



Biomechanical online signature modeling applied to verification

Jânio Coutinho Canuto

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**DOCTORAT EN CO-ACCREDITATION
TELECOM SUDPARIS ET L'UNIVERSITE EVRY VAL D'ESSONNE**

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Ecole doctorale: Sciences et Ingénierie

Présentée par

Jânio Coutinho Canuto

**Pour obtenir le grade de
DOCTEUR DE TELECOM SUDPARIS**

**BIOMECHANICAL ONLINE SIGNATURE MODELING
APPLIED TO VERIFICATION**

Soutenue le 08/12/2014

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Abstract

This thesis deals with the modeling and verification of online signatures. The first part proposes a novel biomechanical modeling of the hand movement in relation to the signing gesture. After a review of the main motor control theories available, a model based on the Minimum Jerk criterion was chosen for its optimality for gesture modeling. However, implementing such model for on-line signatures requires segmenting the trajectory into shorter paths (*i.e.*, strokes) that better fit the chosen kinematic model. We therefore propose an adequate iterative signature segmentation method. Both the choice of the model and the development of the segmentation method are strongly based on a tradeoff between reconstruction quality and signal compression.

On the second part, the polynomial model issued from the Minimum Jerk criterion is intentionally degraded. The non-real zeroes of the polynomials are discarded and the effects of this degradation is studied from a biometric verification perspective. We show that the elimination of non-real polynomial zeroes is equivalent to the Infinite Clipping signal processing technique, originally applied to speech signals. On signatures, the preservation of the essential discriminative information was observed on signature verification tasks, as is the case for speech. As a matter of fact, using only an edit distance (Levenshtein distance) and the degraded signature representation (*i.e.*, infinitely clipped), verification error rates comparable to those of more elaborate methods were obtained. Furthermore, the symbolic representation yielded by the infinity clipping technique allows for a conceptual relationship between the number of polynomial segments obtained through the Minimum Jerk-based iterative segmentation and the Lempel-Ziv complexity. This relationship is potentially useful for the quality analysis of online signature signals and can be used for improving the recognition performance.

Resumé

Cette thèse porte sur la modélisation et la vérification des signatures en ligne. La première partie a pour thème principal la modélisation biomécanique du mouvement de la main associée au geste de signer. Un modèle basé sur le critère de Minimum de Secousse (*Minimum Jerk*) a été choisi parmi les diverses théories du contrôle moteur disponibles. Un examen de ces théories est fourni et les principales raisons pour le choix du Minimum de Secousse sont présentées, comme l'obtention d'un modèle analytique indépendant de l'application. Ensuite, le problème de la segmentation des trajectoires de signature en portions plus courtes (*i.e., strokes*) correspondant le mieux au modèle cinématique choisi est étudié, conduisant à l'élaboration d'une méthode de segmentation itérative. Le choix du modèle et de la mise au point de la méthode de segmentation sont fortement basés sur le compromis entre la qualité de reconstruction et la compression du signal.

Dans la deuxième partie, le polynôme issu du critère de Minimum de Secousse est volontairement dégradé. Les zéros non-réels des polynômes ne sont pas pris en compte et les effets de cette dégradation sont étudiés dans une perspective de vérification biométrique. Cette élimination de zéros non-réels du polynôme équivaut à la technique de traitement des signaux connu sous le nom de *Infinite Clipping*, initialement appliquée à des signaux de parole. Pour les signatures, comme pour la parole, on observe que l'information discriminante essentielle est préservée sur des tâches de vérification de signature. En fait, en utilisant seulement une distance d'édition (distance de Levenshtein) et la représentation dégradée de la signature (*i.e., infinitely clipped*), des taux d'erreur de vérification comparables à ceux de méthodes plus élaborées ont été obtenus. En outre, la représentation symbolique donnée par la technique de *clipping* permet une relation conceptuelle entre le nombre de segments de polynômes obtenus par la segmentation itérative basée sur le Minimum de Secousse et la complexité de Lempel-Ziv. Cette relation est potentiellement utile pour l'analyse des signaux de signature en ligne et l'amélioration des systèmes de reconnaissance.

Contents

Abstract	iii
Resumé	v
List of Tables	xi
List of Figures	xiii
Introduction	xv
Movement Modeling Context	xvi
Main Contributions	xviii
Thesis Organization	xviii
 I General Concepts and Literature Review	 1
 1 Biometrics	 3
1.1 Introduction	3
1.2 Anatomy and Operation of a Biometric System	5
1.3 Biometric Features	7
1.4 Performance Analysis of a Biometric System	9
1.5 Vulnerability and Limitations	13
1.6 Multi-Biometric Systems	15
1.6.1 Fusion Levels	17
1.7 Handwritten Signature Recognition	18
1.8 Conclusion	20
 2 Motor Control	 21
2.1 Introduction	21
2.2 Equilibrium Point Theory	21
2.3 Motor Primitives theory	22
2.4 Internal Models Theory	24
2.5 Optimal Control Theory	25
2.5.1 Optimality Criteria	26
2.5.1.1 Energetic Criteria	26
2.5.1.2 Muscular or Neuronal Criteria	27
2.5.1.3 Dynamic Criteria	27
2.5.1.4 Cinematic Criteria	29
2.6 Movement Modelling and Handwriting	32
2.7 Conclusion	34

3	Signature Verification	37
3.1	Introduction	37
3.2	Data Acquisition	37
3.3	Preprocessing	38
3.4	Feature Extraction	39
3.5	Classification	41
3.6	Database Design	44
3.7	Verification Performance	44
3.7.1	Databases Description	44
3.7.1.1	SVC2004 Task 1 (SVC1)	44
3.7.1.2	SVC2004 Task 2 (SVC2)	45
3.7.1.3	MCYT Signature Subcorpus (MCYT)	45
3.7.1.4	Biosecure Signature Dataset 2 (DS2)	46
3.7.1.5	Biosecure Signature Dataset 3 (DS3)	46
3.7.2	Performances on Selected Works	48
3.8	Conclusion	57
II	Developed Methods	59
4	Minimum Jerk Representation of Online Signatures	61
4.1	Introduction	61
4.2	The Minimum Jerk Model	62
4.3	Proposed Method	63
4.3.1	Reconstruction Error	68
4.3.2	Verification Performance	68
4.3.3	Residual Analysis	70
4.3.4	Compression	71
4.3.5	Stability	77
4.3.6	Relationship to Other Methods	78
4.4	Applications of the Minimum Jerk Representation	80
4.4.1	Signature Resampling	80
4.4.2	Signature Complexity Evaluation and Database Segmentation	82
4.4.3	Synthetic Signatures Generation	85
4.5	Conclusion	88
5	Further Simplifications: Infinite Clipping and Signature Verification	91
5.1	Introduction	91
5.2	Infinite Clipping Representation	92
5.3	Strings Matching: The Levenshtein Distance	97
5.4	Signature Verification Experiments	101
5.4.1	Fusion Schemes	101
5.4.2	Quantization levels	102

5.4.3	Feature Sets	105
5.5	Signature Complexity Evaluation: The Lempel-Ziv Complexity	110
5.6	Conclusion	119
6	Conclusion and Perspectives	121
6.1	Conclusion	121
6.2	Future work	124
III	Bibliography and Appendices	127
	Bibliography	129
A	List of Publications	153

List of Tables

1.1	Error probability as a function of database size in an identification task.	7
1.2	Biometric modalities characteristics.	8
3.1	Signature databases characteristics.	48
3.2	Performance results on the SVC1 database.	49
3.3	Performance results on the SVC2 database.	50
3.4	Performance results on the MCYT database.	51
3.5	Performance results on the DS2 database.	52
3.6	Performance results on the BioSecure Signature Evaluation Campaign (BSEC'09) (Houmani et al., 2012).	52
3.7	Performance results on the BioSecure Evaluation of Signature Resistance to Attacks (ESRA'11) (Houmani et al., 2011).	52
4.1	Verification Performance (average EER in %) and standard deviation values (in parenthesis) for each database before and after reconstruction with a SNR_v of 14 dB per segment.	71
4.2	Average compression rate and standard deviation (in parentheses) for each database.	78
4.3	Verification performance (EER in %) for each complexity category. Percentage of users in each category in parentheses.	85
5.1	Different codings for the clipped signal in Figure 5.2.	94
5.2	Conjoint representation of two binary values.	100
5.3	EER(%) and standard deviation (in parenthesis) for the fusion of x and y velocities on each database. Corresponding values for the DTW-based system (Table 4.1) are reproduced to ease comparison	102
5.4	EER(%) and standard deviation (in parenthesis) for the LD-based and the DTW-based systems using x and y velocities.	105
5.5	Average EER for the 8 features (x , y , v_x , v_y , a_x , a_y , j_x , j_y) considered separately for each signature database.	106
5.6	Average EER(%) for each of the 7 pairs of features containing v_y	108
5.7	Best EER(%) and standard deviation (in parenthesis) obtained with the LD-based system for each signature database.	110
5.8	Average EER (in %) and standard deviation (in parenthesis) for (v_y), (v_x, v_y), and the best feature set (see Table 5.7) for each signature database.	111
5.9	Analogous steps between the Minimum Jerk iterative segmentation and the Lempel-Ziv parsing algorithm.	115

List of Figures

1.1	Flux diagram of a generic biometric system.	5
1.2	Inter-class and Intra-class variances concept. a) Low intra-class variance and high inter-class variance: compact well separated clusters. b) High intra-class variance and low inter-class variance: wide clusters without a clear frontier.	10
1.3	Visualization of the thresholding process and the concepts of FAR and FRR.	11
1.4	FAR and FRR as a function of the threshold τ for the score distribution in Figure 1.3. The EER is the crossing point of the two curves.	11
1.5	ROC curve representing the FAR and FRR on Figure 1.4. The EER is the point where the curve crosses the diagonal line (FAR=FRR).	12
3.1	A signature of the DS3 database before and after the removal of the artificial points at the origin.	47
4.1	Reconstruction (red line) of the same signature (blue line) at different SNR levels.	69
4.2	Reconstruction (red line) of the same signature (blue line) at different SNR levels.	72
4.3	Representation quality and compression rate tradeoff for minimum velocity ($n = 1$), acceleration ($n = 2$), jerk ($n = 3$), snap ($n = 4$) and crackle ($n = 5$).	74
4.4	Representation quality and compression rate tradeoff for each database using the Minimum Jerk criterion.	75
4.5	x and y coordinates for a signature on the SVC1 database. Segmentation points are circled in red.	76
4.6	The four basic strokes in (Edelman and Flash, 1987): hook, cup, inverted gamma and oval.	79
4.7	x and y coordinates after upsampling of a signature with sampling discontinuities.	81
4.8	Number of segments as a function of the signature duration for each database along with its correlation coefficient ρ	83
4.9	Signatures of each category and their respective x and y coordinates signals. Dots represent segments limits.	84
4.10	Personal Entropy (Houmani, 2011) as a function of the number of segments for the MCYT database.	86
4.11	Fifteen synthetic variations obtained from a single original signature.	87
4.12	Synthetic signatures obtained from a single original sample using only positive or negative perturbations.	89

5.1	Infinite clipping (red) of a waveform (blue).	93
5.2	Infinite clipping of a waveform and zero-crossing instants.	94
5.3	5 th order polynomial segment. Red dot is a real root. Green circles are local minima and maxima.	95
5.4	Zero-crossings at different order derivatives. Red dots and green circles are x and y directions.	98
5.5	Average EER (solid lines) and region containing 95% of the EER values (dashed lines 1.96 standard deviations apart from the average) as a function of the number of quantization levels for each database.	104
5.6	Verification performances (EER) for the 8 features (x , y , v_x , v_y , a_x , a_y , j_x , j_y) considered separately for each signature database.	106
5.7	Verification performances (EER) for the 7 pairs of features containing v_y	107
5.8	Verification performances for the best sets of 1 up to 8 features for each signature database.	109
5.9	Two views of the subset of a 3-points ensemble that can be represented without error by a first order polynomial (red plane) and the increased subset due to error tolerance (blue dots).	116
5.10	Average number of MJ segments and relative LZ complexity for each user.	118
5.11	Segments obtained for the same signature through the modified LZ parsing (black circles) and the MJ representation (red dots).	119

Introduction



Handwritten signature verification is a behavioral biometric modality that is performed through natural and instinctive gestures. It has been used for many centuries as a mean for identity verification and is thoroughly accepted both socially and juridically. It is widely used on bank checks, letters, contracts, and all sorts of administrative documents for identification or assuring the good faith and will of the person. Due to the large number of documents that must be verified in a limited time, manual signature verification is unpractical in many applications, leading to the search and design of automatic signature verification systems.

Signature representation is highly dependent on the type of device used for data acquisition. Generally, static (off-line) signature verification systems use imaging devices such as scanners and cameras providing gray scaled images. Even if off-line systems present advantages on some applications (*e.g.*, forensic analysis, check verification), they are more challenging to design than dynamic (on-line) signature verification systems (Impedovo and Pirlo, 2008) because of the relative scarcity of discriminative information. Therefore, dynamic signature verification is more often considered as a biometric measure for resources access. This work deals with the latter type of system and focuses specifically on *dynamic signature representation*.

In fact, this thesis is part of a series of works on dynamic signatures verification developed at the Intermedia team of Télécom SudParis EPH department. Several works on verification systems and signature quality evaluation have been done by the team over the past years. However, few works deal with the first step of the verification system (*i.e.*, signature representation), this motivated the research direction adopted in the present work, which will focus explicitly on the proposition of a new signature representation.

On-line signature verification systems usually adopt graphic digitizers, tablet PCs or PDAs as acquisition devices. These devices produce time varying data about pen tip kinematics, pressure, and orientation. After proper preprocessing (*e.g.*, filtering, normalization, re-sampling), these input signals can either be directly used, be fitted by mathematical functions, or modified (*e.g.*, differentiated, integrated, combined) to provide more informative signals. This approach, in which time-series are used, is said to be function-based and is often associated with different sorts of temporal axis de-

formation techniques (*e.g.*, dynamic time warping (Kholmatov and Yanikoglu, 2005), longest common subsequence (Gruber et al., 2010)) to model signature variability.

A second approach uses a single feature vector to encode each signature’s characteristics. Feature extraction from acquired signals is performed using various techniques such as spectrum analysis, wavelet decomposition, and cross correlation. More basic global features are also used, such as total signing time, signature dimensions and dimension ratios, amount of zero crossings, maximal, minimal, average, and dispersion of velocity, acceleration, curvature, pressure, or pen orientation.

Features are often separated in different classes regarding whether they are shape or dynamics-related, skilled or random forgery discriminative, locally or globally descriptive, or of a continuous, discrete or quantized nature. In most cases, verification systems use different types of complementary features through some kind of fusion.

Global features can be made local if applied to elements of a *segmented signature*. Using local features to perform a stroke-by-stroke signature comparison is sometime seen as a different approach which is then referred as stroke-based or regional approach. Although this decomposition in more basic elements (*e.g.*, strokes, components, segments) raises a segmentation problem, it has shown to lay good results.

Finally, it is worth mentioning that these distinct approaches may either be used by themselves or be combined to best capture writers’ specificities from input data. These usual representations are directly linked to the signature verification problem, associated to a particular matching algorithm, and do not take into account the particular fact that signatures are the result of voluntary hand movements. A more thorough discussion of signature verification systems and each of their components is provided in Chapter 3.

Movement Modeling Context

In this work, a novel signature representation based on a psycho-physiological model of human movement production is proposed. This representation has the advantage of being invariant in regard of cultural or language differences, whereas systems based on visual characteristics often need to be tailored for Chinese, Arabic, European, or American signatures. Furthermore, since the chosen representation is based on a generic human movement model, it can be further used in any application involving handwritten trajectories and not only to signature verification (for instance, pathological behavior detection could be envisaged). The next paragraphs overview some of the human movement control models and lay down some ground rules that have been used to choose an adequate model for signature representation.

Several computational models have been proposed in the literature to explain how the central nervous system generates and controls the kinematics of human movements. Some of them describe movements through analytical expressions, while others proceed through the numerical resolution of a system of differential equations. The use of an equilibrium hypothesis has also been firmly rooted from a neurophysiologic

point of view. Finally, the usage of a minimum principle as basis for solving indeterminacy in human movement control has also been widely discussed in the literature using many different variables as cost functions, such as movement time, acceleration, jerk, snap, torque changes, and energy.

In face of such a variety of movement models, some guidelines were devised in order to develop the on-line signature representation. Four criteria have been considered: (1) the model should have an analytical form for an easy use in analysis and synthesis; (2) it should be able to represent complex movements; (3) the signature representation should have a tunable reconstruction error; (4) finally, signature model should be parsimonious, providing a compressed representation.

None of the available human movement control models are able to satisfy these criteria at once. As a matter of fact, most of the models in the literature are aimed at representing a single stroke and thus are not capable of representing complex movements, such as those of signatures. The minimum jerk model is one of the most commonly used in the movement control literature and has been proven to provide good results on a wide range of scenarios, even if not considered before for signature modeling. In addition, it provides a simple analytic form for the modeled trajectories.

As a first novelty of this work, an iterative segmentation/representation method based on the minimum jerk criterion is proposed where the desired representation quality is an input parameter. This can be seen as an extension of the minimum jerk model for complex trajectories and gives a representation that complies with the four desired criteria.

Driven by complexity reduction and simplification objectives, the Minimum Jerk signature model is intentionally degraded by ignoring all non-real zeros of the polynomial segments yielded by the minimum jerk model. This provides an extremely compressed symbolic representation that is directly linked to the Infinite Clipping signal processing technique, originally applied to speech signals. Through biometric verification experiments it was verified that for signatures, as for speech, the essential discriminant information about the signature's owner is kept even after this strong degradation of the signal.

Finally, a conceptual relationship between the Lempel-Ziv complexity, computed over the symbolic representation yielded by the Infinite Clipping, and the number of segments found through the Minimum Jerk signature model. The Lempel-Ziv parsing algorithm segments the input string based on previous samples. Meanwhile, the Minimum Jerk model segments the trajectory using 5th order polynomials. It is proposed that these polynomials, on the MJ-based representation, performs a role similar to that of the past examples, on the LZ parsing algorithm. Besides the theoretical interest, this relationship corroborates the use of Minimum Jerk segments as a measure of signature complexity.

Main Contributions

In this thesis two new representation techniques for online handwritten signatures are proposed. Contrary to most biometrics works, development of a better verification system is not the main goal; this thesis aims at the development of a new application independent online signature model based on a human movement control model.

The main contributions of this work can be summarized as follows.

- An original online signature model based on the Minimum Jerk principle.
- A new automatic segmentation method based on the Minimum Jerk principle.
- A novel signature symbolization method based on the Infinite Clipping technique.
- A conceptual relationship between the Lempel-Ziv complexity and the number of Minimum Jerk segments.

Thesis Organization

The rest of this thesis is divided in two parts: the first part contains three chapters dealing with general concepts and literature review related to the works developed on the second part, which presents the developed methods along with conclusions and perspectives of future work.

In Chapter 1 general notions regarding biometric systems are presented. Its main components, functions are discussed, along with the techniques used for performance assessment. Some general problems regarding biometric verification are pointed out along with the possible solutions provided by information fusion techniques. And a brief introduction to the handwritten signatures biometrics is provided.

In Chapter 2 the main theories regarding human movement planning are studied, with an emphasis on the Minimum Jerk Model, an Optimum Control theory-based method that provides the tools used in chapter 4 to develop the signature representation proposed in this work. A review of handwritten movement representation methods is performed.

In Chapter 3, a study of online signature verification systems is presented, analyzing the techniques adopted in each of the main components of a biometric system: data acquisition, preprocessing, feature extraction, classification and database design (as described in Chapter 1). Then, the dynamic signatures databases adopted in this thesis are described and state-of-the-art results for each of them are presented. Along with these results, a brief description of the systems developed on each work is provided.

The second part of the thesis describes our original contributions and details the two novel representation methods developed by the author. Chapter 4, presents the

first one, which is based on the Minimum Jerk model. The proposed algorithm yields not only a piecewise polynomial representation but also a signature segmentation technique based on the dynamics of human movement. Following the imposed requirements, this model is able to represent a signature trajectory with any desired reconstruction error.

As a matter of fact, the reconstruction error is a parameter of the modeling algorithm and a compression rate as high as 78% is obtained while maintaining a reconstruction quality of 15 dB SNR_v (signal to error ratio of the velocity profiles). On this regard, this model is analogous to the jpeg image compression; while the jpeg is based on psychophysiological aspects of the human vision the signature model is based on aspects of the human movement. This adjustable representation quality is an improvement over other handwriting models found in the literature, since the user can choose the suitable representation quality level for his/her application. Another advantage over existing techniques is that the proposed algorithm provides an automatic segmentation that is a direct consequence of the movement model, without the use of segmentation heuristics or manually inserted via-points.

Three applications of this model are proposed: signature resampling, signature complexity evaluation and generation of synthetic signatures. Resampling is a common technique used in online signature systems, since time functions feature vectors usually have different lengths amongst samples. Using the proposed model it is possible to easily perform a resampling while keeping the dynamics characteristics of the movement.

Quality measures for biometric samples have been studied for several years. Such measures can be used to improve acquisitions or even to adapt the system parameters to a given user category, improving the overall system performance. The number of segments found by the Minimum Jerk signature model can be used as a complexity measure that is linked both to the signature's shape and dynamic properties.

The analytical form of the proposed representation allows for an easy generation of synthetic signatures through the addition of random perturbations to the parameters of the model. Synthetic signatures generation has been studied in the literature (Galbally et al., 2012) aiming at the resolution of a frequent problem on biometric applications: the limited number of available samples.

Finally, in Chapter 5 another signature representation is proposed as a simplification of the previous one. This representation is an adaptation of a widely used technique for speech compression, the Infinite Clipping. Unlike the previous method, the reconstruction quality of this technique is always very low, since all amplitude information is disregarded. Considering that two bytes are used to store each coordinate at each sampling instant, this model yields a compression rate of at least 94% for the signatures present on the studied databases.

The Infinitely Clipped representation yields a symbolic sequence that, when used along with the Levenshtein distance matching technique, despite all information loss, yields verification performances comparable to those of more elaborate systems. This

is a hint that there is much redundancy on the features commonly used for signature verification.

Since this representation yields a good verification performance and does not allow for the reconstruction of the original signature, it might be adequate for signature verification tasks; this loss of the original signature actually protects the data stored by the system because no forgery can be produced from the available clipped representation.

Last, a modified version of the relative Lempel-Ziv complexity algorithm is proposed, taking into account other users signatures as references. It is noted that the Lempel-Ziv parsing algorithm is very similar, in concept, to the Minimum Jerk segmentation algorithm proposed in Chapter 4. This relationship between the two segmentation methods is supported by the observation that Lempel-Ziv complexity (*i.e.*, number of segments found using the Lempel-Ziv parsing) is close to the number of segments obtained using the Minimum Jerk segmentation. These observation corroborate the use of the number of Minimum Jerk segments as a measure of signature complexity, as proposed in Section 4.4.

Part I

General Concepts and Literature
Review

CHAPTER 1

Biometrics

1.1 Introduction

The word *biometrics* is formed by the junction of two Greek words [βίος (life) and μετρικός (measurement)] meaning “measurement of life”, or what best reflects its current use; it is the measurement of biological data. Although being used in several different contexts, such as medicine and biology, this word has become more and more known into our everyday life as a synonym to identity verification.

Traditional authentication methods are usually based on possession (*e.g.* cards, badges) or knowledge (*e.g.* passwords, secret phrases). These systems have several problems: cards can be lost or forgotten, resulting in frustration to the user, or still stolen and/or cloned, causing security breaches. Passwords, likewise, can be forgotten, shared or broadcasted in an unauthorized way, resulting in the same aforementioned problems. Moreover, simple passwords can be easily guessed while over complicated passwords can be hard to memorize, which usually leads the user to write it down somewhere, making it even more likely for someone to find it.

Biometrics, on the other hand, is the science of establishing a person’s identity based on physiological features, such as face, iris, fingerprint, smell or genetic code; or behavioral traits such as signature, voice, keystroke dynamics or gait (Jain et al., 1999, 2004c; Bolle et al., 2003). Therefore, it is an alternative to traditional authentication methods, being a technique that takes into account not “what you own” or “what you know” but “who you are” instead, which is precisely the question that needs to be answered for identity establishment. Since many of the physiological and behavioral traits are almost unique to each individual, biometrics yields a more reliable authentication system than cards, keys or passwords (Jain et al., 2000; Vielhauer and Dittmann, 2006).

Technology advances, especially on transportation and communication, along with the ever growing worry about frauds and safety, have made reliable identity authentication a necessity in a wide range of applications; this phenomenon has been stimulating the research on biometrics over the years (Rood and Jain, 2003). Because of this increasing need, the use of biometric authentication on security systems has become a worldwide tendency (Boyer et al., 2007; Prabhakar et al., 2007; Zhang et al., 2005; Frischholz and Dieckmann, 2000), being found in airports, forensic investigation, personal computers and phones, physical access (*e.g.* gyms, schools, hospitals, theme

parks), financial transactions and fraud prevention on elections. This buzz around the theme has pushed the development and implementation of systems that are more robust and in larger scale.

This tendency, however, is not always welcome by society, putting biometrics in the center of a great debate with “Orwellian questions” concerning privacy (Davies, 1994). Questions that still do not have a definitive answer, such as: “Can people be tracked?”, “Will their financial and social profile be traced?”, “What are the consequences of exposition and/or sharing of an individual biometric data?”, have been causing discomfort in some people regarding the use of large scale biometric solutions.

Some studies already propose measures to ease these problems (Kenny and Borking, 2002; Rejman-Greene, 2005), such as the use of personal cards to store and process biometric data (*e.g.* e-passport) to eliminate the need of having all users’ information stored on the authentication site, but this brings back some of the problems associated to traditional authentication techniques (loss/theft/cloning of cards). Besides technical solutions, many governments and associations are working on the development of laws and regulations to avoid trading, appropriation or unauthorized processing of biometric data.

Since Francis Galton pioneer works, who has proposed the first standardized system for fingerprint authentication, until the current use of chemistry and informatics in the identification of genetic codes, biometrics has suffered great transformations from the technological point of view, mainly due to the development of digital computers, but its theoretical basis are still rooted on statistics and pattern recognition (Duda et al., 2000; Theodoridis and Koutroumbas, 2006). In fact, despite the continuous advances, biometrics still present, from a scientific point of view, many open questions relative to theoretical models used in the preprocessing, in the features extraction, in the optimization of classification machines parameters and in the combination of information from different sources.

In addition to all these factors, the continuously growing requisites and expectation from users regarding biometric systems, that have been featured in scientific fiction movies since the end of the sixties (*e.g.* 2001: A Space Odyssey by Stanley Kubrick in 1968) as flawless authentication methods, makes the research in this area even more challenging (Jain et al., 2004b).

This Chapter presents some general basic concepts regarding Biometric Systems. Section 1.2 presents the main components of a reference system and how they work. Section 1.3 discusses the desired properties of biometric features. In Section 1.4 the performance assessment of biometric systems is studied. In Sections 1.5 and 1.6 are discussed some problems regarding biometric systems and how they can be partially overcome through the use combined systems. Finally, Section 1.7 gives an introduction into signature verification systems, which are the object of study of this thesis. The reader that is already familiarized with biometrics might want to skip this chapter.

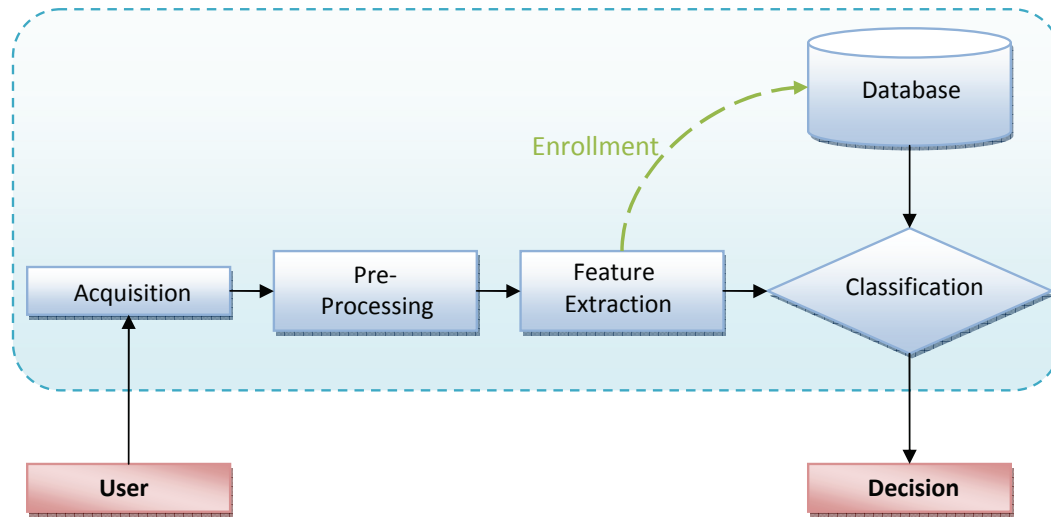


Figure 1.1: Flux diagram of a generic biometric system.

1.2 Anatomy and Operation of a Biometric System

A biometric system can be seen as a pattern recognition machine that a) acquires biometric data from an individual; b) performs some preprocessing; c) extracts relevant features; d) compares the features to an existing reference and; e) executes an action based on the comparison result. Therefore, there are five main parts in this system, each of them with enough scientific challenges to be considered as a separated research domain by itself: data acquisition (sensing), preprocessing, feature extraction, classification and database design. In Figure 1.1 a flux diagram of a generic biometric system is presented.

A detailed description of each component, along with its particularities and existing technologies would be extremely long. Therefore, we present a generic vision of the role performed by each of them in the system.

- a) **Data Acquisition:** this component defines the human-machine interaction and it is, therefore, essential to the performance of the system as a whole. An ill-designed interface can cause acquisition flaws and a low acceptance by the users.
- b) **Preprocessing:** after acquisition, a preprocessing of the signal is generally performed, typically techniques for enhancing characteristics or regions of the signal. Beyond that, a quality evaluation of the acquired data can be performed and a new acquisition can be demanded in case a sample has unacceptable quality.
- c) **Feature Extraction:** its role is to extract a set of relevant characteristics that are

discriminant enough to identify an individual with as low an error rate as possible. During the enrollment stage these features are stored in a database and are usually known as references or templates.

- d) Classification: during the test stage the features obtained on the previous step are compared to the stored templates, generating scores. Based on this score a decision is made which is the output of the system. It is worth noting that the quality of the input data directly affects these scores.
- e) Database Design: The development and maintenance of the database is crucial for the system's security and users' privacy. On large scale systems it is necessary to develop efficient search and clustering techniques in order to make it practical (time wise).

As it can be noted from the components description and Figure 1.1, we can identify two distinct phases during the system's operation: the enrollment phase, when the reference data are stored, and the test phase or query, when a newly acquired entry is compared to the references (Jain et al., 2007; Vielhauer and Dittmann, 2006).

- a) Enrollment: This step consists in acquiring biometric data, extracting its features and storing them on the database (or personal user card) so that it can be later used on the query phase. The reference template model can be generated from a single sample or from several samples. Some systems store several models per user in order to compensate for the intrinsic data variation, such as pose and illumination in photos. In general, enrollment is a supervised step, where a system administrator verifies the identity of the user through non-biometric ways (*e.g.* identity documents) before enrolling him/her.
- b) Query: In this step the user has his/her biometric data once again acquired and processed, but now it is compared to the previously stored template. Later, a label is assigned to the newly acquired sample by the classification component.

The query phase may still be sub-divided into two modes: authentication and identification. The authentication mode consists in validating the claimed identity. In this case, the system compares the newly acquired sample to a single reference in order to determine if they belong to the same person or not. This is the most common operation mode in access control applications for two main reasons: a) a 1 : 1 comparison is safer than a comparison to the whole database, since the error probability on the latter case grows at least exponentially with the size of the database; b) since it is a faster process (a single comparison), it is possible to use more elaborated feature extraction and comparison algorithms, with a lower error rate and, possibly, a higher computational cost per verification.

On the second query mode, identification, the user does not need to say who he/she is, the system must determine, amongst all users enrolled in the database, whose

Table 1.1: Error probability as a function of database size in an identification task.

Database Size	$P_E = 0.10\%$	$P_E = 0.01\%$	$P_E = 1.00\%$
10	09.56%	1.00%	0.10%
100	63.40%	9.52%	1.00%
1000	99.99%	63.23%	9.52%
10000	100.0% ¹	99.99%	63.21%

sample was acquired. It is also possible, instead of returning a single identity as an answer, to give a set of identities that resemble the newly given sample along with their similarity scores. This operation mode is usually found in surveillance applications such as searching for a face amongst a list of wanted people, or in personalized services, such a call center where the user is automatically recognized by his/her voice. This is a $1 : N$ relationship, which brings the need to use high speed algorithms and efficient search methods so that the system works on acceptable time.

Supposing the existence of N users on the database, and that the users are mutually independent (*i.e.* there is no superposition on the feature space amongst different users), and that the probability for any type of error (see Section ?) in a single comparison is P_E , it is easy to notice that the probability of performing all comparison without incurring in an error is $(1-P_E)^N$, in other words, for a big database it is virtually guaranteed that an error will happen. Notice that as the number of users increase the probability of superposition of user features also grows, therefore P_E will grow. In Table 1.1 are presented some values for the error probability as a function of the database size, notice that a system having a 1% error probability for each comparison is not capable of performing satisfactorily on an identification task.

1.3 Biometric Features

The design of a biometric system is a multifaceted problem, each biometric feature has its own pros and cons and, therefore, the choice of a particular feature depends on more than its classification performance (Jain et al., 2007; Vielhauer, 2005; Wijesoma et al., 2001). In (Jain et al., 1999), the main factors that affect the choice of a biometric feature for a given application are identified.

- a) Universality: As many users as possible should have the biometric feature in question;

¹The error probability tends to 100% however the actual value is $1 - 2.25 \times 10^(-44)$.

Table 1.2: Biometric modalities characteristics.

Biometric Modality	Universality	Uniqueness	Permanence	Collectability	Acceptability	Circumvention
Face	High	Low	Medium	High	High	Low
Fingerprint	Medium	High	High	Medium	Medium	High
Hand Geometry	Medium	Medium	Medium	High	Medium	Medium
Keystroke	Low	Low	Low	Medium	Medium	Medium
Hand Veins	Medium	Medium	Medium	Medium	Medium	High
Iris	High	High	High	Medium	Low	High
Retina	High	High	Medium	Low	Low	High
Facial Thermogram	High	High	Low	High	High	High
Voice	Medium	Low	Low	Medium	High	Low
DNA	High	High	High	Low	Low	Low
Signature	Low	Low	Low	High	High	Low

- b) Uniqueness: The feature must be distinct enough amongst users so that it is possible to correctly classify them;
- c) Permanence: Ideally, the biometric trait should be time invariant. On a more realistic scenario, variations are accepted as long as they do not significantly affect the system performance;
- d) Collectability: The acquisition must cause a minimum discomfort to the user;
- e) Acceptability: Users must be willing to provide the biometric feature;
- f) Circumvention: Refers to amount of work needed to reproduce and therefore fool the system.

Even if many biometric systems are currently in use, it is worth noting that no biometric feature is capable of satisfying all these requirements for all application scenarios (Jain et al., 2000). Therefore, the choice of a biometric trait is strongly dependent on the application in mind since it involves not only technical difficulties but also social and cultural issues (Jain et al., 2000; Vielhauer and Dittmann, 2006; Veeramachaneni et al., 2005). In Table 1.2 these requirements are presented in qualitative terms for several biometric modalities (Jain et al., 2007).

Biometric modalities can be roughly divided in two classes that were already cited: physiological and behavioral. The first ones are based on biological traits such

as fingerprint, face shape, hand geometry, retinal vein pattern and iris texture. The last ones consider, as the name suggests, behavioral traits such as voice acoustic patterns, signatures and typing dynamics (Jain et al., 2007; Vielhauer and Dittmann, 2006; Boyer et al., 2007; Zhang et al., 2005; Veeramachaneni et al., 2005). Behavioral traits are usually more susceptible to time variations, because they depend not only on the physical conditions but also on the psychological conditions of the user.

Besides choosing the adequate modality for the target application, the design of a biometric system should also consider other desirable characteristics such as performance, cost and speed (Veeramachaneni et al., 2005; Huang and Yan, 2000).

1.4 Performance Analysis of a Biometric System

On the biometrics context it is very rare to find two samples that yield exactly the same features set. Many factors are responsible for these differences such as sensor imperfection, changes in the biometric trait itself (*e.g.* facial hair changes face appearance), in the ambient (*e.g.* lightning) and/or variations in the user-system interaction (*e.g.* variations on the orientation of the hand or on the opening between fingers in a hand geometry system). In fact, the occurrence of a perfect match of all these factors is so rare that it usually indicates a forgery attempt that is usually called a replay attack, when someone tries to use a copy of the biometric trait presented by an authentic user.

