



Signature alignment based on GMM for on-line signature verification



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ABSTRACT

On-line handwritten signatures are collected as real-time dynamical signals, which are written on collective devices by users. Since writing environments are always changed, fluctuations can be caused by signature size, location and rotation angle which being various at each inputting. Signatures should be effectively aligned before verification, which can diminish deviations caused by these fluctuations. In this study, we propose a method of signature alignment based on Gaussian Mixture Model to obtain the best matching. In verification, a modified dynamic time warping with signature curve constraint is presented to improve the efficiency. Weight factors are dynamically assigned to features, which depend on coefficient of variation, to improve the robustness. Several experiments are implemented on the open access on-line signature databases MCYT and SVC2004 Task2. The best performances can be provided with equal error rates 2.15% and 2.63%, respectively. Experimental results indicate the effectiveness and robustness of our proposed method.

1. Introduction

As requirements of information security and identity verification increase, biometrics is gaining popularity as a more trustable alternative to password based security systems. On-line handwritten signature verification is one of the most acceptable technologies of biometrics due to the fact that on-line handwritten signatures have long been established as the most widespread means of personal verification. The signatures are difficult to be imitated and forged because they are unique and consistent for a given period. Experimental results presented in relevant literatures have indicated that the accuracy of on-line signature verification is not lower than other biometrics [1,2].

On-line signature verification could generally be divided into two groups, i.e., parametric approach and functional approach. In parametric approach, signatures are represented by series of parameters or vectors. Several common parameters have been extensively used, such as position, displacement, numbers of pen ups and pen downs, speed, acceleration, pen down time ratio, aspect ratio, etc. [1–4]. When functional approach is concerned, signatures are usually characterized in terms of time functions, some of the most commonly used functions are position trajectory, velocity, acceleration, centripetal acceleration, pressure, direction of pen movement, azimuth angle and altitude angle etc. [1,2,5,6]. Generally, it would obtain higher accuracy and reliability because the functional approach contains more dynamic information [2,4,6]. But functional approach often requires heavy computation during the process of matching or dissimilarity evaluation and it is less

efficient in most cases.

In verification process, the authenticity of a test signature is evaluated by matching its features against those stored in knowledge base for a given individual. There are some commonly used verification methods, such as template matching methods [7,8], statistics based methods [9–11], and structure based methods [12–14].

On-line handwritten signatures are collected as real-time dynamical signals and are presented as time series. During the process of collection, dynamic information of signatures is stored, such as position trajectory, timestamps, pen down and up status, pressure, azimuth and altitude angle, etc. By reasons of internal or psychological and external environments changes, there are fluctuations of size, location and rotation angle of signatures within the same user at different inputs. Furthermore, from the perspective of the kinematic, signatures are rapid and skilled human actions which mainly determined by the dynamics of muscle system. Signatures will not keep higher consistency for a long time since the writing habits and external environments changes. In this study, it is necessary to reduce the influence of fluctuations caused by variances of size, location and rotation angle, which could worsen the performance of verification. Thus, it is very important to effectively align the test signatures to references before verification.

The motivations of our work are emphasized on reducing the inconsistencies of signatures and improve the effectiveness of verification. Contributions of our work can be mainly described from three facts.

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- In order to reduce the fluctuations of various size, location and rotation at different inputs, we introduce the Gaussian Mixture Model (GMM) into signature alignment. According to GMM, The alignment of reference and test signature is considered as a probability density estimation problem. The reference is treated as GMM centroid, and test signature is aligned to the reference by maximum likelihood estimation. The optimal solution can be solved by Expectation Maximization (EM) algorithm.
- In order to improve the efficiency of on-line signature verification, we propose a modified dynamic time warping with signature curve constraint (DTW with SCC). In DTW with SCC, features are not matched by DTW directly. Instead, features are matched with the location constraints, which are inherent in two matching signature curves. The dissimilarity of features between test signature and reference is evaluated by distance dissimilarity probability. Not only DTW dynamic programming but also complete information of signatures is considered in our proposed method.
- In order to improve the robustness of verification, we introduce the coefficient of variation (CV) into feature weight factor assignment in verification stage. Considering various writing habits, features may have different effects on on-line signature verification. To emphasize on these diverse influences, different weight factors will be assigned dynamically to features depend on CV values.

2. Related works

Methods of signature alignment include size, location and rotation angle matching. In most of research works, signatures are aligned by size, location and rotation angle respectively. In methods of size alignment, **max-min normalization** and **z-score normalization** [15–17] are most used. Methods of location and rotation angle alignment are mainly mapping the location and rotation angle of test signatures onto the references coordinate system. The location alignment commonly uses the initial point and the signature centroid as the reference point [18,19]. While the rotation angle of signatures are aligned by minimum moment of inertia to reference system [19,20]. In addition, some researches pointed out that it should be necessary to normalize the sample points of signatures, i.e., signature curves should be re-sampled by equal interval distance [21–23]. From these points of view, test signatures and references should contain the same sample points after re-sample, which can reduce the complexity during matching or comparison in verification.

Iterative Closest Point (ICP) algorithm [24] is a well-known heuristic method for rigid point set in image analysis and pattern recognition due to its simplicity and low computational complexity. Assuming the initial position of two point sets is adequately close and the two point sets are roughly aligned, ICP iteratively assigns the correspondences based on a closest distance criterion and finds the least-squares rigid transformation relating the two point sets. Nonetheless, ICP is also sensitive to outliers and missing points during the alignment. To overcome the ICP limitations, many improved methods are proposed [25–28]. Out of these, probabilistic methods are more popular due to their abilities of dealing with the outliers and missing points during the matching. Recently, the methods of alignment based on Gaussian Mixture Model (GMM), such as **coherent point drift (CPD)** [29] and **robust point matching (RPM)** [30,31], are developed. In these methods, CPD and RPM treat one point set as the GMM centroid with equal isotropic covariance, the alignment of two point sets is altered to the centroid of GMM matching by maximum likelihood estimation, and the optimal solution can be obtained by expectation maximization (EM) algorithm. Besides, other optimization algorithms, such as kinematic wave model, hydrodynamic and zero inertia, etc., have been developed for designing and managing complex systems [32–37].

