

# On-line signature verification based on stroke matching

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## Abstract

*Stability and style-variation are important characteristics in handwriting analysis and recognition. This paper describes a stability modelling technique of handwritings in the context of on-line signature verification. With this technique, the stability and style-variation characteristics are deduced from the dynamic warping relationship between the sequences of basic handwriting strokes of the reference samples. Reliability measures of the extracted signature features are incorporated into the signature segmentation, model-building, and verification algorithms, so that stable handwriting features are emphasized in the signature matching process, while style-variations for less stable features are intentionally tolerated. The generated signature model consists of a structure description graph of the handwriting components and their stability information. A signature is accepted by the model if it is close to a permissible path within the weighted graph. A novel feature of the technique is its ability to refine the correspondence relation of the handwriting during model-building and signature verification. This ability enables the verification and partial correction of segmentation errors to reduce the number of false rejections while maintaining the system security level and keeping the number of reference samples manageable.*

## 1 Introduction

Signature is a mean of personal identity authentication and verification. Its use has been well established, especially in legal and commercial environments. It is highly desirable to automate the process for the accurate identification of genuine handwritings and the detection of forged ones. For this reason, many research and development efforts have been invested over the last decades [1, 2].

Flexible pattern matching techniques are continuously being investigated. Regional correlation, elastic matching by dynamic time warping, skeleton tree matching [3], signal correlation [4], hidden Markov modelling [5], and neural network techniques [6] have been applied to on-line signature verification. In addition to the pattern matching problem, one also face the problem of selecting optimal prototypes and constructing accurate signature models for verifi-

cation. This is where the analysis of pattern correlation between reference signatures, i.e. stability characteristics, becomes valuable. The standard deviation is a convenient and generic stability indicator for parametric and also for functional features on a region-by-region basis. An alternative stability characteristic for on-line signature verification has been proposed by G. Congedo *et al.*, which makes use of the dynamic time warping function between the sample points of two signature trajectories [7]. In their approach, a Direct Matching Point (DMP) is used to indicate a small region where no significant distortion exists between the trajectories. Stability indices are formulated based on the detection of DMP, which is used to select optimal references.

It seems appropriate to extend the stability estimation technique to handwriting strokes, in order to obtain structural level stability and to take advantage of handwriting-component based verification strategies. This paper describes such a technique. Signatures are first segmented into basic handwriting strokes. Matching between signatures is implemented using dynamic warping applied to the respective stroke sequences. The stability characteristics of the strokes are obtained, and are utilised to weight the importance of each stroke in verification. A novel feature of the technique is its ability to refine the segmentation and the correspondence relation of handwriting strokes. This ability enables the verification and partial correction of segmentation errors, to reduce the number of false rejections while maintaining high security level.

## 2 Stability feature extraction

Stroke-based stability measurement requires the signature to be segmented into basic handwriting units or pen-strokes. In this instance, segmentation of the on-line acquired signature is performed according to the handwriting motion breaks. The transition points near the handwriting motion velocity zero-crossings and corresponding to high curvature peaks are chosen as the segmentation points [8]. The initial segmentation is obtained on an individual signature basis. Over- or under-segmentation could be expected due noise and imperfections in the data collection process. To construct an accurate signature model using a limited number of reference samples, a segmentation verification and refinement technique is derived.

## 2.1 Stroke stability estimation

Inspired by the sample-point stability estimation technique by G. Congedo *et al.* [7], a method of extracting stability information on handwriting strokes is implemented. It is based on the analysis of the dynamic coupling between the chains of handwriting strokes in reference signatures.

For a set of genuine reference samples  $R = \{S^i | i = 1, \dots, n\}$ , the stability of a single specimen  $S^r \in R$  is formulated with respect to the other signatures  $S^v \in R, r \neq v$ . Assume a signature is represented as a list of segmented basic handwriting units, i.e.,

$$\begin{aligned} S^r &= s_r(1) + \dots + s_r(p) + \dots + s_r(n_r), \\ S^v &= s_v(1) + \dots + s_v(q) + \dots + s_v(n_v). \end{aligned} \quad (1)$$

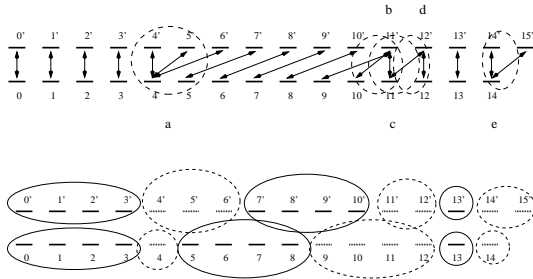
The dynamic warping procedure generates the coupling sequence,  $W(r, v) = (i_1, j_1), \dots, (i_k, j_k), \dots, (i_K, j_K)$ , between the basic units of  $S^r$  and  $S^v$ .  $(i_k, j_k)$  denotes a coupling between  $s_r(i_k)$  and  $s_v(j_k)$ . The accumulated global distance,  $D(S^r, S^v) = \sum_{k=1}^K d(s_r(i_k), s_v(j_k))$ , is to be minimised by the warping algorithm.