This variability observed on the features extracted from the same person is called intra-class variance, while differences between samples of two different people are called inter-class variance. A good biometric trait presents small intra-class variance and large inter-class variance, generating compact and well separated clusters on the feature space, which allows for a good classification performance. This concept is illustrated in Figure 1.2

The scores obtained by the comparator might be of two types: similarity or dissimilarity which, as their name suggest, represent opposite situations. Similarity scores measure how much two samples resemble each other while dissimilarity measures represent how much they differ, the latter being a distance measure. It is always possible to convert similarity measures in dissimilarities and vice-versa. Throughout the rest of this text the term “score” will always refer to dissimilarities unless otherwise specified.

Given the scores, the system decides if the user is genuine or an impostor through a thresholding operation: scores below a given threshold τ are labeled as genuine and scores above this threshold are labeled as impostors.

We will call the scores resulting from the comparison of two samples from the same person as Genuine Scores and those resulting from the comparison of samples from two different people as Impostor Scores. The decision taken by the system might incur in two types of error: A False Acceptance, when an Impostor Score is below the threshold τ , or a False Rejection when a Genuine Score is above τ .

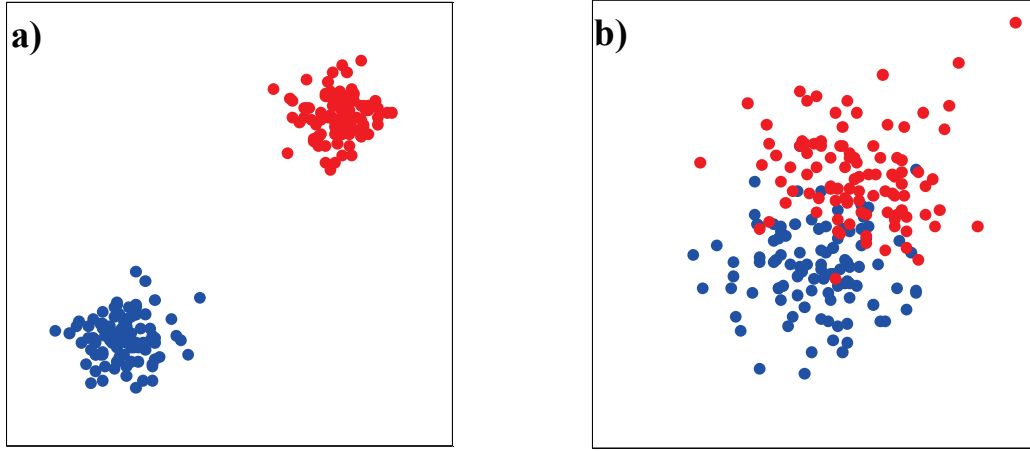


Figure 1.2: Inter-class and Intra-class variances concept. a) Low intra-class variance and high inter-class variance: compact well separated clusters. b) High intra-class variance and low inter-class variance: wide clusters without a clear frontier.

The False Acceptance Rate (FAR) of a biometric system is defined as the fraction of impostor scores below the threshold; it is an estimation of the probability of occurrence of this kind of error. In an analogous way the False Rejection Rate (FRR) is defined as the fraction of genuine scores that exceed the adopted threshold.

The complements of these two probabilities estimations are, respectively, the Correct Acceptance Rate (CAR) and the Correct Rejection Rate (CRR). Therefore we have $CAR = 1 - FAR$ and $CRR = 1 - FRR$.

With a sufficiently large number of scores one could estimate the Probability Density Functions (PDF) of both sets, genuine and impostor, and analytically derive the FAR and the FRR. Let $p(s|genuine)$ and $p(s|impostor)$ be the conditional score PDFs for the genuine and impostor cases, respectively. Then, for a given threshold τ we have

$$FAR(\tau) = \int_{-\infty}^{\tau} p(s|impostor)ds$$

$$FRR(\tau) = \int_{\tau}^{\infty} p(s|genuine)ds.$$

In Figure 1.3 we present a visual interpretation of these concepts. It is easy to notice that a change in the threshold τ changes the values of the error rates; however, for a given system, it is not possible to lower both kinds of error at the same by changing the threshold. In Figure 1.4 we present FAR and FRR for the distributions shown in Figure 1.3 as a function of the threshold τ .

It is also common to use a single curve to summarize the behavior of FAR and FRR as a function of the threshold. The Receiver Operating Characteristic (ROC)

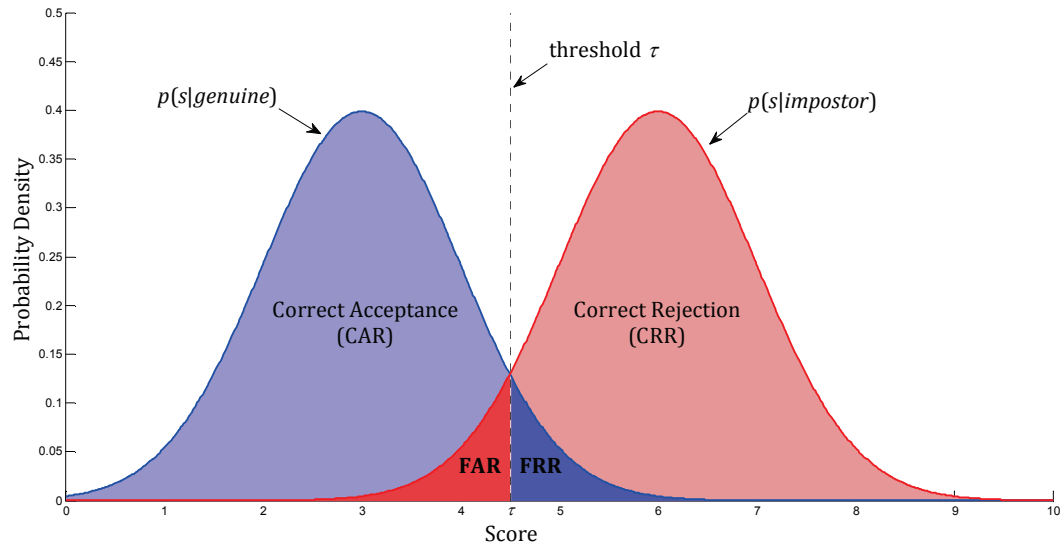


Figure 1.3: Visualization of the thresholding process and the concepts of FAR and FRR.

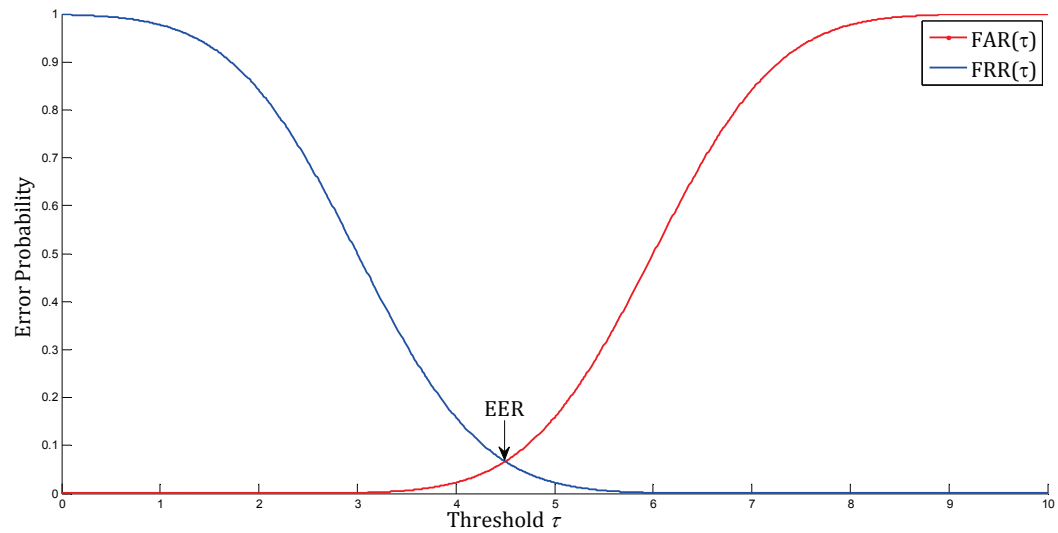


Figure 1.4: FAR and FRR as a function of the threshold τ for the score distribution in Figure 1.3. The EER is the crossing point of the two curves.

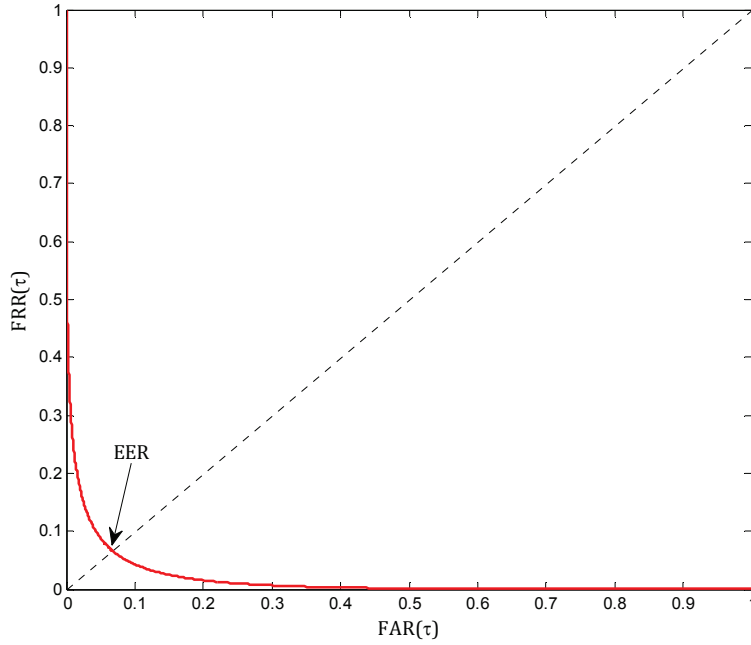


Figure 1.5: ROC curve representing the FAR and FRR on Figure 1.4. The EER is the point where the curve crosses the diagonal line (FAR=FRR).

curve (Egan, 1975) shows the values of FRR x FAR for different thresholds. The ROC curve for the FAR and FRR curves in Figure 1.4 is shown in Figure 1.5.

It is also possible to summarize the performance of a system using a single number, such as the EER (Equal Error Rate) or the d' value. The EER is the point of the ROC curve in which FAR and FRR are equal, therefore, a lower EER is a synonym of a better overall performance. The EER is indicated both in Figures 1.4 and 1.5.

The d' value cited before represents the distance between the means of the genuine and impostor probabilities distributions in unities of standard deviation, it is defined as (Neyman and Pearson, 1933)

$$d' = \frac{(|\mu_{genuine} - \mu_{impostor}|)}{\sqrt{\frac{1}{2} (\sigma_{genuine}^2 + \sigma_{impostor}^2)}}$$

where μ and σ are the mean and the standard deviation, respectively. The bigger d' , the greater is the separation between genuine and impostor scores and, therefore, a better system performance. For the distributions in Figure 1.2, for instance, (a) has $d' = 14.14$ and (b) has $d' = 2.24$. However, d' is very susceptible to the presence of outliers, especially if there are not enough data to properly estimate the standard deviations and means.

It is interesting noting that the occurrence of false acceptances and rejections is not uniformly distributed on the user's population. As the reader might imagine, some people are easier to recognize than others, with more distinct characteristics. Doddington et al. (1998) identified four user categories (known as Doddington zoo) based on these inherent differences:

- a) Sheep: Users whose biometric features are very distinct from the others and have a low intra-class variance, resulting in low FAR and FRR.
- b) Goats: Users with high intra-class variance, causing a high FRR.
- c) Lambs: These users have low inter-class variance, their features superimpose to those of other users, causing a high FAR.
- d) Wolves: Users who are skilled in manipulating their biometrics to emulate those of other users. The presence of this kind of people causes an increase on the system's FAR.

Besides classification errors, there are also acquisition errors (Failure to Acquire - FTA) and enrollment errors (Failure to Enroll - FTE) which result in general from sensor flaws or inadequate human-machine interaction. If the system has a sample quality evaluation module, the quality threshold might affect these two kinds of errors along with the perceived FAR and FRR. If the module accepts only high quality samples the system might present a low FAR and FRR however, the frequent errors in acquisition and enrollment due to this high quality standard might degrade the user experience of the system.

All errors discussed so far are crucial parameters on the design of a biometric system and usually guide the choices taken afterwards. Besides that, depending on the target application, different types of errors might be more or less tolerated: in a military installation, for instance, it is usually better to have a high rejection rate than false acceptances, since the consequences of non-authorized access might be too dangerous. On an amusement park it is better to keep the clients satisfied and one might prefer to have some false acceptances than making clients try over and over to access the park. The same system could be used on both cases (*e.g.* fingerprint authentication) but with different choices of the decision threshold τ .

In addition to error rates and the aforementioned issues regarding biometric traits, more practical factors such as cost, ease of use, sensor quality and speed also affect the suitability of a given system to an application.

1.5 Vulnerability and Limitations

With the proliferation of biometric solutions in many applications it is important to understand the vulnerabilities and limitations of these systems. The performance of a

biometric system is affected by many factors including noise, intra-class variations and incorrect user-system interaction (Bolle et al., 2003). We now list the main difficulties found on the development of a biometric solution.

- a) Noise: The collected sample might present noise due to the operating environment, the sensor and/or variations on the biometric traits itself. This kind of problem tends to increase the system's FRR.
- b) Non-Universality: It might be impossible for the system to acquire biometric data from some individuals in the target population, which yields FTA and FTE errors. To avoid such cases it is necessary to include exceptions on the algorithms or even a backup authentication system.
- c) Performance Limit: A biometric system cannot be continuously improved through successive refinements of the feature extraction and comparison modules. There is an implicit limit to the performance of any biometric system. Three possible reasons for that are (Jain et al., 2004b):
 - a. Limited Information: The amount of information available in a biometric trait is naturally limited. The hand geometry, for instance, has less discriminant information than fingerprints (Pankanti et al., 2001).
 - b. Limited Representation: The ideal representation for a biometric trait must retain all discriminative information. Existing feature extraction systems typically based on simplistic models of the biometric data are not capable of that, resulting in the inclusion of redundant and outlier data and the exclusion of relevant features. As a consequence, a fraction of the feature space cannot be correctly treated by the system, resulting in authentication errors.
 - c. Limited Comparator: Given a representation, an ideal comparator should perfectly model the relationships between different patterns of the same user. In practice, however, the comparators do not have such capabilities, resulting in low performance.
- d) Attacks: Behavioral traits such as voice (Eriksson and Wretling, 1997) and signature (Harrison, 1981) are vulnerable to forgery attacks by impostors capable of emulating the authentic users traits. Physiological traits might be forged through the use of artificial representations. Fingerprints can be modeled in synthetic materials such as plastic dough (Matsumoto et al., 2002; van der Putte and Keuning, 2001). Attacks such as these can undermine the security provided by the system and consequently mitigate their benefits (Ratha et al., 2001).

Some of the limitations of the biometric systems considered up to now can be overcome through the use of multiple sources of biometric information. This can be achieved through the fusion of multiple biometric systems that have different characteristics or multiple feature extraction and classification algorithms operating on the

same biometric trait, on both cases we call this a multi-biometric system (Ross et al., 2006; Jain and Ross, 2004; Hong et al., 1999).

Such evidence accumulation methods can yield a better performance of the system as whole while augmenting the population coverage and making attacks harder to perform.

1.6 Multi-Biometric Systems

Information fusion is a research field that attracts the interest of scholars on many areas including weather forecast (Palmer, 2000), objects tracking (Blum and Zheng, 2005) and robot navigation (Abidi and Gonzalez, 1992). The principle of problem solving through the combination of several specialists has received a lot of attention from the scientific community, in fact, the theory of Multiple Classifier Systems (MCS) has been studied in many works such as (Kuncheva, 2004; Kittler et al., 1998; Xu et al., 1992; Ghosh, 2002).

In biometrics, the consolidation of evidences from multiple sources is an efficient way of improving the performance of the authentication system. Some of the first multi-biometric systems described in the literature combined face and voice (Chibelushi et al., 1994; Brunelli and Falavigna, 1995) in such way that in addition to having a better performance they were also able to cover a larger fraction of the population. An example of a multi-biometric system currently in use is the FBI Integrated Automated Fingerprint Identification System (IAFIS), which uses the fingerprints of several fingers to identify criminal suspects. Some advantages of multi-biometrics (Ross et al., 2006) are listed below:

- Reduction of the non-universality problem;
- Easier filtering or indexation of large databases;
- Harder for an impostor to fool the system;
- Noise reduction;
- Easier surveillance and tracking of individuals when a single trait might not suffice.

A multi-biometric system can be seen as a fault tolerant system that can keep operating even when some biometric sources become less reliable due to a sensor failure, algorithmic problem and/or deliberate user manipulation. The concept of fault tolerance is especially useful on large scale systems involving a great number of users, such as immigration control on airports.

The design of a multi-biometric system is guided by many factors which include: 1. human-machine interface, 2. the compromise between the cost of introducing new

sources and the performance aim, 3. the chosen biometric sources, 4. the fusion level (*i.e.* the type of information to be combined), and 5. the adopted fusion method.

Based on the nature of the sources used for fusion, multi-biometric systems can be classified in six categories (Ross et al., 2006): multi-sensor, multi-algorithm, multi-instance, multi-samples, multi-modal, and hybrid.

- a) Multi-sensor: Employs several sensors to acquire a single biometric trait. Some examples found in literature are the use of many cameras to photograph the person face (Lee et al., 2004a); the combination of infra-red sensors with visible light sensors to get face information (Kong et al., 2005; Chen et al., 2005; Socolinsky et al., 2003); use of multi-spectral cameras for iris, fingerprint or face acquisition (Marcialis and Roli, 2004). The use of several sensors in some cases can result in the acquisition of complimentary information capable of improving the system's performance.
- b) Multi-algorithm: The use of several feature extractors and/or classification algorithms might also improve the system's performance. Multi-algorithm systems compile the data from several extractors or classifiers operating over the same sample set. The design of such systems does not require new sensors and therefore have a lower production cost than other multi-biometric systems. On the other hand, the introduction of new algorithms can highly increase the computational complexity, eventually making the system inviable. Ross et al. (2002) describe a fingerprint verification system that uses both minutiae and texture information to represent and classify images.
- c) Multi-instance: These systems use multiple instances of the same biometric trait, being also known as multi-unit systems. The IAFIS system, aforementioned, is an example of such fusion modality.
- d) Multi-samples: A single sensor can be used to acquire several samples of the same biometric trait in order to compensate for variations that might occur on the measured characteristic or even to obtain a more complete representation of it. A crucial question here is the determination of the number of samples that should be collected. It is important that these samples represent both the variability and the typicality of the biometric trait of the individual.
- e) Multi-modal: Are based on multiple biometric traits. Physically uncorrelated traits usually result in greater performance gains than correlated traits. The design of such systems also requires new sensors, along with the development of an adequate interface capable of integrating all the desired modalities. A great problem of this kind of system is the "curse of dimensionality": the inclusion of new biometric modalities augments the dimension of the problem while the number of samples remains constant, which makes it harder to correctly train the classifiers (Duda et al., 2000).

- f) Hybrids: This term is used to describe systems that combine a subset of the five aforementioned cases (Chang et al., 2005). In (Brunelli and Falavigna, 1995), for instance, a system using two voice recognition algorithms along with three face recognition algorithms is described.

It is also possible to fuse biometric and non-biometric data to increase the system security. In (Teoh et al., 2004) a system uses pseudo-random numbers printed on a personal card along with a set of facial features, using these numbers to choose a subset of features that is specific to each user, called BioCode. When there is a suspicion that the biometric information of an individual was compromised a new card is issued, revoking the previous authenticator. The use of biometric and non-biometric authenticator in tandem is a powerful way of increasing safety however some of the inconvenient of traditional authentication methods come back.

A particular category of multi-biometric systems is the one that employs primary biometrics traits, such as face or fingerprints, with secondary biometric traits, known as soft biometrics, such as sex, height, weight or eyes color. Secondary attributes are not distinct enough to identify a user, since it is shared by many people, however, used along with primary attributes the performance of the system can be significantly improved (Jain et al., 2004a).

Secondary attributes can also be used to filter large biometric databases, limiting the number of comparisons needed in an identification task. If it is known that the target is a “Latin Man”, for instance, the system can restrict its search only to the entries that have such labels. Similarly, secondary biometric traits can be used on surveillance applications to decide if it is needed to collect primary biometric information of a given individual. Development of automatic techniques for the determination of secondary biometric traits is one of the biometric research fields.

1.6.1 Fusion Levels

On pattern recognition systems, such as biometric systems, the amount of information available for decision making decreases as we proceed through each module of the system. Based on the type of information available on each module, different levels of fusion can be defined. Sanderson and Paliwal (Sanderson and Paliwal, 2004) divide the several fusion levels in two big categories: pre-classification and post-classification. This is because the amount of information is drastically reduced after the classification. Pre-classification fusion schemes usually need new classification techniques to be developed, since classifiers used for individual sources might not be adequate to the task, which brings additional challenges to this kind of fusion. Pre-classification category includes fusion techniques on sensors and data, while post-classification include score, ranking and decision fusion.

For binary classifiers such as those used on biometric verification tasks, it is easy to show that the last fusion level (decision level) is not very useful. Let S_1 and S_2 be two mutually independent verification systems. Let $FAR_1(\tau_1)$, $FRR_1(\tau_1)$,

$FAR_2(\tau_2)$ and $FRR_2(\tau_2)$ be the false acceptance and rejection rates for systems S_1 and S_2 , respectively. We will now analyze the two simplest combinations of a binary classifier: union and intersection.

- a) Union: In this case the use is said to be genuine if it passes on either test. So the user is only rejected if he fails both tests

$$FRR_U(\tau_1, \tau_2) = FRR_1(\tau_1)FRR_2(\tau_2).$$

And the false acceptance can be given by the complement of the probability that no test cause false acceptances.

$$FAR_U(\tau_1, \tau_2) = 1 - [1 - FAR_1(\tau_1)][1 - FAR_2(\tau_2)]$$

$$FAR_U(\tau_1, \tau_2) = FAR_1(\tau_1) + FAR_2(\tau_2) - FAR_1(\tau_1)FAR_2(\tau_2)$$

- b) Intersection: The use will be authenticated only if he passes both tests. With a similar thinking to the previous case we have

$$FAR_I(\tau_1, \tau_2) = FAR_1(\tau_1)FAR_2(\tau_2)$$

and

$$FRR_I(\tau_1, \tau_2) = FRR_1(\tau_1) + FRR_2(\tau_2) - FRR_1(\tau_1)FRR_2(\tau_2)$$

On both cases a gain on a type of error is followed by a loss on the other. If both systems are operating at the EER point the total error of the system (*i.e.* FAR + FRR) will be greater or equal to the total error of the best system and less or equal to the total error of the worst system, being equal only if both system have the same performance. However, these are not the only fusion possibilities, a vast theory on this subject is available in the literature.

It is worth noting that using union and intersection rules generate more liberal (low rejection) or restricts (low acceptance), respectively. Depending on the application in mind, such compromise solution between the two types of error might be tolerated.

1.7 Handwritten Signature Recognition

The way a person signs his/her name is known to be a distinct individual trait (Nalwa, 1997; Lee et al., 1996). Signature has a very special place amongst other biometric modalities (Fairhurst, 1997; Fairhurst and Kaplani, 2003; Leclerc and Plamondon, 1994; Pirlo, 1994) mainly for being the identification modality most used throughout time. This method is commonly used by governmental, legal and financial institutions (Wijesoma et al., 2001; Nanavati et al., 2002) for authentication. Besides, signature verification does not require invasive measures, only the contact with the writing

device. The sum of these factors causes signatures to have a good acceptance amongst users (Plamondon and Srihari, 2000).

Signature is the result of a complex psycho-physical process that depends both on the psychological state of the writer and the conditions under which this process occurs. The signature of a person can significantly vary even in successive acquisition. Even if some theories have been proposed to explain the writing mechanism (Plamondon, 1995a,b; Plamondon and Guerfali, 1997; Plamondon, 1998; Plamondon et al., 2003) and the process of ink deposition (Doermann and Rosenfeld, 1995; Franke et al., 2002; Franke and Rose, 2004, 2006), signature verification is still an open challenge.

Besides the fact that signatures usually present a high intra-class variance, skilled forgers are capable of reproducing signatures with enough precision to fool the verification systems (Harrison, 1981). Along with these challenges, verification is usually realized based on few reference samples (Plamondon, 1994) what makes it even harder to obtain a proper model of the subjacent process.

Signature verification involves aspects of disciplines ranging from anatomy to engineering, passing through neuroscience and computation (Miller, 1994). For this reason, this field attracts researchers from many fields, working both for universities and enterprises, for the scientific challenges or for the valuable applications that the field might offer (Newham, 2000). The growth of Internet and electronic commerce along with the proliferation of PDAs, smartphones and tablet devices, has shed a new interest on automatic signature verification since it is an obvious choice on such devices. The creation of specific laws that have already been approved on many countries (Wijesoma et al., 2001; Lei et al., 2005) and the attention drawn by many institutes and associations to the standardization of data exchange formats for signatures (ANSI, 2005; ISO, 2013, 2014) are evidence of this interest. The goal of such efforts is to ease the integration of verification technologies on different devices with the intent of generating complete solutions for a wide range of commercial applications such as banking, insurance, hospitals, security and electronic commerce.

Signature recognition can be divided in two distinct modalities, static and dynamic. The static case refers to “traditional” signatures done with some writing device on a surface (*e.g.* checks, recipes, documents, paintings) while the dynamic case uses suitable electronic devices such as digitizers and tactile surfaces to acquire the movement of the writing device as a time series.

A skilled forger with access to an original signature and a little training is capable of copying a signature with enough details to fool even human specialists. However, copying the speed and acceleration of the strokes, the pressure on the pen tip or even the way of holding a pen are much harder tasks. This new information causes dynamic signatures systems to have a greater discriminating capability than static ones. Besides dynamic information, online signatures as they are also known have the advantage of requiring less storage space, since only an array of positions is stored instead of the whole image.

Another important point is that traditional signatures as they are currently used

do not provide any pro-active security. In banks, for instance, signatures are only verified if there is a protestation or when suspicious transactions are detected (*e.g.*, exceptionally high amounts) since the verification of every signature would make the financial system extremely slow. This is another kind of problem that could be solved or at least reduced through the use of dynamic signatures, since the verification could be realized as the writing occurs, instead of being acquired on a physical media (*i.e.*, paper) to be digitized and posteriorly processed.

Online signature verification is further discussed in Chapter 3

1.8 Conclusion

In this chapter general notions regarding biometric systems were presented. Its main components and functions were discussed, along with the techniques used for performance assessment. This allows for the reader to become familiar with the framework under which this work is developed. Some general problems regarding biometric verification are pointed out along with possible solutions provided by information fusion techniques.

Finally, a brief introduction to the handwritten signatures biometrics, the modality focused in this thesis, is provided. This particular modality is the most commonly used on administrative and financial documents and has a high social acceptance as means for assuring the identity and will of the signer. A more detailed discussion of handwritten signature verification can be found in Chapter 3 and references therein.

As stated in the Introduction chapter, this thesis deals with the particular problem of signature representation. Thus, even if biometric verification experiments are performed in order to evaluate some aspects of the proposed model, development of an improved verification system is not the main goal of this work.

On the next chapter, a review of the motor control theories is performed. This provides the basis for the development of the proposed signature model.

CHAPTER 2

Motor Control

2.1 Introduction

As previously stated (Section 1.7), modeling signature trajectories is a challenging enough matter by itself for scientific research. This chapter starts by describing some theories related to general motor control in Sections 2.2 through 2.5 and then, in Section 2.6 motor control theories used in the literature for describing the writing mechanism are discussed. A good review on motor control theory for human movements can be found in (Berret, 2008) and (Rosenbaum, 2009).

There are four main theories for motor control in the literature: the equilibrium point theory, the motor primitives theories, the internal models theory and the optimal control theory. These theories are not completely independent and some superposition can be found amongst them. The first theory proposes that the viscous-elastic properties of the muscles generate the movement. The second suggests that the central nervous system (CNS) generates movements using motor primitives stocked in certain neural centers and combine them in order to simplify the control of the thousands of degrees of freedom of the muscle-skeleton system. The third theory proposes formal explanation for how the CNS generates the motor commands in a proactive fashion and integrates sensorial feedback in order to correct errors. Finally, the last theory says that our movements are the result of an optimization process and that the selected movement satisfies a certain optimality criterion. Most of the works described in this Section study the movement of an articulated arm on reaching, point-to-point, movements.

2.2 Equilibrium Point Theory

This theory states that movement generation is mainly explained by the mechanical properties of the muscle-skeleton system. Mechanical equilibrium refers to a system state in which the resulting force vector is null. The primary idea of this theory was proposed in (Feldman, 1966). It was observed that the muscular system has static characteristics similar to those of a non-linear spring.

As an example, imagine two identical springs S_1 and S_2 with spring constant k . Suppose that a mass M is attached between the springs, therefore under identical

opposing forces ($F = k\Delta l$) in an equilibrium state. Now imagine that it is possible to abruptly change the length of one of the springs, the mass will then move to a new equilibrium position.

The idea is that the length of the muscles could be a variable controlled by the CNS in order to generate movements. According to this hypothesis, movement would be created by a change in the lengths of the agonists and antagonists muscles, therefore causing a change of the equilibrium point.

This abrupt change of the equilibrium point is a simplified version of the equilibrium point theory and there are several experimental observations that prove it to be wrong, as for instance, the relative invariance of the movement if we attach a mass to the arm of a subject (Atkeson and Hollerbach, 1985). A more elaborated version of this theory proposes that the CNS actually specifies an equilibrium point trajectory that gradually moves to a final position. In (Flash, 1987) it is proposed that the CNS plans a straight virtual trajectory between the departing point and the endpoint but the observed movements are curves due to the action of inertial forces. Theoretical paths predicted by this model are relatively close to what is observed in practice; however, in order to obtain such good results, the spring constant must be almost 3 times larger than actual physiological values.

An alternative would be to have a virtual trajectory that is more complex than a straight line. It was found that virtual trajectories built from experimental data are rather complex (Gomi and Kawato, 1996) and therefore it is needed to determine which criteria are used by the CNS in order to choose a virtual trajectory. Some authors tried to explain that such complex trajectories come from an ill modeling of the neuromuscular system (Kistemaker et al., 2007; Gribble et al., 1998). Despite their effort, this theory is now considered obsolete by many scientists.

The main issue with the equilibrium point theory is that in order to perform fast movements a physiologically impossible elastic coefficient is needed (Gomi and Kawato, 1996). Also, in order to solve some of the degrees of freedom problems an optimality criterion must guide the choice of certain properties of the movement. The minimal interaction principle seems to define a unique solution amongst the many possible solutions provided by the equilibrium point theory (Feldman et al., 2007).

2.3 Motor Primitives theory

Synergy is a basic concept for this theory (Bernstein, 1967); it can be roughly defined as a preprogrammed muscle activations sequence that performs a basic movement, even though this definition varies from author to author. This basic concept can also be applied to cinematic, dynamic or neuronal variables. A review on motor primitives can be found in (Flash and Hochner, 2005).

On the cinematic level, it was shown in (Alexandrov et al., 1998) a strong covariation between the angles on the ankle, knee and hips while performing trunk bending exercises. It is as if the CNS imposed constraints over these three angles, not allow-

ing them to vary independently. This behavior was also observed in other studies on whole body movement (Thomas et al., 2005; Kaminski, 2007). Many authors have found that on a marching cycle, the elevation angles of the foot, tibia and femur covariate on a plane and describe a characteristic curve that is similar both for cats and humans (Lacquaniti et al., 1999).

The same kind of result has been observed on EMG data. In (Torres-Oviedo et al., 2006) muscular synergy is defined as the vector of muscular forces implicated in the reactional postural adjustment; it was found that five synergies allow for postural equilibrium regulation on cats when there is a translation or rotation of the standing base. Other studies have defined synergies as the time series from which it is possible to reproduce the EMG activation of several muscles. Many studies showed that tasks such as locomotion, arm movement and hand posture can be summarized by a few typical activations patterns (synergies) (d’Avella et al., 2003, 2006, 2008; Ivanenko et al., 2004, 2005; Weiss and Flanders, 2004). It is worth noting that these synergies were identified by several different algorithms, consequently, they are not an artifact of the chosen extraction method (Tresch et al., 2006). A more complete review on muscular synergies can be found in (Poppele and Bosco, 2003) and (Bizzi et al., 2008).

Some studies showed that these muscular and cinematic synergies have a neuronal cause, identifying some preprogrammed movements on the spinal cord and sometimes on the cortical level (motor primitives) (Mussa-Ivaldi and Bizzi, 2000; Graziano et al., 2002). On experiments on a frog, they found motor primitives capable of moving a limb to a certain position on the Cartesian plane no matter what the departing position, the neural network on the spinal cord codes a force field that converges to a single equilibrium point. The linear combination of these motor primitives allow for the creation of a great variety of movements (Mussa-Ivaldi and Bizzi, 2000).

This organization of the movement in motor primitives could allow for the CNS to simplify the control of the thousands of degrees of freedom of the muscular-skeletal system. The existence of a limited motor repertoire stocked in certain neural networks could allow for the CNS to generate complex movements, under the hypothesis that it can combine the motor primitives in an adequate fashion. In (Nori and Frezza, 2005) a formalization of this problem on the context of control theory was proposed along with methods for the choice of a minimum number of motor primitives while keeping system controllability (i.e., to go where we want in a given time). It was shown that the choice of motor primitives could be the result of an optimality criterion adopted by the CNS.

This control mode consisting in building commands from pre-existent blocks is strongly linked to the CNS and seems fundamental to understand the solutions found by nature to control such complex dynamic systems. It is an approach that follows a principle similar to language construction: from letters to words, from words to phrases, and so on.

2.4 Internal Models Theory

This theory is based on the idea that the brain stores an internal representation of the environment and the body thus allowing for the prediction of the results of the actions. This concept issued from automation and control theory seems ideal for motor control and planning but the existence of such internal models on the brain is still the cause of debates on the neuroscience community. A review of this theory can be found in (Wolpert and Ghahramani, 2000).

In order to produce a movement without sensorial feedback (e.g. with eyes shut), the CNS needs to find the adequate sequence of muscular activation based on the initial posture and the desired target and duration of movement. It is the inverse model that gives the brain such competence (Kawato et al., 1987). This model is capable of adapting itself to changes in the body (e.g. growth) and the action context. Studies have tested the adaptation capability of subjects when movements are affected by an unexpected force. An exterior force was applied to the subject's arm while moving on the horizontal plane, an adaptation phase was necessary for the subject to accomplish the pointing task with success. If this supplementary force is removed a new period of adaptation is needed and it is proof of the construction of an internal model in the CNS. Moreover, subjects were capable performing movements different from that of the adaptation phase, proving that the learning process actually generates a representation of the force field (Shadmehr and Mussa-Ivaldi, 1994; Gandolfo et al., 1996).

Another type of model present in the CNS is the direct model. The motor orders sent by neural centers can be used to predict the behavior of the system, and therefore know if the target will be achieved with success or not. This model compares the sensorial feedbacks with the predicted signals and generates an error signal to correct the motor orders (Wolpert et al., 1995). The existence of neuronal paths allowing certain brain areas to have access to a copy of motor order has been observed in mental imagery tasks, therefore subjects can significantly improve motor tasks performance by mental stimulation only (Gentili et al., 2006). This kind of training is common amongst accomplished athletes (Driskell et al., 1994) and musicians (Aleman et al., 2000), and also useful in physical rehabilitation (MacIver et al., 2008).

The optimal feedback control theory (Todorov, 2004; Scott, 2004) is based on this internal model concept and tries to minimize the effects of delays and noise present in the system. Here the internal model is an optimal feedback controller and the direct model is an optimal state estimator, according to the formalism of the optimal control theory.

The direct model is used on closed loop control, while the inverse model allows for an open loop control. Even if it is admitted that both models co-exist, it is not evident to know when sensorial feedbacks are integrated and really affect the motor output. For instance, the model in (Desmurget and Grafton, 2000) proposes that the sensorial feedback is integrated towards the end of the movement in order to adjust

the final position. Whichever way it works, the CNS seems to be organized to plan, execute and correct movements and also adapt itself to changes in the environment.

A recurrent debate in neuroscience is if the brain has an internal model for gravity, i.e. an internal representation of the Newton laws. Many studies show that this seems to be the case and that an area of the brain close to the vestibular cortex codes the gravitational acceleration and could be used proactively to predict objects movements on the gravitational field (McIntyre et al., 2001; Indovina et al., 2005). Astronauts have difficulties to catch objects launched in their direction on their first experiences with micro-gravity and many adaptation days are required to correctly evaluate how the absence of gravity affects the movement of the objects. In fact, without an internal model of the physical laws the sensorial feedback would be of little efficacy to accomplish such motor tasks. This is supported by the difficulties we have to understand accelerated body movements that violate the rules of our motor repertoire (Pozzo et al., 2006).

