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A Novel Multiple Distances Based Dynamic Time Warping Method for Online Signature Verification

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Abstract. In this paper, a novel Multiple Distances Based Dynamic Time Warping (MDB-DTW) method is proposed for signature verification. In order to obtain more discriminative and complementary information, we take accounts of the multiple distance measurements on the Euclidian distance based DTW path. In addition, two classifiers (SVM-based classifier and PCA-based classifier) are adopted to fuse the useful information and remove the noise from the multiple dissimilarity vector space. The comprehensive experiments have conducted on three publicly accessible datasets MCYT-100, SUSIG and SVC-task2 with the obtained EER results are 1.87%, 1.28% and 6.32% respectively, which further demonstrates the robust and effectiveness of our proposed MDB-DTW method.

Keywords: Online Signature Verification; Multiple Distance Measurements; Dynamic Time Warping; Biometrics

1   Introduction

Automatic signature verification has been an active research area due to its social and legal acceptance, and the written signatures are also in widespread use as a personal authentication method. There are many types of research on signature verification [1-3] while it still remains a challenging task, owing to the large intra-class variations and, when considering skilled forgeries, small inter-class variations [4].

There are two different kinds of signatures depending on different data formats [5]. The off-line signature verification mainly deals with the signature images scanned from documents and papers. While the on-line signature verification utilizes specific devices like touch screens and digital tablets to capture dynamic time sequences (e.g. x, y coordinates and pressure, etc.). Therefore, it can utilize richer dynamic information with more accurate results comparing with the off-line mode. When considering the forged signatures, it can be divided into two categories, namely random and skilled forgeries. It's obvious that the skilled forgeries are more

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challenging due to its small inter-class variations and thus, we will focus on the skilled forgeries for on-line signature verification.

For the on-line signature verification system, the users first should be registered with genuine samples, referred as a reference set. Then, when a user presents a signature referred as a test sample, claiming to be a particular individual, the test sample will be compared with the reference set of that claimed individual. If the dissimilarity score is above a predefined threshold, this test sample will be rejected as a forgery.

So far many methods have been proposed to extract discriminative features and design effective classifiers for on-line signature verification. J. Fierrez et al. [6] proposed a function-based feature set, including three basic and four extended time sequences and applied this 7-dimension feature vector into a HMM-based model. To alleviate the instability of the signature length, Fischer et al. [7] utilized distance normalization as well as the DTW algorithm to verify a user. A well-designed SVM classifier is used in [8] and won the first prize in the first international signature verification competition. There are also various DTW-based signature verification algorithms. For example, Sharma et al. [9] exploited the information from the DTW cost matrix, while in [10], a GMM-DTW method was proposed to extract discriminative features.

In this paper, we propose a simple but effective feature fusion strategy based on multiple distance measurements and dynamic time warping algorithm (MDB-DTW). This strategy utilizes seven different kinds of distance measurements to extract discriminative information and then two different classifiers are implemented for making full use of the obtained information for the final decision, respectively.

The rest of the paper is organized as follows: Section 2 introduces the proposed MDB-DTW method, including seven different distance measurements, fusion strategy and two different classifier structures. The experimental results and analysis are presented in Section 3 and followed by conclusion in Section 4.

2 The MDB-DTW method

In this section, we will introduce the novel feature fusion strategy for the multiple distances based dynamic time warping algorithm. We first calculate the DTW dissimilarity and the aligned DTW path based on the Euclidian distance. With the Euclidian distance based aligned DTW path, we can calculate other six different distances based DTW dissimilarity and fuse them into a SVM-based classifier and a PCA-based classifier separately.

2.1 The original DTW dissimilarity

To align two sequences more precisely, we first extract a 7-dimension feature vector $[x_i, y_i, p_i, \theta_i, v_i, \rho_i, \alpha_i]$ in Table 1 for each ith sequence point [6] before implementing the DTW algorithm. The dot superscript in Table 1 can be calculated by formula (1).

$$\dot{f}_i = \frac{\sum_{\varepsilon=1}^{2} \varepsilon \left(f_{i+\varepsilon} - f_{i-\varepsilon} \right)}{2 \cdot \sum_{\varepsilon=1}^{2} \varepsilon^2} \quad (1)$$

Table 1 The description of the features

Features	Formulas
Path-tangent angle θ	$\theta_i = \arctan\left(\dot{y}_i / \dot{x}_i\right)$
Path velocity magnitude v	$v_i = \sqrt{\dot{x}_i^2 + \dot{y}_i^2}$
Log curvature radius ρ	$\rho_i = \log\left(v_i / \dot{\theta}_i\right)$
Total acceleration magnitude α	$\alpha_i = \sqrt{\dot{v}_i^2 + \left(v_i \cdot \dot{\theta}_i\right)^2}$

x, y, p denotes the (x, y) coordinates and the pressure.

