A DSmT Based Combination Systems for Handwritten Signature Verification

Nassim Abbas
Youcef Chibani
Bilal Hadjadji

Originally published as Nassim Abbas, Youcef Chibani and Bilal Hadjadji, *A DSmT Based Combination Systems for Handwritten Signature Verification.* Compilation of: N. Abbas and Y. Chibani, "SVM-DSmT Combination for Off-Line Signature Verification," IEEE International Conference on Computer, Information and Telecommunication Systems (CITS), Amman, Jordan, pp. 1-5, May 14-16, 2012., and of N. Abbas and Y. Chibani, "SVM-DSmT combination for the simultaneous verification of off-line and on-line handwritten signatures," International Journal of Computational Intelligence and Applications (IJCIA), vol. 11, no. 3, 2012, and reprinted with permission.

Abstract: *The identification or authentication from the handwritten signature is the most accepted biometric modality for identifying a person. However, a single handwritten signature verification (HSV) system does not allow achieving the required performances. Therefore, rather than trying to optimize a single HSV system by choosing the best features or classifier for a given system, researchers found more interesting to combine different systems. In that case, the DSmT is reported as very useful and powerful theoretical tool for enhancing the performance of multimodal biometric systems. Hence, we propose in this chapter a study of applying the DSmT for combining different HSV systems. Two cases are addressed for validating the effective use of the DSmT. The first one is to enhance the performance of off-line HSV systems by associating features based on Radon and Ridgelet transforms for each individual system. The second one is associating off-line image and dynamic information in order to improve the performance of single-source biometric systems and ensure greater security. Experimental results conducted on standard datasets show the effective use of the proposed DSmT based combination for improving the verification accuracy comparatively to individual systems.*

1.1 Introduction

Biometrics is one of the most widely used approaches for identification and authentication of persons [1]. Hence, several biometric modalities have been proposed in the last decades, which are based on physiological and behavioral characteristics depending on their nature. Physiological characteristics are related to anatomical properties of a person, and include for instance fingerprint, face, iris and hand geometry. Behavioral characteristics refer to how a person performs an action, and include typically voice, signature and gait [1, 2]. Therefore, the choice of a biometric modality depends on several factors such as nonuniversality, nonpermanence, intraclass variations, poor image quality, noisy data, and matcher limitations [1, 3]. Thus, recognition based on unimodal biometric systems is not always reliable. To address these limitations, various works have been proposed for combining two or more biometric modalities in order to enhance the recognition performance [3, 4, 5]. This combination can be performed at data, feature, match score, and decision levels [3, 4].

However, with the existence of the constraints corresponding to the joint use of classifiers and methods of generating features, an appropriate operating method using mathematical approaches is needed, which takes into account two notions: uncertainty and imprecision of the classifier responses. In general, the most theoretical advances which have been devoted to the theory of probabilities are able to represent the uncertain knowledge but are unable to model easily the information that is imprecise, incomplete, or not totally reliable. Moreover, they often lead to confuse both concepts of uncertainty and imprecision with the probability measure. Therefore, new original theories dealing with uncertainty and imprecise information have been introduced, such as the fuzzy set theory [6], evidence theory [7], possibility theory [8] and, more recently, the theory of plausible and paradoxical reasoning developed by Dezert-Smarandache theory (DSmT) [9, 10, 11]. The DSmT has been elaborated by Jean Dezert and Florentin Smarandache for dealing with imprecise, uncertain and paradoxical sources of information. Thus, the main objective of the DSmT is to provide combination rules that would allow to correctly combine evidences issued from different information sources, even in presence of conflicts between sources or in presence of constraints corresponding to an appropriate model (i.e. free or hybrid DSm models [9]).

The use of the DSmT has been used justified in many kinds of applications [9, 10, 11]. Indeed, the DSmT is reported as very useful and powerful theoretical tool for enhancing the performance of multimodal biometric systems. Hence, combination algorithms based on DSmT have been used by Singh et al. [12] for robust face recognition through integrating multilevel image fusion and match score fusion of visible and infrared face images. Vatsa et al. proposed a DSmT based fusion algorithm [13] to efficiently combine level-2 and level-3 fingerprint features by incorporating image quality. Vatsa et al. proposed an unification of evidence-theoretic fusion algorithms [14] applied for fingerprint verification using level-2 and level-3 features. A DSmT based dynamic reconciliation scheme for fusion rule selection [15] has been proposed in order to manage the diversity of scenarios encountered in the probe dataset.

Generally, the handwritten signature is considered as the most known modality for biometric applications. Indeed, it is usually socially accepted for many government/legal/financial transactions such as validation of checks, historical documents, etc [16]. Hence, an intense research field has been devoted to develop various robust verification systems [17] according to the acquisition mode of the signature. Thus, two modes are used for capturing the signature, which are off-line mode and on-line mode, respectively. The off-line mode allows generating a handwriting static image from the scanning document. In contrast, the on-line mode allows generating dynamic information such as velocity and pressure from pen tablets or digitizers. For both modes, many Handwritten Signature Verification (HSV) systems have been developed in the past decades [17, 18, 19]. Generally, the off-line HSV systems remains less robust compared to the on-line HSV systems [16] because of the absence of dynamic information of the signer.

Generally, a HSV system is composed of three modules, which are preprocessing, feature generation and classification. In this context, various methods have been developed for improving the robustness of each individual HSV system. However, the handwritten signature verification failed to underline the incontestable superiority of a method over another in both steps of generating features and classification. Hence, rather than trying to optimize a single HSV system by choosing the best features for a given problem, researchers found more interesting to combine several classifiers [20].