2.5 Optimal Control Theory

All approaches for motor control presented so far need at some point the use of an optimality criterion. Therefore, optimal control theory seems to be the ideal tool to solve such problem. This theory allows for partially solving the problem of redundancy on the sensorimotor system through the imposition of optimality criteria along with biomechanical and anatomical constraints already imposed by evolution.

Optimal control theory is a well-known mathematical theory with applications in many fields of science, such as biology, economy, automation, robotics and chemistry. There are discrete and continuous versions of it.

For the discrete case, a first method was developed in the fifties on the United States known as Dynamic Programming due to Bellman (1957). This method is based on the concept that the choice of the optimal control leading to the next state is independent of the choices that led to the present state. This method suffers from the “curse of dimensionality” problem, which means that it needs too many resources and computing time for high dimensional problems.

On the continuous case, this same principle is generalized under the form of the Hamilton-Jacobi-Bellman (HJB) equation that usually leads to the resolution of second order nonlinear partial differential equations. Meanwhile, in Soviet Union, Pontryagin et al. (1964) developed a Maximum Principle that gave a powerful formalism to solve a large range of problems. The Euler-Lagrange equation can be seen as a special case of the Pontryagin Maximization Principle (PMP). PMP gives a necessary condition while solving the HJB equation gives a sufficient condition.

A complete introduction to optimal control theory can be found in (Kirk, 2012), for a behavioral neuroscience approach see (Todorov, 2006), for a geometrical approach refer to (Agrachev and Sachkov, 2004).

2.5.1 Optimality Criteria

The minimization principles for movement modeling can be roughly divided in four categories: energetic criteria (e.g. minimum total work), muscular and neural criteria (e.g. minimum effort), dynamic criteria (e.g. minimum torque-change), and kinematic criteria (e.g. minimum jerk). Amongst the many criteria, Minimum Jerk and Minimum Torque-Change are the most used in the movement modeling literature and we will pay a special attention to them since we will be using the Minimum Jerk throughout this work. A review on these criteria can be found in (Engelbrecht, 2001; Todorov, 2004).

2.5.1.1 Energetic Criteria

Many models propose the minimization of energetic criteria for movement planning. It seems reasonable to think that energy cost minimization constraints have appeared throughout evolution (Bramble and Lieberman, 2004). However, despite the supposed pertinence of such criteria there are few conclusive results on this topic.

First it is needed to define what “consumed energy” means; it could be mechanical energy or metabolic energy, or even the energy consumed in the form of heat (Nishii and Murakami, 2002). The quantity measuring the energy provided by a force during a movement is the work. This is a well-known measurement in physics but it has some problems, for instance, the work of a conservative force is independent of the path, which is not good when one wants to plan movements.

Many authors have tried to circumvent these difficulties. (Soechting et al., 1995) propose the minimization of the peak of positive work. Their model could predict the final posture of an arm with four degrees of freedom but needed the addition of very constraining hypothesis such as that the peak movement speed always happens exactly halfway through the execution of the action.

(Alexander, 1997) proposes the minimization of the metabolic energy needed to move the arm. He uses a muscular model and evaluates the metabolic power developed by the active muscles and then, by integration over the movement duration, he gets an approximation of the metabolic energy. (Anderson and Pandey, 2001) also uses metabolic energy as the optimality criterion but applies it to walking movements.

In (Kang et al., 2005) a method for solving the inverse cinematic problem (finding angular displacements based on the trajectory) based on the minimization of the total work produced by the articulation torques is proposed. However, their method does not minimize the global absolute work; it minimizes only the amount of work needed to pass from an intermediate posture to another in an iterative algorithm similar to the dynamic programming principle.

In (Nishii and Murakami, 2002) the positive work is proposed as optimality criterion. This theory is based on interesting results for insects’ movements (Nishii, 2000, 2006). However, these authors have chosen to neglect negative work and essentially

consider slow movements. Their cost function is given by

$$C_{Nishii} = \int_0^T \omega(\tau \dot{\theta}) + \alpha \tau^2 dt,$$

where τ is the motor couple, $\dot{\theta}$ is the angular speed and α is a constant.

The function ω is defined as: $\omega(x) = 0$ for $x < 0$ and $\omega(x) = x$ for $x \geq 0$. It considers therefore only the positive work, by doing so the authors make their cost function non-differentiable in $\tau = 0$.

2.5.1.2 Muscular or Neuronal Criteria

These criteria use very detailed models of the neuromuscular system, with the advantage of being closer to reality. However, several parameters related to the neuromuscular system need to be controlled leading to a prohibitive computational complexity. The dimension of the working space is significantly increased and avoiding the multitude of local minima found by numerical solutions of the optimal control problem becomes a tough challenge.

In (Guigon et al., 2007) is suggested that the most of the redundancy problems on movement planning can be solved by minimizing the number of neuronal commands needed to perform the task. They model the arm biomechanics in a precise way and use the separation principle, assuming that the CNS controls inertial and gravitational forces independently. The controlled objects are the motoneuron activities $(u_i)_{i=1..N}$, therefore the quantity to be minimized is

$$E^2 = \sum_{i=1}^N \int_0^T u_i^2 dt.$$

This is an energetic quantity in the sense of signal theory but its physical meaning is not clear, that is why this kind of model is usually referred by the term minimum effort.

It is worth that if the value of the effort E^2 is fixed to a constant it is possible to find the corresponding time T . According to the authors this explains how the CNS chooses a “natural movement speed” that is usually requested by scientists to subjects in behavioral neurosciences experiments. In the presence of noise it is possible to use a minimum variance estimator to find a solution that minimizes the error on the final position (Harris and Wolpert, 1998).

2.5.1.3 Dynamic Criteria

The most well-known criterion in this category is the minimum torque change (MTC). This model was proposed in (Uno et al., 1989) and minimizes the torque variations on the articulations in order to protect the muscle-skeletal system and generate smooth

movements. Their studies considered the movements of a bi-articulated arm on the horizontal plane.

Consider an articulated arm with n segments. Let x be the position vector, v the speed vector and τ the torque vector. Using $u = \dot{\tau}$ as the control variable and $X = (x, v, \tau)$ as state variable, we can write the dynamic equation as $\dot{X} = f(X, u)$. The problem is to move from an equilibrium position X_0 to another one X_F in fixed time T while minimizing

$$C_{TC} = \frac{1}{2} \int_0^T \sum_{i=1}^n \left(\frac{d\tau_i}{dt} \right)^2 dt,$$

which can be solved using Lagrange multipliers (Kirk, 2012). This set of differential equations is a necessary condition for a minimum to exist.

$$\begin{cases} \dot{X} = f(X, u) \\ \dot{\psi} = - \left(\frac{\partial f}{\partial X} \right)^T \cdot \psi \\ u = \psi_\tau \end{cases}$$

where ψ denotes the Lagrange-multiplier vector with $3n$ components and ψ_τ represents its n -dimensional part which corresponds to τ . The problem now is to solve this first order differential equation system and finding the initial values of the Lagrange-multipliers.

The MTC solution generates curved trajectories and asymmetric speed profiles on the horizontal plane. However, for certain movements, this model produces speed profiles with two peaks (Biess et al., 2007), which does not match the experimental results for pointing movements between two targets (these experiments present a bell shaped speed profile). It is worth noting that two-peaked speed profiles were found in pointing tasks using via-points (Viviani and Flash, 1995).

A modified version of this model, including friction terms was proposed in (Nakano et al., 1999), the Minimum Commanded Torque Change (MCTC). The cost function is the same as that of the MTC, but the torques τ are the net torques at each articulation, considering friction.

The minimum torque was considered as optimality criterion for movements with a single degree of freedom on previous works (Nelson, 1983). The amount to be minimized was

$$C_T = \frac{1}{2} \int_0^T \sum_{i=1}^n \tau_i^2 dt.$$

This criterion was classified at the time as energetic, because certain studies showed that the muscular power required for displacing a limb is proportional to τ^2 (Hatze

and Buys, 1977). However, this does not correspond to the actual mechanical energy spent for moving body segments.

The minimum isometric muscle torque-change (Kashima and Isurugi, 1998) proposes that the CNS can control this variable. Using the muscle model in (Hill, 1951) it is defined that the torques at the articulations τ_i depend on the torques due to the muscular contractile forces τ_{ISO_i} and the angular speed $\dot{\theta}_i$. The cost function on this case is

$$C_{ISO} = \frac{1}{2} \int_0^T \sum_{i=1}^n \left(\frac{d\tau_{ISO_i}}{dt} \right)^2 dt.$$

In (Biess et al., 2007) several models are brought together using the separation principle, notably the minimum jerk (Flash and Hogan, 1985), minimum torque change (Uno et al., 1989) and the minimum work peak (Soechting et al., 1995), forming the Geodesic model. This model proposes that the CNS plans the movement in two stages, the first stage is a spatial planning and the second stage plans the temporal aspect of the movement. For moving from an initial to a target location it is assumed that the CNS choses the shortest path over a Riemann variety with a particular metric, this metric is in fact the inertia matrix of the mechanical system. The temporal aspect is planned stating that the resulting path is dictated by the Minimum Jerk. This model seems to work fine on a three dimensional space but not much on a plane, generating paths with a much greater curvature than those found in experimental data.

2.5.1.4 Cinematic Criteria

The simplest cinematic criterion is that of the Minimum Time (Nelson, 1983), however, most of our movements are not done in such fashion and bang-bang solutions are obtained, i.e. the maximum torques that muscles can develop are always achieved. Even if this criterion is plausible for saccadic eye movements it seems very inappropriate for hand movements, for instance.

Other cinematic criteria include all the range of cost functions that propose to explain the smooth aspect of the movement. These models have cost functions for a movement on the (x, y) plane that are of the form

$$C_n = \frac{1}{2} \int_0^T \left(\frac{d^n x}{dt^n} \right)^2 + \left(\frac{d^n y}{dt^n} \right)^2 dt.$$

In (Richardson and Flash, 2002) these criteria are studied up to $n = 10$, and it was found that the case $n = 3$ seems to be the most appropriate for human movements, corresponding to the Minimum Jerk which will be further detailed ahead on this section. In general, solutions for these criteria are polynomials of order $(2n - 1)$.

The case $n = 2$ is the Minimum Acceleration, this criterion has been rejected because it does not generate the horizontal tangents on the beginning and end of

the speed profile, usually found on experimental data. In (Ben-Itzhak and Karniel, 2008) constraints are imposed over the control allowing for the reconciliation of the Minimum Acceleration with the experimental data, solving the problem of non-differentiability on the extremities of the movement.

The case for $n = 5$, corresponding to the minimum Snap is used in (Mellinger and Kumar, 2011) for trajectory generation and control of quadrotors. The case where $n = 5$ (Minimum Crackle) was studied in (Dingwell et al., 2004) to explain the human control of non-rigid objects. This model was tested on a manipulation task of a mass tied to a spring and it was found that all the criteria that maximize the smooth aspect of the movement produce acceptable results.

In (Wada et al., 2001) this kind of criteria is applied to angle space, on the Minimum Angle Jerk model. The cost function in this case is

$$C_{AJ} = \frac{1}{2} \int_0^T \sum_{i=1}^n \left(\frac{d^3 \theta_i}{dt^3} \right)^2 dt,$$

where $(\theta_i)_{i=1..n}$ are the angles at the articulations. The minimum angle jerk predicts straight trajectories on the angle space and the solutions are given by

$$\Theta(\tau) = \Theta^S + (\Theta_0 - \Theta_F)(-10\tau^3 + 15\tau^4 - 6\tau^5),$$

where $\tau = t/T$ and $\Theta = (\theta_i)_{i=1..n}$. If the initial posture Θ_0 is known during movement planning, the selection of the final pose Θ_F is a complementary problem (Rosenbaum et al., 1995; Vaughan et al., 1998). This model allows for the selection of a movement for systems with n degrees of freedom, while the Cartesian space criteria, such as the Minimum Jerk, still need inverse cinematic and inverse dynamic steps in order to determine all angular displacements.

We now give further details on the Minimum Jerk (MJ) criterion, since this is the most used criterion on the movement planning literature and it will be the base for the signature representation we propose in Chapter 4.

Human movements present the fundamental feature of being smooth, i.e. with little trembling, therefore, generating as little trembling at the finger level as possible could be one of the objectives of the CNS in order to gain precision and protect articulations and tendons (Flash and Hogan, 1985). The Minimum Jerk is therefore based on the idea that the CNS produces smooth movements that minimize the trembling of the final effectors on the Cartesian space. The initial formulation of this problem was as follows: let (x, y) be the trajectory of the effector (e.g. finger) in a horizontal plane. The problem is to move from an equilibrium point (x_0, y_0) to another (x_F, y_F) in a fixed time T , while minimizing the cost function

$$C_J = \frac{1}{2} \int_0^T \left(\frac{d^3 x}{dt^3} \right)^2 + \left(\frac{d^3 y}{dt^3} \right)^2 dt.$$

This is clearly a cinematic problem and does not depend on the dynamic properties of the system or the environment. The resolution of this problem is simple

and can be done using Euler-Lagrange equations. Let $L(x, y, \dot{x}, \dot{y}, \ddot{x}, \ddot{y}, x^{(3)}, y^{(3)})$ be the Lagrangian of C_J . Using the generalized Euler-Lagrange equation (one for each variable) we have

$$\begin{aligned}\frac{\partial L}{\partial x} - \frac{d}{dt} \frac{\partial L}{\partial \dot{x}} + \cdots + (-1)^n \frac{d^n}{dt^n} \frac{\partial L}{\partial x^{(n)}} &= 0 \\ \frac{\partial L}{\partial y} - \frac{d}{dt} \frac{\partial L}{\partial \dot{y}} + \cdots + (-1)^n \frac{d^n}{dt^n} \frac{\partial L}{\partial y^{(n)}} &= 0\end{aligned}$$

Therefore we have that

$$\begin{aligned}\frac{d^3}{dt^3} \frac{\partial L}{\partial x^{(3)}} &= 0 \\ \frac{d^3}{dt^3} \frac{\partial L}{\partial y^{(3)}} &= 0\end{aligned},$$

which means that

$$\begin{aligned}\frac{d^6 x}{dt^6} &= 0 \\ \frac{d^6 y}{dt^6} &= 0\end{aligned}$$

The solutions of the problem are therefore fifth order polynomials, with coefficients that can be determined by the acceleration, speed and position at the starting and end points. If we consider the starting and ending speed and acceleration to be null and the start and end points to be, respectively, (x_0, y_0) and (x_F, y_F) we have

$$\begin{cases} x(\tau) = x_0 + (x_F - x_0) (10\tau^3 - 15\tau^4 + 6\tau^5) \\ y(\tau) = y_0 + (y_F - y_0) (10\tau^3 - 15\tau^4 + 6\tau^5) \end{cases},$$

where $\tau = t/T$.

In this case the model predicts a straight trajectory in the Cartesian plane for the end effector. It is easy to see that speed profiles are symmetric and smooth. This model suggests a cinematic planning of the movement, and solves only the lowest level of the problem, which is finding the trajectory of the effector. The initial formulation of the MJ used movements on the horizontal plane for an arm with two degrees of freedom (shoulder and elbow), in this case it is possible to know the angles and forces on the articulations from the minimum jerk trajectory through inverse dynamics.

It is worth noting that the minimum jerk has been successfully used to reproduce the two-thirds power law (stipulating that when we draw an ellipse we follow the law $v = \alpha \kappa^{-1/3}$ where v is the speed of the tip of the crayon, α is a constant and κ is the curvature of the ellipse). The name “two-thirds” power law comes from the original formulation of the law in terms of angular velocity.

Using the peak to average velocity ratio as a single scalar projection of the velocity profiles, it was also found that the MJ is best suited criterion. Indeed, previous experimental evidences (Hogan, 1984) showed that this ratio is about 1.8 (with 10% standard deviation) for reaching movements; amongst the quadratic derivative cinematic criteria, MJ yields a ratio of 1.875 for this class of movements.

As stated before, some works point that the Minimum Jerk is unable to produce asymmetric velocity profiles (Berret, 2008; Feng et al., 2002; Djioua and Plamondon, 2010), however this is only true if velocity and acceleration at both the beginning and the end of the movement are null, which is not a requirement of the model itself. Furthermore, in (Berret, 2008) it is noted that MJ predictions are not in agreement with experimental data when the movement occurs on the vertical plane or when the target is not a single point but an infinite set of points instead (a straight line, for instance); however MJ predictions work properly on the horizontal plane for point-to-point movements. These conditions can both be assumed for a writing movement that we are interested in the present work.

This criterion is the most used on the movement control literature, even it does not gives all the forces on a multi-articulated arm it is very effective on the determination of the end effector trajectory and the generation of natural-like movements being used in robotics (Pattacini et al., 2010) and rehabilitation (Amirabdollahian et al., 2002), for instance.

2.6 Movement Modelling and Handwriting

Handwriting is one of the most complex motor skills, having one of the longest learning processes known to humans. It coordinates a great number of components, not only from the hand and the forearm but also from the entire body, determining a posture that has affects the written production (Hamstra-Bletz and Blote, 1990; Sassoon, 1993). As such, handwriting provides scientists with a unique experimental window into motor expertise. The production of handwriting requires a hierarchically organized flow of information through various transformations (Ellis, 1988; Teulings et al., 1986). The writer starts with the intention to write a message (semantic level) which is then transformed into words (lexical and syntactical level). When individual letters (graphemes) are known, the writer still has to select a specific letter shape (allograph). Below this level, allographs are transformed into movement patterns, which is the focus of this Section.

A survey of the literature yields numerous models that capture several features of trajectory information. They can roughly be classified into two categories: symbolic and continuous models. Symbolic models apply some optimization algorithms over a segment of the trace defined as a stroke according to more or less arbitrary criteria (Edelman and Flash, 1987; Bullock et al., 1993; Teulings, 1996; Grossberg and Paine, 2000; Plamondon and Guerfali, 1998; Plamondon and Djioua, 2006). A stroke represents a basic movement unit of varying length and shape executed by the motor

system in a feedforward control mode. (Teulings, 1996) captured the notion of movement unit with the term “ballistic stroke”. The process of handwriting itself may be then viewed as the concatenation of strokes in space and time. This piecewise process involves a graphic motor buffer where the corresponding motor patterns (Viviani and Terzuolo, 1982) are eventually translated into appropriate neural commands (Ellis, 1982; Patterson and Wing, 1989).

In (Edelman and Flash, 1987) handwriting trace is modeled as the concatenation of four prototypical strokes: a hook, a cup, an inverted gamma and an oval. The letter ‘a’, for instance, was viewed as a concatenation of oval and hook. The minimum jerk model (or the minimum snap model) is then applied to construct the trajectory from the start point to the via-points, situated approximately in the middle of the planned trajectory, and to the end point of a stroke. This model offers an excellent fit for the prototypical strokes as well as for letters, provided that, beforehand, the actual trace is separated into successive strokes. The main disadvantages of this model are the need of arbitrarily defined via-points and a previous segmentation step.

The Adaptive VITEWRITE model (Grossberg and Paine, 2000) is a neural network handwriting learning and generation system that joins together the mechanisms from cortical VITE (Vector Integration to Endpoint) and VITEWRITE trajectory generation models (Bullock and Grossberg, 1988) with the cerebellar spectral timing model from (Fiala et al., 1996). This combination creates a single system capable of both reactive as well as memory based movements. AVITEWRITE model successfully explained the psychophysical and neurobiological data about how synchronous multi-joint reaching trajectories could be generated at variable speeds. The AVITEWRITE model was used to simulate the key psychophysical and neural data of movements: unimodal bell shaped velocity profiles, scaling with preservation of letter’s shape and velocity profiles and the two-thirds power law relation between angular velocity and curvature. The main issue of this model is the great complexity of its implementation.

A symbolic model is presented in (Schomaker, 1991) where movement is represented by strokes chaining, where strokes are defined as a combined acceleration and deceleration movement unit for a spatial axis in Cartesian space with a near sinusoidal velocity profile. Furthermore, this model assumes x and y commands to be linked together, in contrast to findings that show independence between the two axis (Burton et al., 1990).

(Plamondon, 1998) presents a bottom-up model using delta-lognormal synergies referring to the authors’ definition of the velocity of a muscle synergy as a Gaussian function of the movement parameters that varies logarithmically in time. Therefore it is not surprising that bell shaped profiles similar to human velocity profiles are found. More recently, in (Plamondon and Djoua, 2006), a family of models derived from the Kinematic Theory of Human Movement (Plamondon, 1995a,b, 1998; Plamondon et al., 2003) is presented. It provides a multi-level representation paradigm to analyze both the trajectory and the velocity of strokes with a progressive amount of detail. In this work, log-normal impulse responses are used to describe the synergetic action

of neuromuscular networks.

Continuous models generate traces that are the outcome of a nonstop generative process, usually oscillatory, which is modulated parametrically every now and then in a mode that mixes feedback and feedforward control (Stark, 1995). The feedforward mechanism of generation is fused with feedback mechanisms of updating, so that the desired trajectory is obtained. The first continuous trajectory formation in handwriting as a combination of two linear oscillators is found in (Hollerbach, 1981). The model assumed that each antagonist muscle pair behaves as a harmonically moving mass-spring system. Handwriting is thus generated through the combined action of the pair of oscillators set in an orthogonal fashion. The addition of a translational motion from left to right at a constant speed, typical of most western scripts, separates the strokes/letters. Even being crude and incomplete, this model is still the basis for several subsequent oscillatory models.

An extension of the oscillatory model considering that the movement emerges from a non-linear coupling of the orthogonal oscillators is found in (Athenes et al., 2004). Due to this nonlinearity, several stable modes of synchronization between the oscillators were expected to arise, according to the principles of dynamic pattern theory (Kelso, 1984; Schöner and Kelso, 1988). This model could predict the degradation of handwriting in adverse situations (Sallagoity et al., 2004).

In (Gangadhar et al., 2007) a neural network model of handwritten stroke generation in which stroke velocities are expressed as a Fourier-style decomposition of oscillatory neural activities is presented highlighting the role of the basal ganglia. This model was used for Parkinsonian movements, being capable of representing phenomena as micrographia, bradykinesia and tremors (Gangadhar et al., 2008).

Finally, the parsimonious oscillatory model (André et al., 2014) bases itself on Hollerbach's model but it is symmetric in x and y . Despite knowing that the movement axes are usually independent, this model bets in a simplified approach that has the benefits of providing an analytic solution for extracting parameters from the trace, hence an inexpensive computation. Despite its simplicity, this model is still provides representation as good as those of the more complex models.

Amongst these models only the sigma-lognormal model (O'Reilly and Plamondon, 2009; Galbally et al., 2012; Plamondon et al., 2014), based on the kinematics theory of rapid human movement, has been used for signature modeling. By contrast, we propose using the minimum jerk model as described in (Viviani and Flash, 1995), which to our knowledge has not yet been applied to signature representation. Signatures are a particular case of handwriting, where there is no semantic or syntactical level; usually signatures combine, along with letters, a drawing component.

2.7 Conclusion

In this chapter the main theories regarding human movement planning are studied, with an emphasis on the Minimum Jerk Model. This model is an Optimum Control

theory-based method that provides the basis for the development of the signature representation proposed in Chapter 4.

A review of handwritten movement representation methods is also provided. It was noticed that there is, up to author's knowledge, a single other signature representation method based on a human movement model. From a movement modeling point of view, as there is still an intense debate in the research community about which is the more adequate model for representing human movements, the signature representation proposed in this work can neither be considered as better or worse than the Sigma-Lognormal representation. It is an alternative approach based on a different movement model.

On the next chapter, a review of the signature verification literature is provided, focusing on the dynamic (on-line) signature category. The main approaches adopted for each component of a biometric system are discussed for the on-line signature case. This gives the reader the necessary basis for understanding the analysis and applications performed in Chapters 4 and 5. In addition to this literature review, the on-line signature databases used in this thesis are described and performances of state-of-the-art systems for each database are provided.

Signature Verification

3.1 Introduction

Signature has a long tradition as a method to prove one's identity (legal documents, banking transactions) and it is one of the most widespread means of personal verification, if not the most widespread. In the wider field of handwriting verification, the signature modality is the one that has attracted more research efforts and that has produced more scientific publications. Several extensive reviews on this topic can be found in the literature, works until 1988 can be found in (Plamondon and Lorette, 1989) and up to 1993 in (Leclerc and Plamondon, 1994). Subsequent works up to 2000 are surveyed in (Plamondon and Srihari, 2000). A very comprehensive survey containing more than 350 references of more recent works (until 2008) is found in (Impedovo and Pirlo, 2008).

Being a behavioral biometric, signatures depend both on the psychophysical state of the signer and the conditions under which the signing process occurs. Therefore, signature verification still remains an open challenge since a signature is judged based only on a few reference samples (Plamondon, 1994).

Following the general scheme of a biometric system discussed in Chapter 1 (see Figure 1.1), we discuss each step (i.e., data acquisition, preprocessing, feature extraction, classification and database design) from the point of view of the automatic signature verification systems found in the literature. Section 3.2 presents the main aspects of data acquisition; Section 3.3 discusses the most common preprocessing techniques. In Section 3.4 the main features used for signature verification are listed followed by the main techniques for classification in Section 3.5 and some considerations regarding database design in Section 3.6. Finally, in Section 3.7, we present the state of the art systems' performances for the databases used in this work, along with a description of each database.

3.2 Data Acquisition

According to acquisition method, handwritten signatures can be of two categories: static (offline) or dynamic (online). Offline systems perform data acquisition after the writing process has been completed, and the signature is represented as an image.

On the other hand, dynamic systems use devices that generate electronic signals representative of the signature during the writing process, providing a spatiotemporal representation of the signature. In this work we will be dealing with online signatures, therefore we will only discuss the specifics of this acquisition category.

Traditionally, online signatures are acquired through digitizing tablets. Initially, digitizer tablets were composed by a special support and pen basically made out of plastic, which strongly changed the friction forces usually experienced while signing with a traditional pen over a paper and, in addition, gave no visual feedback of what was being written. Many efforts have been made to produce electronic pens that are more acceptable to users, such as writing supports with screens that give an immediate feedback. Some devices have ink cartridges and the paper can be posed over the digitized support for a more natural feeling, these devices also have the advantage of acquiring both online and offline data at the same time. Digitizing tablets use the interaction between the pen and the support to capture several aspects of the writing process, such as position, speed, acceleration, inclination of the pen, and pressure on the tip of the pen.

Recently, handheld digitizers, such as smartphones and tablets, are becoming increasingly popular. In this case, acquisition is performed by a touch-sensitive surface, possibly with the aid of a stylus for a more natural writing experience (Krish et al., 2013). However, such devices suffer not only with the different friction forces but also with a posture problem, since signing can be performed while standing or even walking. Furthermore, touch-sensitive surfaces are not capable of acquiring movements that are performed when the pen is not touching the surface, which can carry important discriminative information (Sesa-Nogueras et al., 2012).

Other approaches capture handwriting by computer vision techniques. For instance, a special stylus with a small camera is used in (Nabeshima et al., 1995). The stylus also has a sensor for detecting the pressure applied on the ballpoint.

Alternative approaches that do not use a special stylus can also be found in the literature, such as those using a hand-glove device (Tolba, 1999) for movement capture, a video camera focused on the user while writing with a normal pen (Munich and Perona, 2003) or even mouse-based signature verification (Ahmed and Traore, 2007).

Development of such variety of acquisition technologies poses new problems concerning device interoperability, especially on distributed systems where the test signature sample could be acquired on a mobile device, for instance, while the template was acquired on a digitizing tablet or even on a different mobile device.

3.3 Preprocessing

Typical preprocessing procedures include noise reduction, smoothing, signature normalization and segmentation. Signature normalization is used to standardize signatures in the domain of position, size, orientation, and time duration (Igarza et al.,

2004).

Segmentation is a crucial preprocessing step that strongly influences all the successive phases of signature verification; we will pay more attention to this particular step since we also propose a segmentation technique in this work. Signatures produced by the same writer can greatly differ from each other making segmentation a complex task. Because of this, specific attention has been devoted to signature segmentation, and several techniques have been proposed. We can divide these techniques in four categories according to which principle they are based on: pen-up/pen-down signals, velocity analysis, perceptual relevant points and dynamic time warping.

A common and very simple segmentation technique is based on the consideration that a signature is as a sequence of writing units delimited by abrupt interruptions. Thus, pen-up/pen-down signals are used to segment a signature into components (Dimauro et al., 1994). Some approaches use only the in-air strokes for signature verification, since those strokes can be memorized by the computer but are invisible to humans, increasing the difficulty of being imitated (Xuhua et al., 1996; Sesa-Nogueras et al., 2012).

Segmentation techniques based on velocity analysis use different approaches, ranging from simple detection of null velocity (Dolfing et al., 1998) to curvilinear velocity signals. The stroke identification step on the Sigma-Lognormal model (Plamondon et al., 2014) can be placed on such category.

A different class of segmentation methods comprises those based on the detection of perceptually important points. The importance of a point is determined by the rate of change of the writing angle around it. We can also include in this category techniques based on the detection of geometric extremes (Lee et al., 2004b).

In order to allow the segmentation of many signatures into the same number of segments, dynamic time warping has been widely used (Rhee et al., 2001). Furthermore, combinations of different techniques can also be found in the literature, in (Qu et al., 2004) a combination of pressure (first category), velocity (second category) and angle change (third category) is used for segmentation.

3.4 Feature Extraction

Features used for automatic signature verification can be divided on two main categories: time functions and scalar parameters. Time function features provide local information while parameters usually represent global information. However, such global parameters can also be made local, or regional, through the use of the aforementioned segmentation techniques. It is easy to see that function features convey more information than parameters, since the last ones try to explain a global behavior of the signature through a single scalar value, but they usually require more time-consuming procedures for matching (Plamondon and Lorette, 1989; Impedovo and Pirlo, 2008). In this section we list the most common features found in the automatic signature verification literature.

The most common function features found in the literature are: position, velocity, acceleration, pressure, pen inclination and azimuth angles. Position function is provided directly by the acquisition device whereas velocity and acceleration functions can be provided by both the acquisition device (Bunke et al., 2011) or numerically derived from position time function. In (Lei and Govindaraju, 2005) it was found that signing velocities, and consequently total signing time, are amongst the most consistent features, along with pen azimuth angle. On this work it was also found that pressure function, despite being almost impossible for a forger to deliberately copy, can significantly vary for the same writer. Some works use the dependencies between features, notably pressure and velocity as a new feature (Khalid Khan et al., 2006). Furthermore, pen posture (inclination and azimuth angles) have been successfully considered to improve systems' verification performances (Van et al., 2007). It is also possible to use time series motifs, extracted from function features (Buza and Schmidt-Thieme, 2010) for signature verification or even local fractal information, known as Hölder functions (Canuto and Lee, 2010; Canuto, 2010).

Regarding scalar parameters, a complete list would be too long. In (Lee et al., 1996) a set of 49 parameters is used and in (Nanni and Lumini, 2006) a total of 100 parameters can be found. Amongst the most common global parameters we can cite the total signing time, maximum, average and minimum values of time functions (e.g. position, velocity), number of pen-downs/pen-ups, and coefficients obtained from mathematical tools as Fourier or wavelet transforms. It is worth remembering that all these global functions can be made local (component-based) through the use of segmentation techniques.

Whatever feature set is considered, evidence that an individual's signature has different distinctive features has increased the studies on feature selection. This interest is also led by the fact that system efficiency, processing cost, and memory requirement are dependent on the size of the feature set (Ketabdar et al., 2005; Richiardi et al., 2005). Feature selection can also be used for renewability of user templates, it should be possible to revoke a compromised template and reissue a new one (new set of features) based on the same biometric data (Argones Rua et al., 2012). Several techniques have been proposed for feature selection based on principal component analysis, self-organizing maps and analysis of feature variability. Feature selection was also used for finding features that are best suited for distinguishing skilled forgeries or random forgeries (Rhee et al., 2001). Another possible approach for feature selection is assigning different weights to each feature (Kim et al., 1995).

Finally, recent works are interested in measuring the signatures' quality, showing that there is a link between quality and verification performance. Many criteria have been considered as quality measures such as stability, complexity, readability and entropy. In fact, it is easy to imagine that complex signatures which are stable through time are easier to correctly classify, since they should present low intra-class variability and, due to their complexity, are hard to imitate. A good review on this subject can be found in (Houmani, 2011).

In (Brault and Plamondon, 1989) complexity is defined by the difficulty in reproducing each portion of the signature while stability is defined by intra-class variance. (Dimauro et al., 2002) proposes uses DTW to calculate the stability of a signature, counting the number of direct correspondences. In (Müller and Henniger, 2007) the term quality is introduced and two evaluation methods are proposed, one linked to the verification performance and another one linked to the stability. (Richiardi, 2008) uses a Gaussian Mixture Model (GMM) and Mahalanobis distance to access quality. In (Galbally et al., 2011) two parameters of the Sigma-Lognormal model are used as a quality measure. Finally, in (Houmani, 2011) a new quality measure based on Hidden Markov Models (HMM) that is linked both to complexity and stability, called Personal Entropy, is proposed. It is worth noting that complexity measures usually have a high correlation with the total signing time (Brault and Plamondon, 1993).

These measure allow for the selection of the best reference signatures (Di Lecce et al., 1999), for controlled data acquisition, through the acceptance of samples based on quality criteria, (Brault and Plamondon, 1989) and even for the adaptation of the template signature through time (Kato et al., 2006).

Other types of approaches relate the stability of some features to physical characteristics of signers, such as age. These approaches have shown that some other features change significantly according to the signer age group such as total execution time, velocity and acceleration (Guest, 2006; Gomez-Barrero et al., 2013), it was noticed that using the sigma-lognormal model, signatures on elderly people present a greater number of strokes with shorter durations. However it is worth noting that these changes were not observed for a single person through time, but for different people of certain age categories, which could reflect not only physical changes but cultural changes as well.

3.5 Classification

Authenticity of test signatures is evaluated by matching their features against those stored in the reference set developed during the enrollment phase. Several approaches for signature matching and classification have been proposed in the literature and we discuss a few of them in this Section. The reader can find a comprehensive list on this subject in (Impedovo and Pirlo, 2008).

When parameters features are used, statistical-based techniques are generally chosen. The most common approaches use Mahalanobis distance (Quan et al., 2006), when the full covariance matrix is available, and Euclidean distance (Nanni, 2006). Membership functions (Qu et al., 2004) and hamming distance (Guru and Prakash, 2009) have also been used.

When time functions are considered the matching problem can be complicated due to the fact that function features usually do not present the same length amongst different signature samples, even for the same writer. The most common approaches used for signature matching using function features include the DTW (Kholmatov and

Yanikoglu, 2005; Pascual-Gaspar et al., 2009; Canuto, 2010) matching and statistical modeling through Gaussian Mixture Models (GMMs) (Canuto, 2010) or Hidden Markov Models (HMMs) (Fierrez-Aguilar et al., 2005; Van et al., 2007). Other approaches include Neural Networks (Cpałka et al., 2014; Cpałka and Zalasiński, 2014), due to their capabilities of learning and generalization, and string or graph matching, usually related to structural representation of signatures (Schimke et al., 2004).

As its name suggests, DTW allows for the compression or expansion of the time axis of two time sequences representative of the signatures to obtain the minimum of a given distance value (Theodoridis and Koutroumbas, 2006). More precisely, let $R = r_1, r_2, \dots, r_M$ and $T = t_1, t_2, \dots, t_N$ be two time sequences where possibly $M \neq N$. The optimal DTW alignment minimizes a cumulative distance measure consisting of local distances between aligned samples. The DTW distance, $D(M, N)$, is computed using dynamic programming through the following recursion:

$$D(i, j) = \min \begin{cases} D(i, j-1) + w_i \times d(i, j) \\ D(i-1, j) + w_d \times d(i, j) \\ D(i-1, j-1) + w_s \times d(i, j) \end{cases},$$

where $d(i, j)$ is a distance measure between the i^{th} reference point and the j^{th} testing point, w_i , w_d and w_s are the insertion, deletion and substitution weights respectively, and $D(0, 0) = 0$. A detailed discussion on DTW, which was initially used in the field of speech processing, is beyond the scope of this chapter, further information can be found in (Theodoridis and Koutroumbas, 2006). Although the superiority of DTW has not been proven with respect to other comparison techniques, some works show that DTW usually has a better performance than other techniques when only position information (x and y) is available (Houmani et al., 2012, 2011).

