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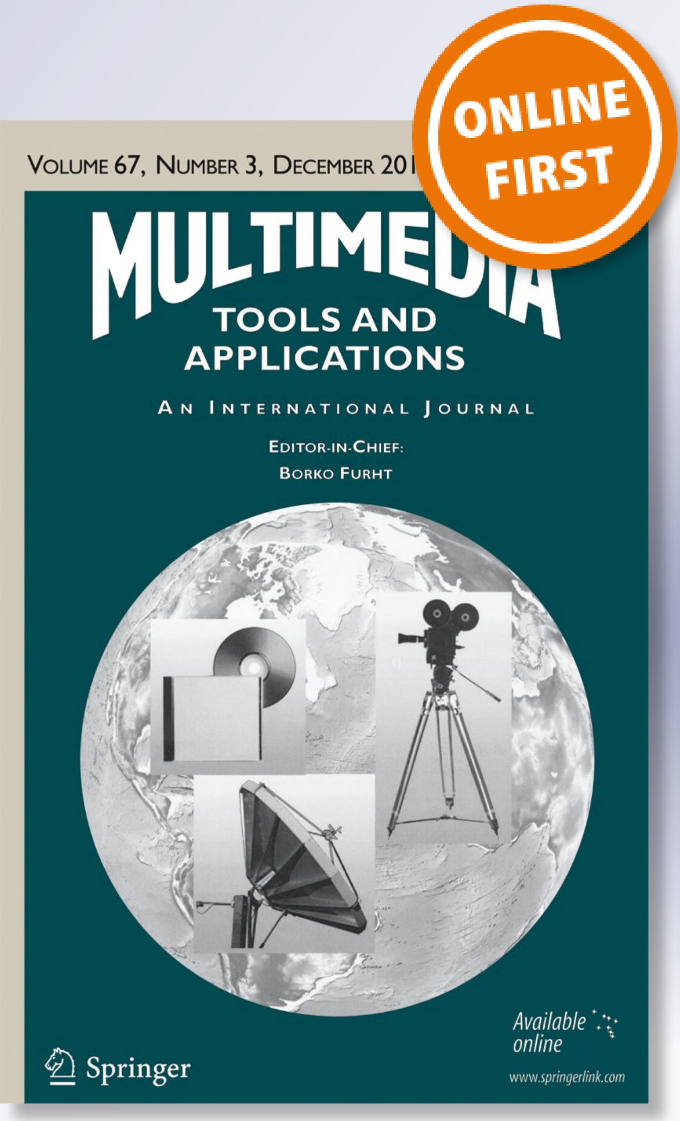

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A comprehensive overview of feature representation for biometric recognition

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Abstract

The performance of any biometric recognition system heavily dependents on finding a good and suitable feature representation space where observations from different classes are well separated. Unfortunately, finding this proper representation is a challenging problem which has taken a huge interest in machine learning and computer vision communities. In the this paper we present a comprehensive overview of the different existing feature representation techniques. This is carried out by introducing simple and clear taxonomies as well as effective explanation of the prominent techniques. This is intended to guide the neophyte and provide researchers with state-of-the-art approaches in order to help advance the research topic in biometrics.

Keywords Biometrics · Feature representation · Dimensionality reduction · Feature selection · Decomposition learning

1 Introduction

Over the few past decades, biometric security is increasingly becoming an important tool to enhance security and brings greater convenience. Nowadays, biometric systems are widely

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used by government agencies and private industries. Though a growing effort has been devoted in order to develop robust biometric recognition systems that can operate in various conditions, many problems still remain to be solved, including the design of techniques to handle varying illumination sources, occlusions and low quality images resulting from uncontrolled acquisition conditions [1, 70, 73, 78, 81]. Indeed, doing this efficiently and completely represents a continuous challenging problem which took the effort and attention of researchers.

Biometric recognition consists in determining the identity for a given person based on his/her physiological or behavioral characteristics [5, 76]. A large variety of biometric modalities including face, iris, gait, keystroke and palmprint have been studied providing different rates of robustness, accuracy and user acceptability [29, 79, 80]. Given the goal of recognizing individuals based on their features, the main task of an automated recognition system can be divided into three basic subtasks: the description subtask which generates features of a person using feature extraction techniques, mapping raw features into another discriminative space where different persons are well separated by feature representation techniques and finally the classification subtask which assigns the identity to new person based on those features and a trained classifier (see Fig. 1).

With the recent advances in machine learning techniques; the goal of this paper is to familiarize the biometrics researchers to the prominent methods and ways of machine learning for feature representation and its correct research methodology. Section 2 introduces the assumptions of a good representation. Section 3 presents the main dimensionality reduction techniques. Section 4 describes the prominent feature selection approaches. Section 5 reports decomposition learning. Section 6 explains the classification. Section 7 reports the discussions. Finally, Section 8 gives our conclusion.