Recently, approaches for combining classifiers have been proposed to improve signature verification performances, which led the development of several schemes in order to treat data in different ways [21]. Generally, three approaches for combining classifiers can be considered: parallel approach [22, 23], sequential approach [24, 25] and hybrid approach [26], [27]. However, the parallel approach is considered as more simple and suitable since it allows exploiting the redundant and complementary nature of the responses issued from different signature verification systems. Hence, sets of classifiers have been used, which are based on global and local approaches [28, 29] and feature sets [30, 31], parameter features and function features [32, 33], static and dynamic features [34, 35]. Furthermore, several decision combination schemes have been implemented, ranging from majority voting [23, 36] to Borda count [37], from simple and weighted averaging [38] to Dempster-Shafer evidence theory [37, 39] and Neural Networks [40, 41]. The boosting algorithm has been used to train and integrate different classifiers, for both verification of on-line [42, 43] and off-line [44] signatures.

In this research, we follow the path of combined biometric systems by investigating the DSmT for combing different HSV systems. Therefore, we study the reliability of the DSmT for achieving a robust multiple HSV system. Two cases are considered for validating the effective use of the DSmT. The first one is to enhance the performance of off-line HSV systems by associating features based on Radon and Ridgelet transforms for each individual system. The second one is associating off-line image and dynamic information in order to improve the performance of single-source biometric systems and ensure greater security. For both cases, the combination is performed through the generalized biometric decision combination framework using Dezert-Smarandache theory (DSmT) [9, 10, 11].

The chapter is organized as follows. We give in Section 1.2 a review of sophisticated Proportional Conflict Redistribution (PCR5) rule based on DSmT. Section 1.3 describes the proposed verification system and Section 1.4 presents the performance criteria and datasets of handwritten signatures used for evaluation. Section 1.5 discuss the experimental results of the proposed verification system. The last section gives a summary of the proposed verification system and looks to the future research direction.

1.2 Review of PCR5 combination rule

Generally, the signature verification is formulated as a two-class problem where classes are associated to *genuine* and *impostor*, namely θ_{gen} and θ_{imp}, respectively. In the context of the probabilistic theory, the frame of discernment, namely Θ, is composed of two elements as: $\Theta = \{\theta_{gen}, \theta_{imp}\}$, and a mapping function $m \in [0, 1]$ is associated for each class, which defines the corresponding mass verifying $m(\emptyset) = 0$ and $m(\theta_{gen}) + m(\theta_{imp}) = 1$.

When combining two sources of information and so two individual systems, namely information sources S^1 and S^2, respectively, the sum rule seems effective for non-conflicting responses [3]. In the opposite case, an alternative approach has been developed by Dezert and Smarandache to deal with (highly) conflicting imprecise and uncertain sources of information [9, 10, 11]. For two-class problem, a reference domain also called the frame of discernment should be defined for performing the combination, which is composed of a finite set of exhaustive and mutually exclusive hypotheses. Example of such approaches is PCR5 rule.

The main concept of the DSmT is to distribute unitary mass of certainty over all the composite propositions built from elements of Θ with $\cup$ (Union) and $\cap$ (Intersection) operators instead of making this distribution over the elementary hypothesis only. Therefore, the hyper-powerset D^Θ is defined as $D^\Theta = \{\emptyset, \theta_{gen}, \theta_{imp}, \theta_{gen} \cup \theta_{imp}, \theta_{gen} \cap \theta_{imp}\}$. The DSmT uses the generalized basic belief mass, also known as the generalized basic belief assignment (gbba) computed on hyper-powerset of Θ and defined by a map $m(.) : D^\Theta \longrightarrow [0, 1]$ associated to a given source of evidence, which can support paradoxical information, as follows: $m(\emptyset) = 0$ and $m(\theta_{gen}) + m(\theta_{imp}) + m(\theta_{gen} \cup \theta_{imp}) + m(\theta_{gen} \cap \theta_{imp}) = 1$. The combined masses m_{PCR5} obtained from $m_1(.)$ and $m_2(.)$ by means of the PCR5 rule [10] is defined as:

$$m_{PCR5}(A) = \begin{cases} 0 & \text{if } A \in \Phi \\ m_{DSmC}(A) + m_{A\cap X}(A) & \text{otherwise} \end{cases} \tag{1.1}$$

Where

$$m_{A\cap X}(A) = \sum_{\substack{X\in D^{\Theta}\setminus\{A\} \\ c(A\cap X)=\emptyset}} \left[\frac{m_1(A)^2\, m_2(X)}{m_1(A)+m_2(X)} + \frac{m_2(A)^2\, m_1(X)}{m_2(A)+m_1(X)} \right]$$

and $\Phi = \{\Phi_{\mathcal{M}}, \emptyset\}$ is the set of all relatively and absolutely empty elements, $\Phi_{\mathcal{M}}$ is the set of all elements of D^{Θ} which have been forced to be empty in the Shafer's model $\mathcal{M}$ defined by the exhaustive and exclusive constraints, $\emptyset$ is the empty set, and $c(A \cap X)$ is the canonical form (conjunctive normal) of $A \cap X$ and where all denominators are different to zero. If a denominator is zero, that fraction is discarded. Thus, the term $m_{DSmC}(A)$ represents a conjunctive consensus, also called DSm Classic (DSmC) combination rule [9], which is defined as:

$$m_{DSmC}(A) = \begin{cases} 0 & \text{if } A = \emptyset \\ \sum_{(X,Y\in D^{\Theta}, X\cap Y=A)} m_1(X) m_2(X) & \text{otherwise} \end{cases} \tag{1.2}$$

1.3 System description

The combined individual HSV system is depicted in Figure 1.1, which are composed of an off-line verification system, an on-line or off-line verification system and a combination module. s_1 and s_2 define the off-line and on-line or off-line handwritten signatures provided by two sources of information S^1 and S^2, respectively. Each individual verification system is generally composed of three modules: pre-processing, feature generation and classification.