As we all know, the signature length is variable even written by the same user. Therefore, the dynamic time warping is a suitable and efficient method to align two sequences with different lengths. Specifically, for two sequences $S = \left(s_{1,z}, s_{2,z}, \ldots s_{n,z}\right)$ and $T = \left(t_{1,z}, t_{2,z}, \ldots t_{n,z}\right)$, the distance matrix d can be calculated by formula (2) based on Euclidian distance where z denotes the zth feature dimension. Then the DTW dissimilarity $D(m,n)$ and the aligned DTW path W (Fig. 1) can be calculated by (3).

$$d(i,j) = \sum_{z=1}^{k} \left\| s_{i,z}, t_{j,z} \right\|_2 \quad (2)$$

$$D(i,j) = d(i,j) + min \begin{cases} D(i, j-1) \\ D(i-1, j-1) \\ D(i-1, j) \end{cases} \quad (3)$$
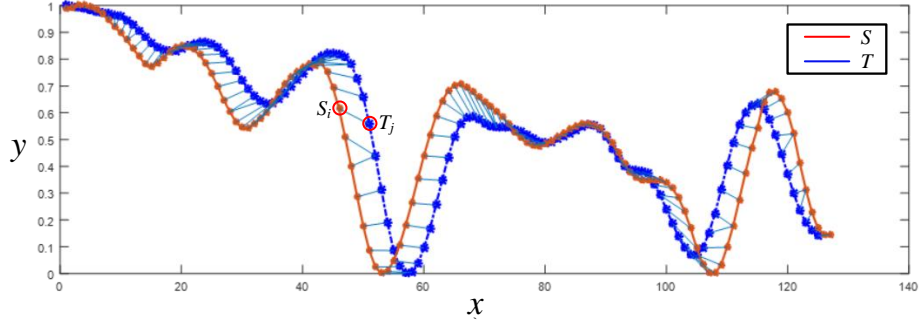

Fig.1 The pair points of the aligned DTW path

2.2 The multiple distances based DTW dissimilarity

As we have observed that different distance measurements have different characteristics in measuring sequences and multiple distance measurements can comprise a complementation group, which can gain more powerful discriminative ability for signature verification, so we proposed to use multiple distance measurements in this paper. Besides, we have made an assumption that the Euclidian

distance based DTW can well align two sequences for two reasons: a) the Euclidian distance is the simple and straightforward way for understanding; b) it could achieve better results in the single distance based signature verification system. Therefore, we choose it to align the signature sequences for verification.

To make full use of the Euclidian distance based aligned DTW path, we finally choose another six different distance measurements as listed in Table 1 to calculate $d(i,j)$ in (2). Considering the characteristic of different measurements, we divide these seven distance measurements into 2 groups, namely ==absolute numerical group== and ==shape distribution group==. The absolute numerical group mainly focuses on the numerical distance between two sequences, while the shape distribution group lays emphasis on the sequence shape and statistical distribution. Hence, the signature sample will be characterized more precisely by our proposed two different group descriptors.

Table 1 Introduction of seven distance measurements

Group	Distance No.	Formula
Absolute numerical measurement	1. Euclidian distance	$d(i,j) = \left\| S_i - T_j \right\|_2$
	2. Manhattan distance	$d(i,j) = \left\| S_i - T_j \right\|$
	3. Chebyshev distance	$d(i,j) = \max_z \left\| S_{iz} - T_{jz} \right\|$
	4. Standardized Euclidian distance	$d(i,j) = \sqrt{\sum_z \dfrac{(S_{iz} - T_{jz})^2}{std\left(\left[S_{iz}, T_{jz}\right]\right)}}$
Shape distribution measurement	5. Cosine distance	$d(i,j) = 1 - \dfrac{S_i \cdot T_j}{\sqrt{\sum_i S_i^2}\sqrt{\sum_i T_i^2}} = 1 - \dfrac{\langle S, T\rangle}{\|S\| \cdot \|T\|}$
	6. Correlation coefficient	$d(i,j) = 1 - \dfrac{\sum_i (S_i - \bar{S}_i)(T_i - \bar{T}_i)}{\sqrt{\sum(S_i - \bar{S}_i)}\sqrt{\sum(T_i - \bar{T}_i)}} = 1 - \dfrac{\langle S - \bar{S}, T - \bar{T}\rangle}{\|S - \bar{S}\| \cdot \|T - \bar{T}\|}$
	7. Bhattacharyya coefficient	$d(i,j) = \dfrac{1}{4}\dfrac{(\bar{S}_i - \bar{T}_j)^2}{\mathrm{var}(S_i) + \mathrm{var}(T_j)} + \dfrac{1}{2}\log\left(\dfrac{\mathrm{var}(S_i) + \mathrm{var}(T_j)}{2 \cdot \sqrt{\mathrm{var}(S_i) \cdot \mathrm{var}(T_j)}}\right)$

