%	96.43%	95.83%
Correct matching pairs of the proposed method are <i>equal to</i> those of 2D method	8.33%	4.39%	4.93%	2.38%	0%
correct matching pairs of the proposed method are <i>less than</i> those of 2D method	2.78%	6.14%	6.34%	1.19%	4.17%
Average correct matching rate based on 2D-DTW method	92.66%	93.41%	93.63%	92.68%	94.75%
Average correct matching rate based on the proposed method	95.85%	96.05%	96.90%	97.04%	98.03%

The first part of Table 2 shows that they are 88.73~96.43% of tests in 5 subsets that correct matching pairs of the proposed method are more than those of 2D-DTW. Especially, in the subsets of 25~30 and more than 30 natural strokes, they are 96.43% and 95.83% respectively that correct matching pairs of the proposed method are more than those of 2D-DTW. In the second part of Table 2, we can see that the average correct matching rates based on the proposed method are all higher than those based on 2D-DTW method in five subsets. A higher correct matching rate is very important, because incorrect segment matching pairs would decrease the performance of the whole system directly. With the number of a signature's nature-strokes becoming larger, the average correct matching rate of the proposed method also increases, but that of 2D-DTW method has not a obvious change. This is because that the classical DTW algorithm does not take the incorrect segmentation into account. In the proposed method, we filter not only the incorrect segmentation but also some incorrect matching pairs by BBMDTW and 2D regression. Therefore, the correct matching rate of the proposed method is higher than that of 2D-DTW method for most of the testing samples, especially, for those complex signatures.

V. Conclusion

An improved method of critical point correspondence is introduced in this paper. The aims of the proposed method are that improve the precision of the flexible matching and increase the number of correct matching pairs. The critical point is detected in 1D instead of 2D, and then 5 simple and novel features are defined to describe each 1D segment. An improved DTW algorithm, bidirectional backward-merging DTW(BBMDTW), is introduced for the flexible matching of two 1D curves. Since the backward-mergence and bidirectional searching are introduced into the classical DTW algorithm, the incorrect segmentation and the local incorrect matching can be filtered, and the precision of the flexible matching is increased. At last, two 1D matching paths are regressed to a 2D matching, because the 2D signature curve has more physical appearances and can better represent the written action of a writer. The experiments show that the proposed method obtains better results in the matching precision and the number of correct matching pairs.

The proposed method is a part of on-line signature verification system. Many verification methods can be used in next stages of a system, after the segment matching path are produced by the proposed method.

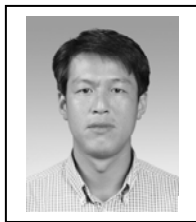
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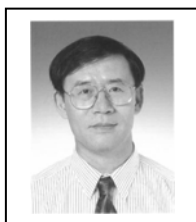
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