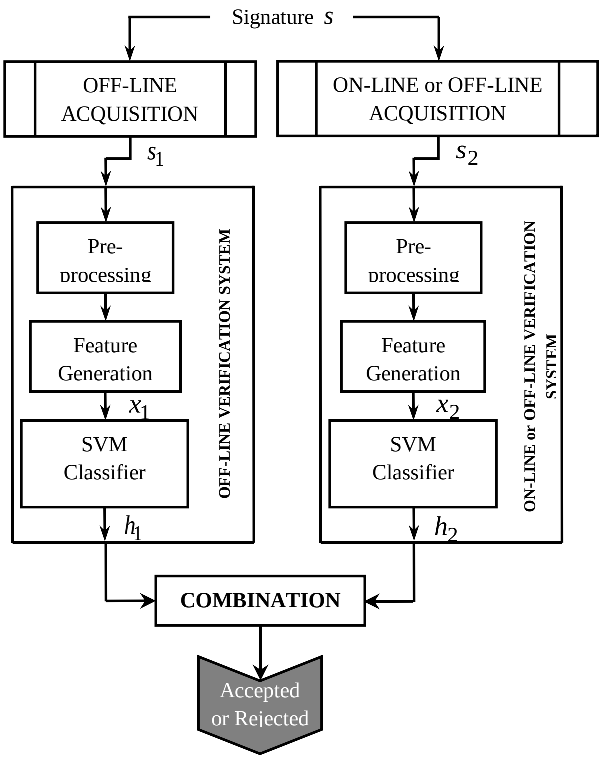


Figure 1.1: Structure of the combined individual HSV systems.

1.3.1 Pre-processing

According the acquisition mode, each handwritten signature is pre-processed for facilitating the feature generation. Hence, the pre-processing of the off-line signature includes two steps: Binarization using the local iterative method [45] and elimination of the useless information around the signature image without unifying its size. The pre-processing steps of a signature example are shown in Figure 1.2. The binarization method was chosen to capture signature from the background. It takes the advantages of locally adaptive binarization methods [45] and adapts them to produce an algorithm that thresholds signatures in a more controlled manner. By doing this, the local iterative method limits the amount of noise generated, as well as it attempts to reconstruct sections of the signature that are disjointed.

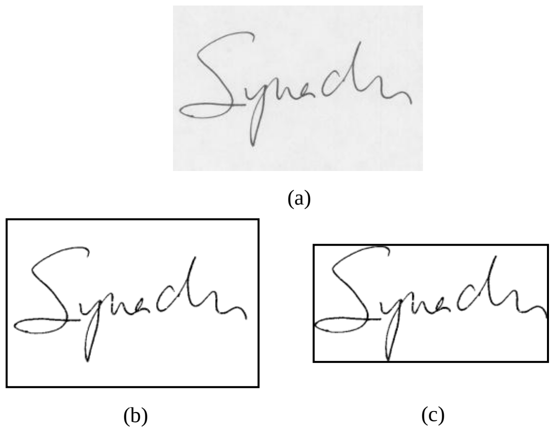


Figure 1.2: Preprocessing steps: (a) Scanning (b) Binarization
(c) Elimination of the useless information.

While the on-line signature, no specific pre-processing is required. More details on the acquisition method and pre-processing module of the on-line signatures are provided in Refs. [46] and [47].

1.3.2 Feature generation

Features are generated according the acquisition mode. In the combined individual HSV systems, we use the uniform grid, Radon and Ridgelet transforms for off-line signatures and dynamic characteristics for on-line signatures, respectively.

a. Features used for combining individual off-line HSV systems

The first case study for evaluating the performance of the proposed combination using DSmT is performed with two individual off-line HSV systems. Features are generated from the same off-line signature using the Radon and Ridgelet transforms. The Radon transform is well adapted for detecting linear features. In contrast, the Ridgelet transform allows representing linear singularities [48]. Therefore, Radon and Ridgelet coefficients provide complementary information about the signature.

- **Radon transform based features:** The Radon transform of each off-line signature is calculated by setting the respective number of projection points N_r and orientations N_θ, which define the length of the radial and angular vectors, respectively. Hence, a radon matrix is obtained having a size $[N_r \times N_\theta]$ which provides in each point the cumulative intensity of pixels forming the image of the off-line signature. Figure 1.3 shows an example of a binarized image of an off-line signature and the steps involved for generating features based on Radon transform. Since the Radon transform is redundant, we take into account only positive radial points $\}\}N_r/2\} \times N_\theta\}$. Then after, for each angular direction, the energy of Radon coefficients is computed to form the feature vector x_1 of dimension $\}1 \times N_\theta\}$. This energy is defined as:

$$E_{\theta}^{rad} = \frac{2}{N_r} \mathop{}_{r=1}^{N_r/2} T_{rad}^{2}(r, \theta \;\; , \theta \in \{1, 2, \dots, N_\theta\} \qquad (1.3)$$

where T_{rad} is the Radon transform operator.

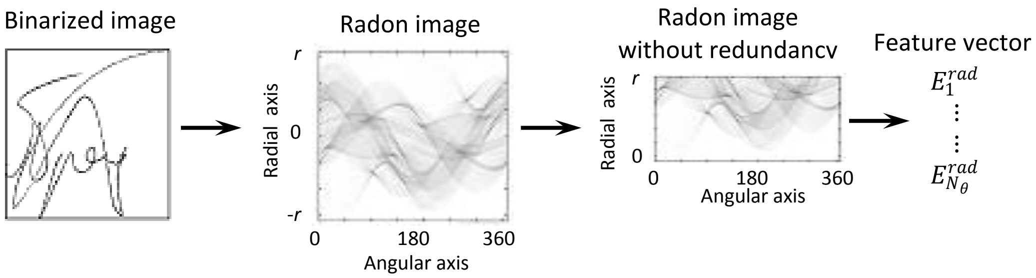


Figure 1.3: Steps for generating the feature vector from the Radon transform.