The multiplicity of the stroke-coupling is defined here as the number of occurrences of a stroke reference in the warping path. Let  $(p, q) \in W(r, v)$  be a coupling between  $s_r(p)$  and  $s_v(q)$ . The multiplicities  $m^p$  and  $m^q$  are,

$$\begin{aligned} m^p &= \text{card}\{(i_k, j_k) \in W(r, v) \mid i_k = p\}, \\ m^q &= \text{card}\{(i_k, j_k) \in W(r, v) \mid j_k = q\}. \end{aligned} \quad (2)$$

A Direct Matching Stroke (DMS) of the  $r$ -th signature is a pen-stroke segment which has a one-to-one coupling with a pen-stroke segment of the  $v$ -th signature, i.e.

$$s_r(p) \text{ is DMS} \iff m^p = m^q = 1. \quad (3)$$



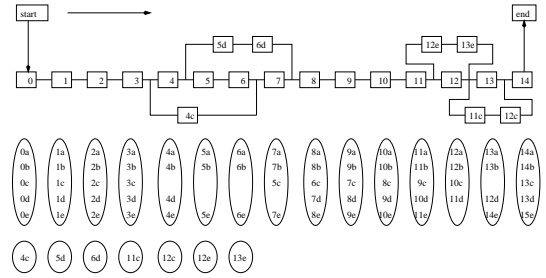
**Figure 1. Identifiable patterns within the dynamic warping output. The stable DMS-coupling patterns, i.e. the one-to-one matchings, are circled with solid lines. Others non-DMS couplings, i.e. one-to-many matchings, are circled with dotted lines.**

The stable-coupling chains, i.e. the chains of uninterrupted DMS coupling, give useful indications of stability. They represent highly skilled sub-groups of pen-strokes

which can be expected to be present in most genuine signatures. In the following, the identified DMS and non-DMS couplings (Figure 1) are utilised in the refinement of signature model.

## 2.2 Structural model building

Structural Description Graph (SDG) is a visually appealing scheme for organising the complex statistical features and structural relations in on-line acquired signatures. It has been utilised by G. Dimauro *et al.* to model handwriting strokes separated by pen-lifts [9]. Similarly, SDG is used here to describe the organisation of the motion-segmented handwriting strokes. For each enrolled signature, a SDG is constructed by identifying the finite set of pen-stroke clusters from the reference samples.



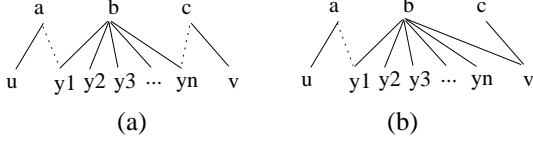
**Figure 2. The Structural Description Graph of a signature model. Each ellipse enclosed group is a stroke cluster.**

The dynamic warping sequences are algorithmically transformed into a SDG (Figure 2). In the transformation, the strokes in the template signature are treated as initial cluster centers. The strokes in the other reference signatures under DMS coupling are grouped directly with these centers. The non-DMS coupled strokes are extrapolated as branches from the main trunk, which then become separate clusters. The branch returns to the main trunk when DMS coupling resumes. The stability indices  $SI$  associated with these clusters are given as the ratio of the numbers of strokes in the clusters over the number of total reference signatures. The uninterrupted DMS coupling sequences are also well presented in the SDG.

## 2.3 Segmentation verification

The non-DMS patterns are further analysed with a segmentation verification process, to decide on how the strokes can be best correlated. Consider the typical non-DMS coupling examples in Figure 1. There are a few possibilities that need to be considered. First it is possible that the stroke may simply need to be repeated several times as detected

by dynamic warping. It is also possible that over- or under-segmentation for one of the signatures occurs. The neighbouring strokes need to be combined before matching to the corresponding region. Finally, the regions under comparison may differ sufficiently, that after eliminating the possibilities of shorter range coupling, a combined long stroke in one signature has to be coupled with a combined long stroke in another signature.