2 Feature representation

The performance of any recognition system is heavily dependent on finding a good and suitable feature representation space which should satisfy the following assumptions [9]:

- Smoothness: in a high density region, if two points $\mathbf{x}_1$ and $\mathbf{x}_2$ are near $\mathbf{x}_1 \approx \mathbf{x}_2$, their outputs by a decision function f are more probable to be close $f(\mathbf{x}_1) \approx f(\mathbf{x}_2)$. This assumption implies also that in case two points are connected by a high density path, their outputs are also likely to be close also. On the other hand, if they are connected by a low density path, then their outputs don't need to be close.
- Cluster: the data tend to be organized in discrete clusters, and points in the same cluster are more likely to share the same class label. The cluster assumption does not mean the data from each class forms a single and unique compact cluster, but rather that we may not observe data from two different classes within the same cluster.
- Manifolds: curse of dimensionality represents a huge problem for many discriminative learning algorithms since the distances tend to be less meaningful and representative. The manifold assumption implies that, the initial data of high dimension reside in a manifold of lower dimension integrated in the ambient space to overcome the curse of dimensionality problem.
- Sparsity: a feature vector $\mathbf{x}$ is called sparse if most of its entries are zeros. Sparse representations are able to extract the hidden structure and provide a simple interpretation of the input data. Furthermore, it has been found that biological vision is based on sparse representations [68].

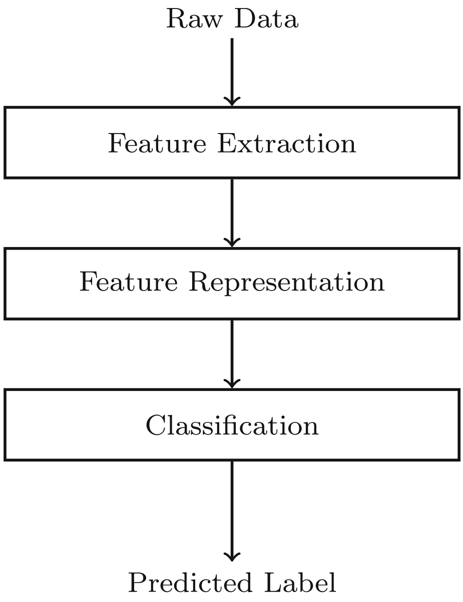

Fig. 1 Scheme of a conventional recognition system

- Temporal and spatial coherence: spatially nearby or consecutive (temporally close) observations tend to share the same value ($\mathbf{x}_t \approx \mathbf{x}_{t+1}$). The simultaneous temporal and spatial changes should be penalized.

We envision feature representations under three points of view: dimensionality reduction, feature selection and decomposition learning (see Fig. 2).

3 Dimensionality reduction

Analyzing high-dimensional data is a difficult problem, since the high-dimensional spaces have geometrical properties that are very complex and hardly interpretable compared to low-dimensional ones. Furthermore, learning a good model needs enough data, while the number of learning data should grow exponentially with the dimension which causes the so called curse of dimensionality [98, 100]. Dimensionality reduction aims to find a transformation mapping the original data residing in a high-dimensional space into a lower one able to capture and preserve the intrinsic characteristics of the initial data. It helps in classification, visualization and compression since it has ability if well designed, to reduce the undesirable

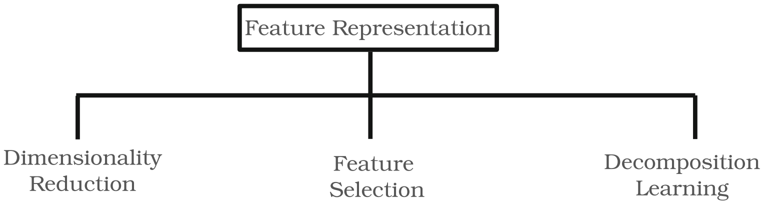

Fig. 2 Taxanomy of feature representation approaches

effects of high-dimensional spaces [39]. Related techniques can be broadly divided into two main groups, linear and non-linear. We briefly introduce hereafter the prominent linear and non-linear methods.

3.1 Linear dimensionality reduction

Given n d-dimensional samples $\{\mathbf{x}_i\}_{i=1}^{n}$ stored in matrix $\mathbf{X} \in \mathbb{R}^{d\times n}$ and a dimensionality choice $r < d$, linear dimensionality reduction aims to find a linear matrix transformation $\mathbf{P} \in \mathbb{R}^{r\times d}$ by optimizing an objective function J such that the high-dimensional $\mathbf{X}$ is mapped into low-dimensional data $\mathbf{Z} = \mathbf{P}\mathbf{X} \in \mathbb{R}^{r\times n}$. Linear dimensionality reduction methods can be formulated as an optimization problem over a manifold matrix [19] as follows:

$$\begin{cases} \min\limits_{\mathbf{M}\in\mathbb{R}^{d\times r}} & J(\mathbf{M},\mathbf{X}) \\ \text{s.t} & \mathbf{M}\in\mathcal{M} \end{cases} \tag{1}$$

The objective function J and the manifold matrix $\mathbf{M}$ try to capture the desired and relevant characteristics. In some linear dimensionally techniques, the matrix $\mathbf{M}$ is imposed to be orthogonal, hence $\mathcal{M} = \{\mathbf{M} \in \mathbb{R}^{d\times r} : \mathbf{M}^T\mathbf{M} = \mathbf{I}\}$. In this particular case the manifold $\mathcal{M}$ is noted $\mathcal{O}^{d\times r}$.