When template matching approaches are considered, **dynamic time warping (DTW)** is commonly used for signature matching. DTW is a

nonlinear optimization method, which is widely used in on-line signature verification. DTW provides normalization and alignment as a computational technique to make the best matching between two signatures, which might produce different sample points. During the process of DTW matching, it allows the time axes to compressed or expanded of two signatures to obtain the minimum distance. In this sense, DTW is able to solve the problem of signature matching very well in most cases [7,8,38]. However, heavy computation is one of the defects of DTW when sampled points included in signatures were increased. During the process of DTW matching, distances of all sampled points included in two signatures are calculated at first, and then the optimal path is planned by dynamic programming to obtain the minimum distance between the two signatures. The DTW will decrease efficiency of on-line signature verification. Some researchers proposed modified methods to improve the efficiency of DTW [8,39–41]. Most of these works mainly emphasize on the data reduction, and some information of signatures might be discarded during the verification.

3. Alignment for on-line signature

To reduce the influences of inconsistency on the performance of on-line signature verification, test signatures should be aligned to reference coordinate system before verification. These inconsistencies are mainly caused by variations of the size, location and rotation angle at different inputs.

3.1. Signature alignment with size

Size of signatures should be aligned due to variable size at each input, and these variations will increase the dissimilarities between test signatures and references. The commonly used method of size alignment (Size-alignment) is max-min normalization to standardize the size of signature [16–18].

$$\hat{s}_{size}(n) = \frac{s(n) - s_{min}}{s_{max} - s_{min}} \quad (1)$$

where, $\hat{s}_{size}(n) = (\hat{x}(n), \hat{y}(n))$ is normalized signature after size alignment, $s(n) = (x(n), y(n))$, $n = 1, 2, \dots, N$ is original signature before size alignment, $s_{min} = \min_{n=1,2,\dots,N} s(n)$ and $s_{max} = \max_{n=1,2,\dots,N} s(n)$. N is total number of sampled points of the signature.

3.2. Signature alignment with location

As stated, locations of signature are different on the collective device at each input, and these fluctuations may also increase the dissimilarities between the test signatures and references. Thus, locations of signature should be aligned before verification. The signature location may be mainly aligned by signature center (Center-alignment) or signature centroid (Centroid-alignment) [18,20,42].

Locations of signature can by aligned by signature center as

$$\hat{s}_{center}(n) = s(n) - s_{center} \quad (2)$$

where, $\hat{s}_{center}(n)$ is the signature after location alignment with signature center, $s_{center} = (s_{max} - s_{min})/2$, s_{max} and s_{min} are defined as above.

Location of signatures can be aligned by signature centroid as

$$\hat{s}_{centroid}(n) = s(n) - s_{centroid} \quad (3)$$

where, $\hat{s}_{centroid}(n)$ is the signature after location alignment with signature centroid, $s_{centroid} = \frac{1}{N} \sum_{n=1}^N s(n)$ is the centroid of signature curves.

3.3. Signature alignment with rotation angle

Fluctuations in orientation of signature can produce noise in the stage of verification. Thus, after size and location alignment, signatures

should be aligned by rotate the signature coordinate axes with a suitable reference angle to the standard reference coordinate system [19,20,43,44]. The coordinate axes of signatures can be rotated by means of a rotation matrix as bellow

$$\hat{x}(n) = x(n) \cdot \cos(\alpha) - y(n) \cdot \sin(\alpha) \quad (4)$$

$$\hat{y}(n) = x(n) \cdot \sin(\alpha) + y(n) \cdot \cos(\alpha) \quad (5)$$

where, $\hat{x}(n)$ and $\hat{y}(n)$ are the new signature curves after rotation angle alignment, $x(n)$ and $y(n)$ are the original signature curves, α is the reference rotate angle, which can be calculated as bellow

$$\alpha = \frac{1}{2} \arctan\left(\frac{2I_{xy_centroid}}{I_{y_centroid} - I_{x_centroid}}\right) \quad (6)$$

where, $I_{xy_centroid}$, $I_{x_centroid}$ and $I_{y_centroid}$ are the moments of inertia referred to the reference centroid, which can be calculated as,

$$I_{xy_centroid} = I_{xy0} - Nx_{centroid}y_{centroid} \quad (7)$$

$$I_{x_centroid} = I_{x0} - Ny_{centroid}^2 \quad (8)$$

$$I_{y_centroid} = I_{y0} - Nx_{centroid}^2 \quad (9)$$

$$I_{xy0} = \sum_{n=1}^N x(n)y(n) \quad (10)$$

$$I_{x0} = \sum_{n=1}^N y^2(n) \quad (11)$$

$$I_{y0} = \sum_{n=1}^N x^2(n) \quad (12)$$

3.4. Signature alignment based on GMM

As previous methods of signature alignment being used, signatures are aligned sequentially by size, location and rotation angle. The accumulative errors will decrease similarities during the matching process. At this point, we propose a probabilistic method of signature alignment based on Gaussian Mixture Model (GMM-alignment). According to GMM-alignment, the size, location and rotation angle of test signature can be effectively aligned to reference.

Let $s^{ref}(n) = (x^{ref}(n), y^{ref}(n))$ and $s^{test}(m) = (x^{test}(m), y^{test}(m))$ be reference signature and test signature, respectively, where, $n = 1, 2, \dots, N$ and $m = 1, 2, \dots, M$ are sampled points included in $s^{ref}(n)$ and $s^{test}(m)$. (x, y) denotes the signature curve. GMM-Alignment considers two point sets of reference and test signatures as a probability density estimation problem, where, the reference is represented as the **centroid of GMM**, and test signature is considered as the data points set to be aligned. Test signature $s^{test}(m)$ becomes the GMM centroid of reference signature $s^{ref}(n)$ through the transformation $\Gamma(s^{test}(m), \theta)$. At the optimum, the test signature $s^{test}(m)$ and reference signature $s^{ref}(n)$ are aligned and the correspondence is obtained by the maximum of the **GMM posterior probability**. The GMM probability density function is given as

$$p(s^{ref}(n)) = \sum_{m=1}^M \omega_m p(s^{ref}(n) | \Gamma(s^{test}(m), \theta), \sigma^2) \quad (13)$$

where, $p(s^{ref}(n) | \Gamma(s^{test}(m), \theta), \sigma^2) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{\|s^{ref}(n) - \Gamma(s^{test}(m), \theta)\|^2}{2\sigma^2}\right)$ denotes the density distribution probability of Gaussian components. σ^2 is the equal **isotropic covariance**, assuming the equal membership probability for all GMM components. ω_m denotes the weight factors of uniform distribution, and $\sum_{m=1}^M \omega_m = 1$. For simplicity, set all points included in $s^{test}(m)$ be equal weighted, i.e., $\omega_m = 1/M$. $\Gamma(s^{test}(m), \theta) = s_c R s^{test}(m) + t$ denotes the transformation function applied to $s^{test}(m)$, where

$\theta = \langle s_c, R, t \rangle$ is a set of transformation parameters, s_c denotes scaling factor, R is rotation matrix, and t denotes translation vector.