**Figure 3. General case of non-DMS coupling from stroke-warping. Stroke  $b$  is the non-DMS coupling under consideration. Case (a) is a simple one-to-many matching enclosed by DMS couplings at both ends, and case (b) is a many-to-many matching due to an extra link between  $b$  and  $v$ . The dotted lines indicate other permissible matchings under dynamic warping.**

Non-DMS coupling patterns can generally appear in the forms listed in Figure 3. Let  $b(y_1, y_2, \dots, y_n)$  denote all the possible configurations that can be generated for the one-to-many relation  $b \rightarrow (y_1, y_2, \dots, y_n)$ . In the following, ‘ $\rightarrow$ ’ denotes ‘is matched to’, and ‘+’ denotes ‘is concatenated with’. For  $n = 1$ ,  $b(y_1)$  is simply  $b \rightarrow y_1$ . For  $n = 2$ ,  $b(y_1, y_2)$  represents  $\{b \rightarrow y_1, b \rightarrow y_2\}; \{b \rightarrow y_1 + y_2\}$ . Configurations for higher orders of  $n$  are generated recursively by expressions involving lower order terms. For example,  $b(y_1, y_2, y_3)$  is equivalent to  $\{b \rightarrow y_1, b(y_2, y_3)\}; \{b \rightarrow y_1 + y_2, b(y_3)\}; \{b \rightarrow y_1 + y_2 + y_3\}$ . The general case  $b(y_1, y_2, y_3, \dots, y_n)$  represents  $\{b \rightarrow y_1, b(y_2, y_3, \dots, y_n)\}; \{b \rightarrow y_1 + y_2, b(y_3, \dots, y_n)\}; \dots; \{b \rightarrow y_1 + y_2 + \dots + y_n\}$ .

The rules of generating the configurations for case (a) of Figure 3 are:

- $a \rightarrow u, b(y_1, y_2, \dots, y_n), c \rightarrow v;$
- $a \rightarrow u + y_1, b(y_2, \dots, y_n), c \rightarrow v;$
- $a \rightarrow u + y_1, b(y_2, \dots, y_{n-1}), c \rightarrow y_n + v;$
- $a \rightarrow u, b(y_1, y_2, \dots, y_{n-1}), c \rightarrow y_n + v.$

In case (b) of Figure 3, they become:

- $a \rightarrow u, b(y_1, y_2, \dots, y_n), c \rightarrow v;$
- $a \rightarrow u + y_1, b(y_2, \dots, y_n), c \rightarrow v;$
- $a \rightarrow u + y_1, b(y_2, \dots, y_n, v), c \rightarrow v;$
- $a \rightarrow u, b(y_1, y_2, \dots, y_n, v), c \rightarrow v.$

The  $a \rightarrow u$  and  $c \rightarrow v$  couplings may not always be present. This happens when the one-to-many relation is at one end of the stroke sequence, in which case these terms are discarded in the list of rules. The distances at sample point level of each possible configuration in these cases are evaluated, and the likelihoods of the configurations are ranked accordingly. In cluster refinement, the most likely configuration is chosen, and the model graph is refined so that uncertainties in the initial SDG are removed.

#### Algorithm of stroke-match refinement

- For signature  $S^r \in R$ , obtain the stroke-coupling sequences  $W(r, v), \forall S^v \in R, v \neq r$ , with dynamic warping.
- From each  $W(r, v)$ , calculate the multiplicities of strokes in  $S^r$  and  $S^v$ , and identify the DMS and non-DMS in the sequence. The stroke whose multiplicity  $m = 1$  is a DMS, otherwise a non-DMS.
- For each non-DMS, perform the following segmentation verification procedure.
  - Derive the possible stroke configurations according to rule set for case (a) and case (b) in Figure 3, and calculate their matching distances.
  - Select the most likely configuration according to the least distance.
- Re-generate the SDG model from the refined coupling. Re-calculate the stability indices of the input signature strokes.

### 3 Signature verification

The online signature verification algorithm adopts a multi-stage strategy. Global features, such as the aspect ratio, the total time duration, and the low-resolution 2-D bitmap features, are used to filter the random and less skillful signature forgeries. While establishing the correspondence of handwriting strokes by the dynamic warping procedure, the presence or absence of the reference pen-strokes are examined, i.e. a structural feature verification is performed. The functional distance is then accumulated to generate an overall matching score for the input signature against the model.