The relation between the projection matrix $\mathbf{P}$ and $\mathbf{M}$ will change depending on the used method. Indeed, there are many techniques in linear dimensionality reduction such as, Principal Component Analysis (PCA) [65], Linear Discriminant Analysis (LDA) [30], Independent Component Analysis (ICA) [37] and Factor Analysis (FA) [88]. The objective function J differs according to desired properties or assumptions (supervised or not, gaussian assumption, statistical independence, etc) encoded by these techniques.

3.1.1 Principal component analysis

Principal Component Analysis (PCA) is an unsupervised linear dimensionality reduction technique initially formulated as the minimization of the residual errors between the original and the projected data [16, 54, 55, 65]:

$$\begin{cases} \min\limits_{\mathbf{M}\in\mathbb{R}^{d\times r}} & \left\|\mathbf{X}-\mathbf{M}\mathbf{M}^T\mathbf{X}\right\|_F^2 \\ \text{s.t} & \mathbf{M}\in\mathcal{O}^{d\times r} \end{cases} \tag{2}$$

The problem 2 can be equivalently reformulated as variance maximization of projected data [10] leading to:

$$\begin{cases} \min\limits_{\mathbf{M}\in\mathbb{R}^{d\times r}} & -\text{tr}\,(\mathbf{M}^T\mathbf{X}\mathbf{X}^T\mathbf{M}) \\ \text{s.t} & \mathbf{M}\in\mathcal{O}^{d\times r} \end{cases} \tag{3}$$

The solution $\mathbf{M}$ corresponds to the r leading principal eigenvectors of $\mathbf{X}\mathbf{X}^T$ and we get the projection matrix $\mathbf{P} = \mathbf{M}^T$. The size of covariance matrix $\mathbf{X}\mathbf{X}^T$ is proportional to the dimensionality of the data which could lead to the tedious calculation of the eigenvectors when the initial data has very high-dimensionality. There have been some extensions of the PCA, such as Kernel PCA [85] a non-linear extension, probabilistic PCA [82, 94] and sparse PCA [20, 42, 113].

3.1.2 Linear discriminant analysis

Linear Discriminant Analysis (LDA) is a supervised technique which aims to project the data in lower subspace where the data from different classes are well separated. In other terms, the LDA seeks to minimize the intra-class variations and to maximize the between-class variations. It is formulated by the following problem [28]:

$$\begin{cases} \max\limits_{\mathbf{M}\in\mathbb{R}^{d\times r}} & \dfrac{\text{tr }(\mathbf{M}^T\Sigma_B\mathbf{M})}{\text{tr }(\mathbf{M}^T\Sigma_W\mathbf{M})} \\ \\ \text{s.t} & \mathbf{M}\in\mathcal{O}^{d\times r} \end{cases} \tag{4}$$

with

$$\Sigma_W = \sum_{i=1}^{n}(\mathbf{x}_i-\boldsymbol{\mu}_{c_i})(\mathbf{x}_i-\boldsymbol{\mu}_{c_i})^T \qquad \Sigma_B = \sum_{i=1}^{n}(\boldsymbol{\mu}_{c_i}-\boldsymbol{\mu})(\boldsymbol{\mu}_{c_i}-\boldsymbol{\mu})^T \tag{5}$$

where $\boldsymbol{\mu}$ and $\boldsymbol{\mu}_{c_i}$ respectively represent the mean of the whole dataset and the mean of class c which the sample $\mathbf{x}_i$ belonging to. The projection matrix $\mathbf{P} = \mathbf{M}^T$.

3.1.3 Independent component analysis

Independent Component Analysis (ICA) is a linear higher-order method which does not impose the orthogonality constraint and with assumption that the components are as independent as possible. Compared to uncorrelatedness of linear PCA, the statistical independence represents a stronger condition to represent the data. ICA tries to find a matrix $\mathbf{P}\in\mathbb{R}^{r\times d}$ which is able to capture the independent sources $\mathbf{Z}\in\mathbb{R}^{r\times n}$ from the initial data $\mathbf{X}\in\mathbb{R}^{d\times n}$ where $\mathbf{Z} = \mathbf{PX}$. The majority of ICA implementations deal with dimension preserving case where the projection $\mathbf{P}$ is such that $d = r$ (in this case, the ICA is not seen as a dimensionality reduction method since it preserves the dimensionality of the initial data).

To use the ICA as dimensionality reduction method, an undercomplete version $r < d$ is needed. There are several works which tried to undercomplete the ICA using a preprocessing step [2, 21, 67, 103, 110]. A possible preprocessing is PCA, which reduces the dimensionality of the initial data to $r < d$, after that the conventional ICA is applied to the resulting data [41] which leads to a projection in a low-dimensionality space with statistical independence. Note also that there are also overcomplete versions of the ICA when $r > d$ [91] mainly applied to blind source separation task.