According to GMM-alignment, the test signature $s^{test}(m)$ can be maximally approximated to the reference $s^{ref}(n)$ through the transformation for obtaining the maximum likelihood. The correspondence probability between $s^{test}(m)$ and $s^{ref}(n)$ can be estimated by joint probability distribution,

$$P(s^{ref}(n) | \Gamma(s^{test}(m), \theta)) = \prod_{n=1}^N p(s^{ref}(n) | \Gamma(s^{test}(m), \theta), \sigma^2) \quad (14)$$

where, $P(s^{ref}(n) | \Gamma(s^{test}(m), \theta))$ is transformation parameter model with $\Gamma(s^{test}(m), \theta)$ and σ^2 , and it can be solved by the maximum likelihood estimation or equivalently by minimized the negative log-likelihood function,

$$\Theta(\Gamma(s^{test}(m), \theta), \sigma^2) = - \sum_{n=1}^N \log \left(\sum_{m=1}^M P(m) p(s^{ref}(n) | \Gamma(s^{test}(m), \theta), \sigma^2) \right) \quad (15)$$

To obtain the best matching of test signature $s^{test}(m)$ being aligned to reference signature $s^{ref}(n)$, it should find the optimal transformation $\Gamma(s^{test}(m), \theta)$ to minimize the $\Theta(\Gamma(s^{test}(m), \theta), \sigma^2)$. Obviously, it is nonlinear function of $\Theta(\Gamma(s^{test}(m), \theta), \sigma^2)$ about $\Gamma(s^{test}(m), \theta)$, and the optimum solution can be estimated by **Expectation Maximization (EM)** algorithm. The basic idea of EM is (1) E-step: compute the posteriori probability $P_{old}(m | s^{ref}(n))$ of GMM components by the Bayes' theorem using the old estimate parameter values of $\Gamma_{old}(s^{test}(m), \theta)$ and σ_{old}^2 ; (2) M-step: the new parameter values can be estimated by minimizing the negative log-likelihood function,

$$\Theta(\Gamma(s^{test}(m), \theta), \sigma^2) = \frac{1}{2\sigma^2} \sum_{n=1}^N \sum_{m=1}^M P_{old}(m | s^{ref}(n)) \cdot \|s^{ref}(n) - \Gamma(s^{test}(m), \theta)\|^2 + N_p \log(\sigma^2) \quad (16)$$

where, $N_p = \sum_{n=1}^N \sum_{m=1}^M P_{old}(m | s^{ref}(n))$. $P_{old}(m | s^{ref}(n))$ is the posterior probabilities of GMM components, and can be calculated by previous parameter values,

$$P_{old}(m | s^{ref}(n)) = \frac{\exp\left(-\frac{1}{2} \frac{\|s^{ref}(n) - \Gamma(s^{test}(m), \theta)\|^2}{\sigma_{old}^2}\right)}{\sum_{m=1}^M \exp\left(-\frac{1}{2} \frac{\|s^{ref}(n) - \Gamma(s^{test}(m), \theta)\|^2}{\sigma_{old}^2}\right) + 2\pi\sigma^2 \frac{1}{M-1} \frac{M}{N}} \quad (17)$$

Actually, the signature curves alignment can be simplified by the minimizing the square error between the reference $s^{ref}(n)$ and transformed test signature $\Gamma(s^{test}(m), \theta)$

$$\arg \min \left(\sum_{n=1}^N \sum_{m=1}^M \|s^{ref}(n) - \Gamma(s^{test}(m), \theta)\|^2 \right) \quad (18)$$

It is the multi-parameter optimization problem, i.e. parameter t and s_c can be optimized with constrains of R , while R can be estimated by singular value decomposition (SVD).

4. DTW matching with SCC

When template matching approaches are considered, DTW is commonly used for signature matching. In DTW algorithm, a full distance matrix, which includes all distances between sampled points contained in two signatures, should be calculated at first. Then the optimal path is planned by dynamic programming to obtain the minimum distance. It would be heavy computation and inefficiency when sampled points included in signatures increasing. We propose a modified method based on DTW with **SCC** for signature distance dissimilarity evaluation. In DTW with SCC, features are not matched by DTW directly. Instead, features are matched with the location constraints, which are inherent in two matching signature curves. The location constraint can be obtained by optimal path, which is dynamic

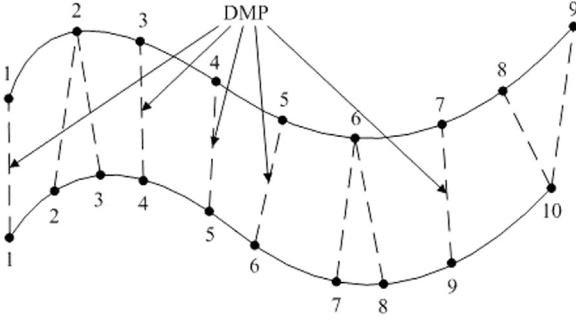


Fig. 1. DTW matching path of two sequences.

programming planned during the DTW matching of the two signature curves.

For a given user, test signature curve $s^{test}(m)$ is matched with reference signature curve $s^{ref}(n)$ by DTW at first. Optimal matching path is obtained by dynamic programming, i.e., $W_{path} = w_1, w_2, \dots, w_r, \dots, w_R$, where, $w_r = (w_{s^{ref}}(r), w_{s^{test}}(r))$ denotes the matching pairs on the DTW path, which is called the SCC in our work. $w_{s^{ref}}(r)$ and $w_{s^{test}}(r)$ are matching points on the path included in reference and test signature curves, respectively. $r = 1, 2, \dots, R$, and R is the length of the optimal path of DTW. During the DTW matching, there might be one-to-one matching points and one-to-many matching points, out of these, the one-to-one matching points are called direct matching points (DMP). Generally, DMP indicates higher similarity and more consistent between two matching signatures. The DMP during the process of DTW matching is shown in Fig. 1.