Gaussian mixture models are a technique for probability density function modeling. The problem can be stated as follows: let $\mathbf{X} = \mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n$ a set of D dimensional samples of a unknown pdf $p(\mathbf{x})$. It is assumed that there is an approximation for $p(\mathbf{x})$ given by a mixture of Gaussian distributions

$$\hat{p}(\mathbf{X}|\Theta) = \sum_{k=1}^M \alpha_k G(\mathbf{X}|\mu_k, \Lambda_k),$$

where $G(\mathbf{X}|\mu_k, \Lambda_k)$ is the k^{th} Gaussian kernel with mean vector μ_k and covariance matrix Λ_k , α_k is the corresponding weight coefficient, and Θ are the parameters of the mixture ($\mathbf{A} = [\alpha_1, \dots, \alpha_M]$, $\mathbf{M} = [\mu_1, \dots, \mu_M]$, $\mathbf{C} = [\Lambda_1, \dots, \Lambda_M]$). This pdf model has its parameters adjusted in order to maximize the logarithm of the likelihood, then the optimum parameters set is

$$\Theta_o = \underset{\Theta}{\operatorname{argmax}}(\log p(\mathbf{X}|\Theta)).$$

A well-known method for solving this problem is the Expectation-Maximization algorithm (Dempster et al., 1977). Another method for pdf estimation is the non-

parametric Parzen Windows method (Parzen, 1962) that can also be seen as regularized GMM in a parametric perspective (Montalvão and Canuto, 2008). Further details on pdf estimation models, including the GMM can be found in (Theodoridis and Koutroumbas, 2006) and (Duda et al., 2000).

Recently, intensive research has been devoted to HMMs. A Hidden Markov Model is a double stochastic process based on the existence of a set of hidden states that are not directly observable. This model is composed by two stochastic processes, a hidden process that is a Markov chain representing the states of the model and sequence of observations. An HMM is characterized by its number of states, the transition matrices that state the probability for changing between states, the initial state distribution and the probability law of emission of a given observation in a given state. On continuous HMMs, this probability laws are usually approximated by GMMs. The optimization of the model's parameters is commonly done using the Baum-Welch algorithm, based on the EM algorithm. Another important method related to HMMs is the Viterbi algorithm, based on dynamic programming principle, that can determine the likelihood of a given observation sequence being generated by the model and the best sequence of states that generates this sequence. Further details on HMMs can be found in (Rabiner, 1989) and (Papoulis and Pillai, 2002). Concerning signature verification, most approaches use the left-to-right topology, since most handwritten signatures have a single writing direction (Van et al., 2007; Fierrez-Aguilar et al., 2005).

Neural Networks have been widely used for automatic signature verification for a long time. Although NNs have demonstrated good generalization capabilities, they require large amounts of learning data that are usually not available. To this purpose, the use of synthetically generated signatures has also been proposed (Galbally et al., 2012).

Structural approaches are not very common in online signatures verification and concern string, graph, and tree matching techniques. However, performance results obtained using such techniques are not promising as compared to other techniques (See Table 3.4) (Schimke et al., 2004).

In addition to all these techniques, multiexpert approaches have been investigated in recent years to improve signature verification performance (Yanikoglu and Kholmatov, 2009; Nanni, 2006; Nanni and Lumini, 2008; Nanni et al., 2010). Several decision combination schemes have been implemented, ranging from majority voting to simple and weighted averaging. Multiexpert approaches have also been used for stroke-based signature verification. This approach can lead to lower error rates compared to global approaches, since a large amount of personal information is conveyed in specific parts of the signature. Furthermore, the verification at stroke level can be performed by DTW, considering multiple function features for stroke representation in order to verify both the shape and dynamics of each part of the signature (Bovino et al., 2003).

3.6 Database Design

Along with the matching techniques, attention has been given to database design. A common problem in online signature verification is the lack of sufficient reference data to characterize a given signature. Thus, specific research has been devoted to the generation of additional training samples from the existing ones by convolutions (de Oliveira et al., 1997), spectral analysis (Galbally et al., 2009b) and generative models (Galbally et al., 2012).

The differences in signatures of people from different cultures have also required the development of specifically designed solutions. Specific approaches have been proposed in the literature for Chinese (Xiao and Dai, 1998) signatures, which can consist of independent symbols, as well as Arabian/Persian (Chalechale et al., 2003) signatures, which are cursive sketches usually independent of the person’s name. As the need for cross-cultural applications increase, “soft biometrics” can be used to store writers nationality and script language in order to adapt the verification approach to each context (Wolf et al., 2006).

3.7 Verification Performance

Several works list their performance results throughout the literature using different datasets. In this thesis we will be working with five public databases (SVC2004 Tasks 1 and 2, Biosecure Signature Datasets DS2 and DS3, and MCYT Signature Subcorpus). We start this Section by providing a description of these databases, followed by a list of verification performances achieved on a selection of works on these datasets.

Unlike physiological biometrics, the use of skilled forgeries for evaluation is crucial to behavioral biometrics such as handwritten signatures. Since this is the most challenging type of forgery, we chose to list in this Section only results on this kind of attack. All datasets used in this work provide a set of skilled forgeries in which users had access to an original signature of other users and trained to imitate them.

3.7.1 Databases Description

3.7.1.1 SVC2004 Task 1 (SVC1)

This database was used for the first signature verification competition in 2004 (SVC2004) (Yeung et al., 2004). This database is originally comprised of 100 users, with 20 genuine signatures and 20 skilled forgers of each, however, only 40 users are publicly available. Each data contributor was asked to provide 20 genuine signatures. For privacy reasons, the contributors were advised not to use their real signature. Instead, they were suggested to practice a new signature until it remained consistent, both spatial and time wise, over different acquisitions.

In the first session, each contributor provided 10 genuine signatures using a Wacom Intuos tablet at a sampling rate of 100 Hz. They were also encouraged to get used to the acquisition device before providing the definitive signatures. Moreover, contributors could discard a signature if they were not satisfied with it. In the second session, which took place at least one week after the first one, each contributor provided another 10 genuine signatures.

Skilled forgeries for each user were provided by five four other users (5 samples each) in the following way: using a viewer, a contributor could replay a video of the writing sequence of the target signature, in such way that they could observe not only the shape but the dynamics of the process. Contributors were advised to practice until they were confident to proceed to the actual acquisition.

Signatures are mostly in English and Chinese, even though most of the contributors are of Chinese nationality. On this first task, only x and y coordinates time functions are provided. Despite being capable of collecting the in-air movements using the Wacom Intuos tablet, all points of the signature that had zero pressure were removed. Therefore, the temporal distance between points is not regular and the time of acquisition of each point is also provided.

3.7.1.2 SVC2004 Task 2 (SVC2)

This dataset is very similar to the SVC1, but it also provides pen pressure (p), azimuth (az) and altitude (alt) angles time functions. All the considerations regarding data acquisition protocol on the SVC1 database are also valid here. However, this dataset is comprised of different people than SVC1.

3.7.1.3 MCYT Signature Subcorpus (MCYT)

The MCYT Spanish project, oriented to the acquisition of a bimodal database including fingerprints and signatures was completed by late 2003 with 330 subjects (Ortega-Garcia et al., 2003). However, only a subcorpus of 100 users is freely available and is used on this work.

A Wacom Intuos A6 USB tablet was used for data acquisition. The pen resolution is 100 lines per millimeter, and the precision is 0.25 mm. The maximum detection height is 10 mm (in-air movements are also considered), and the capture area has 127 mm height and 97 mm width. As for the SVC2 database, this tablet provides x and y coordinates, pressure, azimuth and altitude angles time functions at a sample frequency of 100 Hz. This frequency respects the Nyquist sampling criterion, since maximum frequencies of the underlying biomechanical movements are always under 20 Hz (Baron and Plamondon, 1989).

Each contributor produces 25 genuine signatures, and 25 skilled forgeries are produced for each user. These skilled forgeries are provided by 5 different users by observing the static image of the target signature, training to copy them before providing the valid sample. In this way, shape-based skilled forgeries with natural dynamics

are obtained. The acquisition protocol is as follows: contributor n provides a set of 5 samples of his/her genuine signature and then 5 skilled forgeries of user $n - i$, where i is the iteration number. This procedure is repeated 5 times, producing 5 skilled forgeries for users $n - 1$, $n - 2$, $n - 3$, $n - 4$ and $n - 5$ and 25 genuine samples. This procedure aims at simulating a multi-session acquisition through breaks between genuine acquisitions.

3.7.1.4 Biosecure Signature Dataset 2 (DS2)

This online signature database was acquired in the context of the BioSecure (Biometrics for Secure Authentication) European excellence network. This network grouped 30 partners from 17 European countries and performed the acquisition of this database on 12 different research laboratories. It contains data from 667 contributors acquired on a digitizing tablet. However, only a subset of 210 users is publicly available (Ortega-Garcia et al., 2010) and will be used on this work.

Signatures on this dataset were acquired through a Wacom Intuos 3 A6 tablet. This device's resolution is 200 lines per millimeter, and the precision is 0.25 mm. The maximum detection height is 13 mm (in-air movements are also considered), and the capture area has 270 mm height and 216 mm width. The sampling frequency was once again set to 100 Hz and the same five time functions are available: x and y coordinates, pressure, azimuth and altitude angles. To provide a more natural experience, the pen was equipped with an ink cartridge and a paper was posed over the tablet surface.

Two distinct acquisition sessions were realized at least two weeks apart. At each session 15 genuine samples and 10 skilled forgeries were provided by each contributor. The acquisition protocol was as follows: contributor n provided 5 genuine signatures followed by 5 skilled forgeries of contributors $n - 1$ (or $n - 3$ for the second session), then 5 more genuine signatures followed by 5 skilled forgeries of contributors $n - 2$ (or $n - 4$ for the second session), and finally 5 other genuine samples. In order to produce skilled forgeries, contributors were able to watch a video reproduction of the target signature, as in SVC2004 databases, and could train for several minutes before providing the definitive samples.

3.7.1.5 Biosecure Signature Dataset 3 (DS3)

This database was also part of the acquisition efforts of the BioSecure network of excellence and contains data from 713 contributors acquired on a mobile platform, but only a subset of 240 users is publicly available and will be used on this work.

Signatures on this dataset were acquired using a HP iPAQ hx2790 PDA, with a touch screen resolution of 1280 x 960 pixels and a sampling frequency of 100 Hz. Three time functions are available: x and y coordinates, and pressure.

As for the DS2 dataset, signatures were also acquired in two distinct sessions, performed at least six weeks apart. The acquisition protocol was the same used for

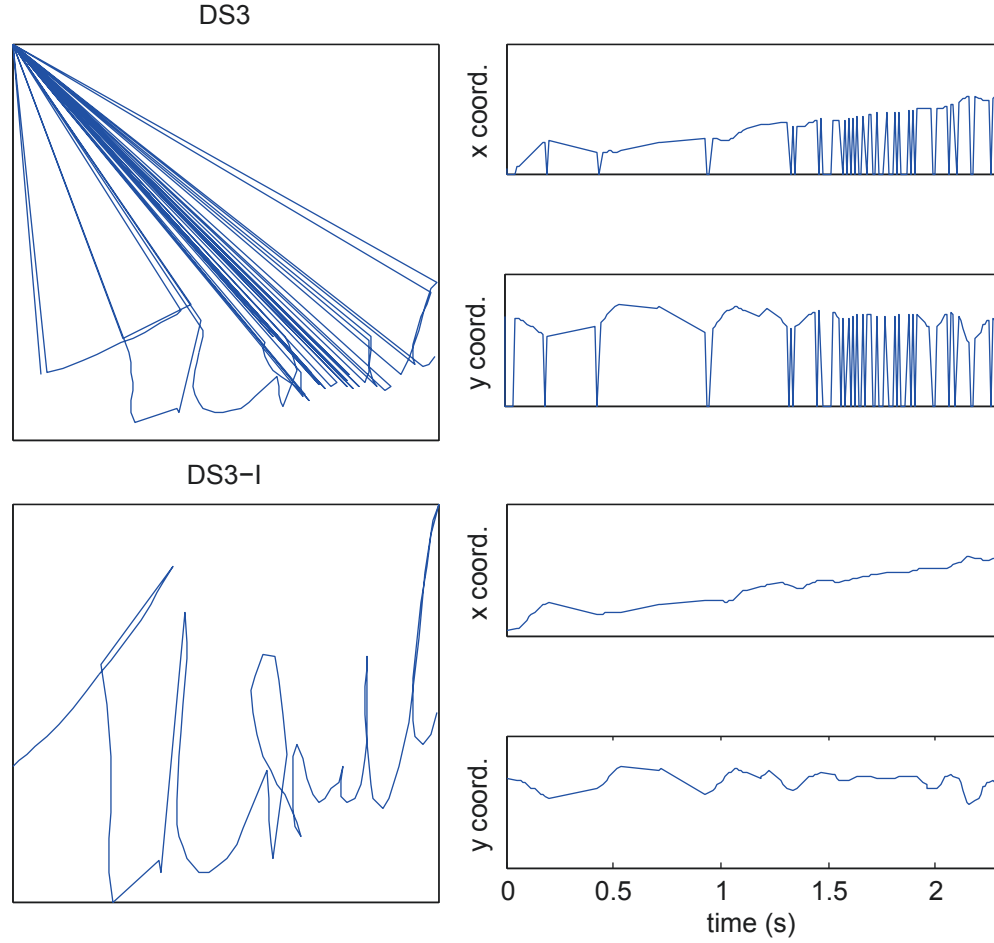


Figure 3.1: A signature of the DS3 database before and after the removal of the artificial points at the origin.

the DS2-210 database. In order to produce skilled forgeries, contributors were able to watch a video reproduction on the PDA screen and could even trace over the target signature image.

Data is only acquired when there is a contact between the stylus and the touch-sensitive surface of the PDA. In addition to that, the system record an occurrence of a point at the origin $(0,0)$ of the Cartesian space whenever a pen-up occurs. This is the only database in which some kind of pre-processing will be used, consisting on the removal of such artificial position recordings. This modified database will be denoted as DS3-I on the text. In Figure 3.1 are shown a signature from the DS3 database before and after the removal of these points.

Table 3.1 summarizes the characteristics of the five public datasets used. As it

Table 3.1: Signature databases characteristics.

Database	Acquisition Device		Users	Genuines	Forgeries	Sessions	Features
SVC1	Wacom Tablet	Intuos	40	20	20	2	x, y
SVC2	Wacom Tablet	Intuos	40	20	20	2	x, y, p, az, alt
MCYT	Wacom A6 USB Tablet	Intuos	100	25	25	1	x, y, p, az, alt
DS2	Wacom 3 A6 Tablet	Intuos	210	30	20	2	x, y, p, az, alt
DS3	HP hx2790 PDA	iPAQ	240	30	20	2	x, y, p

was said before, this work deals mainly with trajectory-related aspects of signatures, therefore only x and y coordinates will be used, even if more information is provided by the acquisition devices. Time functions derived from position information will also be used, such as velocity and acceleration.

3.7.2 Performances on Selected Works

A fair comparison between different automatic signature verification systems is always difficult. Each system component discussed so far play a role on the authentication performance. Furthermore, slight changes on the testing protocol can significantly affect the final result. All verification systems listed here use five genuine signatures for the reference set.

In Tables 3.2 to 3.7 results of several works on databases SVC1, SVC2, MCYT, DS2 and DS3 respectively are provided. Since they were the first publicly and freely available online signature databases, SVC and MCYT datasets are those more widely used in the literature. BioSecure databases are publicly available but not for free, therefore most of the results found in the literature use the 382 users set which is not public but was used for signature competitions in 2009 (Houmani et al., 2012) and 2011 (Houmani, 2011). Results are listed in alphabetical order of the authors; a brief description of each selected work is provided at the end of this Section.

The SVC2004 competition testing protocol used writer-specific thresholds instead of a global threshold. This procedure usually yields better average performances and greater standard variations. The EERs reported on such scenario are the averages for the error rates obtained for each user. However, some selected works using these databases chose to use global thresholds. Therefore, on Tables 3.2 and 3.3 we indicate individual or global threshold by (I) or (G) after the reported performance. Notice that only few works provide reports on the SVC1 Database, because only x and y information is available in this case. Finally, it is worth remembering that the results

Table 3.2: Performance results on the SVC1 database.

Work	Features	Method	EER(%)
(Canuto, 2010)	x, y	DTW	5.60 ± 6.80 (I)
		Parzen	8.40 ± 9.50 (I)
(Fierrez-Aguilar et al., 2005)	14 time functions. User specific normalization	HMM	11.99 ± 17.66 (I)
(Kholmatov and Yanikoglu, 2005)	$\Delta x, \Delta y$	DTW	5.50 ± 7.73 (I)

reported here were performed over the 40 users public subsets of the SVC databases only.

The MCYT database is the bigger freely available dynamic signature database. Due to this fact, this is the database of choice for many recently published works. In Table 3.4 we several approaches are presented. These works were chosen trying to keep a variety of techniques, ranging from methods based on global features to multi-expert systems. In all cases 5 signatures were used as reference set and a global threshold was applied. Special attention must be paid to the results of (Pascual-Gaspar et al., 2009) since only half of the MCYT database was used.

As we said before, only few works on the literature use the BioSecure databases. In fact, we were only able to find four works using the DS2 database (Table 3.5) and no work on the DS3 database. A larger subset of the BioSecure databases, containing 382 users each, were used for signature verification competitions. Tables 3.6 and 3.7 present some competitors that were present on both editions and were also used on other databases.

On the Evaluation of Signature Resistance to Attacks (ESRA'11) competition skilled forgeries were divided into good quality and bad quality forgeries, and results were given separately for each category. In Table 3.7 we present an average of these measurements weighted by the number of samples in each category.

Finally, we now provide a brief description of each of the works figuring on the performance tables in alphabetical order.

(Canuto, 2010) Two verification systems are proposed in this work, one based on DTW and one based on statistical modeling of features. The main goal of this work was to study the usefulness of local multifractal information (Hölder functions) as a biometric feature. Hölder functions are extracted from each x , y and pressure time functions, giving a total of 6 time functions that can be used. On both systems, features have their means removed and signatures are rotated so that their principal direction becomes horizontal.

The first method, based on DTW, uses the Euclidean distance as cost function

Table 3.3: Performance results on the SVC2 database.

Work	Features	Method	EER(%)
(Canuto, 2010)	x, y, p	DTW	3.00 ± 6.10 (I)
			12.8 ± 0.80 (G)
		Parzen	5.50 ± 7.40 (I)
			9.40 ± 0.60 (G)
(Cpalka et al., 2014)	$x, y, p, \Delta x, \Delta y$	Horizontal partitions. Neuro-Fuzzy	11.58 (G)
(Cpalka and Zalasinski, 2014)	$x, y, p, \Delta x, \Delta y$	Vertical partitions. Neuro-Fuzzy	10.70 (G)
(Fierrez-Aguilar et al., 2005)	14 time functions. User specific normalization	HMM	6.90 ± 11.76 (I)
(Gruber et al., 2010)	$\Delta x, \Delta y, \Delta p, az, alt$	SVM-LCSS	6.84 ± 10.18 (I)
(Ibrahim et al., 2010)	$x, y, p, \Delta x, \Delta y$	Partitions. DTW	12.40 (G)
(Kholmatov and Yanikoglu, 2005)	$\Delta x, \Delta y$	DTW	6.96 ± 11.76 (I)
(Pascual-Gaspar et al., 2009)	x, y, p, az, alt and first derivatives	DTW	4.15 (I)
	$\Delta x, \Delta y, p, y$		3.38 (I)
(Pascual-Gaspar et al., 2011)	$x, y, \Delta x, \Delta y, \Delta p$	Partition. VQ	5.00 (I)
			15.50 (G)
(Van et al., 2007)	25 time functions. User specific normalization	GMM Likelihood	8.05 ± 0.26 (G)
		HMM Likelihood	6.86 ± 0.26 (G)
		HMM Segmentation	10.79 ± 0.25 (G)
		HMM Likelihood + HMM Segmentation	4.83 ± 0.20 (G)

Table 3.4: Performance results on the MCYT database.

Work	Features	Method	EER(%)
(Canuto, 2010)	x, y	DTW	6.30 ± 0.60
		Parzen	5.70 ± 0.30
	x, y, p	DTW	4.30 ± 0.20
		Parzen	4.20 ± 0.20
	x, y, p and Hölder functions	DTW	3.70 ± 0.20
		Parzen	3.30 ± 0.10
(Guru and Prakash, 2009)	100 global parameters	Hamming Distance	6.12
(Houmani, 2011)	x, y	DTW	7.81
		HMM	17.87
(Kholmatov and Yanikoglu, 2005)	$\Delta x, \Delta y$	DTW	9.80
(Nanni and Lumini, 2005)	100 global parameters	Cluster of Parzen	8.40
(Nanni, 2006)	100 global parameters	Parzen + PCA	6.5
(Nanni and Lumini, 2008)	DCT coefficients	LPD	9.80
(Nanni et al., 2010)	$\Delta x, \Delta y$	DTW + DTW-SVM	4.96
	local, regional and global features	DTW + HMM + LPD	3.81
(Pascual-Gaspar et al., 2009)	x, y, p, az, alt and first derivatives	DTW	4.21 *
	$\Delta x, \Delta y, p, y$		1.06 *
(Pascual-Gaspar et al., 2011)	$x, y, \Delta x, \Delta y, \Delta p$	Partition. VQ	4.92
(Schimke et al., 2004)	Symbolic description	Levenshtein Distance	10.51 ± 0.13
(Van et al., 2007)	25 time functions. User specific normalization	HMM Likelihood	5.39 ± 0.12
		HMM Segmentation	5.60 ± 0.10
		HMM Likelihood + HMM Segmentation	3.37 ± 0.08
(Yanikoglu and Kholmatov, 2009)	Fourier coefficients	Euclidean Distance	12.11
	$\Delta x, \Delta y$ and Fourier coefficients	Euclidean Distance + DTW	7.22

Table 3.5: Performance results on the DS2 database.

Work	Features	Method	EER(%)
(Cpałka et al., 2014)	$x, y, p, \Delta x, \Delta y$	Horizontal partitions. Neuro-Fuzzy	3.69
(Cpałka and Zalasinski, 2014)	$x, y, p, \Delta x, \Delta y$	Vertical partitions. Neuro-Fuzzy	3.64
(Houmani, 2011)	x, y	DTW	5.94
		HMM	19.14
(Ibrahim et al., 2010)	$x, y, p, \Delta x, \Delta y$	Partitions. DTW	4.58

Table 3.6: Performance results on the BioSecure Signature Evaluation Campaign (BSEC'09) (Houmani et al., 2012).

Work	Features	Method	EER(%)	EER(%)
			on DS2-382	on DS3-382
(Kholmatov and Yanikoglu, 2005)	$\Delta x, \Delta y$	DTW	2.97	4.97
(Pascual-Gaspar, 2010)	$\Delta x, \Delta y$. User specific normalization	DTW	2.20	6.59
(Van et al., 2007)	25 time functions. User specific normalization	HMM Likelihood	4.47	11.27

Table 3.7: Performance results on the BioSecure Evaluation of Signature Resistance to Attacks (ESRA'11) (Houmani et al., 2011).

Work	Features	Method	EER(%)	EER(%)
			on DS2-382	on DS3-382
(Canuto, 2010)	x, y	Parzen	4.74	8.07
	x, y, p		3.97	–
(Kholmatov and Yanikoglu, 2005)	$\Delta x, \Delta y$	DTW	4.37	6.48
(Pascual-Gaspar, 2010)	$\Delta x, \Delta y$. User specific normalization	DTW	4.70	7.21
(Van et al., 2007)	25 time functions. User specific normalization	HMM Likelihood	3.37	9.23

for all cases and unitary weights:

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

where $d(i, j)$ is the euclidean distance between the i^{th} reference point and the j^{th} test point. During verification, a test signature is compared to each reference signature and the resulting distances are averaged. Next, this averaged score is multiplied by a factor based on the length of the signatures; this factor increases the dissimilarity score for signatures whose total length diverges from the average lengths of the reference set.

The second one uses Parzen Kernels, which can be seen as a highly regularized GMM. The imposed constraints are that all kernels have the same weight, available samples are used as Gaussian means, and all kernels are identical and isotropic (all kernels share the same covariance matrix defined as $\mathbf{\Lambda} = \sigma^2 \mathbf{I}$ where \mathbf{I} is the identity matrix). Therefore the only parameter to be adjusted is σ , which is optimized through the method proposed in (Montalvão and Canuto, 2008). A normalized time dimension is also added to the features. In order to penalize signatures that diverge from the reference set, this time dimension is contracted (or expanded) by a factor $k = t_T / \bar{t}_R$, where t_T is the length of the signature and \bar{t}_R is the average length of the signature in the reference set. For this system likelihood is used as score.

(Cpałka et al., 2014) The proposed method is based on four features: x , y , pressure and velocity. First, signatures are divided in four partitions on the basis of pressure and velocity signals. Each partition contains fragments of signature trajectory and a weight is attributed to each partition. Then, all partitions are used in a Neuro-fuzzy classifier for verification.

(Cpałka and Zalasiński, 2014) As for the previous method, x , y , pressure and velocity are the chosen features. First, a base signature is chosen amongst the reference set. All other signatures are aligned in relation to this base signature using DTW to match velocity and pressure signals. The resulting warping is then applied to x and y , and only these features are used for classification. Next, signatures are divided into N partitions of equal length and for each partition a template is created. For verification, the test signature is compared at each partition to the template using Euclidean distance. Finally, partitions are weighted and used in a Neuro-fuzzy classifier. Best results for the SVC2 database used 3 partitions while the best result for the DS2 database used 2 partitions.

(Fierrez-Aguilar et al., 2005) A set of 14 time functions is derived from x , y and p are used as features. Each feature is individually normalized to have zero mean

and unit standard deviation. A left-to-right HMM is trained using the reference signatures; this HMM has only 2 states with multivariate Gaussian Mixtures densities (32 Gaussian kernels per mixture). Likelihood is the similarity score in this system.

(Gruber et al., 2010) In this work the selected features are the speed in x and y direction, pressure variation, and pen inclination angles. The only pre-processing step adopted is mean subtraction. The longest common subsequence (LCSS) matching technique is used to compute the similarity between two signatures. This similarity measure is then used as a kernel function for the SVM. It is interesting noting that the authors also implemented Euclidean Distance and DTW as kernels, but the LCSS presented better results.

(Guru and Prakash, 2009) This method uses a set of 100 global parameter features. Each user template is determined by the average of the features on the reference set plus an interval determined as a function of the standard deviation of these parameters. In a way, this can be viewed as symbolic parameters. The distance between a test signature and a template is simply done by a kind of Hamming distance: if the test parameter lies outside the interval of the template it adds 1 to the distance, otherwise (if it is a match) it does nothing. Therefore no score normalization is needed, since the maximum distance is 100 for all users.

(Houmani, 2011) Two simple verification systems are proposed in this work, one based in a HMM and another based on DTW. On both cases only x and y information are used.

In the first system signatures are modeled by a continuous left-to-right HMM. Each HMM state has a multivariate Gaussian mixture density with diagonal covariance matrix. The number of states is fixed at 6 for all users and each state has 4 Gaussian kernels. The dissimilarity score is computed as the difference between the likelihood of the test signature and the average likelihood of the signatures on the reference set.

The DTW system is similar to the one used in (Canuto, 2010), but in this case the minimum rule is used to select the final dissimilarity score instead of averaging. Furthermore, no penalization based on signature length is adopted.

(Ibrahim et al., 2010) This system is similar to those in (Cpałka et al., 2014; Cpałka and Zalasinski, 2014). Signatures are aligned through a DTW over the velocity profile and then four partitions are generated based on velocity and pressure. Dissimilarities are computed separately for x and y on each partition. Finally, only the most stable partition is used for classification.

(Kholmatov and Yanikoglu, 2005) This method became widely known for being the first placed technique on both test sets of the first signature verification com-

petition (test sets not publicly available). Differences between two consecutive points in x and y ($\Delta x, \Delta y$) are the features chosen for this approach. Signature matching is performed using a DTW with the following recursion:

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

where

$$d(i, j) = \begin{cases} 0 & \text{if } \|x - y\| < \theta \\ \|x - y\| - \theta & \text{otherwise} \end{cases}.$$

Note that it is kept a count of extra points through the addition of γ to the match score at each such point, accounting for the overall speed difference between the two signatures. The test signature is compared to each reference signatures and the resulting values are normalized by three different average distances of the reference set. The resulting three dimensional vector has its dimensionality reduced using PCA and a linear discriminant determines if the signature is genuine or not.

(Nanni and Lumini, 2005) The same 100 global features used in (Guru and Prakash, 2009) are used in this method. Signatures are partitioned into 4 clusters using Fuzzy C-Means to group together signatures with similar parameters. Each user is assigned to the cluster which most of their reference signature belong. For each group, features are ranked according to their capability of discriminating the signers on that cluster. For each signer, 100 Parzen Window Classifiers (PWC) are trained using random sets of the 30 best features of the cluster that the signer belongs to and 100 PWC are trained over the 60 best features of the whole training set. The similarity measure between a test signature and a template is obtained using the max rule.

(Nanni, 2006) Once again the same set of 100 global features is used. 100 PCA descriptors and 100 PWC are trained using 60 randomly chosen features each. The fusion of classifiers of the same type (PCA or PWC) is performed using the max rule. The final similarity scores is obtained using the sum rule.

(Nanni and Lumini, 2008) This method uses y , Δx and azimuth angle as features. Each time function is smoothed and have their first 10 DCT coefficients retained, generating a fixed length feature vector. These DCT values are normalized to zero mean and unit standard deviation and classification is done using a Linear Programming Descriptor (LPD).

(Nanni et al., 2010) This work combines local, regional and global approaches. The global method is the one described in (Nanni, 2006), the regional method is the one described in (Fierrez-Aguilar et al., 2005) and the local method is

the one in (Kholmatov and Yanikoglu, 2005). For the local method, a modified version using a SVM instead of the linear descriptor is implemented and fused with the original method; this fusion by itself already has a good performance (EER 4.96%). This new local method is then combined with the regional and global methods through a weighted sum. The weight assigned to the local method is 6 times greater than those assigned for the other two.

(Pascual-Gaspar et al., 2009) All time functions provided by the tablets (x , y , pressure (p) and inclination angles (az and alt) along with their first derivatives are used in this work. Each feature is normalized to zero mean and unit standard variation. It was found that, for their verification system, the subset $(y, \Delta x, \Delta y, p)$ provided best results. This system uses a simple DTW matching (as described in (Canuto and Lee, 2010)) to compare the test signature to the reference set. The resulting distances are then averaged to give the final dissimilarity score.

(Pascual-Gaspar, 2010) This system is an extension of the one in (Pascual-Gaspar et al., 2009). In this case, the selected feature set is only $(\Delta x, \Delta y)$ and a score normalization procedure is added. The score normalization procedure is user-dependent and takes into account both genuine and random forgeries information. When used on the BioSecure databases, samples from the MCYT database were used as random forgeries.

(Pascual-Gaspar et al., 2011) $(x, y, \Delta x, \Delta y, \Delta p$ and time) is the features set, normalized to zero mean and unit standard deviation in this work. A multi-section Vector Quantization (VQ) is proposed; first signatures are split into N section of equal length and VQ is used to obtain a codebook for each section. This set of N codebooks is used as user template. A distortion measure for each section is computed using the nearest neighbor encoding rule, and the final dissimilarity is computed by the average of these measures.

Even if a multi-section vector quantization method is proposed, best results were obtained using a single section for the MCYT database and 2 sections for the SVC2 database.

(Schimke et al., 2004) The basis for this algorithm is a transformation of handwriting signals into character strings. 22 types of signature events, such as extreme values, gaps and points are defined. This alphabet is then used to parse the signature into a string of events. Dissimilarity measures are computed using the Levenshtein distance (Edit distance), which is a kind of elastic distance for symbolic sequences based on dynamic programming. Further details on the Levenshtein distance can be found in Section 5.3

(Van et al., 2007) This is the reference system used in BioSecure signature verification competitions (BSEC'09 and ESRA'11). Signatures are modeled by a continuous left-to-right HMM. Each HMM state has a multivariate Gaussian

mixture density with diagonal covariance matrix and 4 kernels. The number of states in the HMM is determined as a function of the signatures length, being different for each user. Twenty-five time functions related to the gesture and the shape of the trajectory are used as features. These features are normalized independently for each person to guarantee that their contribution to the emission probability is equally important.

Two scores are used for verification: the first one is related to the likelihood given by the HMM of the claimed identity; the second score is related to the segmentation given by such an HMM. These scores can be used independently or combined using arithmetic mean.

(Yanikoglu and Kholmatov, 2009) Fourier descriptors obtained from each time function (x , y , p , az , alt) are used as features. In order to obtain the same number of descriptors for any two signatures, the shorter signature is padded with zeros prior to the application of the Fourier Transform. These descriptors are normalized and smoothed through averaging of consecutive descriptors. The user template is the average of such descriptors for each dimension. The adopted dissimilarity measure is the Euclidean distance between the test and template feature vectors. This distance is then normalized by a user-specific factor based on the average dissimilarity amongst the signatures on the reference set.

This paper also proposes a fusion of these normalized scores with those issued from the DTW-based system in (Kholmatov and Yanikoglu, 2005) using a simple sum rule.

3.8 Conclusion

A broad study of online signature verification system was presented. Approaches adopted in signature verification were analyzed for each of the main components of a biometric system: data acquisition, preprocessing, feature extraction, classification and database design (as described in Chapter 1). This analysis provides the basis for understanding the evaluations and applications proposed in Chapters 4 and 5. The DTW, described in Section 3.5 is the distance measure adopted for the verification experiments in Chapter 4.

Following this study, the dynamic signatures databases adopted in this thesis are described and performances of state-of-the-art verification systems for each of them are provided. A brief description of each of these systems is also given. These results will be particularly interesting for comparison with the verification results in Chapter 5.

This chapter ends the first part of this thesis, where the basis for the studies developed on the second part are laid. On the next chapter, the main objective of this thesis is developed: an original online signature model based on the Minimum Jerk principle.

Part II

Developed Methods

Minimum Jerk Representation of Online Signatures

4.1 Introduction

Handwritten signatures result from voluntary but typically complex gestures of the human hand. As result of their particularities, in most cultures, these graphically recorded gestures have been used for centuries as means to identity verification. Some less straightforward uses of handwritten signatures analysis may even include neuromuscular disorders detection or daily stress measurement (Caligiuri et al., 2006; O'Reilly and Plamondon, 2012).

Beyond potential applications, modeling gestures behind signatures and developing proper ways for representation of their basic components (i.e., segments) is a challenging enough matter for scientific research. In addition, signature segmentation is a crucial step that strongly influences the performance of signature verification systems and, therefore, a special attention has been drawn into this task over the last few decades (Impedovo and Pirlo, 2008).

Furthermore, the problem of signal segmentation appears in many practical research areas including speech processing, image processing, biomedical and communication applications (Gustafsson, 2000). The observed signal may be composed of several segments, where the number of segments and the transition times are unknown. Several works deal with the problem of determining these unknown parameters as well as a representation for each segment (Djuric, 1994; Han et al., 2004; Fearnhead, 2005; Amar et al., 2014).

In this chapter, we aim at providing new application independent signature representation and segmentation methods, based on psychophysiological evidences that led to the development of the well-known Minimum Jerk principle for movement planning. We focus on dynamic signatures, which are represented as a time series of pen-tip position coordinates acquired through the use of specific recording devices, such as digitizing tablets and smartphones.

Even if signature segmentation is the focus of this work, the proposed technique may be applied to any kind of signal. However, the use of the Minimum Jerk criterion might not be justifiable on other applications, since this criterion is aimed at human movements modeling.

This chapter is structured as follows: in Section 4.2 we give a brief review on the Minimum Jerk model. Section 4.3 presents the proposed approach for signature representation along with an evaluation in terms of reconstruction error, verification performance, residual analysis, compression, and stability. Section 4.4 provides some potential applications of the method, such as signature quality evaluation.

4.2 The Minimum Jerk Model

As stated in Chapter 2, this model is based on the optimal control theory and uses a kinematic criterion to establish which path the central nervous system (CNS) chooses amongst the several possible paths to move the end effector from one point to another.

Human movements present the fundamental feature of being smooth. Therefore, generating as little trembling at the end effector level as possible could be one of the objectives of the CNS in order to gain precision and protect articulations and tendons (Hogan, 1984; Flash and Hogan, 1985). A family of cost functions is proposed to explain this smooth aspect of the movement on the (x, y) plane:

$$C_n = \frac{1}{2} \int_0^T \left(\frac{d^n x}{dt^n} \right)^2 + \left(\frac{d^n y}{dt^n} \right)^2 dt. \quad (4.1)$$

In (Richardson and Flash, 2002) this family of optimality criteria were studied up to $n = 10$, and the authors concluded that the case $n = 3$ seems to be the most appropriate for human movements modeling, corresponding to the Minimum Jerk (MJ). As most works on human movement control, the quality of the representation was accessed through the study of the velocity profiles provided by the model (see Chapter 2). In addition, using a single scalar projection given by the ratio between the maximum and average velocity to characterize velocity profiles it was also found that the MJ is the best suited criterion. Experimental evidences showed that this ratio is about 1.8 (with 10% standard deviation) for point-to-point movements in healthy adults while movement predicted using the MJ model yields a ratio of 1.875.