3.1.4 Factor analysis

Factor analysis (FA) is a generative model which assumes that the observed data have been produced from a set of latent unobserved variables (called here factors). FA can be seen as a more general case of Probabilistic PCA (PPCA) [19, 43] and addresses the following problem:

$$\min_{\mathbf{M}\in\mathbb{R}^{d\times r}} \log|\mathbf{M}\mathbf{M}^T+\mathbf{D}| + \mathrm{tr}\left((\mathbf{M}\mathbf{M}^T+\mathbf{D})^{-1}\mathbf{X}\mathbf{X}^T\right) \tag{6}$$

where $\mathbf{M}$ is the factor loading matrix and $\mathbf{D}$ is a diagonal matrix for the conditional data likelihood $\mathbf{x}_i|\mathbf{z}_i \sim \mathcal{N}(\mathbf{M}\mathbf{z}_i, \mathbf{D})$ representing the observation noise fit. The linear dimensionality reduction mapping of the initial data $\mathbf{X}$ is given by $\mathbf{Z} = \mathbf{P}\mathbf{X}$ where $\mathbf{P} = \mathbf{M}^T(\mathbf{M}\mathbf{M}^T + \mathbf{D})^{-1}$.

3.2 Nonlinear dimensionality reduction

Conventional linear dimensionality reduction techniques, such as PCA and ICA are designed to operate when the observed initial high-dimensionality data is embedded in a low-dimensional linear manifold. However, real world data have a very complex structure and reside generally on nonlinear manifolds [56]. Based on the latter reasons it has been demonstrated that traditional methods are not suitable to deal with such complex structure. Encouraged by the gaps and weakness of linear techniques, numerous nonlinear dimensionality reduction techniques have been introduced. These techniques can be broadly divided into two main groups: local and global. The local approach involves Locally Linear Embedding (LLE) [83] and Laplacian Eigenmaps (LE) [7]; when the global approach involves Isometric Feature Mapping (Isomap) [90] to name a few.

Local methods seek to preserve the local geometry of the observed data; in other terms, these methods try to preserve the neighborhood by mapping the nearby points in the initial high-dimensional manifold to nearby points in low-dimensional one. This is done by approximating each point on the manifold with a combination of its neighbors; and then based on resulting weights, a low-dimensional embedded manifold is constructed. Local approaches have good representational ability, for a larger range of manifolds, whose local geometry is close to Euclidean, furthermore they are computationally efficient [87]. In the other hand, global methods, attempt to preserve the geometry at all scales, mapping nearby points on the manifold to nearby points in low-dimensional space, and faraway points to faraway points. The advantage of the global methods is the ability to give more general and faithful representation of global structure of the data [87].

There have been some works which tried to incorporate strengths of the local methods in the global methods such as Conformal Isomap (C-Isomap) [87]. C-Isomap extends Isomap to be capable to learn the structure of curved manifolds. As a result it is computationally efficient (equals to or better than the existing local approaches such LLE and LE) with good stability and theoretical tractability characteristics of the methods belonging to global approach [87]. In the following we introduce the main concepts of several widely used nonlinear techniques.

3.2.1 Isomap

It attempts to preserve the geometric properties of the data. It was introduced to deal with the problem of classical scaling methods which consider two high-dimensional data points lying in curved manifold as close points whereas they are not really close [96]. Isomap method has three main steps, the first one consists on constructing a neighborhood graph G where each data point $\{\mathbf{x}_i\}_{i=1}^n$ is connected with its neighbors $\{\mathbf{x}_j\}_{j=1}^k$ in the high-dimensional dataset $\mathbf{X} \in \mathbb{R}^{d\times n}$. In second step, Isomap estimates the geodesic distances between all pairs of data points by computing their shortest path in the graph G using Dijikstra's [23] or Floyd's [31] shortest path algorithm. The third and ultimate step consists on applying classical Multidimensional Scaling (MDS) [95] to resulting geodesic distance matrix $\mathbf{D} \in \mathbb{R}^{n \times n}$. It consists in solving the following optimization problem:

$$\min_{\{\mathbf{z}_i \in \mathbb{R}^r\}_{i=1}^n} \sum_{i=1}^{n} \sum_{j=1}^{n} \left({d_{ij}}^2 - \|\mathbf{z}_i - \mathbf{z}_j\|^2 \right) \tag{7}$$

where d_{ij} represents the geodesic distance between $\mathbf{x}_i$ and $\mathbf{x}_j$. $\mathbf{z}_i$ and $\mathbf{z}_j$ stand for the low-dimensional representation of $\mathbf{x}_i$ and $\mathbf{x}_j$ respectively. It has been shown that the solution of the problem is $\mathbf{Z} = \mathbf{U}\Sigma^{\frac{1}{2}}$ issued from the spectral decomposition of the Gram matrix $\mathbf{K}$ which is the double centering of the geodesic distance matrix $\mathbf{D}$.