Consistent penalty factor (SPF) of DTW matching can be defined,

$$K_{DMP} = \frac{N_{DMP}}{\max(N, M)} \quad (19)$$

where, K_{DMP} denotes the SPF of DTW matching, N_{DMP} is number of DMP in DTW matching, N and M are lengths of two signatures, respectively, $N_{DMP} \leq \min(N, M)$. Greater value of K_{DMP} indicates the higher similarity between two signatures.

An example of SCC is also given in Fig. 1. With the optimal path of DTW having been planned, matching pairs on DTW path are obtained as w_r , the length of optimal path $R=11$. Matching points on the path included in reference and test signature curves can be given as $w_{s^{ref}}(r) = \{1, 2, 2, 3, 4, 5, 6, 6, 7, 8, 9\}$ and $w_{s^{test}}(r) = \{1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 10\}$. With SCC, the dissimilarity of feature f_k between reference and test signature can be calculated by,

$$dist_{f_k} = \frac{1}{K_{DMP}} \sum_{r=1}^R |f_k(w_{s^{ref}}(r)) - f_k(w_{s^{test}}(r))| \quad (20)$$

According to the discussions above, not only the complete information of signatures but also the DTW dynamic programming is included in the proposed method of signature distance dissimilarity calculation.

The efficiency of on-line signature verification can be improved by the proposed method. The computational complexity of the proposed method is given by $O(N \cdot M + K \cdot (N + M - 1)) \cong O(N \cdot M)$ as opposed to $O(K \cdot N \cdot M)$ of DTW, where, K denotes the number of features used in on-line signature verification, N and M denote the length of two signatures, respectively.

For a given user, distance dissimilarity probability between test signature and reference signature can be evaluated,

$$P_{diss} = \sum_{k=1}^{N_r} \sum_{i=1}^{N_f} \varpi_k p(f_k | s^{ref_i}) \quad (21)$$

where, $p(f_k | s^{ref_i})$ is distance dissimilarity probability of feature f_k between test signature and the i th reference signature s^{ref_i} . $p(f_k | s^{ref_i}) = \frac{thres_{s^{ref_i}}}{dist_{f_k}}$, $dist_{f_k}$ is distance of feature f_k between test signature and reference s^{ref_i} , which can be calculated by (20). $thres_{s^{ref_i}}$ is threshold

of feature f_k of reference signature s^{ref_i} , which can be given by $thres_{s^{ref_i}} = \mu_{s^{ref_i}} + \beta \sigma_{s^{ref_i}}$, $\mu_{s^{ref_i}}$ and $\sigma_{s^{ref_i}}$ are mean and standard deviation of DTW with SCC distance between reference s^{ref_i} and other reference signatures for a given user. N_r and N_f are number of reference signatures and number of features which are used in verification, respectively. β is an empirical constant being adjusted to obtain EER curves of on-line signature verification. ϖ_k is the weight factor of feature f_k and $\sum_{k=1}^{N_f} \varpi_k = 1$, ϖ_k can be estimated by coefficient of variation (CV) in our work.

Set CV_{f_k} is the coefficient of variation of feature f_k for a given reference s^{ref_i} and is given as

$$CV_{f_k} = \frac{\sigma_{s^{ref_i}}}{\mu_{s^{ref_i}}} \quad (22)$$

where, $\mu_{s^{ref_i}}$ and $\sigma_{s^{ref_i}}$ are defined as above, and set $CV_{f_k} = 1$ when $\mu_{s^{ref_i}} = 0$ in limiting case. CV is a standardized measure of dispersion of a probability distribution. For reference s^{ref_i} of given user, weight factor of feature f_k can be estimated dynamically depend on CV value,

$$\varpi_k = \frac{CV_{f_k}}{\sum_{k=1}^{N_f} CV_{f_k}} \quad (23)$$

Considering various writing habits, features may have different effects on on-line signature verification. To emphasize on these diverse influences, different weight factors can be assigned dynamically to features depend on CV values.

5. Experiments

5.1. On-line signature verification dataset

Two standard on-line signature databases *MCYTSubcorpus100(DB1)* [45] and *SVC2004 Task2* [46] are used in our work, and several experiments are implemented to demonstrate the effectiveness and efficiency of our proposed method. DB1 and SVC 2004 Task2 databases are acquired with WACOM graphic tablet. Dynamic information of each signature is collected and stored, i.e., position in x-axis, position in y-axis, pressure applied by the pen, azimuth angle of the pen, altitude angle of the pen, timestamps and button status.

DB1 consists of 5000 western signatures from 100 users. For each user, there are 50 signatures in all, out of these, 25 signatures are genuine and 25 signatures are skilled forgeries. Since there are no references given directly from DB1, 5 genuine signatures are selected randomly to be used as references, and other 20 genuine signatures and 25 skilled forgeries are used to verification tests. SVC2004 Task2 database consist 1600 signatures from 40 users, including western signatures and Chinese signatures. For each user, there are 20 genuine signatures and 20 skilled forgeries. Out of these, 5 genuine signatures are selected randomly to be used as references, and other 15 genuine signatures and 20 skilled forgeries are used as test signatures. Thus, there are 5900 test signatures from 140 users to be verified in total.

The details of on-line signature verification databases used in our work are described as bellow.