The family of optimality criteria given by Equation 4.1 has as general solution polynomials of order $2n - 1$ (see Chapter 2), therefore the Minimum Jerk path ($n = 3$) follows a fifth order polynomial:

$$\begin{cases} x_t = a_0 + a_1 t + a_2 t^2 + a_3 t^3 + a_4 t^4 + a_5 t^5 \\ y_t = b_0 + b_1 t + b_2 t^2 + b_3 t^3 + b_4 t^4 + b_5 t^5 \end{cases}. \quad (4.2)$$

Several works (Feng et al., 2002; Berret, 2008; Djioua and Plamondon, 2010) point out that the paths predicted by this model are always straight lines with bell-shaped symmetric velocity profiles. However, this is only true if velocity and acceleration at both the beginning and the end of the movement are null. For such strong constraints,

the path on the (x, y) plane for a movement starting in (x_0, y_0) and ending in (x_T, y_T) with a total duration T is given by

$$\begin{cases} x(\tau) = x_0 + (x_T - x_0) (10\tau^3 - 15\tau^4 + 6\tau^5) \\ y(\tau) = y_0 + (y_T - y_0) (10\tau^3 - 15\tau^4 + 6\tau^5) \end{cases},$$

where $\tau = t/T$.

On the other hand, the only constraint imposed by the model itself is the minimization of the jerk. Forcing velocities and accelerations to be null is not the only option for determining the unknown parameters a_i and b_j . Since these are the parameters of a fifth order polynomial, any six points of the trajectory could be used to determine a unique path that respects the minimum jerk condition. Furthermore, if more than six points are known, a curve fitting method can be used to find the best path (*i.e.* the one that minimizes the jerk) for the whole set of points. Note that without the null dynamics constraints, non-straight paths with various velocity profiles can be obtained.

Another criticism of the Minimum Jerk model is that it is only capable of providing the trajectory of the end effector and not the angular displacements of the joints of a multi-articulated arm, which might be a problem in some movement planning scenarios (Berret, 2008). It is important noting that for our target application (*i.e.* representing signatures), gestures have already been performed and we seek a suitable representation for the recorded movements of the end effector.

Despite these criticisms, this is the most commonly used method for movement planning in the literature due to its effectiveness on the determination of natural trajectories for the end effector, requiring very little computational efforts, compared to other methods. This approach has been used in applications ranging from robotics (Pattacini et al., 2010) to human physical rehabilitation (Amirabdollahian et al., 2002) and is widely accepted as a good approximation for movements that occur on the horizontal plane where the gravity force can be disregarded (Berret, 2008).

4.3 Proposed Method

As previously stated (Section 3.3), many works deal with the problem of signature segmentation and their approaches can be divided in four categories according to which principle they are based on: pen-up/pen-down signals, velocity analysis, perceptual relevant points, and dynamic time warping (Impedovo and Pirlo, 2008).

For online signatures, a common and very straightforward segmentation technique uses pressure (or contact) information for determining writing units, which are defined as the written part between a pen-down (*i.e.* pen touches the surface) and a pen-up (*i.e.* pen leaves the surface) movement (Dimauro et al., 1994).

Segmentation techniques based on velocity analysis use different approaches, ranging from simple detection of null velocity (Dolfing et al., 1998) to curvilinear velocity

signals. The stroke identification step present in the Sigma-Lognormal model (Plamondon et al., 2014) can also be placed on such category.

A different class of segmentation methods rely on the detection of perceptually important points. The importance of a point is determined by the rate of change of the writing angle around it. We can also include in this category techniques based on the detection of geometric extremes (Lee et al., 2004b).

In order to allow the segmentation of many signatures into the same number of segments, dynamic time warping (DTW) has been widely used (Rhee et al., 2001). In addition, Combinations of different techniques can also be found in the literature, for instance in Qu et al. (2004) a combination of pressure, velocity and angle change is used for segmentation.

Notice that each of the techniques previously mentioned use a different definition of segment (or stroke) based on arbitrary choices that are usually not linked to any human movement control theory, such as the use of pen-ups/down as segmentation points. An exception to this is the Sigma-Lognormal model (Plamondon et al., 2014), which is based on the observation that velocity profiles on human reaching movements resemble lognormal curves.

The MJ model states that the path chosen by the CNS when performing point-to-point movements is given by a fifth order polynomial (Equation 4.2); however, it is clear that such simple equation is not sufficient to describe a too complex trajectory, such as that of most signatures. In this work we propose a signature representation method that can also be seen as a segmentation technique. Taking into consideration the Minimum Jerk principle and its success on a wide range of scenarios, we propose a new definition for a stroke.

Definition. *Stroke is the longest trajectory segment of an online signature that complies with the Minimum Jerk model.*

In other words, it is a segment of the signature that can be satisfactorily represented by a fifth order polynomial.

Based on this definition and assuming that a signature is a sequence of strokes, we propose a representation in which the signature is modeled by a sequence of polynomials. More formally, for a signature $S(t) = (x_t, y_t)$ where t is the time instant at which samples were acquired and range from 0 to T , assume it was found a set of n pairs (one for each coordinate) of polynomial segments $P_i(t)$, with breakpoints between segments at instants T_i , $i = 1, \dots, n$ and $T_n = T$. Therefore, the proposed model $\hat{S}(t)$ for signature $S(t)$ is defined as:

$$\hat{S}(t) = \begin{cases} P_1(t) & \text{for } t = 0, \dots, T_1 \\ P_2(t) & \text{for } t = T_1, \dots, T_2 \\ \vdots & \\ P_n(t) & \text{for } t = T_{n-1}, \dots, T_n \end{cases}. \quad (4.3)$$

Finding the longest Minimum Jerk segments requires a double optimization; first it is needed to determine how many segments there are and secondly which portions of the signature each segment represents. One could start with a single segment and increment this number one by one, performing an exhaustive search for the best breakpoints at each step. It is easy to see that this is a computationally intense procedure and impractical on a real application since an unacceptable time might be needed to segment some signatures.

To ease the computational burden, we propose an iterative algorithm that yields a piecewise polynomial representation of the trajectory. For a given signature $S(t)$ with total duration T , let x, y be the arrays of coordinates values sampled at time instants τ . The iterative segmentation/representation procedure is defined in Algorithm 1.

Algorithm 1 Minimum Jerk Signature Representation

```

1: procedure SEGMENT( $x, y, \tau, q$ )
2:   Create an empty list of breakpoints  $T$ 
3:   Create an empty list of  $x$  coefficients  $X_c$ 
4:   Create an empty list of  $y$  coefficients  $Y_c$ 
5:   Normalize  $x$  and  $y$  values to the  $(0, 1)$  interval
6:    $i \leftarrow 0$ 
7:    $L \leftarrow 1$ 
8:    $R \leftarrow L + 5$ 
9:    $i \leftarrow i + 1$ 
10:   $x_{fit} \leftarrow x[L, \dots, R] - x[L]$ 
11:   $y_{fit} \leftarrow y[L, \dots, R] - y[L]$ 
12:   $\tau_{fit} \leftarrow \tau[L, \dots, R] - \tau[L]$ 
13:   $X_c[i] \leftarrow$  fit a  $5^{th}$  order polynomial to  $(\tau_{fit}, x_{fit})$ 
14:   $Y_c[i] \leftarrow$  fit a  $5^{th}$  order polynomial to  $(\tau_{fit}, y_{fit})$ 
15:   $T[i] \leftarrow \tau[R]$ 
16:  Compute the fit quality,  $Q$ 
17:  if  $Q > q$  then
18:     $R \leftarrow R + 1$ 
19:    if  $\tau(R) > T$  then
20:      go to 28
21:    else
22:      go to 10
23:    end if
24:  else
25:     $L \leftarrow R$ 
26:    go to 8
27:  end if
28:  return  $T, X_c$  and  $Y_c$ 
29: end procedure

```

The T list contains the timestamp at which segments end, and X_c and Y_c contain the polynomial coefficients that represent the coordinates x and y respectively, for each segment.

We now present a more detailed view of each part of the algorithm. Lines 2 to 4 set up the lists that will contain the representation and segmentation of the signature. Line 5 is a preprocessing step that can be omitted depending on the quality criterion Q adopted. This normalization consists in fitting the signature to a rectangle where the longest size has unit length, but without changing the proportions between x and y (both coordinates are scaled by the same factor).

The L pointer indicates the start of a segment and the R pointer the end; notice that the end pointer starts at $L + 5$ since it is known that a fifth order polynomial can perfectly fit 6 points, without error. Step 9 creates a new entry on the lists that will hold the parameters of the current segment.

Steps 10 through 12 determine the set of points that will be used to find the polynomial fit, notice that both coordinates and time are set to start at 0 through the subtraction of the first elements. Therefore we consider that each segment starts at the origin of the Cartesian plane. Due to this condition the first (independent) coefficient of the polynomials will be always null.

In steps 13 and 14 the polynomial fitting of segment points is performed. We chose to use a simple Least Squares procedure with the added constraint that the polynomial must start and finish on the extreme points of the segment. This constrained fitting procedure can be performed for x and y simultaneously with the following matrix operations. Let \mathbf{t} be a column vector with n timestamps, \mathbf{X} be a $n \times 2$ coordinates matrix:

$$\mathbf{t} = \begin{bmatrix} t_1 \\ \vdots \\ t_n \end{bmatrix}, \quad \mathbf{X} = \begin{bmatrix} x_1 & y_1 \\ \vdots & \vdots \\ x_n & y_n \end{bmatrix}.$$

Define the $n \times 6$ matrix of regressors $\mathbf{T} = [\mathbf{t}^0, \mathbf{t}^1, \mathbf{t}^2, \mathbf{t}^3, \mathbf{t}^4, \mathbf{t}^5]$ and the constraints matrices \mathbf{Tc} (2×6) and \mathbf{Xc} (2×2).

$$\mathbf{Tc} = \begin{bmatrix} 1 & t_1 & t_1^2 & t_1^3 & t_1^4 & t_1^5 \\ 1 & t_n & t_n^2 & t_n^3 & t_n^4 & t_n^5 \end{bmatrix}, \quad \mathbf{Xc} = \begin{bmatrix} x_1 & y_1 \\ x_n & y_n \end{bmatrix}.$$

The polynomial coefficients are then given by

$$\mathbf{P} = (\mathbf{T}^T \mathbf{T})^{-1} (\mathbf{T}^T \mathbf{X} - \mathbf{Tc}^T \boldsymbol{\lambda}), \quad (4.4)$$

where the T superscript indicates matrix transposition and $\boldsymbol{\lambda}$ is a 2×2 lagrangian multipliers matrix given by

$$\boldsymbol{\lambda} = (\mathbf{Tc}(\mathbf{T}^T \mathbf{T})^{-1} \mathbf{Tc}^T)^{-1} (\mathbf{Tc}(\mathbf{T}^T \mathbf{T})^{-1} \mathbf{T}^T \mathbf{X} - \mathbf{Xc}).$$

Each column of the 6×2 \mathbf{P} matrix contains the coefficients for one coordinate (x and y).

Given the polynomial coefficients, the approximated curves \hat{x} and \hat{y} are given by **TP**. With the predicted values, we pass to the next step of the algorithm, which is determining the fitting quality parameter Q that specifies if the approximation is acceptable or not. The most straightforward method would be to compute the mean squared error (MSE). Notice, however, that the MSE would be dependent on the scale of the signature, this is why the preprocessing step (5) might be needed.

Other works that deal with human movement modeling use the velocity signal to noise ratio (SNR_v) as a reconstruction quality parameter (Richardson and Flash, 2002; O'Reilly and Plamondon, 2009; Galbally et al., 2012; Plamondon et al., 2014), and this is the same measure we chose to use on our implementation. These works state that a 15 dB SNR_v is good enough for human movement modeling purposes. The velocity signal to noise ratio gives a measurement of the quality of the reproduction of the original velocity profile and is defined as:

$$SNR_v = 10 \log_{10} \left(\frac{\int_0^T v_x(t)^2 + v_y(t)^2 dt}{\int_0^T [v_x(t) - v_{\hat{x}}(t)]^2 + [v_y(t) - v_{\hat{y}}(t)]^2 dt} \right), \quad (4.5)$$

where $v_x(t)$ and $v_y(t)$ are respectively the horizontal and vertical velocities on the original signal and $v_{\hat{x}}(t)$ and $v_{\hat{y}}(t)$ are the horizontal and vertical velocities on the reconstructed signal, respectively. These velocities signals can be estimated from the coordinate and time signals.

Using the chosen fit quality criterion (*e.g.* SNR_v) and a given quality threshold q the algorithms tests the acceptability of the approximation. If the polynomial approximation is acceptable, the length of the segment is increased by adding the next point. If all points in the original signature have already been parsed the segment lists are returned, otherwise the fitting is calculated again including the next point. If the approximation is not acceptable, a new segment starts where the previous one has stopped.

Following this procedure, it was possible to successfully find representations for all signatures on the five databases described in Section 3.7.1. Notice that the 15 dB SNR_v criterion proposed in (O'Reilly and Plamondon, 2009; Galbally et al., 2012; Plamondon et al., 2014) is supposed to be evaluated on the whole signature but we evaluate it segment by segment, which ensures that the SNR_v obtained for the whole signature will be at least 15 dB. It was decided to lower the SNR_v requirement to 14 dB for each segment and finally SNR_v values ranging from 14.7 dB to 21.2 dB were obtained for whole signatures.

Notice that all signature segments found through the procedure in Algorithm 1 start at the origin of the Cartesian plane; therefore, in order to rebuild the whole signature from the reconstructed segments, one just needs to add the x and y coordinates of the last point in the previous segment to the coordinates of the current segment. Consequently, reconstruction also needs to be iterative.

For the original DS3 database, without preprocessing (see Section 3.7.1), it was also possible to obtain a MJ representation. However, due to the severe discontinuities caused by the presence of artificial points at the origin each time there is a pen-up/pen-down movement, the segmentation algorithm was forced to use only 6 points (*i.e.* the minimum number of points required to determine the 5th order polynomial coefficients) for most of the segments. Therefore we will consider only the results on the preprocessed DS3-I database, which removes all such artificial points and consider only actual signature trajectory coordinates.

Finally, we would like to remark that even if this algorithm is aimed at signature modeling it can be applied to any other application that requires signal segmentation. The proposed segmentation algorithm can be easily modified to use segment primitives other than a fifth order polynomial. As a matter of fact, only the fitting procedure and the associated quality measure need to be changed. The iterative procedure can still be used to automatically determine the number of segments and the transition times.

On the following subsections the obtained representations are evaluated in terms of reconstruction error, verification performance, residual analysis, compression, stability, and finally, some comparisons to other signature modeling approaches.

4.3.1 Reconstruction Error

The reconstruction error is the most common method for evaluating the quality of a model; however, as one can notice in the proposed algorithm, reconstruction error is a parameter of our model. This means that any reconstruction error can be achieved yielding different segmentations.

The question that remains is: which reconstruction error should be adopted? As it was previously stated, some works propose that 15 dB SNR_v is adequate for human movement analysis but give no reason for this threshold. We give a possible answer to this question on the residual analysis section.

In Figure 4.1 we provide different reconstructions of the same signature at different SNR_v levels. It is possible to notice that at 15 dB, an almost perfect reconstruction is obtained, giving a hint to why this threshold was chosen by other researchers.

4.3.2 Verification Performance

Another way to verify if there is a loss of information after representation is performing verification experiments. The idea consists in, using the same verification approach, observing the differences obtained on the verification performance using the original data or the reconstructed data.

Since we want to evaluate a trajectory model, we decided to use only x and y information for verification. Therefore, the chosen approach was DTW-based, as the ones in (Canuto, 2010; Houmani, 2011), because DTW approaches usually perform better on systems that rely only on coordinates information for verification (see Section 3.7).

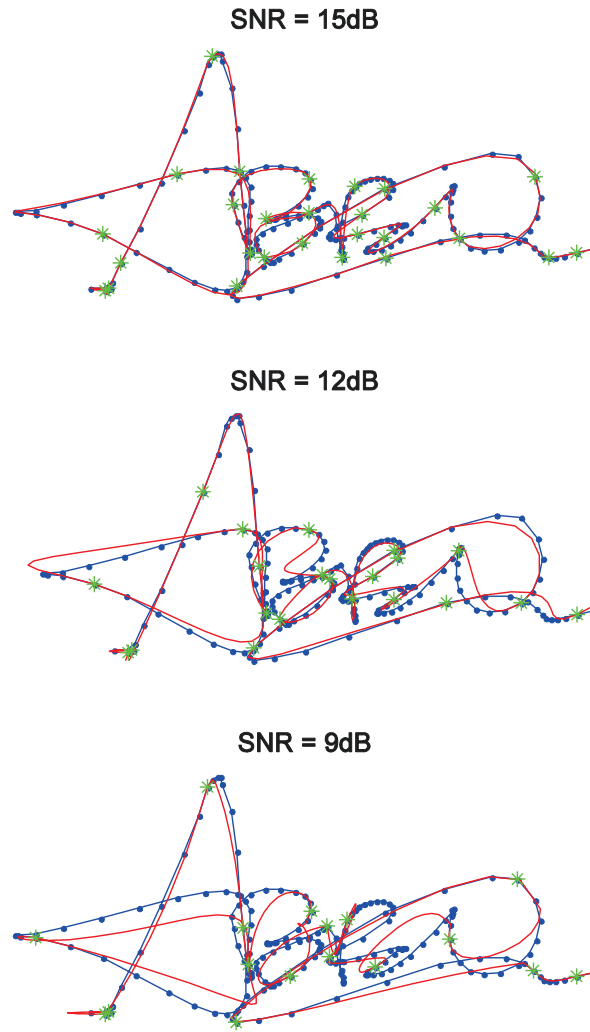


Figure 4.1: Reconstruction (red line) of the same signature (blue line) at different SNR levels.

The chosen DTW implementation uses the Euclidean distance as cost function and unitary weights (see Section 3.5), therefore the DTW distance, $D(M, N)$ between two time series $R = r_1, r_2, \dots, r_M$ and $T = t_1, t_2, \dots, t_N$ is computed through the recursion

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

where $d(i, j)$ is the euclidean distance between the i^{th} reference point and the j^{th} test point, and $D(0, 0) = 0$.

For a given test sample, a DTW distance is computed to each signature of the reference set and the minimum distance is used as dissimilarity score. The verification protocol is as follows: 5 genuine signatures are chosen as reference for each user and genuine scores are obtained from the remaining genuine signatures while impostor scores are computed only in reference to skilled forgeries.

N random samplings with replacement of 5 reference signature are performed. For each sampling k the verification step is performed and an EER_k is computed. This allows to give an idea of the order of magnitude of the measured EER. For the experiments in this thesis $N = 1000$ random samplings were evaluated. Signatures were represented with a quality threshold of 14 dB SNR_v per segment and rebuilt with the same sampling rate as the original ones. EER results are presented as the average of the EERs obtained over the N random samplings and the standard deviation of these EERs.

In Table 4.1 we present the obtained average EERs and respective standard deviations for each database before and after reconstruction for an SNR_v of 14 dB per segment. Notice that the DS3 database figures in this table to show that even if the artificial points added at the pen-up/pen-down pose a problem to signature representation (see Section 3.7.1), they actually help in the verification. These points indirectly add information regarding pen contact to the coordinates time series.

Notice that reconstructed signals usually present an EER that is slightly higher than using the original signals, however, when standard deviations are considered, a significant overlap between the area 1 standard deviation around the average EER before and after reconstruction. Therefore we can conclude that almost no relevant information (regarding the specific task of biometric verification) is lost when modeling signatures at 14 dB SNR_v per segment.

4.3.3 Residual Analysis

Another criterion that can be taken into account for the determination of the thresholds comes from the fact that a good estimator should yield a residue that is a white noise (Donoho, 1981). In other words, everything that can be deterministically modeled should be taken into account by the estimator, while only the random white (unpredictable) errors are left.

Table 4.1: Verification Performance (average EER in %) and standard deviation values (in parenthesis) for each database before and after reconstruction with a SNR_v of 14 dB per segment.

	Original	Reconstructed
MCYT	05.64 (0.31)	05.93 (0.35)
DS2	05.91 (0.38)	06.46 (0.41)
SVC1	12.68 (1.34)	13.07 (1.44)
SVC2	13.24 (0.94)	13.32 (1.00)
DS3	12.11 (0.66)	12.13 (0.78)
DS3-I	17.40 (1.36)	17.39 (1.27)

A simple way for testing for white noise is considering the sample autocorrelation defined for a signal $x_t = x_1, x_2, \dots, x_N$ as:

$$\rho_x(\tau) = \frac{\sum_{i=\tau+1}^N [(x_i - \mu_x)(x_{i-\tau} - \mu_x)]}{\sum_{i=1}^N (x_i - \mu_x)^2},$$

where μ_x is the average of x_t and τ is the lag. In other words it is the correlation between the original signal and a delayed version of itself. Given the severe sample limitation (some signature are only a few tenths of points long), only unitary lag, $\rho_x(1)$, is considered. This means that we are testing if the error follows a first order autoregression, as in the Durbin-Watson statistic (Papoulis and Pillai, 2002).

The autocorrelation sequence is normalized in such way that the zero-lag autocorrelation, $\rho_x(0)$, is 1. We use as a measure of “whiteness” the quantity $W = \rho_x(0)/\rho_x(1)$, with $\rho_x(1) \neq 0$, which becomes $W = 1/\rho_x(1)$ after normalization. The higher the value obtained, the whiter the noise is. This procedure was performed separately for x and y coordinates, yielding W_x and W_y , that were averaged to obtain a single whiteness measure $W = (W_x + W_y)/2$. In Figure 4.2, it is shown the W measure as a function of SNR_v for the whole signature. Notice that we have a noticeable rupture on the curvature around the 15 dB value ($W = 1.075$). This observation could be a hint that we need to have at least 15 dB SNR_v (for the whole signature) in order to obtain a reasonably good estimator.

4.3.4 Compression

An important aspect of the proposed model is that it gives a compressed representation of the signature. As stated before, this method represents a signature as a

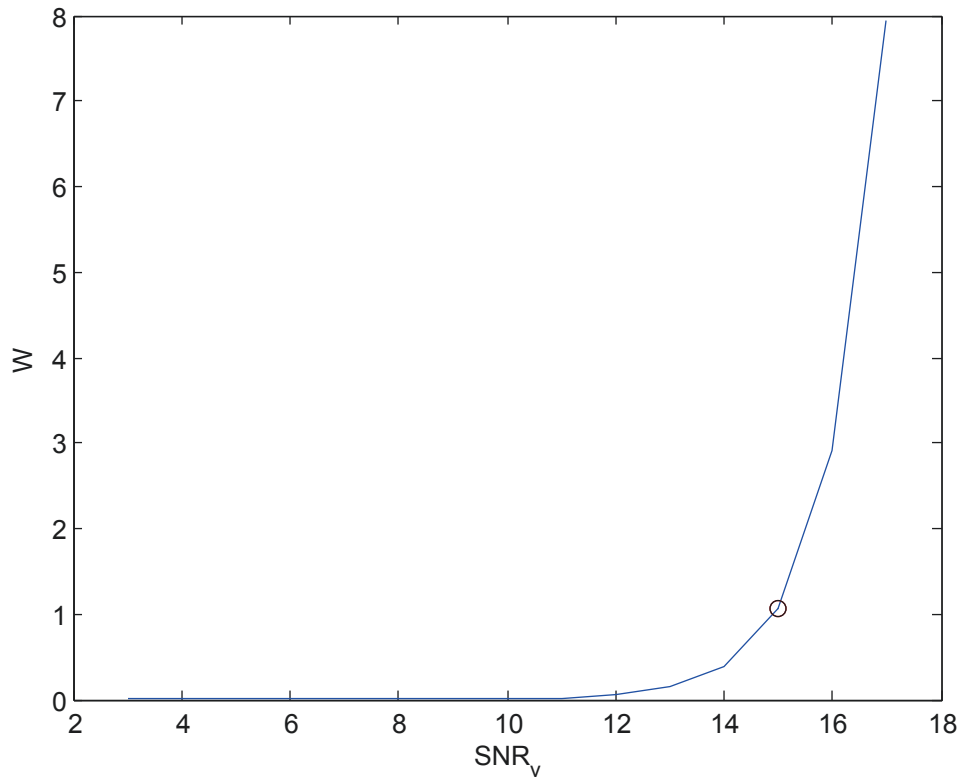


Figure 4.2: Reconstruction (red line) of the same signature (blue line) at different SNR levels.

series of 5th order polynomials. Therefore for each segment we only need to store 10 coefficients, 5 for each coordinate since the first coefficient is always null, and its length. As a result, the fewer the number of polynomials needed to model a signature, the more parsimonious is its representation. We define the compression rate as

$$CR = \frac{S_0 - S_M}{S_0},$$

where S_0 is the number of bytes in the original signature and S_M is the number of bytes needed to represent the signature after modeling, it is considered that 2 bytes are needed to encode each number.

Another important question, besides which reconstruction error should be used is the following: Is the Minimum Jerk the best criterion amongst the family of cost functions defined by C_n ? To answer this question we modified the segmentation algorithm to use the different criteria defined by C_n (Equation 4.1).

In Figure 4.3 we present several reconstruction errors as a function of the compression rate for n ranging from 1 to 5. These values consider signatures from all databases. For a SNR of 15 dB all of the higher order ($n \geq 3$) solutions attain the same compression rate of 73.3%. Notice that the MJ acts as a limit to the compression-quality trade-off. Therefore, according to this criterion, we could consider the MJ to be the most suited criterion for signature representation amongst this family of cost functions C_n , as it was found in (Richardson and Flash, 2002) for human reaching movements.

At this point we would like to note a few differences among the test databases. Signatures collected continuously at a constant sampling rate, such as those in DS2 and MCYT, do not need to keep a record of the timestamps, since the index of the sample already determines the sampling time. On the other hand, signatures with sampling discontinuities such as the SVC1, SVC2 and DS3-I databases need to keep a record not only of the coordinates but the time instant at which they were sampled. Therefore, even if discontinuous sampling might yield less sampling points, it might require more storage space. Generally speaking, for n samples signature, $2n$ numbers are stored to represent the trajectory with continuous sampling and $3n$ numbers are needed when discontinuous sampling is used. However, if the sampling rate is constant between discontinuities, the required storage can be optimized to $2n + d$, where d is the number of discontinuities. In Figure 4.4, the quality-compression tradeoff curves for each database using the MJ criterion are presented.

When only the storage space for coordinates is considered, databases using continuous sampling present a better compression rate (78.1%) than signatures that do not record in-air movements (68.4%). This later category, in addition to having less points, presents discontinuities that can force the proposed algorithm to segment the signature before the quality threshold is reached. In Figure 4.5 is presented the x and y coordinates for a signature on the SVC1 database along with its segmentation points. Notice how several of the discontinuities became segmentation points.

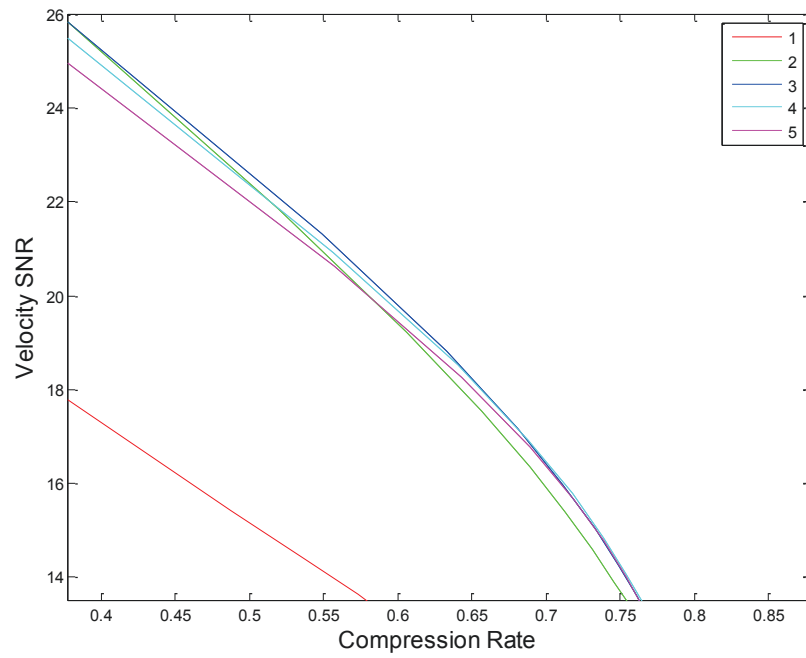


Figure 4.3: Representation quality and compression rate tradeoff for minimum velocity ($n = 1$), acceleration ($n = 2$), jerk ($n = 3$), snap ($n = 4$) and crackle ($n = 5$).

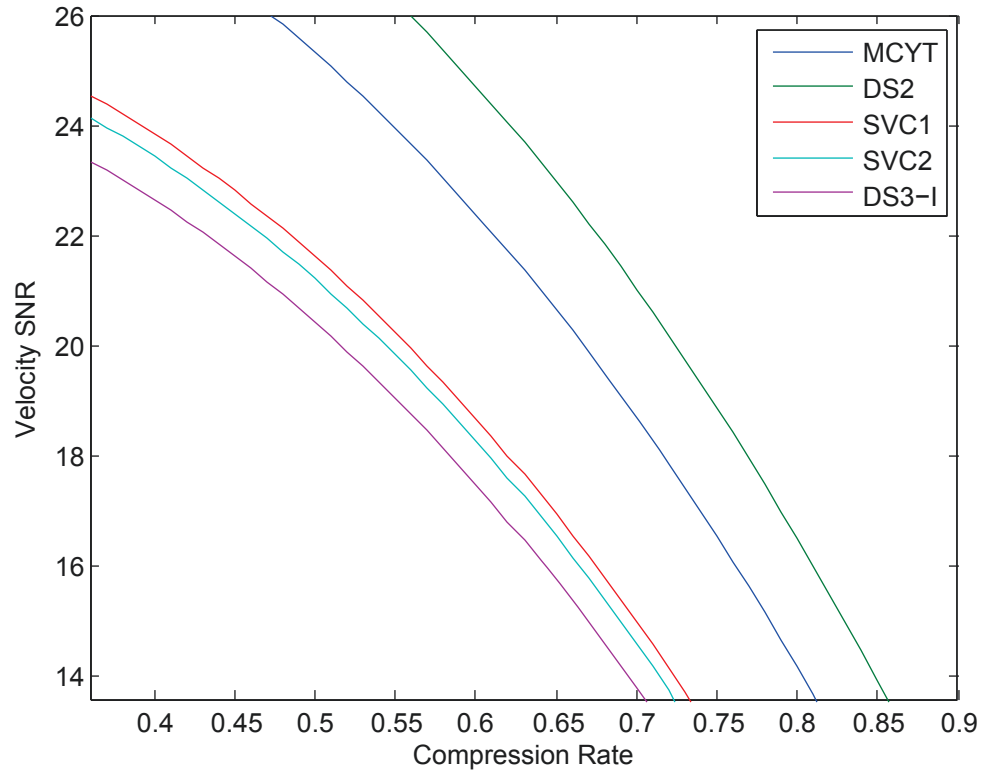


Figure 4.4: Representation quality and compression rate tradeoff for each database using the Minimum Jerk criterion.

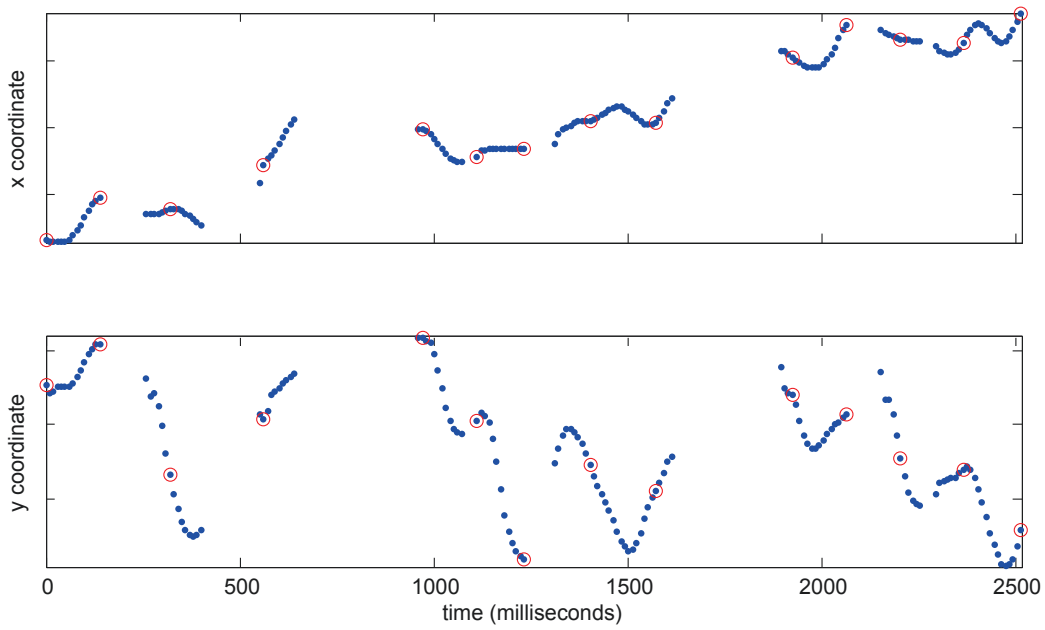


Figure 4.5: x and y coordinates for a signature on the SVC1 database. Segmentation points are circled in red.

Furthermore, it is interesting noting that forgeries present a compression rate about 4.2% higher than their genuine counterparts on all databases. This is an expected behavior, since forgeries are usually performed on a slower pace than genuine signatures they generate more points for the same trajectory. Therefore, more points of the recorded movements are represented by each polynomial.

As a last remark, it was previously stated that the original DS3 database, without preprocessing (see Section 3.7.1) does not yield a good representation because of the artificial discontinuities caused by the points inserted at the origin on pen-ups/down. This compression analysis allows for the observation of this fact. At 15 dB SNR_v the DS3-I database behaves just as the other test databases, however without the preprocessing (removal of the additional points), the compression rate is only of 10.2%. Notice that even if each segment has only 6 points of the original signature (the minimum number of points to uniquely determine a 5th order polynomial, a compression rate of 8.3% is achieved.

4.3.5 Stability

In this section, user stability is defined by the number of polynomials used to describe each of their signatures. Since this number is clearly related to the length of the trajectory, a normalized measure is needed in order to compute the average for all signers in a database. Therefore, it was chosen to use the standard variation of the compression rate, which is already normalized by the length of each signature, in order to evaluate the stability of the number of polynomials found for each user. For these tests only modeling using the MJ (5th order polynomials) at 15 dB SNR_v is considered. It is worth noting that the standard deviations are computed for each signer and then averaged for the whole database.

Once again, signatures on the DS2 and MCYT databases behaved better (lower variability, in this case) than signatures with sampling discontinuities. This is due to the same reason that was previously explained: discontinuities sometimes force the iterative algorithm to create a premature segment, since it can not find a smooth path that includes the discontinuity. Therefore, variations on the occurrence of pen-up/pen-down movements strongly affect the resulting number of segments. In Table 4.2 we present a summary of the average compression rate and standard deviation for each test database.

Notice that a variation coefficient (standard deviation normalized by the mean) around 5% is much lower than the usual variability in the length of a signature, which is consistently around 10% for all databases.

Another criterion related to the stability was investigated; namely, the quality of the representation given by the iterative procedure as related to a global optimization (exhaustive search). Since this is a very intensive computation, tests were performed only over a small subset of 50 signatures, 5 genuine and 5 forgeries from each database. The exhaustive search works as previously described: the number of

Table 4.2: Average compression rate and standard deviation (in parentheses) for each database.

	Genuine	Forgery
MCYT	0.75 (0.03)	0.77 (0.06)
DS2	0.83 (0.02)	0.88 (0.04)
SVC1	0.69 (0.04)	0.73 (0.06)
SVC2	0.69 (0.05)	0.74 (0.05)
DS3-I	0.67 (0.04)	0.70 (0.05)

segments is incremented one by one and, at each iteration, the best distribution of these n segments over the signature is searched, maximizing the SNR_v . The optimum number of segments was defined as the minimum number that yielded a 15 dB SNR_v for the whole signature.

Only 2 signatures had an optimum number of segments different from the number found through the proposed iterative procedure (one from the DS2 dataset and one from the MCYT dataset, both forgeries). However, the difference was only 1 segment less found through exhaustive search. Amongst the other 48 signatures, the distance between the breakpoints found through the iterative procedure and the exhaustive search were compared. 40% of the breakpoints were different, but none of them were more than 5 positions apart. This experiment indicates that the iterative procedure is indeed a good alternative to the exhaustive search.

4.3.6 Relationship to Other Methods

In the literature, two main works can be directly related to the method proposed in this thesis. First, the Sigma-Lognormal model (Plamondon et al., 2014) which is, to the author’s knowledge, the only signature modeling technique based on human movement analysis. This work, based on the kinematic theory of Rapid Human Movement (Plamondon, 1995a,b, 1998; Plamondon et al., 2003) uses log-normal impulse responses to describe the synergistic action of neuromuscular networks.