#### 3.1 Stroke distance metrics

The functional distances between corresponding pen-strokes are computed with the aid of B-spline approximation, adopting the curve distance metrics formulated in reference [10]. Let  $s_r(p)$  be a model curve of  $n$  equi-distance points, and  $s_v(q)$  a corresponding curve in the test pattern,  $s_v(q)$  is reconstructed from its B-spline representation to be of the same dimension  $n$ . The shape change between these curves  $d(s_r(p), s_v(q))$ , is defined to be a measurement of

the elastic deformation in transforming from one curve to the other. It includes three components; the accumulated square of the Euclidean distance between the sample points, the internal strain energy term, and the internal bending energy term.

While transforming from  $s_r(p)$  to  $s_v(q)$ , the Euclidean distance term  $E_d$ , the strain energy term  $S_e$ , and the bending energy term  $B_e$  are given by,

$$\begin{aligned} E_d[l] &= \| S_p[l] - S_q[l] \|^2, \\ B_e[l] &= \left\| \frac{d^2 S_p[l]}{ds^2} - \frac{d^2 S_q[l]}{ds^2} \right\|^2, \\ S_e[l] &= \left\| \frac{dS_p[l]}{ds} - \frac{dS_q[l]}{ds} \right\|^2. \end{aligned} \quad (4)$$

The first and second order derivatives in the above equations are obtained analytically from the cubic B-Spline versions of the curves.

Let  $d[l]$  be the point-wise distance between corresponding samples on  $s_r(p)$  and  $s_v(q)$ .

$$d[l] = \sqrt{\alpha E_d[l] + \beta S_e[l] + \gamma B_e[l]}, \quad (5)$$

where  $\alpha, \beta$  and  $\gamma$  are weighting constants denoting the contributions of the distance components, with  $\alpha + \beta + \gamma = 1$ . The total distance is

$$d(s_r(p), s_v(q)) = \sum_{l=1}^n d[l]. \quad (6)$$

### 3.2 Verification algorithm

The block diagram of the detailed signature verifier is given in Figure 4. In principle, the verification process operates by rectifying the errors in signature segmentation and refining the stroke-correspondence mapping in order to obtain an accurate model. A SDG is built for each reference signature and the collection of all the reference signature SDGs is the signature model. During model building, each of the reference signatures in turn is used as a test input, to generate a set of acceptance thresholds. In the verification phase, an input signature is tested against the SDG models. Utilising the cluster thresholds, the lists of accepted and rejected input strokes, as well as the omitted reference strokes, are generated. The final decision is based on the analysis of these lists.

The input signature is accepted by the signature model if there exists a path within a SDG which is sufficiently similar to the input sequence. The test for such a condition is implemented with a straight-forward strategy, i.e. to generate all the permissible paths within the SDG, and comparing each path against the input sequence. A more efficient strategy would be to perform the dynamic warping and refinement procedure between the SDG main trunk and the input sequence, and then to consider the localized matching with the SDG branches. The former strategy is used for its simplicity.

#### Algorithm of model acceptance testing

- For each SDG<sup>*i*</sup>,  $i \in [1..n]$  in the signature model, create an initial path  $p_j^i$ ,  $j = 0$ , and generate all permissible paths:
- GenPath( $p_j^i, j$ )
  - Add links to path  $p_j^i$  along SDG<sup>*i*</sup>, till the end node is reached or a node with branches is encountered.
  - If the end node of SDG<sup>*i*</sup> is reached, return path  $p_j^i$ ;
  - If encountering a node with branch-outs, create temporary  $p_t = p_j^i$ ; for each branch-out  $\{ j = j + 1$ ; create a new path  $p_j^i$ ; copy  $p_t$  to  $p_j^i$ ; recursively call GenPath( $p_j^i, j$ ); }
- For each path  $p_j^i = s_1^i + \dots + s_r^i + \dots + s_{k_r}^i$ , obtain the distance to the input signature stroke path  $t = s_1 + \dots + s_t + \dots + s_{k_t}$ :
  - Perform stroke-match and refinement to obtain the warping sequence  $W(p_j^i, t)$ ;
  - Perform cluster membership test on the input strokes along  $W(p_j^i, t)$ ;
  - Accumulate the lists of accepted, rejected input strokes, and the omitted reference strokes;
  - Accumulate the weighted global distance  $d_{total}$ ;
  - Make decision on the acceptance for path  $p_j^i$ .
- Make final decision on the acceptance of input signature  $t$ .