Detailed description of DB1

- No. of users: 100
- No. of references: $100 \times 5 = 500$ (*genuines*)
- No. of test signatures:
 - $100 \times 20 = 2000$ (*genuines*);
 - $100 \times 25 = 2500$ (*skilledforgeries*)

Detailed description of SVC2004 Task2

- No. of users: 40
- No. of references: $40 \times 5 = 200$ (*genuines*)
- No. of test signatures:

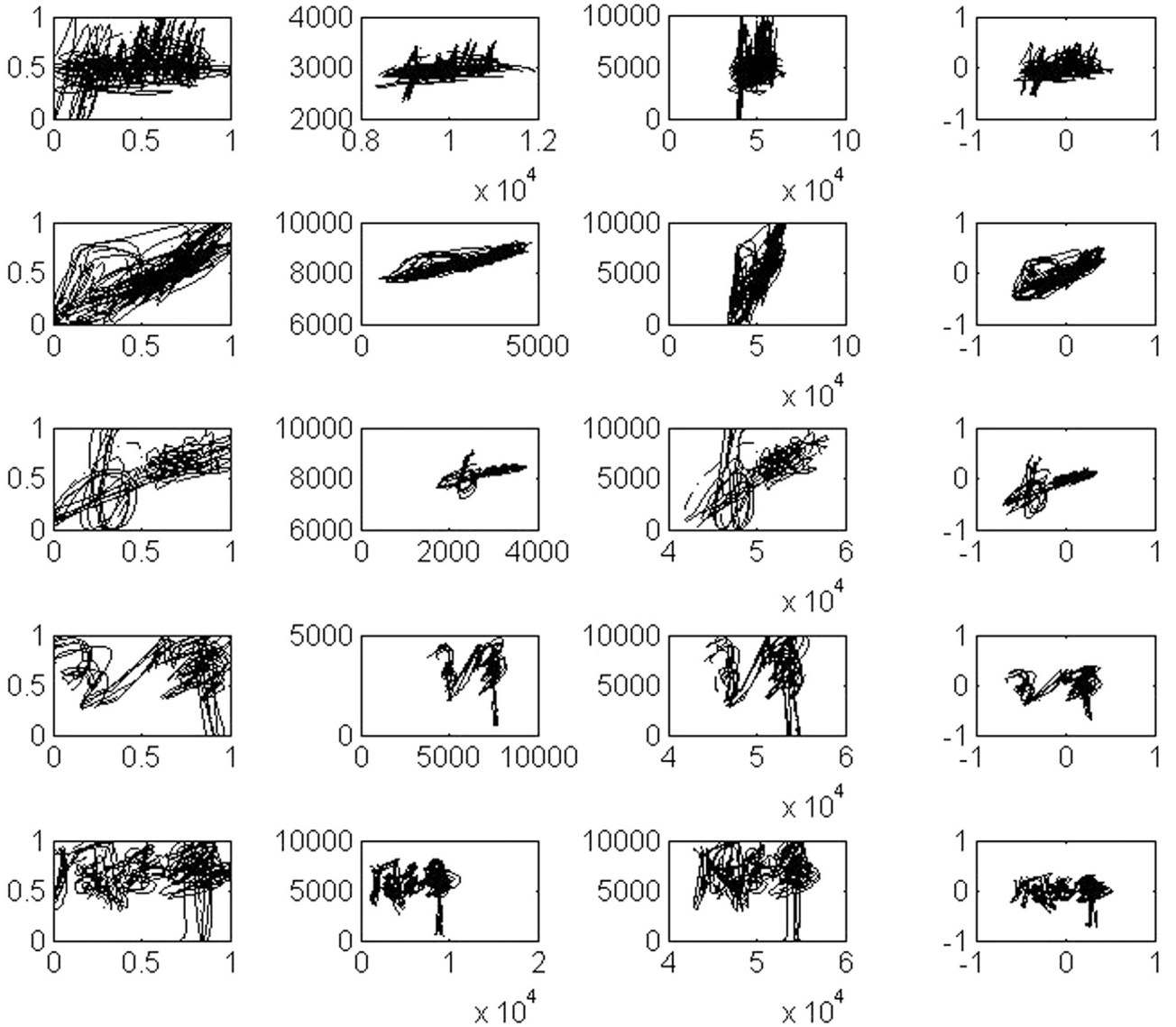


Fig. 2. Genuine signatures from 5 users (from top to bottom) are aligned by different methods, i.e., Size-alignment, GMM-alignment, Center-alignment and Centroid-alignment (from left to right). Where, signature in dash line is reference and signatures in solid line are genuines.

$$40 \times 15 = 600 \text{ (genuines);}$$

$$40 \times 20 = 800 \text{ (skilledforgeries)}$$

5.2. On-line signature alignment

User-20, -30, -80 from DB1 and user-19, -23 from SVC2004 Task2 are chosen randomly to be demonstrated the experiments of alignment. For each user, one reference signature is chosen as the template, while 10 genuine signatures and 10 skilled forgery signatures are also chosen randomly to be aligned to the template. To obtain the optimum matching and maximum similarity, different algorithms of signature alignment are carried, including Size-alignment, GMM-alignment, Center-alignment and Centroid-alignment. Results of signatures alignment are given in Figs. 2 and 3 respectively. In Figs. 2 and 3, signature in dash line denotes the reference signature, which is considered as the template to be aligned, while, signatures in solid line are test signatures.

From the Fig. 2, for genuine signatures alignment, the best matching is obtained by GMM-alignment, and the results of Centroid-alignment are acceptable, but, the worst matching is given by Size-alignment. For skilled forgeries alignment, the same conclusions can be obtained from Fig. 3. The experimental results illustrate

that the best matching between test and reference signatures can be obtained by GMM-alignment. Sub-sequential experiments will indicate that the best alignment could improve the performance of on-line signature verification.

5.3. Feature extraction

5 features are empirically extracted to be used for on-line signature verification, i.e., **Feature** = $\langle f_1, f_2, f_3, f_4, f_5 \rangle$.

1. $f_1 = y(n)$: signature position in y -direction
2. $f_2 = p(n)$: writing pressure
3. $f_3 = v_x(n)$: writing linear velocity in x -direction.
 $v_x(n) = (x(n+1) - x(n-1))/2$. For the initial point and end point, the linear velocity can be calculated $v_x(1) = x(2) - x(1)$ and $v_x(N) = x(N) - x(N-1)$ respectively.
4. $f_4 = v_y(n)$: writing linear velocity in y -direction.
 $v_y(n) = (y(n+1) - y(n-1))/2$. For the initial point and end point, the linear velocity can be calculated $v_y(1) = y(2) - y(1)$ and $v_y(N) = y(N) - y(N-1)$, respectively.
5. $f_5 = a_c(n)$: writing centripetal acceleration. $a_c(n) = (v_x(n) \cdot a_y(n) - v_y(n) \cdot a_x(n)) / v(n)$. where, $a_x(n)$ and $a_y(n)$ are linear acceleration