The sigma-lognormal representation technique is closely related to this work. Instead of fitting fifth order polynomials to the trajectories, or equivalently fourth order polynomials to the velocities, this approach fits lognormal curves to the velocity profiles. However, instead of providing a segmentation that is directly related to the kinematic model itself, the stroke identification step involves the detection of characteristic points on the velocity signals (local maxima, local minima, and inflexion points). Furthermore, optimization of the Sigma-lognormal parameters can be very

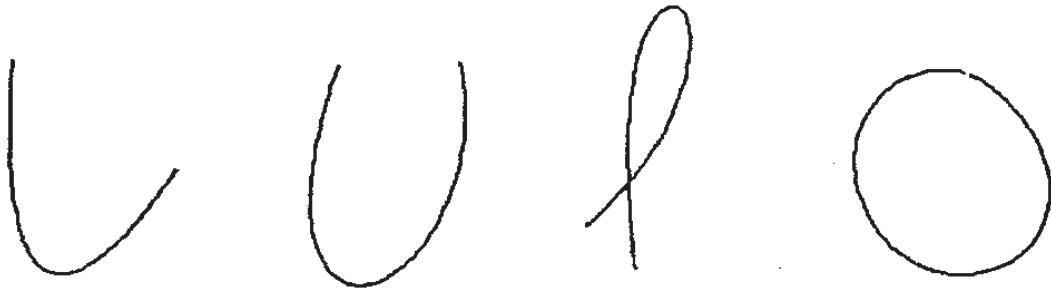


Figure 4.6: The four basic strokes in (Edelman and Flash, 1987): hook, cup, inverted gamma and oval.

computational intensive, since it involves three separate optimization steps.

Another difference between the Sigma-lognormal model and the MJ representation is the number of strokes identified for each signature. The number of lognormal strokes is closely related to the total of local maxima in x and y velocities. Meanwhile, the MJ model can absorb more variations and provides a number of strokes that is about 3.3 times smaller than those of the Sigma-lognormal representation. The stroke identification step on the Sigma-Lognormal model uses one lognormal for each maximum of the velocity profile.

A second representation approach that is closely related to the present work is the one proposed in (Edelman and Flash, 1987). This work deals with western cursive handwriting modeling, instead of signatures, through the concatenation of strokes that are constructed through the Minimum Jerk model. Two main differences must be identified between their method and ours.

First, only four stroke shapes that can be scaled are allowed: a hook, a cup, an inverted gamma, and an oval, as shown in Figure 4.6. The letter ‘a’, for instance, is a concatenation of an oval and a hook. Secondly, in order to create the strokes shapes, null velocities and accelerations are supposed on the extremes of the movement and a via-point is added approximately in the middle of the planned trajectory, these via-points determine the curvature of the stroke. This model offers an excellent fit for cursive letters, provided that, beforehand, the handwritten trajectory is segmented into successive strokes. This simple method works for western cursive writing but can not be directly applied to more complex trajectories such as those of signatures.

Therefore, the main disadvantages of this model are the use of arbitrarily defined via-points and simple stroke shapes in order to create complex trajectories and the need of a previous segmentation step. The method propose in Section 4.3 is capable of solving both of these issues in a joint manner.

Finally, it is interesting pointing out a recent work that is not related to signa-

ture or handwriting representation. The recently published¹ segmentation method proposed in (Amar et al., 2014) also uses a constrained piecewise polynomial segmentation. This work supposes that each segment of the original signal is a polynomial function of known order in the presence of additive Gaussian noise with known variance. These *a priori* information are used to help in the optimization of the number of segments and their transition times. In addition, the maximum number of segments also need to be arbitrarily set. The algorithm proposed in this chapter, on the other hand, is capable of determining all these parameters automatically based only on the representation quality measure adopted.

4.4 Applications of the Minimum Jerk Representation

In this section three additional applications of the proposed model, besides segmentation and compression, are proposed: signature resampling, signature quality evaluation and synthetic signatures generation.

4.4.1 Signature Resampling

A straightforward application of the proposed representation is signature resampling. Several verification methods perform some kind of resampling, either downsampling or upsampling in order to obtain signature samples of the same size (Plamondon, 1994; Impedovo and Pirlo, 2008). Using the polynomial segments it is possible to perform such operations easily while keeping the dynamic properties of the original signal. One just needs to determine the desired number of points when reconstructing each segment using the polynomial equations. Even variable sampling is allowed as long as the extremities of the segments are kept, this is a requirement for the iterative reconstruction of the signature (concatenation of segments).

Resampled signature can be interpreted in two ways. It could simulate an actual change on the data acquisition rate or, especially for signatures on the DS2 and MCYT databases, it can be seen as a velocity modulation. As previously stated, such databases do not require an explicit storage of timestamps, since the acquisition rate is constant. Therefore, an upsampling could be interpreted as a slower movement, and in an analogous way, downsampling can be interpreted as an acceleration.

It is important noting that upsampling operations in the presence of acquisition discontinuities (SVC1, SVC2 and DS3 databases) can lead to a seemingly unnatural movement on these acquisition gaps even while respecting the smoothness requirements of the MJ criterion. In Figure 4.7 an upsampling of a signature that has sampling discontinuities is presented; the final gap of the y coordinate presents a significant curve, while a more straight line would be expected given the previous points.

¹Published on 17th July 2014

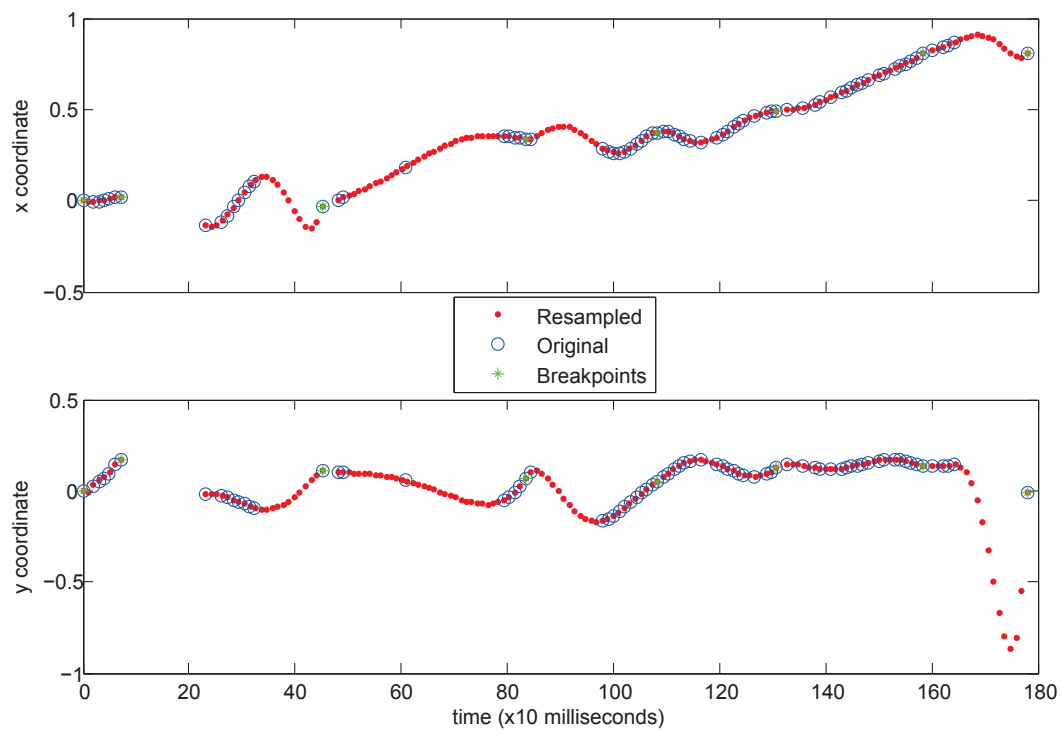


Figure 4.7: x and y coordinates after upsampling of a signature with sampling discontinuities.

Notice that even if for most segments the interpolation creates a reasonable path, the discontinuity on the last segment causes the y coordinate to present a rather strong variation. From a biometric verification perspective, artificial in-air movements were generated for the SVC1, SVC2, and DS3-I databases, it was observed that verification performance using the aforementioned approach (DTW) is negatively affected; the EERs on all databases have increased of 4% on average. Meanwhile, upsampling on the DS2 and MCYT databases had little effect over verification performance.

4.4.2 Signature Complexity Evaluation and Database Segmentation

Since signature segments are based on a piecewise polynomial model that represent “natural” movements according to the Minimum Jerk motor control theory, one should expect that the number of such segments is related to complexity of the signature’s shape and dynamic properties.

In Figure 4.8 it is shown that the number of segments is directly related to the duration of the signature, as expected. As a matter of fact, the correlation coefficient (ρ) between the number of segments and the signature duration is always above 0.74 for all databases. However, the number of segments for a given user is more stable than the length of the signature and therefore provides a more stable categorization of each signer.

Users were divided into three complexity categories, arbitrarily defined as:

$$\text{Complexity} = \begin{cases} \text{High,} & \text{if } \mu_{N_{user}} > \mu_{N_{db}} + 2\sigma_{N_{db}} \\ \text{Low,} & \text{if } \mu_{N_{user}} < \mu_{N_{db}} - 2\sigma_{N_{db}} \\ \text{Medium,} & \text{otherwise} \end{cases} ,$$

where $\mu_{N_{user}}$ is the average number of segments for a given user, $\mu_{N_{db}}$ is the average number of segments for the database and $\sigma_{N_{db}}$ is the standard deviation for the number of segments on the database.

Even if the segments number is highly correlated to the duration of the signature, it is possible to have signatures of the same length in different categories, specially for signature of average length. In this case, the number of segments reflects the complexity of the pen movement dynamics. In Figure 4.9 three signatures, one of each complexity category, are shown along with their x and y coordinates time functions and segmentation points. All three signatures have a total duration of 3.2 s.

Notice that the signature on the “Low” category (in Figure 4.9) has a rather complex appearance due to the end loops. However, its movement is performed on a fluid manner, without fast variations. The three ending loops are represent by only three segments. On the other hand, the other two signatures present several fast variations, generating more segments.

Finally, the segmentation of the databases into complexity classes allows for the use of specific thresholds for each category. This approach yields a better overall verification performance. It can also provide an insight into the classification error

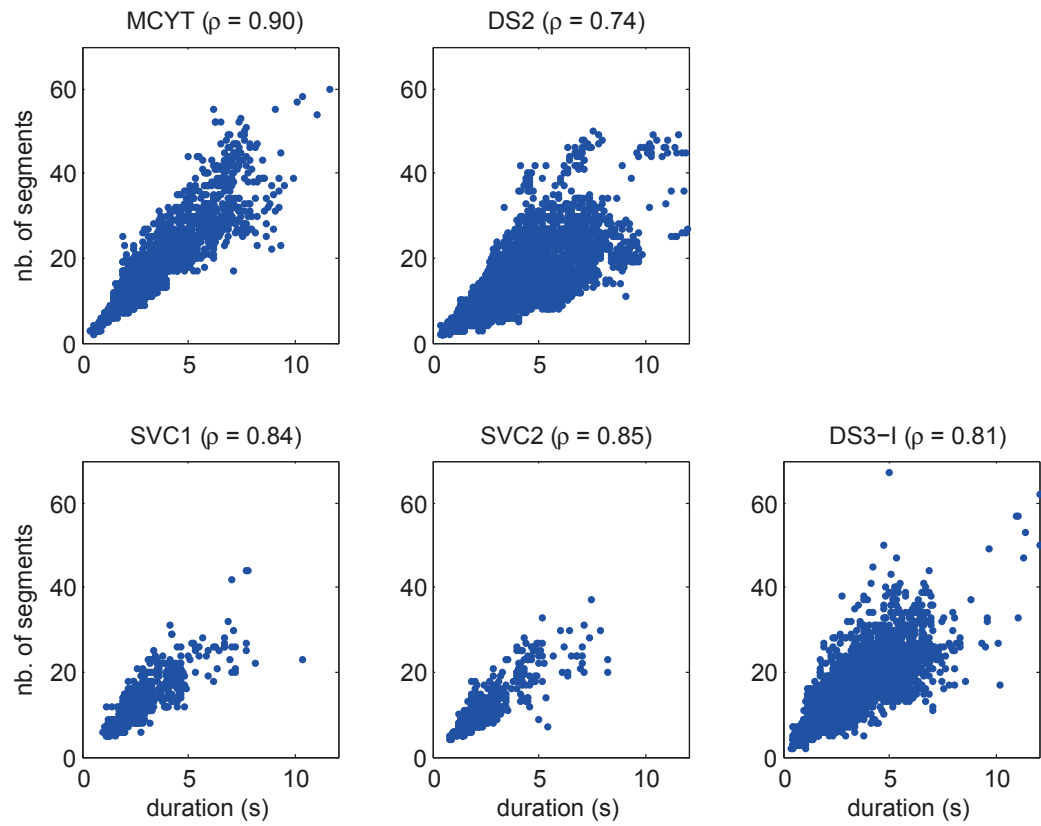


Figure 4.8: Number of segments as a function of the signature duration for each database along with its correlation coefficient ρ .

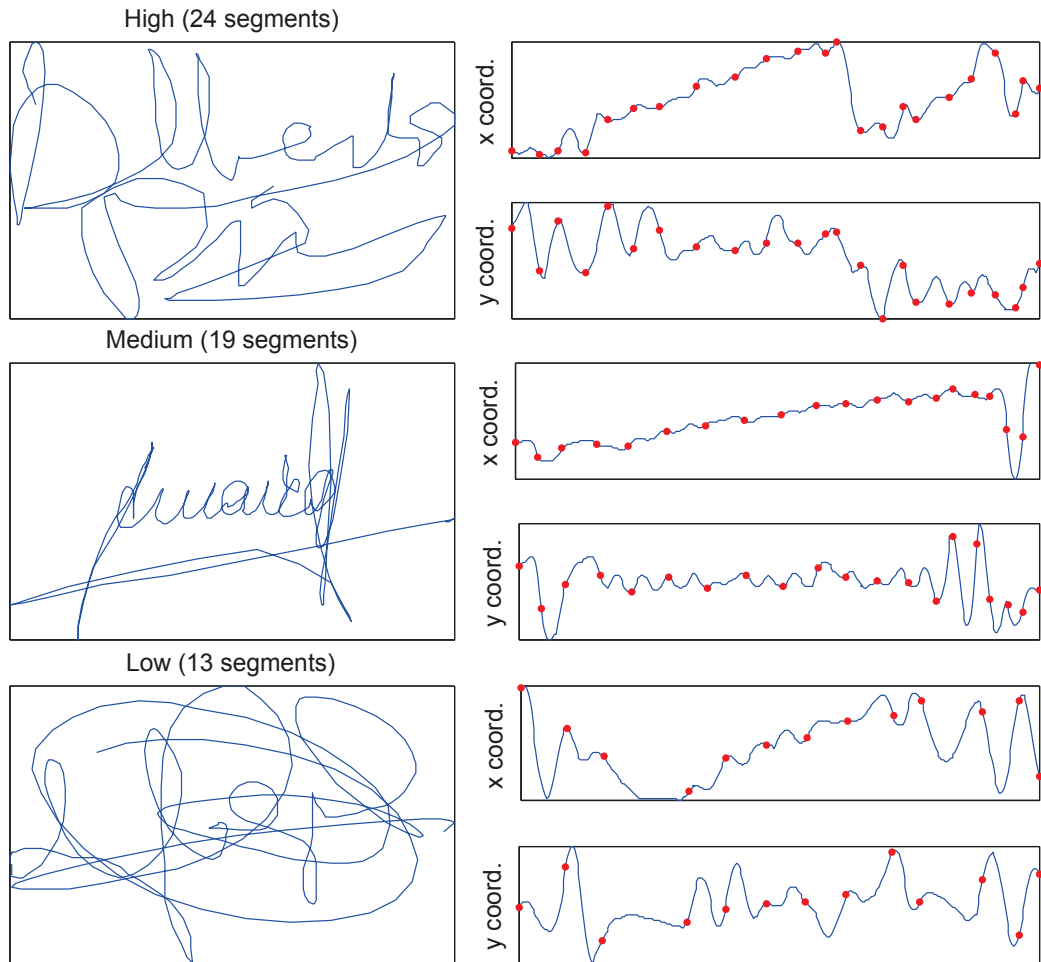


Figure 4.9: Signatures of each category and their respective x and y coordinates signals. Dots represent segments limits.

Table 4.3: Verification performance (EER in %) for each complexity category. Percentage of users in each category in parentheses.

	Low	Medium	High	Average	Original
MCYT	06.90 (36)	04.40 (36)	03.37 (28)	05.01	05.64
DS2	05.54 (35)	05.43 (41)	04.52 (24)	05.20	05.91
SVC1	13.08 (23)	12.56 (60)	11.47 (17)	12.41	12.68
SVC2	14.12 (25)	12.35 (60)	10.17 (15)	12.46	13.24
DS3-I	17.98 (20)	16.14 (61)	14.38 (19)	16.17	17.40

that will be observed for a specific user based on the category its signatures belong to. After a user is already enrolled, this complexity measure can even be used for a fast rejection of random forgeries. In Table 4.3 we present the attained performances for each category and the overall performance obtained by a weighted average of these error rates. The weights adopted for the calculation of the average performance of each database are the percentage of users on each category. For a better comparison, we reproduce the performances for the databases without segmentation.

A consistent behavior can be observed for all databases; verification performance increases as we move through the complexity categories. Signatures that fall on the high category are usually long with complex dynamics, which causes then to be more difficult to forge. Furthermore, a small improvement on the overall performance is obtained using a different threshold for each category.

A similar result was observed in (Garcia-Salicetti et al., 2009; Houmani, 2011) for the MCYT database using another quality criterion. As a matter of fact, the MJ-based complexity is inversely proportional to the Personal Entropy measure proposed in Dr. Houmani’s work. In Figure 4.10 is presented the Personal Entropy as a function of the number of segments for the MCYT database. Categories are indicated both for the number of segments and personal entropy; for the later case, the categorization is that provided in (Houmani, 2011), using an hierarchical clustering algorithm.

These relationships indicate that the number of MJ-based segments can indeed be used as a complexity measure for online signatures.

4.4.3 Synthetic Signatures Generation

Another application of the MJ representation is for the generation of new artificial signatures from original samples. This could help solving a common issue on signature verification applications that is the lack of samples for training classifiers (Galbally et al., 2009a, 2012; Plamondon et al., 2014).

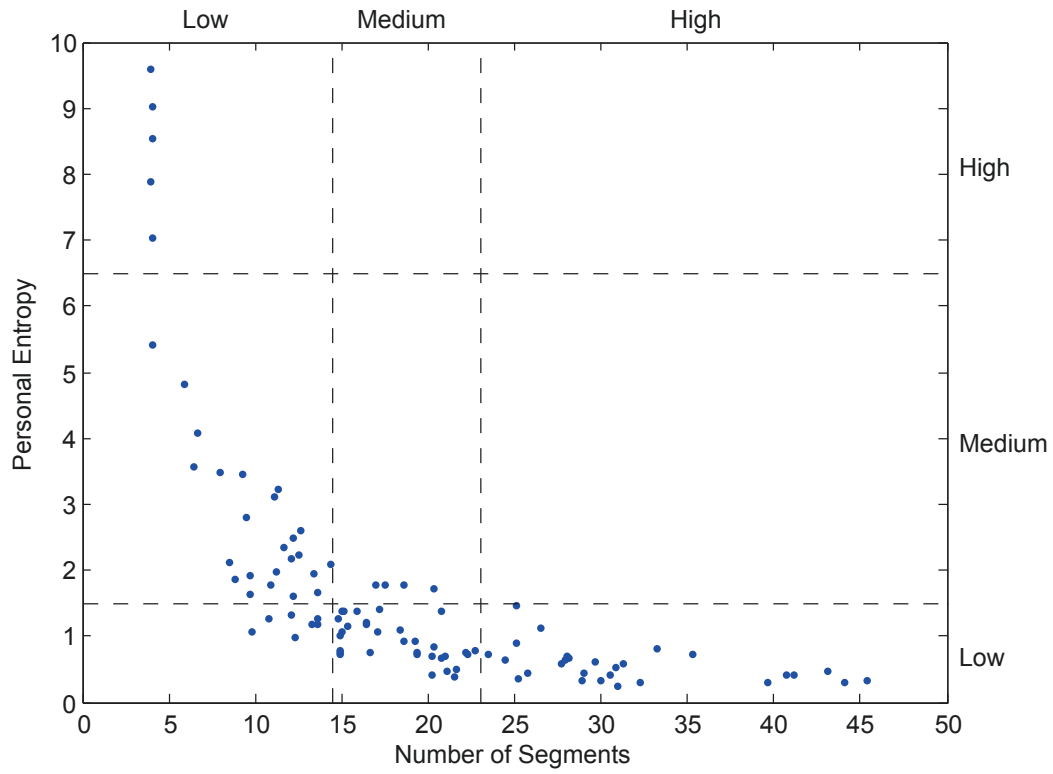


Figure 4.10: Personal Entropy (Houmani, 2011) as a function of the number of segments for the MCYT database.

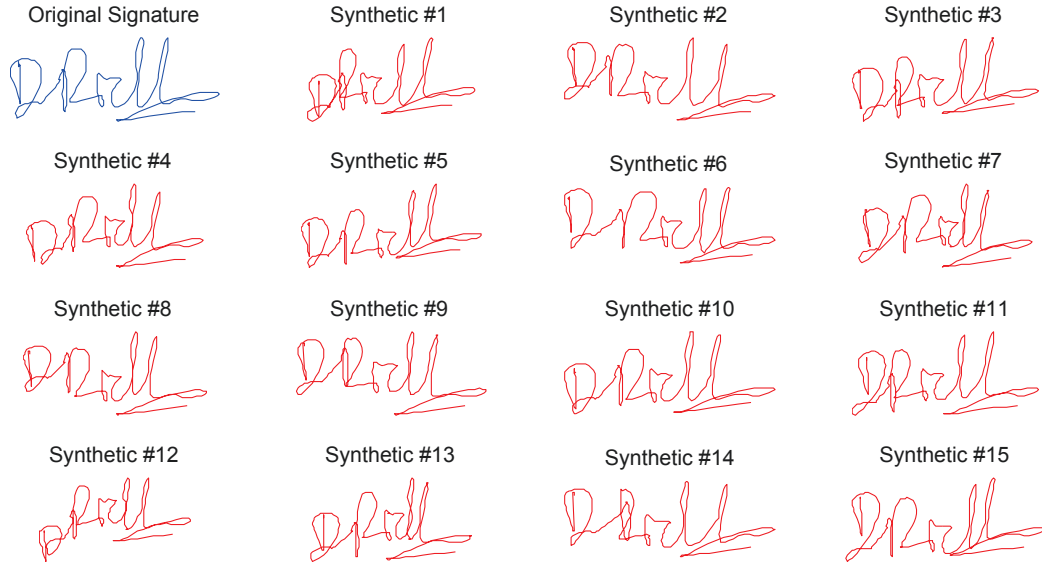


Figure 4.11: Fifteen synthetic variations obtained from a single original signature.

Based on the piecewise polynomial representation proposed in this chapter it is possible to generate artificial variations of a given signature. These variations are obtained through the introduction of perturbations on the polynomial coefficients. In Figure 4.11 several variations obtained from the same model are presented.

The proposed signature synthesis scheme works on a rather straightforward manner. The polynomial representation, $\hat{S}(t)$, of a given signature sample is composed by N segments, $P_k(t)$ (Equation 4.3); each of these segments is composed by 2 time-functions that represent each coordinate through 6 coefficients, a_i, b_j with $i, j = 1, \dots, 6$ (see Equation 4.2). From the N segments, the average of the modulus for each coefficient is computed, μ_{a_i}, μ_{b_j} , these give an idea of the magnitude. Then, each coefficient is modified by the addition of a random perturbation uniformly distributed in $\pm 0.5\%$ of their corresponding averages, this operation can be expressed as:

$$\begin{aligned}\hat{a}_{i_k} &= a_{i_k} + \mu_{a_i} \cdot \mathcal{U}(-1, 1) \cdot 10^{-4} \\ \hat{b}_{j_k} &= b_{j_k} + \mu_{b_j} \cdot \mathcal{U}(-1, 1) \cdot 10^{-4} \quad , \quad i, j = 1, \dots, 6 ; k = 1, \dots, N,\end{aligned}$$

where k indicates the segment number and $\mathcal{U}(-1, 1)$ is a random sample from a uniform distribution in the $[-1, 1]$ interval.

The perturbation magnitude (0.5% of the modulus average) was determined through the visual inspection of several sets of synthetic signatures generated at different perturbation levels. It was desired that synthetic signatures presented a moderate variation but not enough to become unrecognizable.

Notice that by changing only the polynomial coefficients, the synthetic signatures have the same length (*i.e.*, number of points) as the original one. It is possible to change the length of the signatures by performing different resamplings on each segment. For a given representation, $\hat{S}(t)$, each segment has a different length L_k . The standard deviation of these lengths, σ_L is computed and, as for the coefficients, a random perturbation is added to each of the original segments lengths. However, in this case, the perturbation is a sample of a random variable uniformly distributed in $\pm\sigma_L$. Therefore, segments lengths are modified according to:

$$\hat{L}_k = L_k + \sigma_L \cdot \mathcal{U}(-1, 1), \quad k = 1, \dots, N,$$

where k indicates the segment number and $\mathcal{U}(-1, 1)$ is a random sample from a uniform distribution in the $[-1, 1]$ interval.

Experiments on the generation of synthetic signatures by modifying a single coefficient at a time were performed. However, no clear relationship between individual coefficients and overall signature shape could be noticed. On the other hand, as a general rule, it is possible to observe that when exclusively positive perturbations are used, synthetic signatures present a “stretched” trajectory as compared to the original one. Analogously, when only negative perturbations are used, more “compact” trajectories are observed. Twelve synthetic signatures based on a single initial sample are shown in Figure 4.12. Half of these signatures were generated using positive perturbations and half using negative perturbations.

4.5 Conclusion

The main objective of this thesis was developed in this chapter: an online handwritten signature representation based on the Minimum Jerk model. The proposed algorithm performs a fully automated piecewise polynomial modelling of dynamic signatures through an iterative segmentation technique.

Following the design criteria, the proposed model is capable of representing a signature trajectory with any chosen representation error. As a matter of fact, reconstruction quality is the only parameter that needs to be set in order to obtain a signature model. Compression rates as high as 78% are obtained while maintaining a reconstruction quality of 15 dB SNR_v (Equation 4.5). From this point of view, the proposed model can be interpreted as a lossy compression algorithm, such as the jpeg for image compression or the mp3 for audio compression; while the jpeg and mp3 algorithms are based on psychophysiological aspects of human vision and hearing, respectively, the signature model is based on aspects of human movement planning.

This adjustable representation quality is an improvement over other handwriting models found in the literature, since the user can choose the suitable representation quality level for his/her application. Another advantage, as compared to other piecewise representations, is that the proposed method provides an automatic segmentation

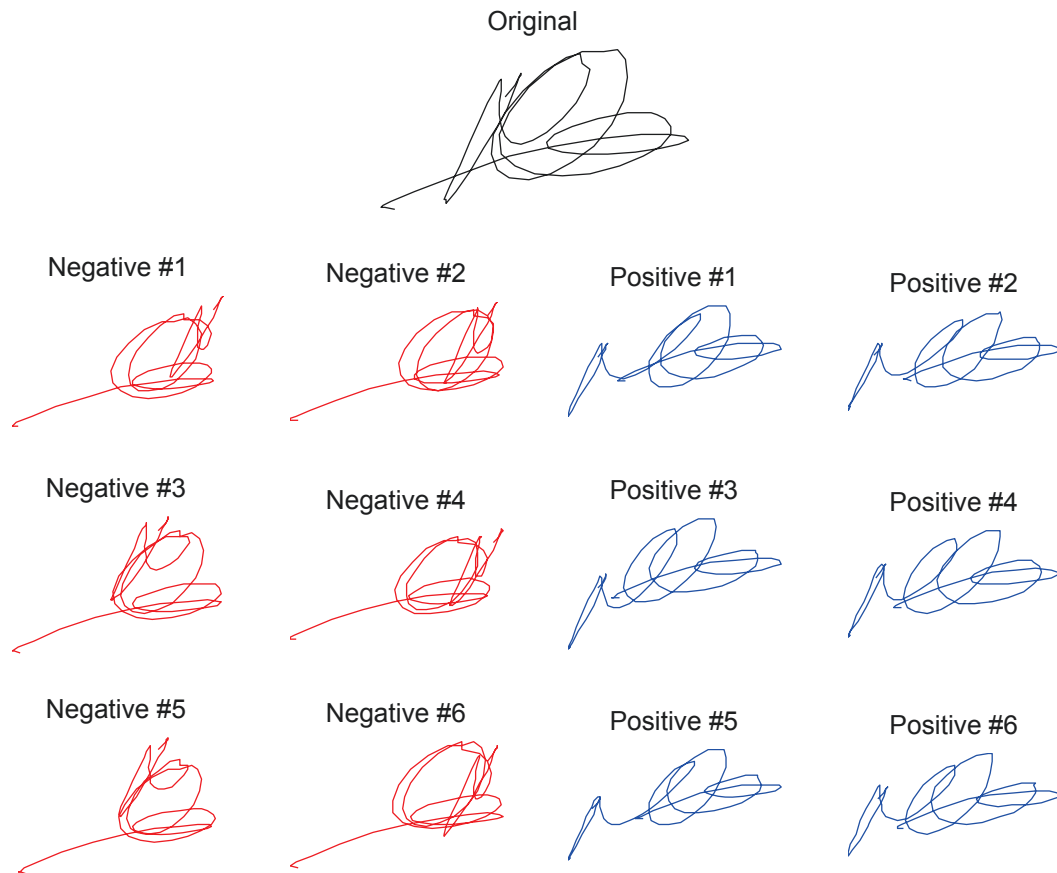


Figure 4.12: Synthetic signatures obtained from a single original sample using only positive or negative perturbations.

that is a direct consequence of the movement model adopted (*i.e.*, Minimum Jerk). Thus, segmentation heuristics or manually inserted via-points are unnecessary.

Three sample applications of the model were proposed: signature resampling, signature complexity evaluation and generation of synthetic signatures. Resampling is a common preprocessing technique in online signature verification systems, since time-functions feature vectors usually have different lengths amongst signatures samples. The proposed model allows to perform resampling easily, while keeping the dynamics characteristics of the movement.

Quality measures for biometric samples have been studied for several years. Such measures can be used to improve the overall system performance, through the rejection of bad quality reference samples or adaption of the system's parameters to a certain user category.

The generation of synthetic signatures has been studied in the literature aiming at the resolution of a frequent problem on biometric applications: the limited number of available samples. A simple generation procedure, based on the MJ-based signature model, was proposed.

The next chapter of this thesis proposes a symbolic representation for online signatures. This representation can be interpreted as a severe simplification of the model developed so far. The goal of Chapter 5 is obtaining a highly compressed representation while maintaining discriminative information. Notice that reconstruction quality is no more a requirement, and the new coding is evaluated from a biometric verification perspective.

Further Simplifications: Infinite Clipping and Signature Verification

5.1 Introduction

Up to this point a signature representation scheme based on a well-established movement planning model, namely the Minimum Jerk, was presented. This model gives a compressed representation of the writing movement that can be used to suit a given application, even if it was originally developed using signature signals.

It was shown in Chapter 4 that the MJ-based signature model is capable of modeling with any given degree of accuracy all details of a signature trajectory. In addition, notice that this modeling algorithm does not require any significant preprocessing step, such as filtering or outlier removal, thus representing as much as possible of the original information.

For verification purposes, however, the details of signature signals might not be helpful at all if they are not adequately taken into account by verification algorithms. As a matter of fact, if the information is irrelevant to the classifier it can be interpreted as noise and will usually negatively affect the classification performance (Skrypnik, 2011); even if performance is not affected, irrelevant features will almost surely increase the computational cost and the number of training samples needed to achieve acceptable error rates.

Due to these reasons, preprocessing and feature selection methods tailored for use with a given classifier are usually adopted in verification systems and their choice has a great impact on the observed performance (Impedovo and Pirlo, 2008).

In this chapter, the online signature verification task is focused. A new symbolic signature representation, that can be interpreted as an extremely simplified version of the Minimum Jerk-based model developed in Chapter 4, is proposed. The main goal of this symbolic representation is obtaining a compressed signature signal while maintaining the essential discriminant information about the signature's owner.

The symbolic sequence obtained through this new method is directly related to the Infinite Clipping signal processing technique, widely used for speech signals as

means of compression (Schroeder, 2004). As for speech, signatures reconstructed from this symbolic representation are severely distorted; however, this simpler signal is still enough for discriminating amongst different signers, as it is observed through biometric verification tasks. This impossibility of obtaining the original data from the proposed representation is actually interesting from a biometric verification perspective since it protects the users' privacy.

This chapter is structured as follows. In Section 5.2 the Infinite Clipping technique is discussed and a link to the proposed MJ-based model is made. Section 5.3 discusses the matching technique adopted for the comparison of these symbolic representations, the Levenshtein Distance. Verification experiments are discussed in Section 5.4. Finally, in Section 5.5 the signature complexity evaluation proposed in Chapter 4 is revisited using a well-known symbolic strings complexity measure, the Lempel-Ziv complexity.

5.2 Infinite Clipping Representation

The Infinite Clipping signal processing technique has been used for speech signals related to compression and non-uniform sampling for transmission and storage purposes. The effects of clipping on speech signals were first studied by Licklider (one of the progenitors of the Internet) and colleagues from 1946 to 1948 (Licklider, 1946; Licklider and Pollack, 1948; Kryter et al., 1947).

The term Infinite Clipping refers to a signal processing technique that saturates the signal (*i.e.*, sets it to a fixed limit), transforming the original waveform into a rectangular wave. Amplitudes in waveforms are converted to either plus or minus one, preserving zero-crossing information but removing all amplitude information. More formally, given an input signal $x(t)$ the infinite clipped output $y(t)$ is given by

$$y(t) = \text{clip}\{x(t)\} = \begin{cases} 1 & \text{if } x(n) \geq 0 \\ -1 & \text{if } x(n) < 0 \end{cases},$$

where the output values 1 and -1 can be interpreted as symbolic values, representing the two amplitude quantization levels. In other words, it is a simple comparator that detects zero-crossings and produces a binary representation of the original signal. In Figure 5.1 is shown an original signal and its clipped version.

The essential though surprising finding observed when applying such technique to speech signals was that despite the fact that it produces a highly distorted waveform, speech is still highly intelligible for human listeners. When comparing the power spectral densities of the original sounds to those of the infinitely clipped signals it was found that the fine structures of the spectra are kept while using the clipped signal (Olofsson, 1980). Nonlinear distortion generates additional frequency components but does not destroy the spectral prominences (formants) and their movements that our ears rely on in decoding the signal. This is an important observation since features

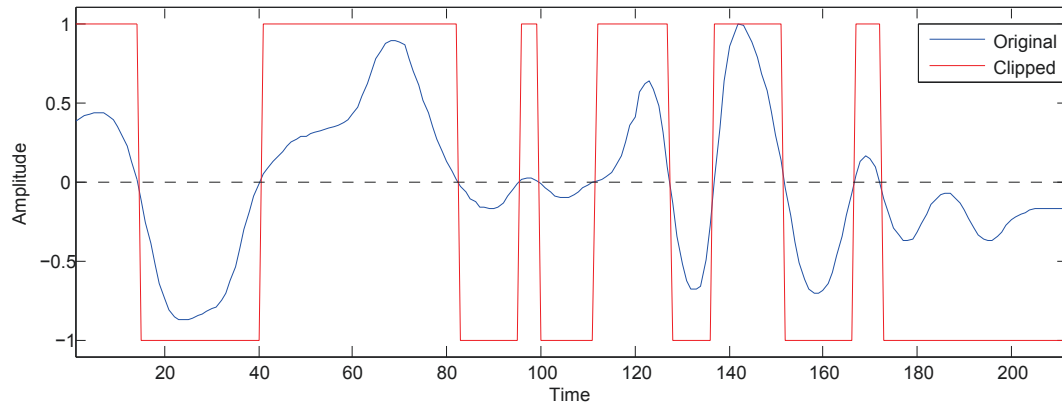


Figure 5.1: Infinite clipping (red) of a waveform (blue).

commonly used for speech and speaker recognition tasks (*e.g.*, mel-frequency cepstral coefficients) are also based on such spectral properties.

This does not mean, however, that amplitude cues do not contribute to speech discrimination. Studies motivated primarily by cochlear implant research found that waveform amplitude also conveys a certain amount of speech information (Van Tasell et al., 1987; Rosen, 1989).

This simple quantization method has many important consequences and interpretations. First, from a signal compression perspective, infinite clipping has a double effect on the memory requests for storage. On one hand, a single bit is needed to represent the signal at each time instant, which could originally be a real-valued number.

On the other hand, since only two output values are possible, if the time instants at which the zero-crossings occur are recorded, or equivalently the duration of each value, the signal can be further compressed depending on its dynamics properties. In the worst case scenario, one bit per time sample will be observed if there is a sign change at each consecutive sample.

In Table 5.1 five possible compressed representations for the clipped signal in Figure 5.2 are proposed.

Another important interpretation for the Infinite Clipping comes from the fact that it detects all zero-crossings of a given signal. In other words, it finds the location of the real roots of the input signal. All the representations in Table 5.1 yield a waveform with the same zero-crossings as those of the original time series.