3.2.2 Locally linear embedding

Locally Linear Embedding (LLE) is a method which aims to preserve the local characteristics and properties of the data. Compared to the methods belonging to global approach such as Isomap, the LLE is less sensitive to short-circuiting problem which happens when the local neighborhood connections shortcut across the manifold [96]. LLE captures the local properties of the manifold around each data point $\{\mathbf{x}_i \in \mathbb{R}^d\}_{i=1}^n$ by expressing $\mathbf{x}_i$ as a linear combination of its k neighbors $\{\mathbf{x}_{ij}\}_{j=1}^k$ with coefficients $\{\mathbf{w}_i \in \mathbb{R}^k\}_{i=1}^n$. Here $\mathbf{x}_{ij}$ represents the j^{th} neighbor of $\mathbf{x}_i$. By doing so, the manifold is assumed to be locally linear which implies that the weights $\mathbf{w}_i$ of $\mathbf{x}_i$ are invariant to different transformations such as translation and rotation, etc. Formally the weights $\{\mathbf{w}_i \in \mathbb{R}^k\}_{i=1}^n$ are first estimated by solving:

$$\begin{cases} \min\limits_{\{\mathbf{w}_i \in \mathbb{R}^k\}_{i=1}^n} \sum\limits_{i=1}^{n} \left\| \mathbf{x}_i - \sum\limits_{j=1}^{k} w_{ij} \mathbf{x}_{ij} \right\|^2 \\ \text{s.t} \quad \sum\limits_{j=1}^{k} w_{ij} = 1 \qquad \forall i = 1, \cdots, n \end{cases}$$

We shall notice that the weights $w_{ij} = 0$ for all samples $\mathbf{x}_j$ not belonging to the k-neighborhood of $\mathbf{x}_i$. Based on the transformation invariance property, the weights $\mathbf{w}_i = [w_{i1}, \cdots, w_{ik}]$ that construct the initial data in high-dimensional space based on its neighbors are also able to reconstruct $\mathbf{z}_i$ from its neighbors in low-dimensional space. Finding the new representation $\{\mathbf{z}_i \in \mathbb{R}^r\}_{i=1}^n$ where $r < d$ is formulated by the following minimization problem:

$$\begin{cases} \min\limits_{\{\mathbf{z}_i \in \mathbb{R}^r\}_{i=1}^n} \sum\limits_{i=1}^{n} \left\| \mathbf{z}_i - \sum\limits_{j=1}^{k} w_{ij} \mathbf{z}_{ij} \right\|^2 \\ \text{s.t} \quad \|\mathbf{z}_i\|^2 = 1 \qquad \forall i = 1, \cdots, n \end{cases} \tag{8}$$

[83] established that the reduced dimension solutions $\{\mathbf{z}_i\}_{i=1}^n$ are obtained by calculating the eigenvectors corresponding to r smallest nonzero eigenvalues of $(\mathbf{I} - \mathbf{W})^T(\mathbf{I} - \mathbf{W})$ where $\mathbf{I} \in \mathbb{R}^{n \times n}$ and $\mathbf{W} \in \mathbb{R}^{n \times n}$ a matrix with entries equal to the weight w_{ij} when i and j are connected in the neighborhood graph and 0 otherwise. Note that there have been some extensions of the LLE such as Orthogonal Neighborhood Preserving Projections [46] and Neighborhood Preserving Embeddings [36].

3.2.3 Laplacian eigenmaps

Laplacian Eigenmaps (LE) aims to find a low-dimensional representation by preserving local properties of the high-dimensional data based on pairwise distances between neighbors. For the latter, LE tries to minimize a cost function based on the sum of the distances between each data point in the low-dimensional space $\{\mathbf{z}_i\}_{i=1}^n$ and its k nearest neighbors $\{\mathbf{z}_j\}_{j=1}^k$. The distance between each data point and its first nearest neighbor contributes more in the cost function than the second and so on. This is made possible by constructing a weighting matrix $\mathbf{W} \in \mathbb{R}^{n\times n}$, where its entries w_{ij} corresponds to the distance between data point $\mathbf{x}_i$ and its k-nearest neighbor using the Gaussian kernel function given by:

$$\begin{cases} w_{ij} = e^{-\frac{\|\mathbf{x}_i-\mathbf{x}_j\|^2}{2\sigma^2}} & \text{if } \mathbf{x}_j \text{ is in the } k\text{-neighborhood of } \mathbf{x}_i \\ w_{ij} = 0 & \text{otherwise} \end{cases} \quad (9)$$

where σ is the bandwith of the Gaussian. The computation of the low-dimensional representation $\mathbf{z}_i$ is obtained through the following optimization problem:

$$\min_{\{\mathbf{z}_i\in\mathbb{R}^r\}_{i=1}^n} \sum_{i=1}^n \sum_{j=1}^n \left\|\mathbf{z}_i - \mathbf{z}_j\right\|^2 w_{ij} \quad (10)$$