- **Ridgelet transform based features:** For generating complementary information of the Radon features, the wavelet transform (WT) is performed along the radial axis allowing generating the Ridgelet coefficients [49]. Figure 1.4 shows an example for generating the feature vector from the Ridgelet transform. For each angular direction, the energy of Ridgelet coefficients is computed taking into account only details issued from the decomposition level L of the WT. Therefore, the different values of energy are finally stored in a vector x_2 of dimension $\}1 \times N_\theta\}$. This energy is defined as:

$$\frac{2}{N_r} \mathop{}_{r=1}^{N_r/2} \qquad E_{\theta}^{rid} = \}T_{r\ id}^{\ 2}\}a, b, \theta\}, \theta \in \}1, 2, \dots, N_\theta\} \quad (1.4)$$

where T_{rid} is the Ridgelet transform operator whereas a and b are the scaling and translation factors of the WT, respectively.

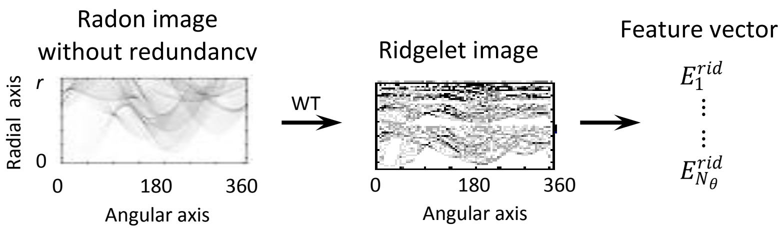
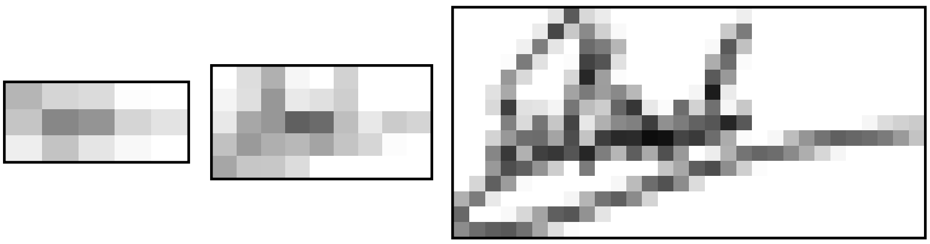


Figure 1.4: Steps for generating the feature vector from the Ridgelet transform.

b. Features used for combining individual off-line and on-line HSV systems

The second case study is considering for evaluating the performance of the proposed DSmT for combining both individual off-line and on-line HSV systems. Features are generated from both off-line and on-line signatures of the same user using the uniform grid (UG) and dynamic characteristics, respectively. The UG allows extracting locally features without normalization of the off-line signature image. On each grid, the densities are computed providing overall signature appearance information. In contrast, dynamic characteristics computed from the on-line signature allow providing complementary dynamic information in the combination process.

- **Uniform grid based features:** Features are generated using the Uniform Grid (UG) [50, 51], which consists to create $n \times m$ rectangular regions for sampling. Each region has the same size and shape. Parameters n and m define the number of lines (vertical regions) and columns (horizontal regions) of the grid, respectively. Hence, the feature associated to each region is defined as the ratio of the number of pixels belonging to the signature and the total number of pixels of images. Therefore, the different values are finally stored in a vector x_1 of dimension $n \times m$, which characterizes the off-line signature image.
  Figure 1.5 shows a 3×5 grid, which allows an important reduction of the representation vector, but it preserves wrongly the visual information. In contrast, a 15×30 grid which provides an accurate representation of images, but it leads a larger characteristic vector. A 5×9 grid seems to be an optimal choice between the quality of representation and dimensionality. Thus, the optimal choice of the grid size for all writers is obviously too important to effectively solve our problem of signature verification. In our case, for all experiments, the parameters n and m of are fixed to 5 and 9, respectively.



$[3 \times 5]$ $[5 \times 9]$ $[15 \times 30]$

Figure 1.5: Visualization of different grid sizes.

- **Dynamic information based features:** For the individual on-line verification system, features are generated using only the dynamic features. Each on-line signature is represented by a vector x_2 composed of 11 features, which are signature total duration, average velocity, vertical average velocity, horizontal average velocity, maximal velocity, average acceleration, maximal acceleration, variance of pressure, mean of azimuth angle, variance of azimuth angle and mean of elevation angle. A complete description of the feature set is shown in Table 1.1.

1.3.3 Classification based on SVM

a. Review of SVMs

The classification based on Support Vector Machines (SVMs) has been widely used in many pattern recognition applications as the handwritten signature verification [35, 52]. The SVM is a learning method introduced by Vapnik et al. [53], which tries to find an optimal hyperplane for separating two classes. Its concept is based on the maximization of the distance of two points belonging each one to a class. Therefore, the misclassification error of data both in the training set and test set is minimized.

Ranking	Feature Description	Ranking	Feature Description
1	$t_n - t_1$	7	$\max\limits_{i=1,\dots,n-2} \frac{dist_{Eucl}\,(Pt_i, Pt_{i+2})}{(t_{i+1} - t_i)^2}$
2	$\frac{{}_{i=1}^{n-1}(dist_{Eucl}\,(Pt_i, Pt_{i+1})}{t_n - t_1}$	8	${}_{i=1}^{n}\left(Pr_i - \frac{{}_{i=1}^{n} Pr_i}{n}\right.^2$
3	$\frac{{}_{i=1}^{n-1}\lvert y_{i+1} - y_i}{t_n - t_1}$	9	$\frac{{}_{i=1}^{n} Az_i}{n}$
4	$\frac{{}_{i=1}^{n-1}\lvert x_{i+1} - x_i}{t_n - t_1}$	10	${}_{i=1}^{n}\left(Az_i - \frac{{}_{i=1}^{n} Az_i}{n}\right.^2$
5	$\max\limits_{i=1,\dots,n-1} \frac{dist_{Eucl}\,(Pt_i, Pt_{i+1})}{t_{i+1} - t_i}$	11	$\frac{{}_{i=1}^{n} Al_i}{n}$
6	$\frac{{}_{i=1}^{n-1}(dist_{Eucl}\,(Pt_i, Pt_{i+1}}{(t_n - t_1)^2}$		

Table 1.1: Set of dynamic features. $s =)Pt_1, Pt_2, \dots, Pt_n)$ denotes an on-line signature composed of n events $Pt_i)x_i, y_i, t_i)$, $x_i, y_i, Pr_i, Az_i, Al_i$ denote x-position, y-position, pen pressure, azimuth and elevation angles of the pen at the i^{th} time instant t_i, respectively.