At this point we can make a link between the Infinite Clipping representation and the Minimum Jerk signature model. As seen in Chapter 4, in order to obtain the MJ model a sequential search for the longer signature segment that obeys the Minimum Jerk law is performed. The MJ approach yields a fifth order polynomial representation

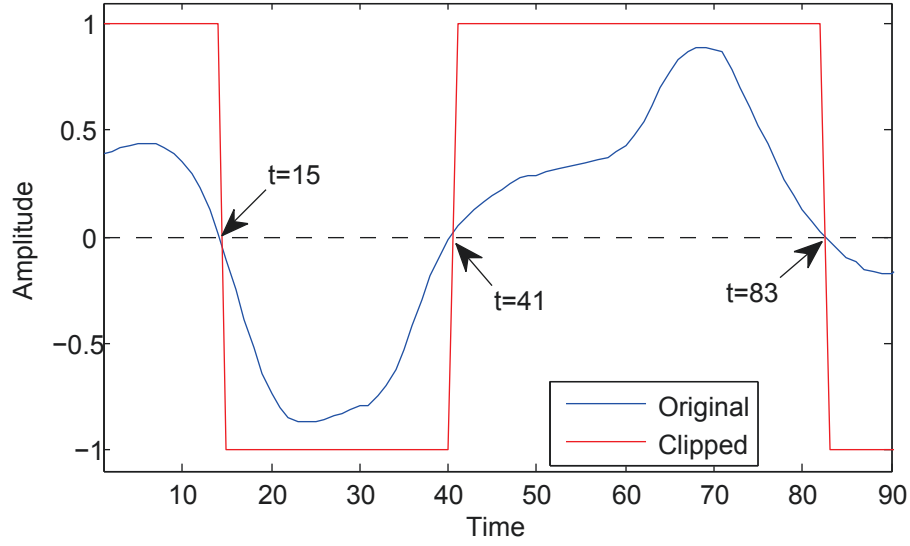


Figure 5.2: Infinite clipping of a waveform and zero-crossing instants.

Table 5.1: Different codings for the clipped signal in Figure 5.2.

Coding Approach	Coded Representation
1 bit per sample	$1, 1, \dots, 1, -1, -1, \dots, -1, 1, 1, \dots, 1, -1, -1, \dots$
Level and crossing time	$(1, 0), (-1, 15), (1, 41), (-1, 83)$
Level and duration	$(1, 15)(-1, 26)(1, 42)(-1, 7)$
1 st level and switch time	$1, 15, 41, 83$
Polynomial	$z(t) = \text{clip}\{-(t - 15)(t - 41)(t - 83)\}$

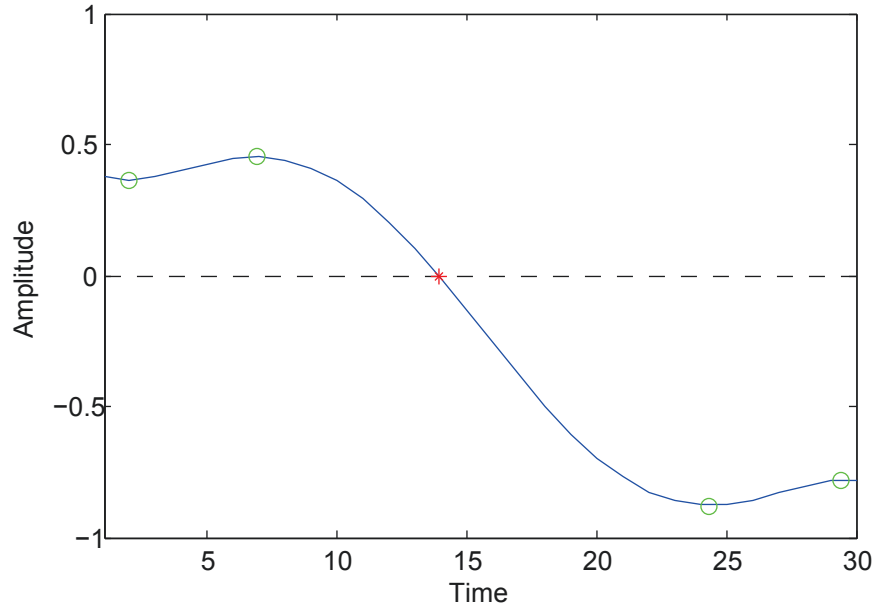


Figure 5.3: 5th order polynomial segment. Red dot is a real root. Green circles are local minima and maxima.

for each segment of the trajectory. Fitting such polynomials to the trajectories is equivalent to finding the five roots (real and/or imaginary) that describe each stroke. Therefore, each segment $s(t)$ is represented as:

$$s(t) = (t - z_1)(t - z_2)(t - z_3)(t - z_4)(t - z_5),$$

where z_i are the polynomial roots.

The Infinite Clipping technique can be seen as an extreme simplification of the polynomial fit, since it specifies only the real roots. Then, it keeps only the zero-crossings and sign information. For instance, the polynomial segment in Figure 5.3 has 5 roots: $0.5 \pm 4.2i$, 14, $31.7 \pm 5.4i$. The complex roots indicate the critical (maxima and minima) and inflection points of the curve while the Infinite Clipping ignores all these details.

It is important noting that zero-crossing conveys little information when observed over x and y coordinate values. For instance, assuming that signatures start at the origin of the Cartesian plane it is highly unlikely that a zero-crossing is observed on the x coordinate for western signatures or Arabic signatures, since both scripts are usually performed in a single direction (left to right for western and right to left for Arabic); for some eastern scripts, such Japanese, the usual direction is top to bottom, therefore no crossings on the y coordinate are observed.

One other possibility is to preprocess the coordinates values in order to center

the signature, through the removal of the means of the coordinates. In such case, zero-crossings represents only if the point is above or below this mean.

An alternative to using coordinate values is employing their first derivatives. First derivative represent velocity information and therefore their zero-crossings correspond to changes in the direction of the movement. One advantage of using velocity signals it that they are insensitive to signature translations. As a matter of fact, it has also been observed that for speech signals differentiating the waveform prior to clipping improves the perceived intelligibility (Licklider and Pollack, 1948).

From a signal processing point of view, differentiation is equivalent to high-pass filtering; therefore, an enhancement of the details of the signal is performed. Since Infinite Clipping ignores all amplitude information, this filtering happens over the frequency information (dynamics) only.

From a polynomial perspective, differentiation allows Infinite Clipping to access some of the complex roots that were hidden before. Every pair of real roots of the original polynomial corresponds to a single real root on its derivative and every pair of imaginary roots of the original polynomial becomes a pair of real roots on the derivative. As a matter of fact, all maxima, minima of the original signal become a real root after differentiation.

Yet another interpretation for the Infinite Clipping coding of the derivative is related to the Bandt and Pompe approach for finding ordinal patterns in time series. The infinite clipping of the derivative is a particular case of their method with an embedding dimension $d = 2$. Formally, for the original signal $x = x_1, x_2, \dots, x_N$, the coded signal $y = y_1, y_2, \dots, y_{N-1}$ is given by

$$y_i = \begin{cases} 1 & \text{if } x_{i+1} \geq x_i \\ -1 & \text{if } x_{i+1} < x_i \end{cases}, \quad i = 1, 2, \dots, N-1.$$

This approach has been successfully used on the calculation of Permutation Entropy, a complexity measure for time-series, on a wide range of applications (Bandt and Pompe, 2002; Morabito et al., 2012).

Based on these observations, one might think that the more we differentiate the signal, the more details will be available (more zero-crossings). However, it is important noticing that successive differentiations also destroy some of the original zeroes and therefore results in an information loss.

When considering the number of zero-crossings on the original signal and each of its derivatives, it is possible to notice that the relative increase in the number of such signal changes (*i.e.*, the number of real roots) is greater for the first derivative. For the considered databases, the first derivatives (velocities) have on average 2.7 times more zero-crossings than the original data, the second derivatives (accelerations) have 1.9 times more signal changes than the first derivatives, and finally the third derivatives (jerks) present 2 times more zero-crossings than the velocities.

In Figure 5.4 we present the zero-crossings obtained at different derivatives orders for one of the signatures on the DS2 database. Red dots indicate zero-crossings on

the x direction and green circles on the y direction.

Notice that zero-crossings of the first derivative represent movement direction changes (corners and inflection points); meanwhile, further order derivatives are harder to give a clear interpretation. The jerk, as a measurement of acceleration variation, presents several zero-crossings near points of low speed that usually present more trembling movements of the hand.

These remarks do not lead to a definitive conclusion about which of the different signals (position, velocity, acceleration, jerk) is the most appropriate for signature verification purposes. This choice is further studied through verification experiments in Section 5.4.

5.3 Strings Matching: The Levenshtein Distance

As discussed in Section 5.2, infinitely clipped signals can be represented in a variety of ways. Even if the coding using only the first state and the signal changes instants is usually the most economic, the fully symbolic representation was chosen. This coding scheme yields a binary string with the same length as those of the original time series, where each element indicates the sign of the original function at that time instant.

This choice was motivated by two interconnected reasons. First, a symbolic string allows for the use of string matching techniques, while the other mixed representations would require further developments on the matching technique. Secondly, using one symbol for each time instant allows for the preservation of some dynamics information such as rhythm and speed while using fully binary coding. Other works, such as (McCabe, 2000; Pippin, 2004; Guru and Prakash, 2009; Reza et al., 2011), use regional or global symbolic features; on the other hand, the chosen binary representation gives a local information, even if this information is reduced to a single bit.

Since signature lengths are usually different even for the same writer, an elastic string matching technique is needed. The well-known Levenshtein distance (Theodoridis and Koutroumbas, 2006), also known as Edit distance, was chosen to perform this task. This dynamic programming string matching approach can be defined as follows. Given two strings $a = a_1, a_2, \dots, a_n$ and $b = b_1, b_2, \dots, b_m$ the Levenshtein distance (LD) between these strings $D_{lev}(a, b)$ is given by $d_{m,n}$ defined by the recurrence

$$d_{i,j} = \min \begin{cases} d_{i,j-1} + w_i \\ d_{i-1,j} + w_d \\ d_{i-1,j-1} + w_s \times D(i, j) \end{cases},$$

where $D(i, j)$ is a distance measure between b_i and a_j , w_i , w_d and w_s are the insertion, deletion and substitution weights respectively. $d_{0,0} = 0$, and $d_{i,0}$ and $d_{0,j}$ are defined as

$$d_{i,0} = \sum_{k=1}^i w_d \quad , \quad d_{0,j} = \sum_{k=1}^j w_i.$$

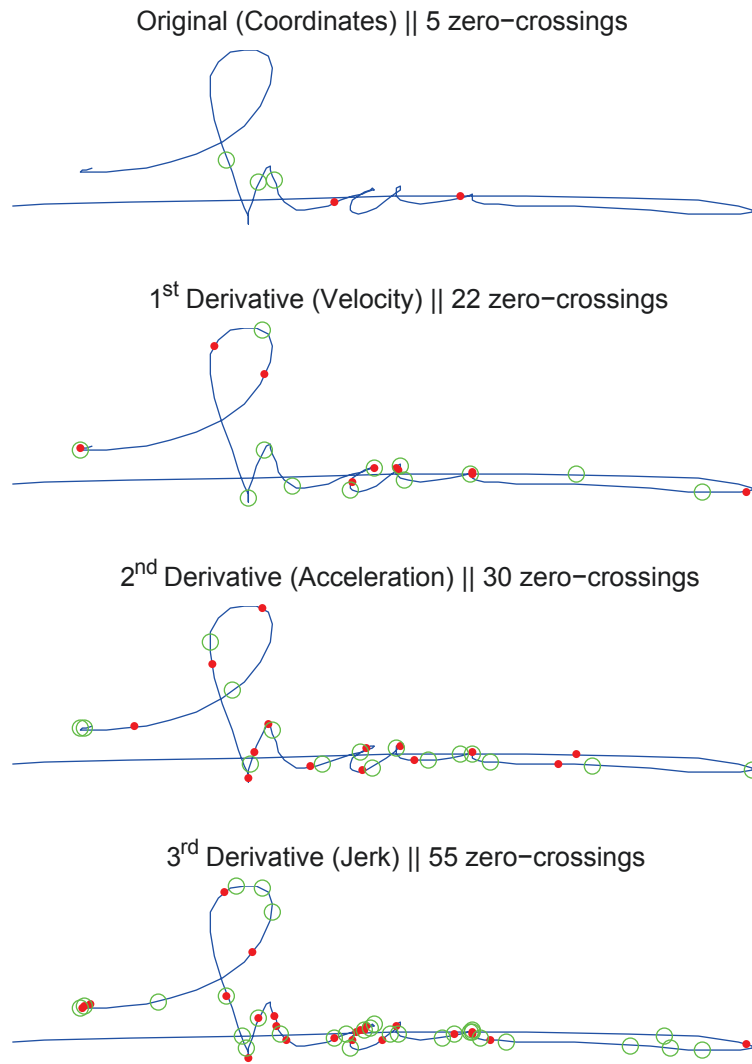


Figure 5.4: Zero-crossings at different order derivatives. Red dots and green circles are x and y directions.

It is interesting noting that the LD and DTW algorithm (see Section 3.5) are very similar. As a matter of fact, LD can be seen as a version of the DTW for symbolic signals (strings). Furthermore, notice how the DTW implementation in (Kholmatov and Yanikoglu, 2005) (see description in Section 3.7.1) is close to the Levenshtein, using a constant penalization for insertions and deletions and providing a tolerance interval for the Euclidean distance measure that can be seen as a localized quantization. Note that this particular implementation, (Kholmatov and Yanikoglu, 2005), is the leading algorithm for online signatures verification when only x and y coordinates information are available.

The most basic version of this algorithm was implemented in this work, with all weights set to one and using the Hamming distance to compare two elements (i.e. $D(i, j) = 1$ if $b_i \neq a_j$ and $D(i, j) = 0$ if $b_i = a_j$). Using these conditions, the recursion can be rewritten as

$$d_{i,j} = \begin{cases} d_{i-1,j-1} & \text{if } a_j = b_i \\ 1 + \min \begin{cases} d_{i,j-1} \\ d_{i-1,j} \\ d_{i-1,j-1} \end{cases} & \text{if } a_j \neq b_i \end{cases},$$

with $d_{i,0} = i$, $d_{0,j} = j$ and $d_{0,0} = 0$. Under such conditions the Levenshtein distance is at most the length of the longer string; therefore it can be easily normalized to the $[0, 1]$ interval. Another important property of this distance measure is that it is at least the difference between the strings lengths, so signatures with different lengths are automatically penalized in the matching.

The Infinite Clipping representation yields two binary strings, one for each coordinate. However, the Levenshtein distance is designed to compare two unidimensional strings. In order to cope with this issue, two possible approaches could be adopted: combining the two binary strings into a single four-symbol string or combining the distances for each coordinate into a single measure.

In the first case (data fusion), a simple equivalence table (Table 5.2) can be used at each time instant. Therefore, two binary sequences x and y defined as:

$$x = [-1, -1, -1, 1, 1, -1, 1],$$

$$y = [-1, -1, 1, -1, 1, 1, -1],$$

would be coded as

$$c = [A, A, B, C, D, B, C].$$

However, derivatives obtained from the original coordinates present less sampling points than the original time series, making it impossible to directly apply this approach when combining information from different order derivatives (e.g. coordinates and velocities); requiring the deletion of points from the longer string or analogously

Table 5.2: Conjoint representation of two binary values.

x coordinate	y coordinate	Combined
-1	-1	A
-1	1	B
1	-1	C
1	1	D

the addition of points on the shorter one. When several reference signature samples are available, the minimum distance is used as dissimilarity score.

For the second combination approach (scores fusion), the following procedure was adopted. For each reference sample i a set of Levenshtein distances is obtained, one for each feature f_d (e.g. $D_{lev,i}^{f_2}$ is the distance between the test signature and the i^{th} reference signature when considering only the f_2 feature). This set of distances can be seen as i vectors on a d -dimensional space. For each vector its norm

$$R_i = \sqrt{\sum_{k=1}^d (D_{lev,i}^{f_k})^2}$$

is computed and the vector with minimum norm $r = \min(R_i)$ is chosen as reference. Finally, a similarity measure is defined as

$$P = \frac{1}{V_d(r)}$$

where

$$V_d(r) = \frac{\pi^{d/2}}{\Gamma(\frac{d}{2} + 1)} r^d$$

and $\Gamma(\cdot)$ is the gamma function.

This procedure is based on a k -Nearest Neighbors (k NN) probability density estimation for $k = 1$. On this kind of estimation, the likelihood is inversely proportional to the volume that encompasses k points in the dataset. Notice that our similarity measure P is inversely proportional to $V_d(r)$ which defines the volume of a d -dimensional sphere of radius r . The radius r , in its turn, is the closest point to the origin of the distances space. Therefore, our similarity measure is proportional to the likelihood of the test sample being genuine.

This procedure provides a general fusion framework in which it is possible to change both the number of reference samples and the number of features used for verification.

5.4 Signature Verification Experiments

In this section three main aspects of the verification scheme proposed on the previous section are studied. First, the equivalence, in terms of verification performance between the two proposed fusion schemes (data and score fusion) is evaluated. Secondly the influence of using different quantization levels other than the two yielded by Infinite Clipping is investigated. Finally, the influence of using different features (position, velocity, acceleration and jerk for each coordinate) on the system's performance is evaluated.

These aspects could be linked to each other (*e.g.*, velocity can be the more informative signal using two quantization levels but not with some other number). Performing verification experiments with all the 22950 combinations of these aspects (*i.e.*, the 2 fusion schemes for each of the 255 features combination using 45 different numbers of quantization levels) for each signature database would require an exceptional amount of time. Therefore, it was decided to first study the MCYT database over a limited range of 10 different numbers of quantization levels, yielding a total of 5100 combinations.

It was observed that such parameters can be analyzed independently in terms of verification performance. Moreover, it was noted that best verification performances are obtained when using two quantization levels and velocity signals, and that the fusion schemes always yield equivalent results. Therefore, when analyzing the number of quantization levels on other databases, only velocities signals are used. In an analogous way, when investigating the best features combination, the number of quantization levels is fixed to two.

Similarly to the verification experiments in Section 4.4, experiments in this section were conducted over the five databases described in Section 3.7.1. For each database, 1000 random samplings with replacement of the 5 reference signatures are performed. For each sampling k a corresponding EER_k is computed. This allows to give an idea of the order of magnitude of the observed EER. Results are presented though the average and standard deviation of the EERs obtained over the random samplings.

5.4.1 Fusion Schemes

In order to evaluate the two proposed fusion schemes, verification experiments were performed and had their performances compared. Since the data fusion of features corresponding to different derivative orders might pose some problems we chose to perform the fusion of two features of the same order. More specifically, this first set of verification experiments considers the fusion of x and y velocities using the Infinite Clipping coding (*i.e.* two quantization levels).

Table 5.3 presents the obtained performances in terms of EERs and their corresponding confidence intervals for each test database.

Notice that neither of the fusion schemes perform better than the other for all data sets. As a matter of fact, similar results are obtained using both approaches,

Table 5.3: EER(%) and standard deviation (in parenthesis) for the fusion of x and y velocities on each database. Corresponding values for the DTW-based system (Table 4.1) are reproduced to ease comparison

Database	Data Fusion	Score Fusion	DTW System
MCYT	04.22 (0.22)	04.31 (0.25)	05.93 (0.35)
DS2	03.16 (0.36)	03.96 (0.33)	06.46 (0.41)
SVC1	11.95 (1.05)	11.93 (1.06)	13.07 (1.44)
SVC2	11.71 (0.97)	12.24 (1.02)	13.32 (1.00)
DS3	07.37 (0.52)	06.54 (0.49)	12.13 (0.78)
DS3-I	09.29 (0.67)	08.17 (0.58)	17.39 (1.27)

with performance values that are less than one and a half standard deviation apart. It is interesting noting that the EERs are lower and more stable in regards to the reference set than the DTW-based system used in Chapter 4; this stability can be seen by comparing the standard deviations of the LD-based system to those of the DTW-based system (values are reproduced in Table 5.3 for an easier comparison). Standard deviations for the DTW-based approach are usually larger than their LD-based counterparts. Note that the usual, more simple, DTW implementation was adopted in this work, and not the one presented in (Kholmatov and Yanikoglu, 2005).

Based on these observations the score fusion approach was chosen for the remaining verification experiments in this chapter. As stated before, this fusion technique can easily deal with any number of features. This property will be particularly useful for the study of different combinations of features in Section 5.4.3.

5.4.2 Quantization levels

Another important question about the proposed system is the following: is the binary string provided by the Infinite Clipping really a good symbolization choice for signature verification? To investigate this issue, several signal representations using different quantization levels were experimented while keeping the same distance metric (Levenshtein distance).

Quantization levels were determined by the division of the range of possible amplitude values for the whole database in an even number of intervals around the origin. If a given feature has M as its maximum absolute value, quantization levels are given

by the intervals defined as

$$\begin{aligned} & \left[-M, -\frac{(L-1)M}{L} \right), \\ & \left[-\frac{(L-k)M}{L}, -\frac{(L-k-1)M}{L} \right)_{k=1}^{L-1}, \\ & \left[\frac{(k-1)M}{L}, \frac{kM}{L} \right)_{k=1}^{L-1}, \\ & \left[\frac{(L-1)M}{L}, M \right] \end{aligned}$$

where L is a positive integer and $2L$ is the number of levels.

For instance, if $L = 1$ the two quantization levels (symbols) are defined as

$$[-M, 0), [0, M] \mapsto (A, B),$$

and for $L = 2$ the intervals are given by

$$\left[-M, -\frac{1}{2}M \right), \left[-\frac{1}{2}M, 0 \right], \left[0, \frac{1}{2}M \right], \left[\frac{1}{2}M, M \right] \mapsto (A, B, C, D).$$

Using a coding alphabet with size ranging from 2 to 90 (*i.e.* L ranging from 1 to 45 on the aforementioned coding scheme), the score fusion procedure and, as for the previous experiments, x and y velocities as feature set, verification experiments were conducted on the test databases. As previously explained, this feature choice is motivated by the fact that they yield a better verification performance and is further discussed in Section 5.4.3.

In Figure 5.5, EERs for each alphabet size are presented. The region between the dashed lines are 1.96 standard deviations apart from the average and contain approximately 95% of the EER values obtained for a particular number of quantization levels.

Note that there is a verification performance degradation with the increase of the number of quantization levels. The only exception to this rule is the MCYT database, that presents a slight improvement around 30 quantization levels. This improvement, however, falls inside the shown interval; on this database, EER for 2 quantization levels is 4.31% with a standard deviation of 0.25% and for 30 quantization levels the average EER is 4.0% with a standard deviation of 0.27%.

In order to compare these results to those of the DTW-based system used in Chapter 4), Table 5.4 shows the performances for the LD-based system using 2 and 90 quantization levels and for the DTW-based system using the x and y first derivatives (instead of coordinates) as feature set.

When 90 quantization levels are used, a significant performance degradation is observed as related to the 2 quantization levels case. However, performances on

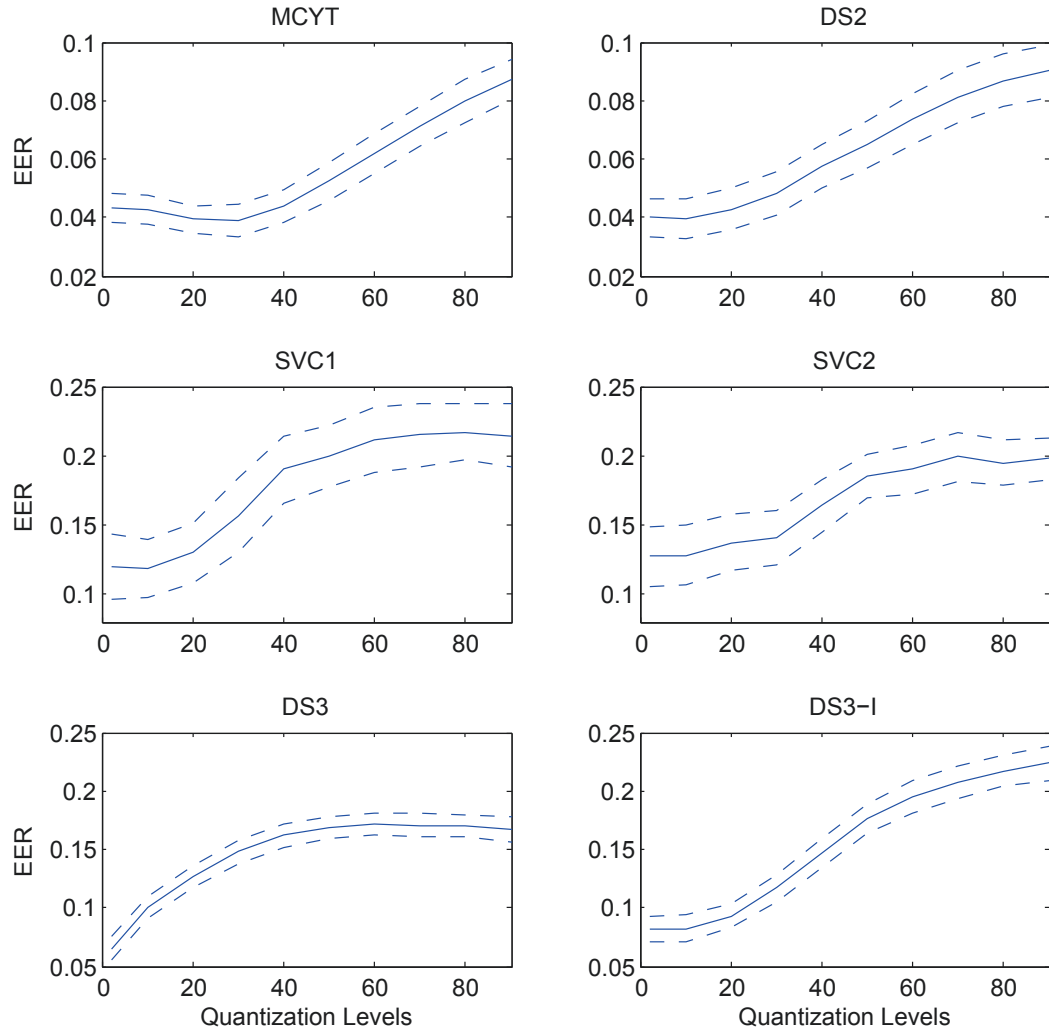


Figure 5.5: Average EER (solid lines) and region containing 95% of the EER values (dashed lines 1.96 standard deviations apart from the average) as a function of the number of quantization levels for each database.

Table 5.4: EER(%) and standard deviation (in parenthesis) for the LD-based and the DTW-based systems using x and y velocities.

Database	LD system (2 levels)	LD system (90 levels)	DTW system
MCYT	04.31 (0.25)	08.71 (0.35)	12.62 (0.39)
DS2	03.96 (0.33)	09.02 (0.45)	16.26 (0.50)
SVC1	11.95 (1.05)	21.42 (1.17)	22.84 (1.41)
SVC2	11.71 (0.97)	19.77 (0.74)	23.57 (0.93)
DS3	07.37 (0.52)	16.71 (0.56)	14.62 (0.50)
DS3-I	09.29 (0.67)	22.38 (0.74)	24.13 (0.87)

the LD-based system are better than those of the DTW-based system when velocity signals are used.

Based on the results of the verification experiments performed so far it is now possible to provide an answer to the question that started this section. Is the binary string provided by the Infinite Clipping really a good symbolization choice for signature verification? Yes, or at least it is for the signature databases considered in this thesis.

5.4.3 Feature Sets

Up to this point, x and y velocities have been used as features, but an important question needs to be answered: is this really the best feature set to be used with the Infinite Clipping coding? To answer this question, derivatives up to third order have been computed from the recorded x and y coordinates time series provided by the acquisition devices. A set of eight features are then available, two for each direction: coordinates (x, y) , velocity (v_x, v_y) , acceleration (a_x, a_y) and jerk (j_x, j_y) .

Based on the results of the previous sections, a basic Infinite Clipping (2 quantization levels) is performed and a score fusion procedure is adopted in order to compare the verification performance using different feature sets. First, each of the eight features is considered separately, Figure 5.6 and Table 5.5 present the performances obtained using each feature on each signature database.

When independently considered, the y velocity signal provides the best verification performance for all the considered databases. A similar behavior is observed on all databases: a performance improvement after the first differentiation, and a degradation of performance for the successive steps.

It is interesting pointing out to the reader the fact that, for the database acquired

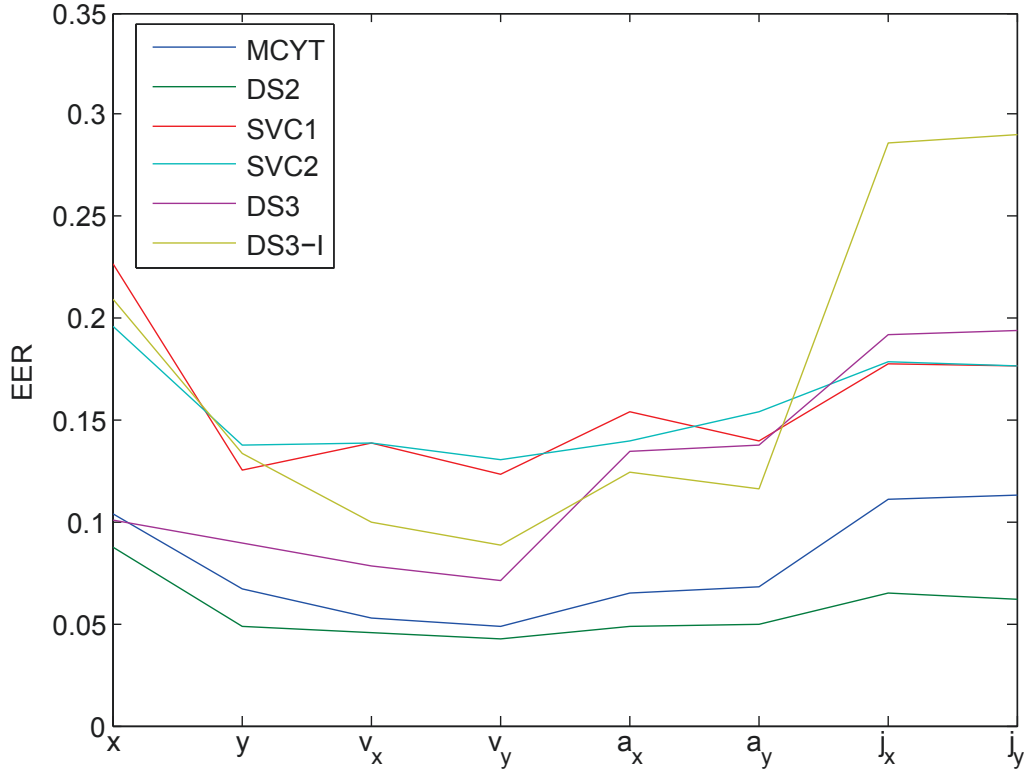


Figure 5.6: Verification performances (EER) for the 8 features (x , y , v_x , v_y , a_x , a_y , j_x , j_y) considered separately for each signature database.

Table 5.5: Average EER for the 8 features (x , y , v_x , v_y , a_x , a_y , j_x , j_y) considered separately for each signature database.

Database	x	y	v_x	v_y	a_x	a_y	j_x	j_y
MCYT	10.35	06.69	05.22	04.89	06.49	06.80	11.10	11.30
DS2	08.74	04.91	04.54	04.28	04.81	04.93	06.47	06.20
SVC1	22.67	12.49	13.89	12.36	15.37	13.94	17.78	17.62
SVC2	19.55	13.74	13.84	13.05	14.00	15.42	17.90	17.64
DS3	10.11	08.98	07.87	07.09	13.51	13.75	19.21	19.35
DS3-I	20.92	13.36	10.02	08.82	12.43	11.59	28.58	29.02

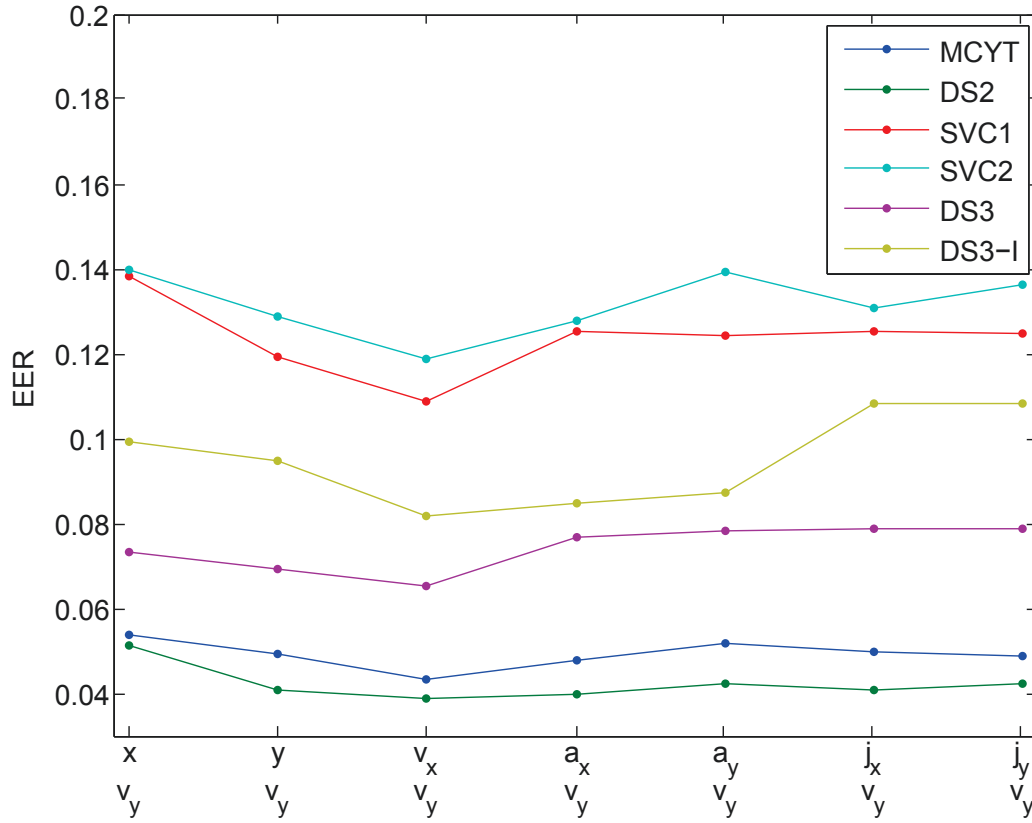


Figure 5.7: Verification performances (EER) for the 7 pairs of features containing v_y .

through a mobile device (DS3) the information loss is already significant for a second order derivative (acceleration) while for the other databases it is more noticeable for the third order derivative (jerk). This reflects the difficulty in keeping a stable hand movement on a mobility environment.

Furthermore, note that y coordinate is more informative, in terms of biometric verification, than x coordinate. This is an expected result, since most of the signatures on the studied databases present fewer direction changes on the horizontal axis than on the vertical axis.

Next, all the 28 possible pairs of features are studied. For an easier interpretation, only results for the 7 pairs containing the y velocity signal are presented in Table 5.6 and Figure 5.7. This choice was based on the fact that this is the most effective feature for signature verification, according to the above mentioned results (Table 5.5).

For all available databases the velocity features are the most informative, yielding

Table 5.6: Average EER(%) for each of the 7 pairs of features containing v_y .

Database	(x, v_y)	(y, v_y)	(v_x, v_y)	(a_x, v_y)	(a_y, v_y)	(j_x, v_y)	(j_y, v_y)
MCYT	05.37	04.92	04.31	04.75	05.18	04.96	04.89
DS2	05.10	04.09	03.86	03.98	04.23	04.07	04.23
SVC1	13.84	11.93	10.88	12.50	12.42	12.54	12.48
SVC2	13.97	12.89	11.86	12.77	13.92	13.09	13.64
DS3	07.32	06.90	06.54	07.67	07.82	07.86	07.89
DS3-I	09.92	09.48	08.18	08.46	08.74	10.80	10.81

the lowest verification error rate. Even when all the other possible pairs are considered, the combination of v_x and v_y is still slightly better than the rest. The SVC1 and SVC2 databases, are the only exceptions, presenting a slightly better performance when using the (y, a_x) and (y, a_y) sets, respectively. This performance improvement of about 0.6% is not significant, since the standard deviation for such databases is around 1%. It is interesting noting that in these databases only artificial signatures have been used during enrollment (see Section 3.7.1), which might have affected the fluency of the signing movement.

This result, in which the (v_x, v_y) set is adequate for all databases, gives a hint that such features have a role, in terms of information, that is pertinent to the writing itself and not to the chosen acquisition device. It is interesting remarking that similar behaviors to those reported in this chapter (*i.e.*, velocity domain as the best representation space for signature verification and superiority of signals that reflect vertical activity) were reported in (Plamondon and Parizeau, 1988) for three different comparison algorithms (DTW, regional correlation and tree matching).