In the cost function, large values of w_{ij} means that the data points $\mathbf{x}_i$ and $\mathbf{x}_j$ have small distance in the high-dimensional space. In other words, nearby points $\mathbf{x}_i$ and $\mathbf{x}_j$ in the high-dimensional space are mapped into low-dimensional space $\mathbf{z}_i$ and $\mathbf{z}_j$ with the lowest distance possible. Defining $\mathbf{Z} = [\mathbf{z}_1, \cdots, \mathbf{z}_n]$, the problem in formula (10) can be reformulated as an eigenproblem [96] as follows:

$$\begin{cases} \min\limits_{\mathbf{Z}\in\mathbb{R}^{r\times n}} \quad 2\mathbf{Z}\mathbf{L}\mathbf{Z}^T \\ \text{s.t} \quad \mathbf{Z}\mathbf{D}\mathbf{Z}^T = \mathbf{I} \end{cases} \quad (11)$$

where the equality constraint removes an arbitrary scaling factor in low-dimensional space, $\mathbf{D}$ is a diagonal matrix with entries $\mathbf{D}_{ii} = \sum_{j=1}^n w_{ij}$ and $\mathbf{L}$ is the graph Laplacian given by $\mathbf{L} = \mathbf{D} - \mathbf{W}$. The solution of the problem is the r eigenvectors corresponding to the r smallest nonzero eigenvalues of generalized eigenvalue problem:

$$\mathbf{L}\mathbf{v} = \lambda\mathbf{D}\mathbf{v} \quad (12)$$

4 Feature selection

Feature selection aims to select a relevant feature subset $\mathcal{S}$ from the original initial set $\mathcal{I}$ ($\mathcal{S} \subset \mathcal{I}$) which is efficiently able to describe the intrinsic characteristics of the input data by reducing the impact of the noise and irrelevant features [15, 17, 57, 58, 72]. In fact dependent features do not give extra information about the data belonging to a class (e.g. when two features are highly correlated, a single one is sufficient to describe the characteristics of the class). In other words, the total information of the data can be captured only from few unique features able to express the discriminative characteristics of each class leading to the reduction of the data dimension [14, 74]. As such feature selection can be seen as an instance of dimension reduction preserving the original variables. Removing irrelevant features requires an efficient feature criterion which measures the relevance of each feature so as to be able to select a feature subset from 2^d possible subsets where d is the cardinality of $\mathcal{I}$. There are three main approaches used in features selection, filter, wrapper and embedded methods [34].

4.1 Filter

Filter methods include non-learning techniques exclusively. Features are ranked according to scores that depend on their relevance according to pre-defined criterion. They are mainly applied before the classification step, to filter out the irrelevant features (for instance features with scores below a threshold are discarded). The notion of feature relevance remains an open question; several definitions have been introduced based on the context of the problem [34, 45, 48]. In our thesis and since we are in classification context, we adopt the definition that presents an irrelevant feature as the independent one of the class label. In other words, a feature is considered irrelevant if it has no information about the class label [49]. In some cases features which have no dependency or correlation with classes serve as noise and eliminating them might lead to improvement in the classification accuracy.

Several criterions have been introduced such as, Pearson correlation coefficients [34] and Mutual Information (MI) [6, 45, 50] which are able to estimate the dependency between a feature and a target (the target can be for instance the class label). The advantage of methods belonging to filter approaches is that they are computationally efficient and avoid overfitting since they do not rely on learning algorithms [34, 50]. However filter methods have also some drawbacks, such as, MI and correlation-based methods which are not able to estimate the correlation between features leading sometimes to correlated features within the same feature subset [40, 53]. Furthermore filter methods are usually not optimal since they do not account for the mechanism of the learning algorithm [3].

4.2 Wrapper

Wrapper methods used a learning algorithm as a black-box. Given the original feature set, all possible subsets obtained by search algorithms are evaluated with a classifier. The prediction performance serves as the selection criterion, and the subset that performs the best is retained. Sadly, evaluating 2^d is an NP-hard problem and can become intractable and computationally intensive when the number of features is very large [45, 64]. Based on that, some simplified algorithms such as Genetic Algorithm (GA) [32] and Particle Swarm Optimization (PSO) [44] have been introduced; they can make a good trade off between computational cost and performance. Methods belonging to wrapper approaches can be broadly divided into, Sequential Selection Algorithms and Heuristic Search Algorithms [14].

In sequential selection algorithms we can find Sequential Forward Selection (SFS) and Sequential Backward Selection (SBS). The first one starts with an empty set and adds one feature at time which gives the maximum classification accuracy. The process is repeated until the number of required features is reached. The second one follows the same steps, however instead of starting with empty set, it starts with the full set and, instead of adding a feature, it removes it. In the heuristic search algorithms we can find algorithms such as GA [32] and its variants such as CHCGA [26] and PSO [44]. The heuristic algorithms have been introduced to avoid exhaustive search and cope against the problem of the greedy methods which do not examine all possible subsets and hence do not guarantee finding an optimal subset.

4.3 Embedded

Embedded methods, as the name suggests, embed feature selection into the learning algorithm. They seek to reduce the computation complexity time needed to evaluate the different feature subsets in order to select an optimal one as in the wrapper methods [14]. Embedded methods have been successfully used in linear problems, by including convex and concave regularization terms [89]. Recently, there have been also some works to extend feature selection methods to group feature selection in both linear and nonlinear models [61]. For sake of simplicity, we suppose that our decision function is linear and applied on $\mathbf{x} \in \mathbb{R}^d$. The definition is given by:

$$f(\mathbf{x}) = \mathbf{x}^T\mathbf{w} + b \tag{13}$$

with $\mathbf{w} \in \mathbf{R}^d$ and $b \in \mathbb{R}$ is the bias. Embedded methods typically attempt to solve the learning problem:

$$\min_{\mathbf{w},b} \frac{1}{n} \sum_{i=1}^{n} L(y_i, f(\mathbf{x}_i)) + \lambda\Omega(\mathbf{w}) \tag{14}$$

where y_i is the label associated with $\mathbf{x}_i$, $\Omega(\mathbf{w})$ is the regularization term and $\lambda > 0$ the regularization parameter. The first term in previous equation expresses data fitting error. Regularization aims to select features and also to avoid the overtraining [59]. This generally leads to better performances of the learned decision function [66].