Basically, SVMs have been defined for separating linearly two classes. When data are non linearly separable, a kernel function is used. Thus, all mathematical functions, which satisfy Mercer's conditions, are eligible to be a SVM-kernel [53]. Examples of such kernels are sigmoid kernel, polynomial kernel, and Radial Basis Function (RBF) kernel. Generally, the RBF kernel is used for its better performance, which is defined as:

$$K(x, x_k) = exp\left(-\frac{x - x_k\|^2}{2\,\sigma^2}\right. \tag{1.5}$$

Where σ is the kernel parameter, $\|x - x_k\|$ is the Euclidian distance between two samples. Therefore, the decision function f: $\mathbb{R}^p \rightarrow \{-1, +1\}$, is expressed in terms of kernel expansion as:

$$f(x) = {}_{k=1}^{Sv}\, \alpha_k y_k\, K(x, x_k) + b \tag{1.6}$$

where α_k are Lagrange multipliers, Sv is the number of support vectors x_k which are training data, such that $0 \leq \alpha_k \leq C$, C is a user-defined parameter that controls the tradeoff between the machine complexity and the number of nonseparable points [54], the bias b is a scalar computed by using any support vector. Finally, test data x_d, $d = \{1,2\}$, are classified according to:

$$x_d \in \begin{matrix} class\,(+1) & \text{if}\, f(x_d) > 0 \\ class\,(-1) & \text{otherwise} \end{matrix} \tag{1.7}$$

b. Decision rule

The direct use of SVMs does not allow defining a decision threshold to assign a signature to genuine or forgery classes. Therefore, outputs of SVM are transformed to objective evidences, which express the membership degree (MD) of a signature to both classes (genuine or forgery). In practice, the MD has no standard form. However, the only constraint is that it must be limited in the range of $[0, 1]$ whereas SVMs produce a single output. In this chapter, we use a fuzzy model which has been proposed in [50, 51, 55] to assign MD for SVM output in both genuine and impostor classes. Let $f(x_d)$ be the output of a SVM obtained for a given signature to be classified. The respective membership degrees $h_d(\theta_i), i = \{gen, imp\}$

associated to genuine and impostor classes are defined according to membership models given in the Algorithm 1 [51]. To compute the values of membership degrees $)h_d, d = 1, 2)$, we consider the two case studies as follows:

- in first case study, the main problem for generating features is the appropriate number of the angular direction N_θ for the Radon transform and the number of the decomposition level L of the WT (Haar Wavelet) in the Ridgelet domain. Hence, many experiments are conducted for finding the optimal values for which the error rate in the training phase is null. In this case, feature vectors are generated from both Radon $(d = 1)$ and Ridgelet $(d = 2)$ of the same off-line signature by setting N_θ and L to 32 and 3, respectively.
- in second case study, we calculate the values $(h_d, d = 1)$ of off-line signature by using the optimal size $[5 \times 9]$ of the grid for which the error rate in the training phase is null. In the same way, we calculate also the values $(h_d, d = 2)$ of on-line signature by using the vector of 11 dynamic features for which the error rate in the training phase is null.

Algorithm 1.

Respective membership models for two classes.

```
if f(x_d) > 1 then
  h_d(θ_gen) ← 1
  h_d(θ_imp) ← 0
else
  if f(x_d) < −1 then
    h_d(θ_gen) ← 0
    h_d(θ_imp) ← 1
  else
    h_d(θ_gen) ← (1 + f(x_d)) / 2
    h_d(θ_imp) ← (1 − f(x_d)) / 2
  end if
end if
```

Hence, a decision rule is performed about whether the signature is genuine or forgery as described in Algorithm 2.

Algorithm 2. Decision making in SVM framework.

if $\dfrac{h_d(\theta_{gen})}{h_d(\theta_{imp})} \geq t$ then

$\quad s_d \in \theta_{gen}$

else

$\quad s_d \in \theta_{imp}$

end if

Where t defines a decision threshold.

1.3.4 Classification based on DSmT

The proposed combination module consists of three steps: i) transform membership degrees of the SVM outputs into belief assignments using estimation technique based on the dissonant model of Appriou, ii) combine masses through a DSmT based combination rule and iii) make a decision for accepting or rejecting a signature.

a. Estimation of masses

In this chapter, the mass functions are estimated using a dissonant model of Appriou, which is defined for two classes [56]. Therefore, the extended version of Appriou's model in DSmT framework is given as:

$$m_{id}(\emptyset) = 0 \tag{1.8}$$

$$m_{id}(\theta_i) = \frac{(1-\beta_{id})\, h_d(\theta_i)}{1+h_d(\theta_i)} \tag{1.9}$$

$$m_{id}(\overline{\theta}_i) = \frac{1-\beta_{id}}{1+h_d(\theta_i)} \tag{1.10}$$

$$m_{id}(\theta_i \cup \overline{\theta}_i) = \beta_{id} \tag{1.11}$$

$$m_{id}(\theta_i \cap \overline{\theta}_i) = 0 \tag{1.12}$$

where $i = \{gen, imp\}$, $h_d(\theta_i)$ is the membership degree of a signature provided by the corresponding source S^d $(d = 1,2)$, $(1-\beta_{id})$ is a confidence factor of i-th class, and β_{id} defines the error provided by each source $(d = 1,2)$ for each class θ_i. In our approach, we consider β_{id} as the verification accuracy prior computed on the training database for each class [14]. Since both SVM models have been validated on the basis that errors during training phase are zero, therefore β_{id} is fixed to 0.001 in the estimation model.