The weight of each template stroke  $s_r^i$  in  $p_j^i$  is calculated by taking into account the length as well as its stability index,

$$weight(s_r^i) = \frac{length(s_r^i) \times SI(s_r^i)}{\sum_{l=1}^{k_r} length(s_l^i) \times SI(s_l^i)}. \quad (7)$$

The weight of each input stroke  $s_t$  is the stroke length over the sum of lengths of all input strokes, assuming they are equally stable,

$$weight(s_t) = \frac{length(s_t)}{\sum_{l=1}^{k_t} length(s_l)}. \quad (8)$$

The total weighted distance is

$$d_{total} = \sum_{l=0}^K weight(s_{w_1}^i) \times d(s_{w_1}^i, s_{w_2}), \quad (9)$$

where  $(w_1, w_2) = W(p_j^i, t)(l)$ .

Assume a pen-stroke  $s_t$  of input signature  $t$  has a matching reference stroke  $s_r^i$  of  $p_j^i$  in the warping sequence  $W(p_j^i, t)$ .  $s_t$  is accepted by  $s_r^i$  cluster if the deviations of its feature values are within the model cluster thresholds. Otherwise it is either rejected if the reference stroke  $s_r^i$  is a DMS, or marked as a style variation in which case the deviation is accumulated in the global distance. In the case that  $s_t$  is rejected,  $s_r^i$  is marked as an omitted stroke by  $t$ . Statistical data are also recorded on whether the uninterrupted chains of DMS in  $p_j^i$  has been broken.

Judgement of whether the input is acceptable to the signature model is based on the following criteria, comparing to the corresponding statistics obtained from the reference signatures.

- the accumulated weights of accepted strokes of  $t$  by  $p_j^i$ ,  $Acc(p_j^i, t)$ ;
- the accumulated weights of rejected strokes of  $t$  by  $p_j^i$ ,  $Rej(p_j^i, t)$ ;
- the accumulated weights of omitted strokes of  $p_j^i$  by  $t$ ,  $Omt(p_j^i, t)$ ;
- the conformance of stable DMS sequences within  $p_j^i$  by  $t$ ;
- the accumulated weighted distance  $d_{total}$ .

#### 4 Experiment result

The online signature data acquisition device is a Summagraphics writing tablet with a 6x6 square-inch opaque active writing area. It operates at a resolution setting of 500 lines per inch, and a reporting rate of 50 coordinate pairs per second. The tablet is attached to the computer via a serial interface. Additional data are collected with Wacom Intuos 4x5 graphics tablet and pen hardware, interfacing through the Wintab driver available from the Wacom Website. It has a handwriting pressure sensor of 1024 levels, and a 200 coordinate pairs per second maximum reporting rate. These additional data are used to study the effectiveness of higher sampling rates.

Data are gathered from 89 people, with 36 using the Wacom tablet. They were asked to write their signatures for enrollment, but a number of participants offered to write practiced names instead of their real signatures. Each such writing is repeated 20 or more times. The first few are used as references and the rest as test samples. They are also asked to forge other people's signatures using the same system in verification mode. The forgery data are used in the false acceptance test. The system displays the target signature for the signer to practice and perform verification interactively. The total number of handwriting samples collected is about 4600, with about 2100 obtained from the Wacom tablet. Sample signatures are shown in Figure 5.

The multi-regional elastic matching algorithm for online signature verification [8] is extended to incorporate the SDG