The regularization $\Omega(\mathbf{w})$ tends to promote peculiar characteristics such as sparsity on $\mathbf{w}$ [101]. Norms and quasi-norms ℓ_p represent one of the most used regularization terms, they are given by:

$$\Omega_p(\mathbf{w}) = \|\mathbf{w}\|_p = \left(\sum_{i=1}^{d} |\mathbf{w}_i|^p\right)^{\frac{1}{p}} \tag{15}$$

with $0 < p \leq \infty$ and $\Omega_p(\mathbf{w})$ is considered as norm for $p \geq 1$. The regularization can be broadly categorized as standard and structured.

4.3.1 Standard regularization

- ℓ_0 - ”pseudo norm”: it counts the number of non zero coefficients in the vector $\mathbf{w}$.
- Convex relaxation: it promotes sparsity on the vector $\mathbf{w}$ using convex regularizers which generally lead to easier optimization problem.
  - Norm ℓ_2: also called Euclidean norm because it is inducted from the dot product. In the case of the linear regression [35], the square of the ℓ_2 regularization is called ridge regression. Notice that sparsity is attained in practice for high values of the regularization parameter λ.
  - Norm ℓ_1: it is known in the linear regression as LASSO (Least Absolute Shrinkage and Selection Operator) [92].

  - Fused Lasso: it penalizes ℓ_1-norm of the difference between two successive coefficients of $\mathbf{w}$ which leads to sparsity of the coefficients difference [93]:

$$\Omega(\mathbf{w}) = \sum_{i=1}^{d-1} \|\mathbf{w}_{i+1} - \mathbf{w}_i\|_1 \tag{16}$$

- Non-convex relaxation: promotes sparsity more strongly than convex regularizers, but it suffers the difficulties brought by local optimums.
  - ℓ_p with $0 < p < 1$: when the sparsity obtained by ℓ_1 is not sufficient and more sparsity is needed, the ℓ_p with $0 < p < 1$ could be applied.
  - Log-sum: introduced in [104] for sparse SVM classification, it is given by:

$$\Omega_\epsilon(\mathbf{w}) = \sum_{i=1}^{d} \log(\epsilon + |\mathbf{w}_i|) \tag{17}$$

  - Minimax concave penalty (MCP): introduced in the context of linear regression [111], it is given by:

$$\Omega_{\lambda,\gamma}(\mathbf{w}) = \begin{cases} \lambda|\mathbf{w}_i| - \dfrac{|\mathbf{w}_i|^2}{2\gamma} & \text{if } |\mathbf{w}_i| \le \gamma\lambda \\ \dfrac{\gamma\lambda^2}{2} & \text{if } |\mathbf{w}_i| > \gamma\lambda \end{cases} \tag{18}$$

Table 1, Figs. 3 and 4 compare the properties of the different regularizers introduced above.

4.3.2 Structured regularization

In some cases, it is interesting to introduce sparsity by group of features based on the previous regularizers [99]. For a linear decision function, the weights of $\mathbf{w} \in \mathbb{R}^d$ can be decomposed intro groups (overlapping or not) $g \in \mathcal{G}$. For instance, when $d = 3$, the partition $\mathcal{G} = \{(1, 2), (3)\}$ contains two groups, the first one includes two variables (1 and 2)

Table 1 Properties of several regularization terms

	Standard regularization		
	Regularity	Convexity	Non convexity
• ℓ_2	✓	✓	–
• ℓ_1	–	✓	–
• Fused lasso	–	✓	–
• $\underset{0<p<1}{\ell_p}$	–	–	✓
• Log-sum	✓	–	✓
• MCP	✓	–	✓
• ℓ_0	–	–	✓

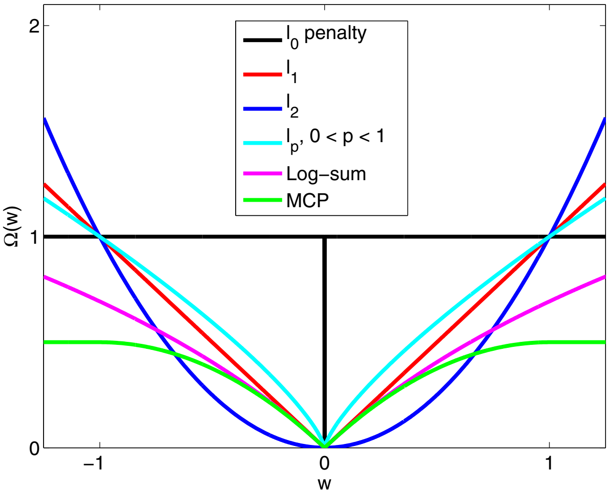

Fig. 3 Comparison of several unstructured regularization terms ($\epsilon = 1$ and $\gamma = 1$ are respectively the parameters of the log-sum and MCP regularizations)

when the second includes only the variable 3. The group regularization applied to the coefficients of **w** based on the mixed norm ℓ_p - ℓ_q is as follows:

$$\Omega_{p,q}(\mathbf{w}) = \sum_{g \in \mathcal{G}} \left(\left\| \mathbf{w}_g \right\|_q \right)^p \tag{19}$$

where $\mathbf{w}_g$ corresponds to the sub-vector of **w** corresponding to variables of the group g.