Note that the same information source cannot provide two responses, simultaneously. Hence, in DSmT framework, we consider that the paradoxical hypothesis $\theta_i \cap \ \theta\}_i$ has no physical sense towards the two information sources θ_{gen} and θ_{imp} . Therefore, the beliefs assigned to this hypothesis are null as given in Equation (1.12).

b. Combination of masses

The combined masses are computed in two steps. First, the belief assignments $(m_{id}(.), i = \{gen, imp\})$ are combined for generating the belief assignments for each source as follows:

$$m_1 = m_{\{gen\}1} \oplus m_{\{imp\}1} \tag{1.13}$$

$$m_2 = m_{\{gen\}2} \oplus m_{\{imp\}2} \tag{1.14}$$

where $\oplus$ represents the conjunctive consensus of the DSmC rule.

Finally, the belief assignments for the combined sources $(m_d(.), d = 1,2)$ are then computed as:

$$m_c = m_1 \oplus m_2 \tag{1.15}$$

where $\oplus$ represents the combination operator, which is composed of both conjunctive and redistribution terms of the PCR5 rule.

c. Decision rule

A decision for accepting or rejecting a signature is made using the statistical classification technique. First, the combined beliefs are converted into probability measure using a probabilistic transformation, called Dezert-Smarandache probability (DSmP), that maps a belief measure to a subjective probability measure [11] defined as:

$$DSmP_{\epsilon}(\theta_i) = m_c(\theta_i) + (m_c(\theta_i) + \epsilon) w_{\mathcal{M}} \tag{1.16}$$

where $w_{\mathcal{M}}$ is a weighting factor defined as:

$$w_{\mathcal{M}} = \sum_{\substack{A_j \in 2^{\Theta} \\ A_j \supset \theta_i \\ C_{\mathcal{M}}(A_j) \geq 2}} \frac{m_c(A_j)}{\sum_{\substack{A_k \in 2^{\Theta} \\ A_k \subset X \\ C_{\mathcal{M}}(A_k) = 1}} m_c(A_k) + \epsilon\, C_{\mathcal{M}}(A_j}$$

such that is a tuning parameter, $\mathcal{M}$ is the Shafer's model for Θ, and $C_{\mathcal{M}})A_k)$ denotes the DSm cardinal [11] of the set A_k . Therefore, the likelihood ratio test is performed for decision making as described in Algorithm 3.

Algorithm 3. Decision making in DSmT framework.

if $\dfrac{DSmP_{\varepsilon}(\theta_{gen})}{DSmP_{\varepsilon}(\theta_{imp})} \geq t$ then
    $s_d \in \theta_{gen}$
else
    $s_d \in \theta_{imp}$
end if

Where t defines a decision threshold and $s = \{s_1, s_2\}$ is the j -th signature represented by two modalities according the case study as follows:

- in first case study, s is an off-line signature characterized by both Radon and Ridgelet features.
- in second case study, s is a signature represented by both off-line and on-line modalities.

1.4 Performance criteria and dataset description

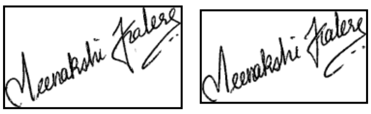
In this section, we briefly describe datasets used and performance criteria for evaluating the proposed DSmT for combing individual handwritten signature verification systems.

1.4.1 Dataset description

To evaluate the verification performance of the proposed DSmT based combination of individual HSV systems, we use two datasets of handwritten signatures: (1) CEDAR signature dataset [57] used for evaluating the performance for combining individual off-line HSV systems and (2) NISDCC signature dataset [58] for the experiments related to the simultaneous verification of individual off-line and on-line HSV systems.

a. CEDAR signature database

The Center of Excellence for Document Analysis and Recognition (CEDAR) signature dataset [57] is a commonly used for off-line signature verification. The CEDAR dataset consists of 55 signature sets, each one being composed by one writer. Each writer provided 24 samples of their signature, where these samples constitute the genuine portion of the dataset. While, forgeries are obtained by asking arbitrary people to skillfully forge the signatures of the previously mentioned writers. In this fashion, 24 forgery samples are collected per writer from about 20 skillful forgers. In total, this dataset contains 2640 signatures, built from 1320 genuine signatures and 1320 skilled forgeries. Figures 1.6(a) and 1.6(b) show two examples of both preprocessed genuine and forgery signatures for one writer, respectively.



(a) Genuine signatures.

(b) Forgery signatures.

Figure 1.6: Signature samples of the CEDAR.

b. NISDCC signature database

The Norwegian Information Security laboratory and Donders Centre for Cognition (NISDCC) signature dataset has been used in the ICDAR'09 signature verification competition [58]. This collection contains simultaneously acquired on-line and off-line samples. The off-line dataset is called "NISDCC-offline" and contains only static information while the on-line dataset which is called "NISDCC-online" also contains dynamic information, which refers to the recorded temporal movement of handwriting process. Thus, the acquired on-line signature is available under form of a subsequent sampled trajectory points. Each point is acquired at 200 Hz on tablet and contains five recorded pen-tip coordinates: x-position, y-position, pen pressure, azimuth and elevation angles of the pen [59] The NISDCC-offline dataset is composed of 1920 images from 12 authentic writers (5 authentic signatures per writer) and 31 forging writers (5 forgeries per authentic signature). Figures 1.7(a) and 1.7(b) show an example of both preprocessed off-line signature and a plotted matching on-line signature for one writer, respectively.