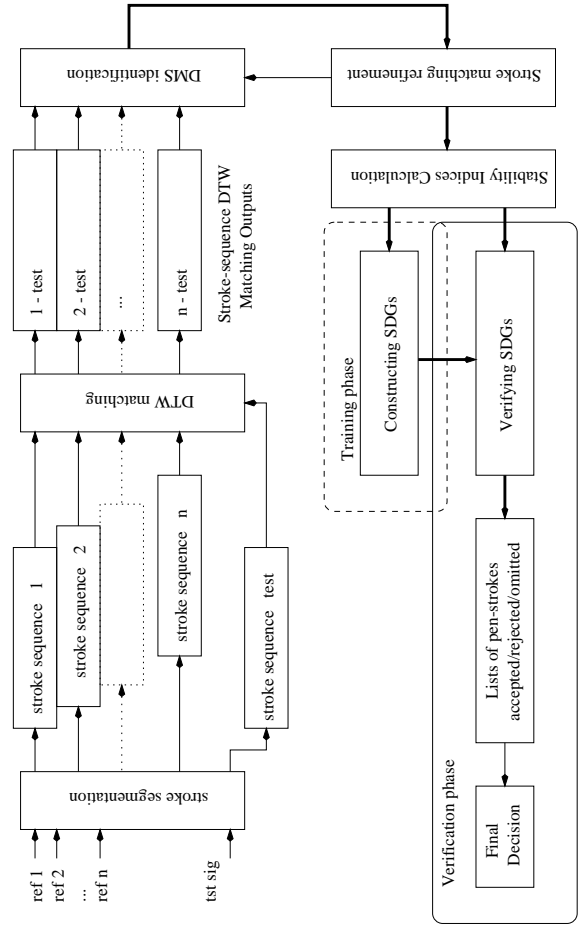


Figure 4. The block diagram of the detailed signature verifier of the on-line signature verification system implemented.

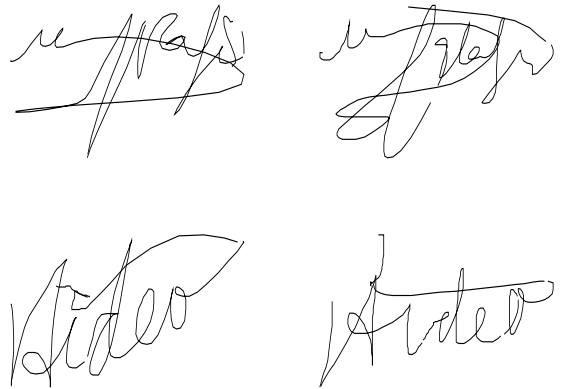
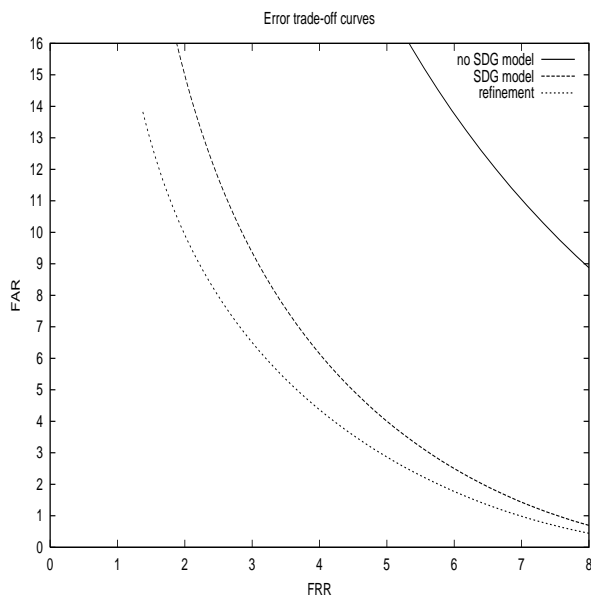


Figure 5. Examples of signatures in the database. Left is genuine and right is forgery.

stability modelling. The system is tested on the experimental database, with five reference signatures in the verification model for each signature class. Varying the number of reference signatures from three to seven gives little deviations to the error trade-off curves shown in Figure 6. However the more reference signatures are used, the more strict the verification threshold controls need to be. Tests on data collected from the Summagraphics tablet and the Wacom tablet show no significant difference in the final result. Thus higher sampling rates than 50Hz does not significantly improve the signature segmentation and matching accuracy in the current form of the algorithm. It can be seen from the trade-off curves that, without SDG models, the equal-error-rate is about 9%; with the addition of SDG model verification, the error rate is reduced to about 5%; and with the introduction of stroke-match refinement, the error rate is reduced again to about 4%.



**Figure 6. The error trade-off curves for the three cases of not using SDG model, using SDG model, and using SDG model with stroke matching refinement.**

## 5 Conclusion

A SDG-based stability modeling technique has been introduced in this paper. It is used to improve a stroke-based on-line signature verification system developed previously. The improvements include stability considerations in the verification score, signature segmentation verification, and signature SDG model building. Style variations are explicitly allowed for by following all permissible paths within the SDGs and therefore a more thorough utilisation of available reference signatures is achieved. While the DTW tech-

nique is an essential part of the proposed signature verification method, it operates on signature segments only. Although the handwriting motion-based signature segmentation technique is adopted here to generate the basis signature segmentation structure, this method is not restricted to motion segmentation. Other segmentation techniques, such as segmenting the signature at perceptually important points, may also be applicable.

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