2.3 The SVM-based and PCA-based classifiers

It cannot be ignored that indeed, these seven distance measurements are highly correlated with each other. In other words, ==the information calculated by multiple distance measurements is overlapped and noisy.== To ==extract the tiny but useful information of a high dimension space==, we first apply the support vector machine (SVM) to the 7-dimension dissimilarity space inspired by [8]. Besides, considering to remove the correlation, we also adopt the principle component analysis (PCA) inspired by [11]. Finally, a distance normalization *DN-1* and a decision formula *ID2* proposed in [12] are used to calculate the decision score as shown by formula (4) and formula (5), respectively. In formula (4), *i* denotes the ith and j^{th} sample in reference

set and test set respectively, l denotes the length of the sample and n denotes the nth subject. In formula (5), the parameters (u_t, σ_t) and (u_r, σ_r) are corresponding to $D_{ref,ref} \sim N(u_r, \sigma_r^2), D_{ref,test} \sim N(u_r, \sigma_r^2)$ respectively. In summary, Algorithm 1 presents the whole procedure of our proposed MDB-DTW algorithm.

Algorithm 1: The MDB-DTW-SVM/PCA algorithm

Inputs: the x, y, p data of reference i^{th} sample R_n^i and test j^{th} sample T_n^j of subject n.

Outputs: the decision score $SCORE_n^j$ of R_n^i and T_n^j.

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1. Extract the 7-D feature vectors F_n^i, F_n^j with $F = [x, y, p, \theta, v, \rho, \alpha]$ in Section 2.1.

2. Calculate the Euclidian distance based DTW dissimilarity $DTW\text{-}DIST_1^{i,j}$ and the corresponding aligned DTW path $W^{i,j}$.

3. **FOR** distance 2 to 7 in Table 1:

    Calculate the other distance based DTW dissimilarity using Euclidian distance based aligned DTW path $W^{i,j}$: $DTW\text{-}DIST_{n,k}^{i,j} = \sum_{w \in W_n^{i,j}} d_k\left(F_n^{i,w_1}, F_n^{j,w_2}\right)$

4. **IF** MDB-DTW-SVM:

    Use $\left[DTW\text{-}DIST^{R,R}, DTW\text{-}DIST^{R,F}\right]_m^*$ as training data to train the SVM model.

    Transform the $DTW\text{-}DIST^{i,j}$ with the SVM model: $Dtrans_n^{i,j} = SVM\left(DTW\text{-}DIST^{i,j}\right)$

   Elif MDB-DTW-PCA:

    Apply PCA algorithm to $\left[DTW\text{-}DIST^{R,R}\right]_r^{**}$ and calculate the PCA coefficient: *coeff*.

    Transform the $DTW\text{-}DIST^{i,j}$ with the *coeff*: $Dpca_n^{i,j} = coeff \times DTW\text{-}DIST_n^{i,j}$.

    Use the first dimension of $Dpca_n^{i,j}$ as $Dtrans_n^{i,j} = \left[Dpca_n^{i,j}\right]_1$.

5. Apply distance normalization to $Dtrans_n^{i,j}$ with formula (4): $Dsn_n^{i,j} = DN\text{-}1\left(Dtrans_n^{i,j}\right)$.

6. Calculate the SCORE by formula (5): $SCORE_n^j = ID2\left(Dsn_n^{R,R}, Dsn_n^{R,j}\right)^{***}$.

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* m denotes the randomly-selected 10 subjects, R,R denotes one randomly-selected pair sequence in reference set, R,F in both reference and test set.