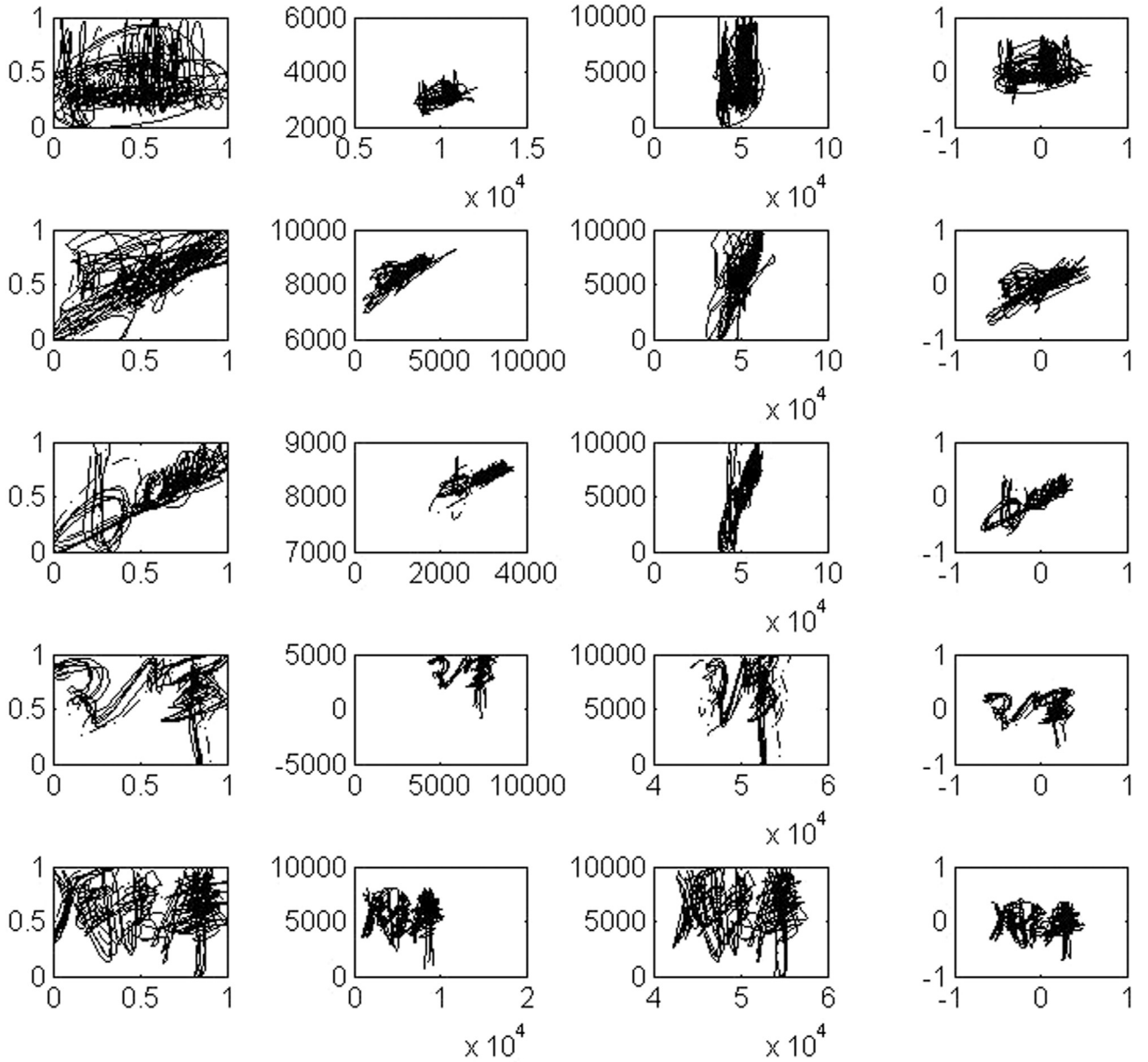


Fig. 3. Skilled forgeries from 5 users (from top to bottom) are aligned by different methods, i.e., Size-alignment, GMM-alignment, Center-alignment and Centroid-alignment (from left to right). Where, signature in dash line is reference and signatures in solid line are skilled forgeries.

in x -direction and y -direction, respectively, which can be calculated by $a_x(n) = (v_x(n+1) - v_x(n-1))/2$ and $a_y(n) = (v_y(n+1) - v_y(n-1))/2$. Similarly, for the initial point and end point, linear acceleration can be calculated by $a_x(1) = v_x(2) - v_x(1)$, $a_x(N) = v_x(N) - v_x(N-1)$, and $a_y(1) = v_y(2) - v_y(1)$, $a_y(N) = v_y(N) - v_y(N-1)$. $v(n)$ is absolute writing velocity, $v(n) = \sqrt{v_x^2(n) + v_y^2(n)}$.

5.4. Experimental results

To demonstrate the effectiveness of our proposed method, the authenticity of 5900 test signatures from 140 users are determined. Error rates of equal error rate (EER), false reject rate (FRR) and false accept rate (FAR) are adopted to evaluate the performance of on-line signature verification. Out of these, EER could indicate the security level of a given biometrics system. Experimental results of different methods of signature alignment are given in Table 1, in which DTW is used as dissimilarity evaluation. From Table 1, there are lowest EER 3.07% and 3.84% can be provided by GMM-alignment method

Table 1

Performance of the system measured with FRR, FAR and EER in % for different alignment methods.

Database	Methods	FRR (%)	FAR (%)	EER (%)
DB1	Size-alignment	5.62	6.22	5.92
	GMM-alignment	2.91	3.23	3.07
	Center-alignment	4.00	7.08	5.54
	Centroid-alignment	5.22	4.08	4.15
SVC2004	Size-alignment	6.88	8.98	7.93
	GMM-alignment	3.56	4.12	3.84
	Center-alignment	6.02	7.88	6.95
	Centroid-alignment	4.57	6.15	5.36

implemented on DB1 and SVC2004 Task2, respectively. Experimental results indicate that it could obtain the max similarity between the test and reference signatures after GMM-alignment. Thus, in our subsequent experiment, GMM-alignment is used for signature

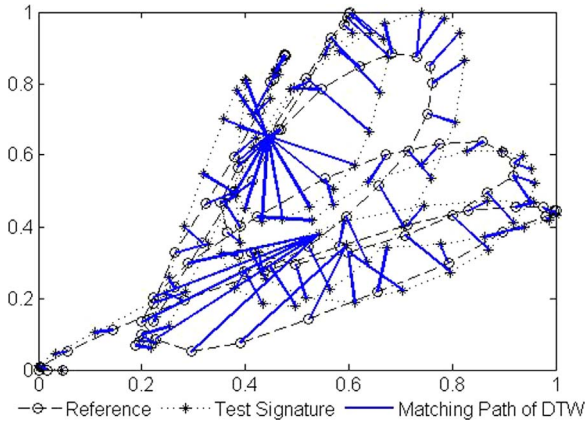


Fig. 4. Signature curves matching path of DTW.