Finally, each of the 255 possible combination of 1, 2, up to 8 features are tested and the best performance for each different number of features is presented in Figure 5.8. Databases acquired through a digitizing tablet (MCYT, DS2, SVC1 and SVC2) have their best performances using the same 6 features set: $(y, v_x, v_y, a_x, a_y, j_y)$. For the DS3 and DS3-I databases, the best results are obtained when using a set of 3 time functions, (y, v_x, v_y) and (v_x, v_y, a_y) , respectively. For the ease of the reader, these optimal results for each database are presented in Table 5.7.

Note that when the artificial points inserted on pen-up/pen-down on the DS3 database are ignored, the signal a_y becomes more informative than y , this is expected since such points encode a certain degree of information about pen pressure into the coordinates data. As a general remark, using information other than the first derivative on this particular verification system is a needless effort since the performance

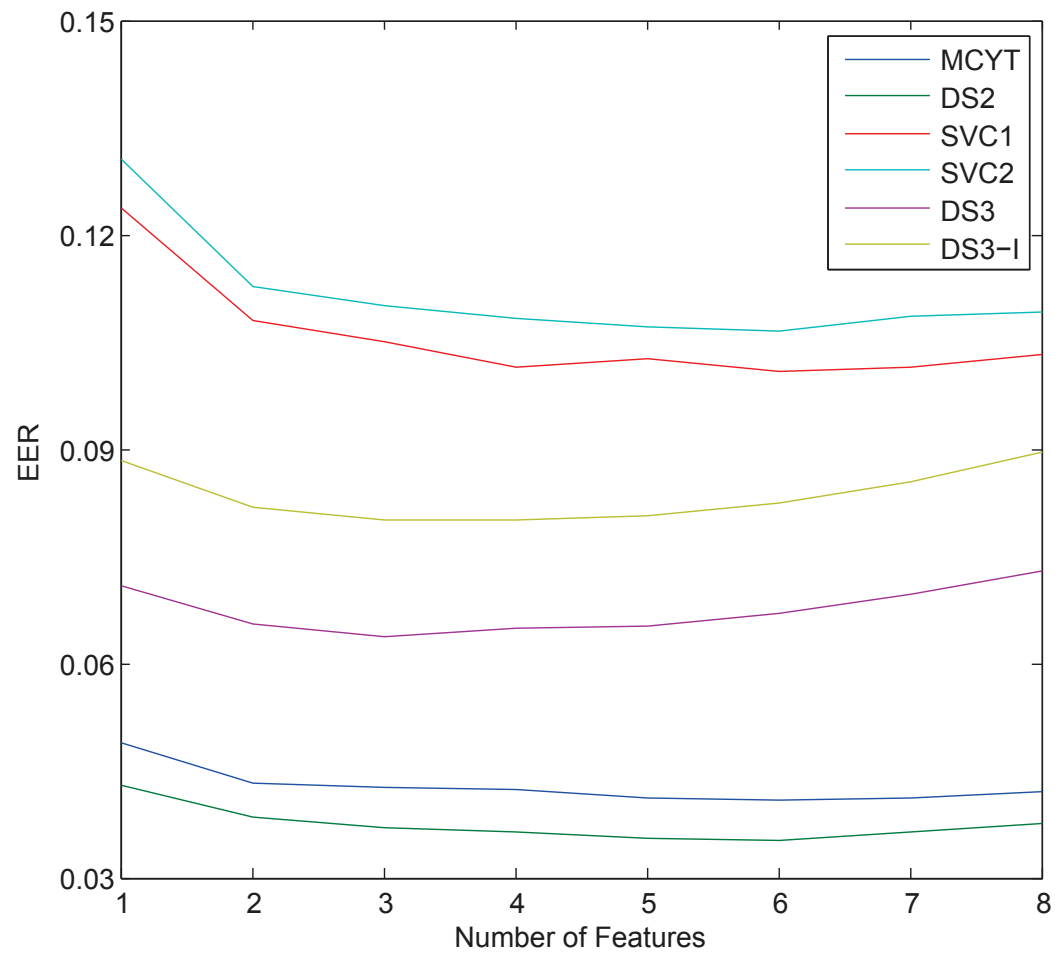


Figure 5.8: Verification performances for the best sets of 1 up to 8 features for each signature database.

Table 5.7: Best EER(%) and standard deviation (in parenthesis) obtained with the LD-based system for each signature database.

Database	Feature Set	EER
MCYT	$(y, v_x, v_y, a_x, a_y, j_y)$	04.08 (0.24)
DS2	$(y, v_x, v_y, a_x, a_y, j_y)$	03.53 (0.42)
SVC1	$(y, v_x, v_y, a_x, a_y, j_y)$	10.08 (1.10)
SVC2	$(y, v_x, v_y, a_x, a_y, j_y)$	10.62 (1.25)
DS3	(y, v_x, v_y)	06.38 (0.51)
DS3-I	(v_x, v_y, a_y)	07.98 (0.55)

improvement is not significant when standard deviation is taken into account. Table 5.8 presents the progression of the performance values with the increase of the number of signals in the feature set.

The verification system proposed in this chapter, despite using very little information (only the sign of the time functions is kept), has a verification performance that is on the same level as the state-of-the-art systems for online signature verification (see Section 3.7). These results suggest that the representation proposed in this chapter, a strong simplification of the MJ signature model of Chapter 4, is indeed adequate for verification purposes.

As a last remark, it is interesting observing that the “lossy” compression provided by the Infinite Clipping can indirectly improve users privacy and the overall system security. If only zero-crossings are stored, it is virtually impossible to reconstruct the original signature; therefore, even in the eventuality of an information leakage no forgery can be generated based on the system’s references.

On the next session, a comparison between the complexity measure proposed in Section 4.4 and the well-known Lempel-Ziv complexity for symbolic sequences is presented.

5.5 Signature Complexity Evaluation: The Lempel-Ziv Complexity

In Section 4.4, the use of the number of MJ segments as a complexity measure for the signatures was proposed. In the present section, another signature complexity measure is proposed based on the symbolic representation provided by the Infinite Clipping technique.

Table 5.8: Average EER (in %) and standard deviation (in parenthesis) for (v_y) , (v_x, v_y) , and the best feature set (see Table 5.7) for each signature database.

Database	(v_y)	(v_x, v_y)	Best feature Set
MCYT	04.89 (0.26)	04.31 (0.25)	04.08 (0.24)
DS2	04.28 (0.37)	03.86 (0.33)	03.53 (0.42)
SVC1	12.36 (1.06)	10.88 (1.05)	10.08 (1.10)
SVC2	13.05 (1.02)	11.86 (0.97)	10.62 (1.25)
DS3	07.09 (0.49)	06.54 (0.52)	06.38 (0.51)
DS3-I	08.82 (0.74)	08.18 (0.67)	07.98 (0.55)

The work developed in this chapter is based on a discrete representation of the signature time series as a symbolic string. In 1976, A. Lempel and J. Ziv (Lempel and Ziv, 1976) proposed an approach for complexity analysis of symbolic sequences known as Lempel-Ziv complexity (LZC). A simplified version of Lempel-Ziv’s approach (Ziv and Lempel, 1978) became widely known as the compression algorithm behind many “zip-like” programs for file compression. It is particularly successful due to its lack of *a priori*, being a universal approach.

The LZ method is based on an iterative search for redundancies on a symbolic string. It looks for the minimum number of unique substrings that form the original sequence. For a given string $x(t) = x_t$ with $t = 1, \dots, N$, the LZ parsing algorithm is defined in Algorithm 2.

Before explaining how the LZ parsing algorithm works, it is needed to remind the definition of a list. This data structure can be understood as a variable size array, in which each element is a symbolic string with possible different sizes (for the case of the LZ algorithm). The appending operation creates a new element at the end of the list and adds some data to this element. Finally, the length of a list is defined as the number of elements it contains. As an example of these concepts, consider an empty list, $L = \{\}$, this list has length zero. If the string ‘*abba*’ is appended to L , it becomes $L = \{\text{‘abba’}\}$ and has length 1, despite the fact that the string has a length of 4. If a second string, ‘*c*’, is appended to L , it becomes $L = \{\text{‘abba’}, \text{‘c’}\}$ and has a length of 2.

The parsing algorithm sequentially scans the input string for blocks that did not occur on the previous samples of the original data. Let a substring x_p, \dots, x_q , with $q \geq p$, be denoted by $x_{p,q}$, the LZ algorithm searches for the occurrence of this substring into the past samples, $x_{1,q-1}$. First, the initial element, x_1 , is appended to the list S . Then, starting from position 2, it is verified whether the substring

Algorithm 2 Lempel-Ziv Parsing

```

1: procedure PARSE( $x$ )
2:   Create an empty list of substrings  $S$ 
3:   Append  $x_1$  to  $S$ 
4:    $p \leftarrow 2$ 
5:   while  $p \leq N$  do
6:      $stop \leftarrow \text{false}$ 
7:      $dp \leftarrow 0$ 
8:     while not  $stop$  do
9:        $T \leftarrow x_p, \dots, x_{p+dp}$ 
10:       $R \leftarrow x_1, \dots, x_{p+dp-1}$ 
11:      if  $T \notin R$  or  $p + dp \geq N$  then
12:        append  $T$  to the list  $S$ 
13:         $p \leftarrow p + dp + 1$ 
14:         $stop \leftarrow \text{true}$ 
15:      else
16:         $dp \leftarrow dp + 1$ 
17:      end if
18:    end while
19:  end while
20:  return  $S$ 
21: end procedure

```

$x_{2,2} = x_2$ was present in the past, $x_{1,1} = x_1$. If it has already occurred, the length of the test substring is increased by one and the substring $x_{2,3}$ is searched for in the past $x_{1,2}$. If it has not occurred (*i.e.*, it is an innovation), the test substring is appended to the list S and a new test substring starting on the next position is initiated, $x_{3,3}$. This search is performed until the test substring reaches the end of the input string. Finally, the Lempel-Ziv complexity is defined as the length of list S .

The inner *while* loop in Algorithm 2 performs the above mentioned search. Notice that the substring T increases at each iteration and, if it is not part of the R substring, it is added as a new unique sequence into list S . Therefore, if x has many redundancies, S will have few elements and its complexity will be low. In an analogous way, a complex signal will have more elements (of shorter lengths) in S .

As an illustration, the parsing procedure for the input string $x = 'abbba'$ is detailed.

- The first element of x , ' a ', is automatically set as the first parsing element, $S = \{'a'\}$.
- Is the substring ' b ' ($x_{2,2}$) part of the substring ' a ' ($x_{1,1}$)?
- No, then ' b ' is appended to the list of parsing elements, $S = \{'a', 'b'\}$.
- Is the substring ' b ' ($x_{3,3}$) part of the substring ' ab ' ($x_{1,2}$)?
- Yes, then the length of the test substring is incremented by one.
- Is the substring ' bb ' ($x_{3,4}$) part of the substring ' abb ' ($x_{1,3}$)?
- Yes, then the length of the test substring is incremented by one.
- The end of x was reached, then ' bba ' ($x_{3,5}$) is appended to the list of parsing elements, $S = \{'a', 'b', 'bba'\}$

Therefore, the string $x = 'abbba'$ is parsed as $S = \{'a', 'b', 'bba'\}$, and has a complexity of 3.

This algorithm has been used for several years and it was even shown that under ergodicity conditions, the normalized LZC (Ziv, 1978) converges almost surely to the Shannon entropy rate of the source from which symbols are drawn (Cover and Thomas, 2006). This convergence, however, requires a rather long string (a few thousand samples for binary sequences). The LZ algorithm was later modified to estimate the relative entropy (Ziv and Merhav, 1993) or to compare two sequences (Montalvão and Canuto, 2014) through the use of another string as reference (*i.e.* the R variable in Algorithm 2).

The MJ-based segmentation, on its turn, relies on a model for human movement derived from the observation of several movement samples. The 5th order polynomial can also be interpreted as a model of the past, since its parameters are adjusted using

pre-recorded signals; it relies on an intrinsic belief on the symmetries/redundancies between past and future, in analogy to the LZ complexity. The iterative MJ-based segmentation procedure defined by Algorithm 1 (Chapter 4) searches for the longest subsequences that can be adequately represented by a 5^{th} order polynomial while the LZ parsing procedure (Algorithm 2) sequentially searches for the longest subsequences that have already been observed on previous samples.

For a better understanding of this relationship between the number of MJ segments and the Lempel-Ziv complexity, both segmentation algorithms are presented in Table 5.9 in five analogous steps.

This parallel analysis clarifies the fact that, while LZ uses actual data to represent the past, and thus reduces the search set, MJ employs a parametric model that represent this past references. As a simple example, consider a symbolic sequence $x = 'abbababbab'$, at some point of the parsing, the LZ algorithm will need to search for the substring $T = 'bab'$ in the reference $R = 'abbaba'$. The considered search space is a subset of the 2^3 set of length 3 strings, formed only by the subsequences present in R (*i.e.*, $'abb'$, $'bba'$, $'bab'$, $'aba'$).

Providing an example for the MJ case, however, would require the visualization of high dimensionality spaces (\mathbb{R}^n , with $n > 6$). To help in the understanding of how the search space is reduced by a polynomial model, a toy example using a first order polynomial is presented. Consider three sequential points acquired at a fixed sampling rate $p_1 = (t_1, y_1)$, $p_2 = (t_2, y_2)$, and $p_3 = (t_3, y_3)$, with $t_2 - t_1 = t_3 - t_2 = \delta t$; it is clear that these points can only be properly represented by a first order polynomial if they are co-linear, in other words, if $2y_2 - y_1 - y_3 = 0$. Even if the three points, p_i , can occur anywhere in a \mathbb{R}^3 space, only the subspace defined by the co-linear condition (the red plane shown in Figure 5.9) can be represented without error by a first order polynomial. With the increase of the fitting error (blue dots in Figure 5.9) this subspace becomes wider, eventually covering the whole \mathbb{R}^3 space (when error tolerance tends to infinity).

This conceptual relationship, shown in Table 5.9, between the iterative segmentation algorithm proposed in Chapter 4 and the well-known Lempel-Ziv complexity supports the claim that Minimum-Jerk based segments can be used as a signature complexity measure, as proposed in Section 4.4.

Note that the LZ algorithm considers only the past of the signal currently being analyzed, while the MJ model employs an analytic representation of the natural movements that are produced by the hand on a certain duration observed for different subjects. In order to have similar conditions to those of the MJ (*i.e.*, use an ensemble of samples from different subjects as reference), we propose a straightforward extension of the Relative Lempel-Ziv Complexity (RLZC) (Ziv and Merhav, 1993). The RLZC computes the complexity of a given string, x , with regards to another string, r , while the modified Lempel-Ziv parsing described in Algorithm 3 uses a set of reference strings instead of a single reference.

For a string $x(t) = x_t$ with $t = 1, \dots, N$, and a set of m reference strings $R =$

Table 5.9: Analogous steps between the Minimum Jerk iterative segmentation and the Lempel-Ziv parsing algorithm.

Step	Minimum Jerk	Lempel-Ziv
1)	Let $x = x_1, x_2, \dots, x_n$, with $n > 6$ be a trajectory segment; if no constraints are imposed, this signal can be in any region of the \mathbb{R}^n space.	Let $x = x_1, x_2, \dots, x_n$ be a symbolic signal, where each symbol can assume Q different values; this signal can be any element of the Q^n set.
2)	The Minimum Jerk model states that x must be in a subspace of dimension 6, which is the dimension of the subspace generated by the columns of the matrix of regressors \mathbf{T} (see Equation 4.4). This search subspace can be increased according to the approximation margin provided by the representation quality parameter.	The Lempel-Ziv parsing algorithm states that x must belong to a subset of Q^n composed by all sequences of n symbols observed on previous samples.
3)	If x is found in this subspace it is incremented by one sample and a new search is performed in the \mathbb{R}^{n+1} space. If it is not found, the signal is segmented.	If x is found in this subset it is incremented by one sample and a new search is performed in the Q^{n+1} set. If it is not found, the signal is segmented.
4)	Constraints to the search space are based on an empirical parametric model obtained through the observation of several signal samples acquired on previous experiments (past, on a wider sense).	Constraints to the search space are based on an empirical non-parametric model obtained through the observation of previously acquired signal samples.
5)	Signal complexity is defined as the number of segments given by the search space constraints.	Signal complexity is defined as the number of segments given by the search space constraints.

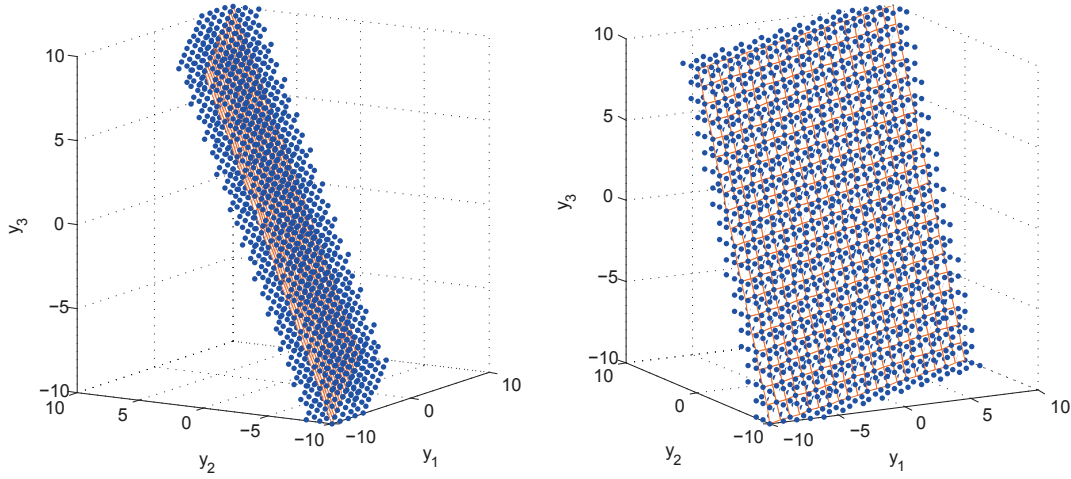


Figure 5.9: Two views of the subset of a 3-points ensemble that can be represented without error by a first order polynomial (red plane) and the increased subset due to error tolerance (blue dots).

$\{r_1(t), r_2(t), \dots, r_m(t)\}$ where each $r_i(t)$ is a sequence of possible different lengths, the parsing of $x(t)$ relative to R is defined by Algorithm 3. This algorithm works similarly to the original Lempel-Ziv parsing, previously described (Algorithm 2). The main difference is that the occurrence of the test string, T , is verified for each of the r_i in R , and not only on the past of the input sequence. As for the Lempel-Ziv complexity (Algorithm 2), the relative Lempel-Ziv complexity of x with respect to R is given by the length of the parsing elements list, S .

As an example, the parsing procedure for the input string $x = 'abbba'$ with respect to the reference set $R = \{'ab', 'bb'\}$ is detailed.

- Is the substring ' a ' ($x_{1,1}$) part of the string ' ab ' (r_1)?
- Yes, then the length of the test substring is incremented by one.
- Is the substring ' ab ' ($x_{1,2}$) part of the string ' ab ' (r_1)?
- Yes, then the length of the test substring is incremented by one.
- Is the substring ' abb ' ($x_{1,3}$) part of the string ' ab ' (r_1)?
- No, then verify the next reference string.
- Is the substring ' abb ' ($x_{1,3}$) part of the string ' bb ' (r_2)?
- No, then ' abb ' is appended to the list of parsing elements, $S = \{'abb'\}$.

Algorithm 3 Modified Lempel-Ziv Parsing

```

1: procedure PARSE( $x, R$ )
2:   Create an empty list of substrings  $S$ 
3:    $p \leftarrow 1$ 
4:   while  $p \leq N$  do
5:      $stop \leftarrow \mathbf{false}$ 
6:      $dp \leftarrow -1$ 
7:     while not  $stop$  do
8:        $dp \leftarrow dp + 1$ 
9:        $T \leftarrow x_p, \dots, x_{p+dp}$ 
10:      if  $T \notin R$  or  $p + dp \geq N$  then
11:        append  $T$  to the list  $S$ 
12:         $p \leftarrow p + dp + 1$ 
13:         $stop \leftarrow \mathbf{true}$ 
14:      end if
15:    end while
16:  end while
17:  return  $S$ 
18: end procedure

```

- Is the substring ‘ b ’ ($x_{4,4}$) part of the substring ‘ ab ’ (r_1)?
- Yes, then the length of the test substring is incremented by one.
- The end of x was reached, then ‘ ba ’ ($x_{4,5}$) is appended to the list of parsing elements, $S = \{‘abb’, ‘ba’\}$

Therefore, the string $x = ‘abbba’$ is parsed as $S = \{‘abb’, ‘ba’\}$, and has a relative complexity of 2 with respect to the reference set R .

In order to compute this relative complexity for each signature sample of a given user, the genuine samples of all the other signers in the database are used as references. In other words, innovations (*i.e.*, sequences that do not occur in the references) of a particular signature sample are searched with respect to an ensemble of reference signatures provided by different people. Only velocities signals were parsed, since it was noted that they are the most informative signals when using the binary coding issued from the Infinite Clipping. The choice of using several different signers as reference was guided by the intuition that, as the MJ model proposes, there is an underlying process that is pertinent to the human movement itself and is common to all signers.

In Figure 5.10 is presented the average number of segments found through the MJ approach and the relative LZ complexity average for all the signatures of each user on the databases. The correlation coefficient ρ between the two measures is also provided.

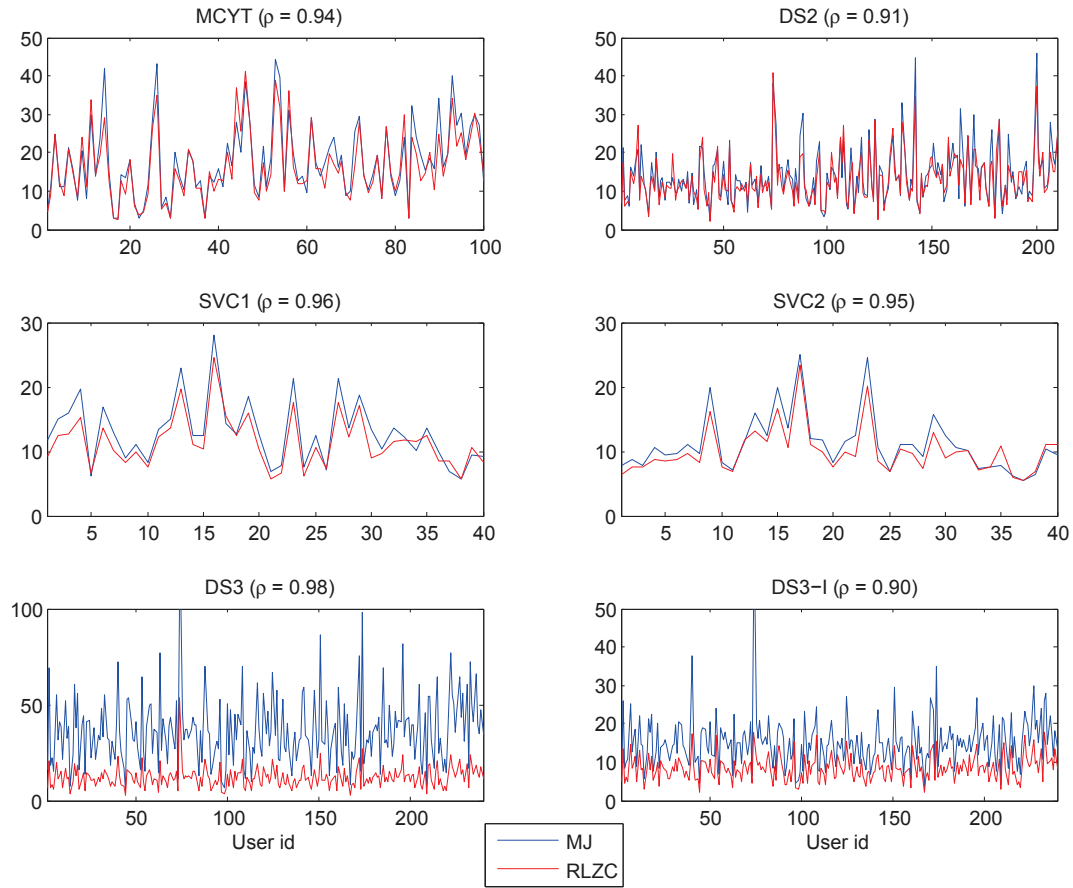


Figure 5.10: Average number of MJ segments and relative LZ complexity for each user.

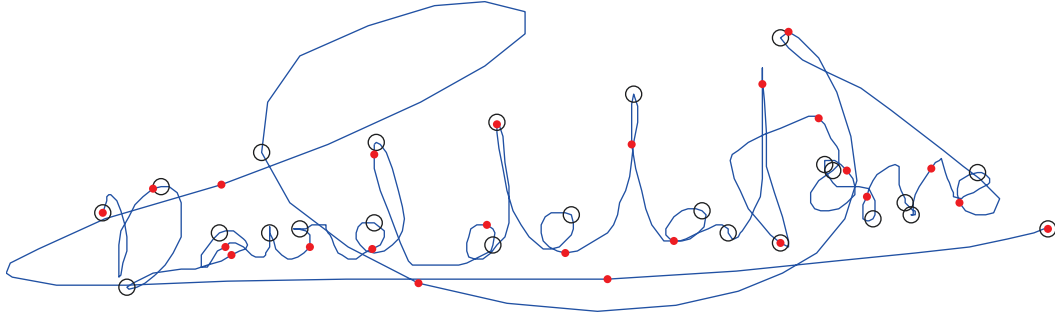


Figure 5.11: Segments obtained for the same signature through the modified LZ parsing (black circles) and the MJ representation (red dots).

First, note that there is a high correlation between the two complexity measures, which supports the use of the number of MJ segments as a complexity measure, as proposed in Section 4.4. It is also interesting noting that the DS3 database, the only one acquired through a mobile device, is the one that presents the greatest difference between the number of segments and relative LZ complexity; indicating that the mobility situation can significantly affect the smoothness of the writing movement, which is directly linked to the MJ criterion.

As for the number of MJ segments, the LZ complexity is very stable for a given user with a standard deviation of plus or minus 1.5. This allows for a good estimation of user complexity even when few reference signatures are available.

Finally, the modified LZ parsing procedure might also be used as a segmentation technique. However, even if the number of segments is close to that obtained by the MJ method, such segments may have different lengths. Figure 5.11 shows a signature for which the same number of segments is found using both segmentation algorithms (LZ and MJ). The position and length of the segments obtained by the MJ-based approach (red dots) and the LZ method (black circles) can be quite different. The similarity in the number of segments (Figure 5.10) is interesting, however, because despite the fact that the non-parametric model used by the LZ has only access to the clipped version of the velocity signals, it seems to capture the essential regularities of the signature.

5.6 Conclusion

In this chapter a novel signature representation, based on the Infinite Clipping signal processing technique is presented. This representation can be interpreted as a simplified version of the method proposed in Chapter 4. Unlike the previous method,

the reconstruction quality for this technique is always very low, since amplitude information is ignored, but compression rates above 94% are obtained for the studied signature databases.

In order to compare symbolic sequences obtained through the Infinite Clipping representation, the Levenshtein distance was adopted as matching technique. It was observed that verification performances are on the same level as those found in the literature for more elaborated systems (see Tables 3.4 to 3.7), despite the loss of amplitude information. This suggests that there is much redundancy in the features commonly used for signature verification.

An important aspect of this representation is that it does not allow for the reconstruction of the original signature, which might be an improvement for signature verification systems security. The destruction of the original signature protects the stored data from forgeries and also the users' privacy.

On the last section, the well known Lempel-Ziv complexity measure for symbolic sequences was studied. A conceptual relationship between the Lempel-Ziv parsing algorithm and the Minimum Jerk iterative segmentation, in which the 5th order polynomials of the MJ model perform a role similar to that of the past references of the LZ parsing algorithm, is presented. This relationship corroborates the use of the number of MJ segments as a signature complexity measure. Based on these relationships, a modified version of the relative Lempel-Ziv complexity algorithm was proposed, taking into account signatures from other users as references. This complexity measure is defined as the number of subsequences that do not appear on the reference samples.

It was noted that the Lempel-Ziv complexity value is very similar to the number of Minimum Jerk segments obtained by the representation in Chapter 4. This similarity between complexity values, using either the MJ or the LZ algorithms, reinforce the validity of the conceptual relationship previously presented (Table 5.9).

In the next chapter, final conclusions are drawn and the contributions of this work are summarized. Finally, several research perspectives related to the methods and results obtained in this thesis are proposed.

Conclusion and Perspectives

6.1 Conclusion

In this thesis two new representation techniques for online handwritten signatures have been proposed. The first technique is based on a well-known human movement control model, namely the Minimum Jerk. Three requirements were imposed to this representation: (1) it should have an *analytical form* for an easy use in analysis and synthesis, (2) it should provide a *compressed* coding, and (3) a *good reconstruction* of the original signal should be possible.

The second representation is based on the Infinite Clipping signal processing technique, used mainly for speech compression, and can be interpreted as a simplification of the first proposed representation. The goal was to obtain a signature representation as compressed as possible while preserving the essential discriminant information about the signature's owner. Unlike the previous method, based on the Minimum Jerk, reconstruction quality is not a requirement.

In Chapter 1 general notions regarding biometric systems were presented. Its main components, functions were discussed, along with the techniques used for performance assessment.

Next, in Chapter 2 the main theories regarding human movement planning were studied, with an emphasis on the Minimum Jerk Model, an Optimum Control theory-based method that provides the tools used in chapter 4 to develop the signature representation proposed in this work.

In Chapter 3, a study of online signature verification systems was presented, analyzing the techniques adopted at each of the main components of a biometric system. Then, the dynamic signatures databases adopted in this thesis were described and state-of-the-art results for each of them were presented.

The first chapter of the second part, Chapter 4, presented the first main contribution of this thesis: an online handwritten signature representation based on the Minimum Jerk model. The proposed algorithm yields a piecewise polynomial representation for a signature trajectory, obtained through an iterative segmentation/fitting technique. Following the imposed constraints, any desired representation quality can be achieved with a degree of compression that is directly linked to the chosen representation error requirement.

As a matter of fact, reconstruction error is the only parameter needed for the modeling algorithm, and a compression rate as high as 78% is obtained while maintaining a signal to noise ratio of 15 dB when comparing the original and reconstructed velocity profiles. From this point of view, this model can be interpreted as a “lossy” compression algorithm, such as the jpeg for image compression and the mp3 for audio compression; while the jpeg and mp3 are based on psychophysical aspects of the human vision and hearing, respectively, the Minimum Jerk signature model is based on aspects of the human movement control. This adjustable representation quality is a great improvement over other handwriting models found in the literature, since the user can choose the suitable error level for his/her application. Another advantage over existing techniques is that the proposed algorithm provides an automatic segmentation of the signature trajectory that is a direct consequence of the adopted movement model (Minimum Jerk), without the use of segmentation heuristics or manually inserted via-points.

Three applications of this model were proposed: signature resampling, samples complexity evaluation and generation of synthetic signatures. Resampling is a common preprocessing technique used in online signature systems, since time functions feature vectors usually have different lengths amongst signature samples. Using the proposed model it is possible to easily perform resampling while keeping the dynamics characteristics of the movement.

Quality measures for biometric samples have been studied for several years. Such measures can be used to ignore bad quality samples during acquisition or even to adapt the system parameters to a given user category, improving the overall system performance. The number of segments found by the MJ signature model can be used as a complexity measure that is linked both to the signature’s shape and dynamic properties.

The analytical form of the proposed representation allows for an easy generation of synthetic signatures through the addition of random perturbations to the parameters of the model. Synthetic signatures generation has been studied in the literature aiming at the resolution of a frequent problem on biometric applications: the limited number of available samples.

In Chapter 5 another signature representation is proposed. This representation is an adaptation of a signal processing technique used for speech compression, the Infinite Clipping, and can be interpreted as a simplified version of the method proposed in Chapter 4. Unlike the previous method, the reconstruction quality of this technique is always very low, since all amplitude information is disregarded. Considering that two bytes are used to store each coordinate at each sampling instant, this model has a compression rate of at least 94% for the signatures on the studied databases.

The symbolic sequence obtained from the Infinite Clipping representation was used with the Levenshtein distance matching technique. Despite all information loss, it was observed that verification performances on the same level as those found in the literature (see Tables 3.4 to 3.7 and 5.8). This gives an insight that there is a

great deal of redundancy on the features commonly used for signature verification. Despite using biometric verification experiments as tools to analyze and evaluate the proposed representation methods, it is worth remarking that, contrary to most biometrics works, the development of a better verification system was not the main goal of this thesis.

Since this representation yields a good verification performance and does not allow for the reconstruction of the original signature, it might be an improvement for signature verification systems security; this loss of the original signature actually protects the data stored by the system because no forgery can be produced from the available clipped representation.

Finally, based on the binary coding of the signatures, the well known Lempel-Ziv complexity measure for symbolic sequences was used. A modified version of the relative complexity algorithm was proposed, taking into account other signatures as references. The complexity measure is defined as the number of subsequences that do not appear on the reference samples. It was noted that the Lempel-Ziv complexity value is very close to the number of Minimum Jerk segments obtained by the representation in Chapter 4. It is worth remarking that this modified Lempel-Ziv parsing algorithm can also be used as an alternative signature segmentation method, where each segment is a subsequence that contains an innovation (different symbol) as related to the reference samples.

The observed similarities between complexity values and some segmentation points corroborate the conceptual relationship between the Minimum Jerk signature model and the Lempel-Ziv algorithm, presented in Section 5.5, in which the 5th order polynomials of the MJ model perform a role similar to that of the past references on the LZ algorithm.

The contributions of this work can then be summarized as follows:

- An original online signature model based on the Minimum Jerk principle with the following properties:
 - adjustable representation quality,
 - adjustable compression rate (linked to the representation quality).
- A new automatic segmentation method based on the Minimum Jerk principle where:
 - the number of segments reflects signature's complexity.
- A new signature symbolization based on the Infinite Clipping technique in which:
 - discriminative information is kept,
 - original signature shape is lost (privacy improvement),
 - a high compression rate is obtained ($\approx 94\%$).

- A conceptual relationship between the Lempel-Ziv complexity and the number of segments obtained through the MJ signature model.

6.2 Future work

Several work perspectives can be considered. Regarding the Minimum Jerk representation proposed in Chapter 4, a first work would be to perform a more thorough evaluation of the proposed complexity measure on a framework similar to that developed in (Houmani, 2011). This study should also investigate the effects, in terms of performance, of the integration of the complexity measure on the enrollment and classification steps of the verification system.

A second work perspective is the study of the synthetic signatures generation, including a technique to model also pressure information. The generation method can also be improved to provide a better control of the variations and even the generation of synthetic users. A proper modeling of the signatures parameters can lead to the possibility of choosing between the generation of synthetic genuine or skilled forgeries. Furthermore, the influence of these artificial samples on the training of classifiers also needs to be investigated.

A final work perspective based on the Minimum Jerk approach is the diagnostic aid for neuromotor disorders such as Parkinson's disease and dyspraxia. Since the Minimum Jerk principle was developed through the observation of healthy adults, the typical number of Minimum Jerk segments found using the proposed iterative segmentation technique should be affected by these disorders. However, it is likely that standard psychophysical tasks, such as drawing basic shapes, might be more suitable for this application. Unfortunately, no public database of such movements is available, therefore a data acquisition campaign will be needed in order to follow this work path.

With regards to the signature symbolization in Chapter 5, many work perspectives have been envisaged. A first, straightforward, perspective is considering other features, such as pressure on the verification process. This inclusion of additional features can either be done on the Levenshtein distance-based system itself or through the fusion with other verification systems. Since very little information is used by the proposed system and its performance is still comparable to those of more elaborate systems, there should be plenty of room for improvement.

A second working path is related to the verification experiments using different feature sets (Table 5.7). It was observed that the best feature set for the database acquired through a mobile device had half the number of features of the best set for the other databases (acquired using a digitizing tablet). It would be interesting to investigate other datasets acquired on a mobile platform and verify if this observation holds. In such way it could be possible to select an optimal feature set for different acquisition conditions.

Another work perspective related to the verification system based on signature

symbolization is already in progress. It consists on the application of this system to other handmade trajectories (*e.g.*, doodles, drawings) acquired through different devices, such as mouse and touchscreens. A commercial biometric application based on this system is currently being developed by a Brazilian enterprise¹.

Finally, the study of both segmentation techniques (MJ-based and LZ-based) along with verification approaches based on regional features (stroke-by-stroke) is envisaged. This can help determining which technique is more suitable for signature verification tasks. It is also expected that, for the Minimum Jerk segmentation, the length of the stroke can provide a regional measure of complexity; longer segments should correspond to a more smooth region of the trajectory, as a consequence of the Minimum Jerk criterion.

¹<http://www.biostroke.com.br/biomotion/en/biomotion.jsp>

Part III

Bibliography and Appendices

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