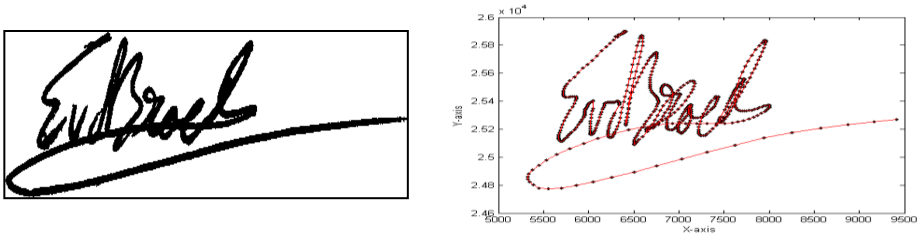


Figure 1.7: Signature samples of the NISDCC signature collection.

1.4.1 Performance criteria

For evaluating performances of the combined individual HSV systems, three different kinds of error are considered: False Accepted Rate (FAR) allows taking into account only skilled forgeries; False Rejected Rate (FRR) allows taking into account only genuine signatures and finally the Half Total Error Rate (HTER) allows taking into account both rates. Thus, Equal Error Rate is a special case of HTER when FRR = FAR.

1.4.2 SVM model

For both case studies, signature data are split into training and testing sets for evaluating the performances of the proposed DSmT based combination of individual HSV systems. Thus, the training phase allows finding the optimal hyperparameters for each individual SVM model. In our system, the RBF kernel is selected for the experiments.

a. SVM models used for combined individual off-line HSV systems

In first case study, the SVM model is produced for each individual off-line HSV system according the Radon and Ridgelet features, respectively. For each writer, 2/3 and 1/3 samples are used for training and testing, respectively. The optimal parameters (C, σ) of each SVM are tuned experimentally, which are fixed as $(C = 19.1, \sigma = 4)$ and $(C = 15.1, \sigma = 4.6)$, respectively.

b. SVM models used for combined individual off-line and on-line HSV systems

In second case study, the SVM model is produced for both individual off-line and on-line HSV systems according the uniform grid features and dynamic information, respectively. For each writer and both datasets, 2/3 and 1/3 samples are used for training and testing, respectively. The optimal parameters (C, σ) for both SVM classifiers (off-line and on-line) are tuned experimentally, which are fixed as $(C = 9.1, \sigma = 9.4)$ and $(C = 13.1, \sigma = 2.2)$, respectively.

1.5 Experimental results and discussion

For each case study, decision making will be only done on the simple classes. Hence, we consider the masses associated to all classes belonging to the hyper power set $D^\Theta = \{\emptyset, \theta_{gen}, \theta_{imp}, \theta_{gen} \cup \theta_{imp}, \theta_{gen} \cap \theta_{imp}\}$ in both combination process and decision making. In the context of signature verification, we take as constraint the proposition that $\theta_{gen} \cap \theta_{imp} = \emptyset$ in order to separate between genuine and impostor classes. Therefore, the hyper power set D^Θ is simplified to the power set 2^Θ as $2^\Theta = \{\emptyset, \theta_{gen}, \theta_{imp}, \theta_{gen} \cup \theta_{imp}\}$, which defines the Shafer's model [9]. This section presents the experimental results with their discussion.

To evaluate the performance of the proposed DSmT based combination, we use two individual off-line HSV systems using the CEDAR database at the first case study. Indeed, the task of the proposed combination module is to manage the conflicts generated between the two individual off-line HSV systems for each signature using the PCR5 combination rule. For that, we compute the verification errors of both individual off-line HSV systems and the combined individual off-line HSV systems using PCR5 rule. Figure 1.8 shows the FRR and FAR computed for different values of decision threshold using both individual off-line HSV systems of this first case study. Table 1.2 shows the verification errors rates computed for the corresponding optimal values of decision threshold of this case study. Here HSV system 1 is the individual off-line verification system feeded by Radon features that yields an error rate of 7.72% corresponding to the optimal value of threshold $t = 1.11$ while HSV system 2 is the individual off-line verification system feeded by Ridgelet features, which provides the same result with an optimal value of threshold $t = 0.991$. Consequently, both individual off-line HSV systems give the same verification performance since the corresponding error rate of HTER $= 7.72\%$ is the same.

The proposed DSmT based combination of individual off-line HSV systems yields a HTER of 5.45% corresponding to the optimal threshold value $t = 0.986$. Hence, the combined individual off-line HSV systems with PCR5 rule allows improving the verification performance by 2.27%. This is due to the efficient redistribution of the partial conflicting mass only to the elements involved in the partial conflict.

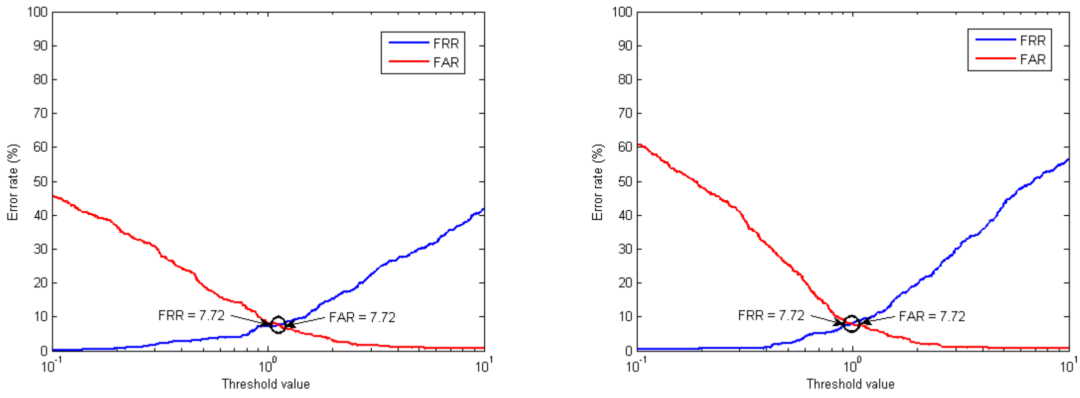


Figure 1.8: Performance evaluation of the individual off-line HSV systems.