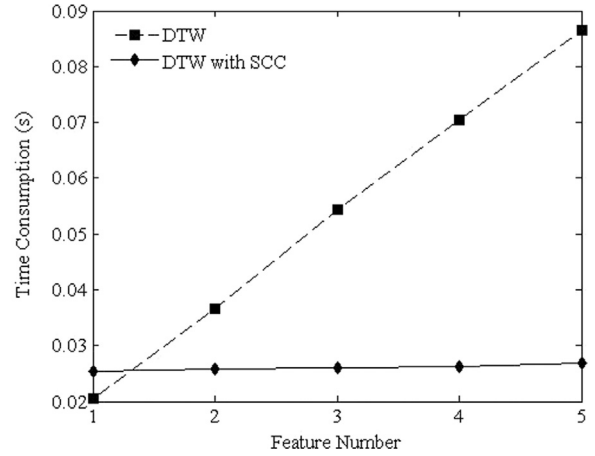


Fig. 6. Comparison of time consumption between DTW and DTW with SCC.

alignment.

As discussed above, it would be heavy computation if sampled points included in signatures were increased when DTW is used as dissimilarity evaluation, and the efficiency of system will be deteriorated. For improving the efficiency, features will not be matched by DTW. Instead, features are matched by DTW with SCC which is inherent in signature curves in our work. The optimal matching path of signature curves can be obtained by two signature curves matching during the process of DTW matching, as shown in Fig. 4. Features are respectively matched by DTW with SCC and DTW are shown in Fig. 5 for comparison. From Fig. 5, features can be matched well by DTW with SCC.

Time consumption of DTW and our proposed modified DTW with SCC is shown in Fig. 6. When DTW with SCC is used, SCC inherent in signature curves should be extracted which is optimized by 2-dimension signature curves matching by DTW, and then features are matched by DTW with SCC. When one feature is used in verification, time consumption of DTW with SCC is 0.025 s which is a little more than 0.021 s of DTW. But as feature number being increased, time consumption of DTW is increased dramatically, but time consumption of modified DTW with SCC is increased slowly. As discussed above, five features are used in our on-line signature verification, time consumption of DTW is 0.088 s as opposed to 0.026 s of modified DTW with SCC.

Performance of the system with FRR, FAR and EER measured in

Table 2

Performances of the system with different methods.

Database	Methods	FRR (%)	FAR (%)	EER (%)
DB1	DTW	2.91	3.23	3.07
	DTW with SCC	2.62	2.88	2.75
SVC2004	DTW	3.56	4.12	3.84
	DTW with SCC	3.24	3.76	3.50

percentage for different methods of dissimilarity evaluation are given in Table 2. From Table 2, when experiments are implemented on DB1, EER=2.75% can be provided by DTW with SCC as opposed to 3.07%, which is provided by DTW. As for SVC2004 Task2, it can be provided EER=3.50% by DTW with SCC as opposed to 3.84% by DTW. The results illustrate that our proposed modified DTW with SCC can provide higher accuracy and more efficient of on-line signature verification.

In Table 3, experiments of weight factor assigning dynamically depending on CV are implemented. Some users are selected randomly to illustrate different weight factors being assigned dynamically to features. From Table 3, we can observe that different weight factors are assigned to different features, while for the same feature, weight factors are also different for different users. There are various dispersions of

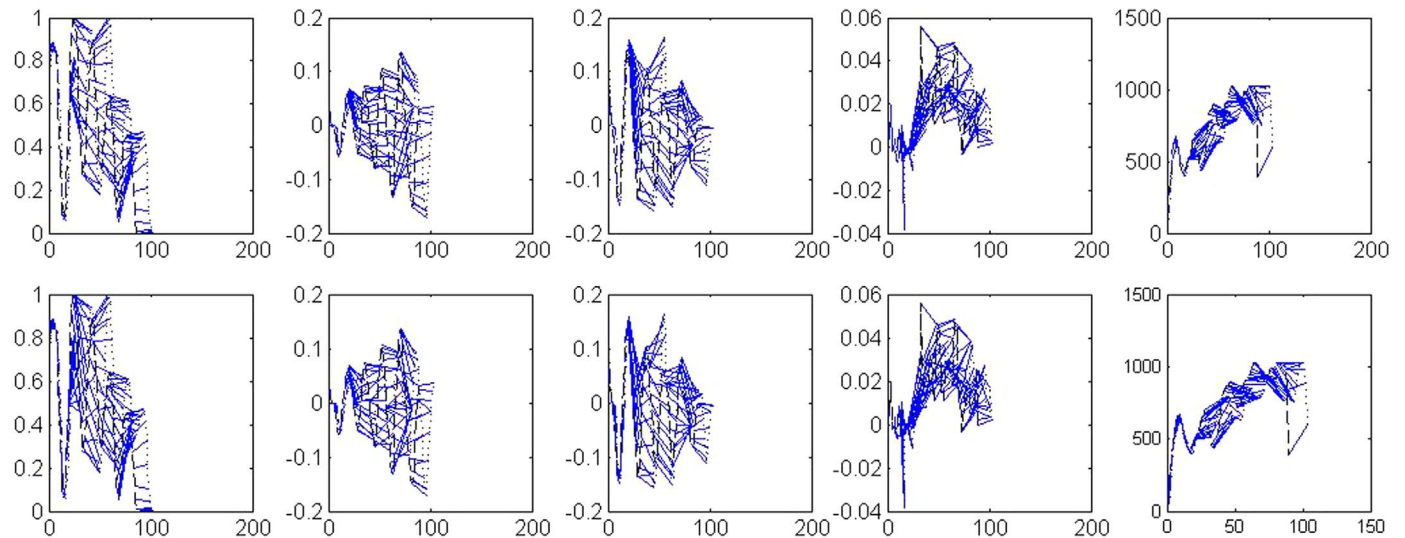


Fig. 5. Features are matched by DTW with SCC(the first row) and DTW(the second row), i.e., f_1, f_2, f_3, f_4 and f_5 (from left to right).