** r denotes 100 randomly-selected subjects (allow repeat), R,R denotes one randomly-selected pair sequence in reference set

*** $Dsn_n^{R,R} \sim N(u_r, \sigma_r^2)$ is calculated via reference set, and $Dsn_n^{R,j} \sim N(u_t, \sigma_t^2)$ is calculated between test sample and reference set.

$$DN\text{-}1: \ dist_n^{i,j} / l_n^j \quad (4)$$

$$ID2: \ D = (u_t - u_r) \times \left(\frac{\sigma_t}{\sigma_r}\right)^{0.4}, \ if \ \frac{\sigma_t^2}{\sigma_r^2} > T1$$

$$D = (u_t - u_r) \times \left(\frac{\sigma_r}{\sigma_t}\right)^{0.4}, \ if \ \frac{\sigma_t^2}{\sigma_r^2} < T1 \quad (5)$$

$$T1 = \left(\frac{(u_r - u_t)^2}{\sigma_r^2} + 1\right) \times 0.7$$

3   The experimental results

Three different online signature databases are used to evaluate our proposed MDB-DTW-SVM and MDB-DTW-PCA algorithm. Also, to make the experimental results more convincing, we set two strict protocols with fixed reference set and test set.

3.1   Database and protocol description

The MCYT-100 database [13] is comprised of 100 subjects and each subject contains 25 genuine samples and 25 skilled forged samples. The SUSIG database [14] consists of 94 subjects, 20 genuine samples and 10 skilled forged samples per subject, and the SVC-task2 [15] database contains 40 subjects, 20 genuine samples and 20 skilled forged samples per subject.

We have defined two protocols P5 and P10 for our experiments. For the protocols, we use the first 5 and 10 genuine samples as a reference set, and the rest of the genuine samples and all of the skilled forged samples of the corresponding subject as the test set, namely P5 and P10 respectively. To compare with other signature verification systems, we have reported the EER under the above-mentioned P5 and P10 protocols.

3.2   The experimental results

The EER results under the P5 and P10 protocols are listed in Table 2. It seems that the original DTW outperforms our proposed MDB-DTW method a little under the P5 protocol for MCYT-100 and SUSIG databases. This is expected because our MDB-DTW aims to dig the minor but discriminative information from the multiple distance measurements and it's reasonable that the more samples we used, the more information our MDB-DTW will capture to enhance the accuracy. The results further confirm our expectations.

Table 2 The EER (%) of the proposed MDB-DTW

Database	MCYT-100		SUSIG		SVC-task2	
Protocol	P5	P10	P5	P10	P5	P10
Original-DTW*	**2.98**	1.95	**1.91**	1.33	6.36	6.71
MDB-DTW-SVM	3	**1.84**	2.04	1.38	**6.26**	6.64
MDB-DTW-PCA	3	1.87	1.99	**1.28**	6.33	**6.32**

* The original-DTW refers to only use Euclidian distance based DTW and *ID2* decision formula in [12].

We also compare our proposed MDB-DTW with other signature verification approaches as listed in Table 3. To be noted that most evaluation protocols choose reference set randomly and thus it's unfair to directly compare the EER results. The randomly-chosen reference set is unreliable while our fixed protocols P5 and P10 are more convincing. In Table 3, our proposed MDB-DTW achieves the state of the art results except for the P5 protocol of MCYT-100 and P10 protocol of SVC-task2, even comparing with the randomly-chosen reference set. What's more, our proposed

MDB-DTW performs well in all three common signature databases, which further demonstrates the robust and effectiveness of our proposed MDB-DTW method.

Table 3 EER (%) summary of different signature verification approaches

Method	EER (%)		
	MCYT-100	SUSIG	SVC-task2
Path-DTW [9]	**2.76^5***	-	7.8^5*
SC-DTW [7]	3.94^5/2.74^{10}	3.09^5/2.13^{10}	-
KL-DTW [12]	3.16^5/2.25^{10}	2.13^5/1.6^{10}	-
DCT + Sparse representation [16]	-	2.98^{10}*	**5.61^{10}***
SVC2004 [15]	-	-	6.9^5
MDB-DTW- SVM [this work]	**3.00^5/1.84^{10}**	2.04^5/1.38^{10}	**6.26^5**/6.64^{10}
MDB-DTW-PCA [this work]	**3.00^5**/1.87^{10}	**1.99^5/1.28^{10}**	6.33^5/**6.32^{10}**

* select the reference set randomly
The superscript 5 and 10 denote the P5 and P10 protocol respectively

4   Conclusions

In this paper, we have proposed a novel MDB-DTW method, to extract discriminative information for signature verification. We found that multiple distance measurements can be complementary to each other and thus via the SVM or PCA method, more discriminative information can be utilized to enhance the accuracy. The experimental results show that our proposed MDB-DTW-SVM/PCA is robust and effective.

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