HSV Systems	**Optimal Threshold**	**FAR**	**FRR**	**HTER**
System 1	1.110	7.72	7.72	7.72
System 2	0.991	7.72	7.72	7.72
Combined Systems	0.986	5.45	5.45	5.45

Table 1.2: Error rates (%) obtained for individual and combined HSV systems.

In the second case study, two sources of information are combined through the PCR5 rule. Figure 1.9 shows three examples of conflict measured between off-line and on-line signatures for writers 3, 7, and 10 of the NISDCC dataset, respectively. The values K_{c3})∈)0.00, 0.35)), K_{c7})∈)0.00, 0.64)), and K_{c10})∈)0.00, 1.00)) represent the mass assigned to the empty set, after combination. We can see that the two sources of information are very conflicting. Hence, the task of the proposed combination module is to manage the conflicts generated from both sources)$K_{cw}, w = 1, 2, \dots, 12$) for each signature using the PCR5 combination rule. For that, we compute the verification errors of both individual off-line and on-line HSV systems and the proposed DSmT based combination. Figure 1.10 shows the FRR and FAR computed for different values of decision threshold using both individual off-line and on-line HSV systems of this second case study. For better comparison, Table 1.3 shows the HTER computed for the corresponding optimal values of decision threshold of this case study.

The proposed DSmT based combination of both individual off-line and on-line HSV systems yields a HTER of 0% corresponding to the optimal threshold value $t = 0.597$. Consequently, the proposed combination of individual off-line and on-line HSV systems using PCR5 rule yields the best verification accuracy compared to the individual off-line and on-line HSV systems, which provide conflicting and complementary outputs.

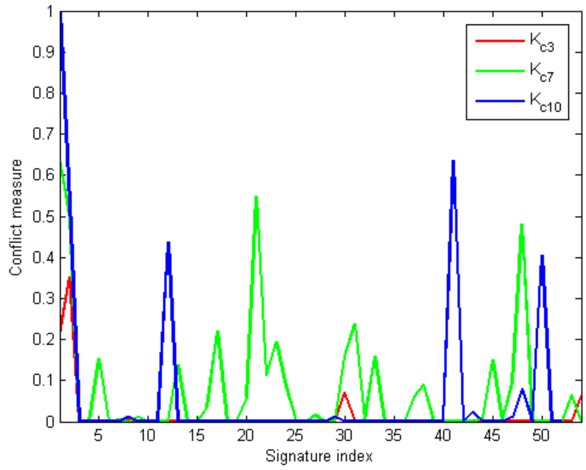
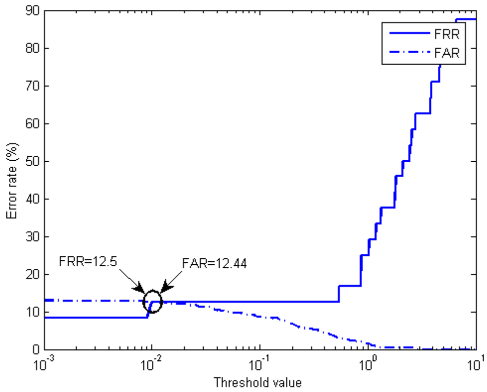
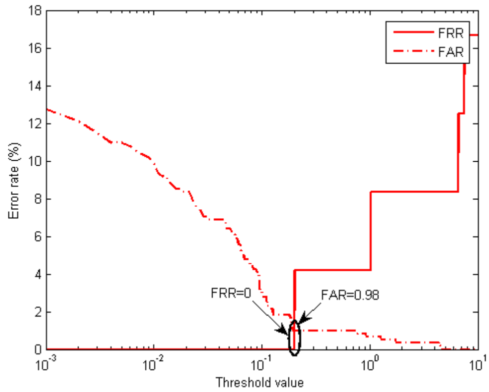


Figure 1.9: Conflict between off-line and on-line signatures for the writers 3, 7, and 10, respectively.



(a) Off-line HSV system 1.



(b) On-line HSV system 2.

Figure 1.10: Performance evaluation of the individual off-line and on-line HSV systems.

HSV Systems	**Optimal Threshold**	**FAR**	**FRR**	**HTER**
System 1	0.012	12.44	12.50	12.47
System 2	0.195	0.98	0.00	0.49
Combined Systems	0.597	0.00	0.00	0.00

Table 1.3: Error rates (%) obtained for individual and combined HSV systems.

1.6 Conclusion

This chapter proposed and presented a new system based on DSmT for combining different individual HSV systems which provide conflicting results. The individual HSV systems are combined through DSmT using the estimation technique based on the dissonant model of Appriou, sophisticated PCR5 rule and likelihood ratio test. Hence, two cases have been addressed in order to ensure a greater security: (1) combining two individual off-line HSV systems by associating Radon and Ridgelet features of the same off-line signature (2) and combining both individual off-line and on-line HSV systems by associating static image and dynamic information of the same signature characterized by off-line and on-line modalities. Experimental results show in both case studies that the proposed system using PCR5 rule allows improving the verification errors compared to the individual HSV systems.

As remark, although the DSmT allows improving the verification accuracy in both studied cases, it is clearly that the achieved improvement depends also to the complementary outputs provided by the individual HSV systems. Indeed, according to the second case study, a suitable performance quality on the individual on-line HSV system can be obtained when the dynamic features of on-line signatures are carefully chosen. Combined to the grid features using DSmT allows providing more powerful system comparatively to the system of the first case study in term of success ratio. In continuation to the present work, the next objectives consist to explore other alternative DSmT based combinations of HSV systems in order to attempt improving performance quality of the writer-independent HSV whether the signature is genuine or forgery as well as in the false rejection and false acceptance concepts.

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