Table 3Weight factors assigned dynamically to feature f_k depend on CV.

Database	User	Weight factor	f_1	f_2	f_3	f_4	f_5
DB1	user-6	CV	0.18	0.38	0.17	0.24	0.24
		ϖ	0.15	0.31	0.14	0.20	0.20
	user-25	CV	0.20	0.28	0.87	0.39	0.38
		ϖ	0.09	0.13	0.41	0.18	0.18
SVC2004	user-10	CV	0.12	0.25	0.26	0.12	0.19
		ϖ	0.13	0.27	0.28	0.13	0.20
	user-19	CV	0.23	0.22	0.20	0.18	0.35
		ϖ	0.19	0.19	0.17	0.15	0.30

Table 4

Performances of the system implemented on DB1 with different strategies. Where, ‘–’ denotes without alignment, ‘GMM’ denotes GMM-alignment.

No.	Alignment	Dissimilarity	Weight factors	EER	σ^2
1	–	DTW	Equal weights	6.23	10.86
2	–	DTW with SCC	Equal weights	6.14	10.23
3	–	DTW with SCC	Dynamic weights	4.45	5.66
4	GMM	DTW with SCC	Dynamic weights	2.15	4.58

Table 5

Performances of the system implemented on SVC2004 Task2 with different strategies. Where, ‘–’ denotes without alignment, ‘GMM’ denotes GMM-alignment.

No.	Alignment	Dissimilarity	Weight factors	EER	σ^2
1	–	DTW	Equal weights	8.42	11.75
2	–	DTW with SCC	Equal weights	8.53	11.68
3	–	DTW with SCC	Dynamic weights	4.85	6.12
4	GMM	DTW with SCC	Dynamic weights	2.63	5.32

features since different writing habits. To improve on-line signature verification, these various dispersions should be emphasized. The experimental result indicates that different weight factors can be assigned to features dynamically depending on their CV values.

Performances of the system with different strategies are given in Tables 4, 5. From Tables 4, 5, for strategy-1, system can provide $EER_{DB1} = 6.23 \pm 10.86\%$ and $EER_{SVC} = 8.42 \pm 11.75\%$ when DTW is merely used without signature alignment while features are equal weights. It is a bit unreliable for biometric identification as strategy-1 is adopted. When strategy-2 is adopted, system can provide $EER_{DB1} = 6.14 \pm 10.23\%$ and $EER_{SVC} = 8.53 \pm 10.68\%$ as DTW with SCC being used to evaluate the dissimilarity between test signature and reference. Accuracy of signature verification is improved a little but the efficiency of system can be improved significantly as demonstrating in Fig. 6. When strategy-3 is adopted, DTW with SCC is used to evaluate the dissimilarity and dynamic weight factors are assigned to features depend on CV. System can provide $EER_{DB1} = 4.45 \pm 5.66\%$ and $EER_{SVC} = 4.85 \pm 6.12\%$. The result illustrate that different features have different influences on signature verification system since the various writing habits. When different weight factors are assigned to features dynamically depend on CV, the EER can be reduced to some extent. When strategy-4 is adopted, signatures are aligned well by GMM-alignment before verification. In verification stage, DTW with SCC is used to improve the efficiency of the system and dynamic weight factors are assigned to features depend on CV, system can provide lowest $EER_{DB1} = 2.15 \pm 4.58\%$ and $EER_{SVC} = 2.63 \pm 5.32\%$ which is reduced significantly. The experimental results indicate that the best performance of on-line signature verification can be obtained when signatures are aligned well and strategy of dynamic weight factor is adopted.

In order to demonstrate the effectiveness of our proposed method, we compare the results of our proposed method with other state-of-

Table 6

Comparative studies of state-of-the-art methods implemented on DB1.

Literatures	Features	Methods	EER (%)
J.M. Pascual-Gaspar [38]	6 features	VQ	2.46
N. Sae-Bae [47]	x, y, r, θ, p	Statistical Distance	4.02
M. Lopez-Garcia [48]	25 features	DTW+GMM	2.74
A. Fishcher [49]	8 features	DTW	3.94
A. Sharma [50]	5 features	DTW+VQ	1.55
Proposed method	y, p, v_x, v_y, a_c	DTW with SCC	2.15

Table 7

Comparative studies of state-of-the-art methods implemented on SVC2004 Task2.

Literatures	Features	Methods	EER (%)
S. Rashidi [39]	14 features	Modified DTW	3.62
A. Sharma [50]	5 features	DTW+VQ	2.73
K. Cpalka [51]	x, y	Neuro-Fuzzy	10.70
W. Khoh [52]	x, v, v_y, ϕ	DWT-DFT+SVM	4.92
Y. Liu [53]	Coefficients of DCT	Sparse representation	3.95
Proposed method	y, p, v_x, v_y, a_c	DTW with SCC	2.63

the-art methods. It is difficult to make comparisons between different methods based on different database. Hence, we just compare the performance of systems which are carried out on DB1 and SVC2004 Task2. The best results methods carried out both on DB1 and SVC2004 Task2 are taken for comparative studies. Performances of state-of-the-art methods implemented on DB1 and SVC2004 Task2 are given in Tables 6, 7. From the results, our proposed algorithm can provide lowest EER value on DB1 in most cases except literature [50], but can provide lowest EER value on SVC2004 Task2 among state-of-the-art methods. Results illustrate that it can obtain higher accuracy with fewer features by our proposed method of on-line signature verification.

6. Conclusions

In this article, we presented a method of signature alignment based on GMM for on-line signature verification. Considering internal and external writing environments being always varied, signatures were effectively aligned to references by GMM-alignment before verification for improving performance of the system. A distance probability was proposed to evaluate the dissimilarity between test signatures and references. Since diverse writing habits and various dispersions of features, different weight factors were assigned dynamically to feature depend on CV values. To improve the efficiency of algorithm, a modified DTW with SCC was presented. Open access signature databases MCYT and SVC2004 Task2 were used in our work, and several experiments were implemented. Experimental results illustrated that the best matching could be obtained by our proposed GMM-alignment method. The best error rates $EER_{DB1} = 2.15\%$ and $EER_{SVC} = 2.63\%$ were provided, respectively, which demonstrated the effectiveness and robustness of our proposed method.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.patcog.2016.12.019>.

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