In the structured regularization, we can find the mixture ℓ_1 - ℓ_2 (also called the group Lasso), it represents the most known mixture of norms which applies the norm ℓ_1 to the sum of the ℓ_2 of each group leading to sparsity on the groups [4, 109]. There are some variants

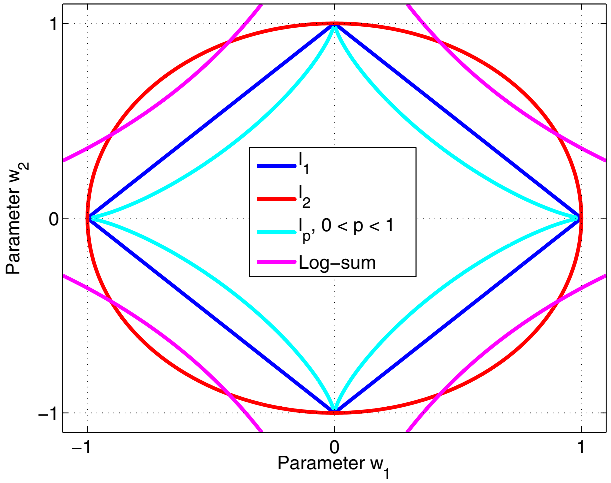

Fig. 4 Illustration 2D for several regularization terms

such as ℓ_p - ℓ_q where $0 < p < 1$ able to promote more sparsity. In the family of structured regularization, we can also find the group fused Lasso [12, 75, 77], which penalizes ℓ_1-norm of the difference between two successive groups of variable which leads to sparsity of groups difference. It is given by:

$$\Omega(\mathbf{W}) = \sum_{i=1}^{d-1} \|\mathbf{w}_{i+1} - \mathbf{w}_i\|_1 \tag{20}$$

where $\mathbf{w}_i$ is the i^{th} group corresponding to the i^{th} row of $\mathbf{W}$.

5 Decomposition learning

Instead of selecting most relevant features or learning a mapping of the data in low dimensional another trend of feature representation attempts to find a sparse decomposition of the data over a learned dictionary. The problem of sparse decomposition has known growing interest. A very interesting task in this field is dictionary learning which attempts usually to design a dictionary capable to capture all or most information of the signal with a linear combination of a small number of elementary signals called dictionary atoms. Different from conventional predefined dictionaries such as wavelet basis, wavelet packet basis, Gabor atoms or Discrete Cosine Basis, dictionary learning allows more representation flexibility and efficiency in reconstruction and classification [22, 106]. Searching for the sparse representation of a signal over a dictionary is achieved by optimizing an objective function that consists of two terms: one that measures the reconstruction error and the other that measures the sparsity of the representation. Dictionary learning has been applied for different applications, such as image denoising [24, 60], inpainting [25, 60], clustering [18, 105] and classification [62].

It has been shown that the conventional dictionary learning algorithm is rather adapted for signal construction than classification [47]. Therefore, researchers introduced novel approaches more adapted for signal classification by taking the class label in consideration. Dictionary-based classification can be broadly divided into two main groups [47]:

- Discriminative dictionaries, such as Meta-face learning [107] and dictionary learning with structured incoherence [69].
- Discriminative coefficients, such as supervised dictionary learning [62], discriminative K-SVD [112], label consistent K-SVD [38] or fisher discriminant dictionary learning [108].

5.1 Conventional dictionary learning

Let n d-dimensional signals $\{\mathbf{x}_i\}_{i=1}^n$ stored in $\mathbf{X} = [\mathbf{x}_1 \cdots \mathbf{x}_i \cdots \mathbf{x}_n\ ] \in \mathbb{R}^{d\times n}$. The conventional learning approach attempts to find a dictionary (possibly overcomplete) of K atoms $\mathbf{D} = [\mathbf{d}_1 \cdots \mathbf{d}_k \cdots \mathbf{d}_K] \in \mathbb{R}^{d\times K}$ and the sparse coefficients $\mathbf{A} \in \mathbb{R}^{K\times n}$ corresponding to the representation of $\mathbf{X}$ over $\mathbf{D}$ by minimizing the following objective function:

$$\begin{cases} \min\limits_{\substack{\mathbf{D}\in\mathbb{R}^{d\times K}\\ \mathbf{A}\in\mathbb{R}^{K\times n}}} \|\mathbf{X} - \mathbf{DA}\|_F^2 + \lambda \|\mathbf{A}\|_1 \\ \\ \text{s.t} \quad \|\mathbf{d}_k\|_2^2 \leq 1 \quad \forall k = 1, \cdots, K \end{cases} \tag{21}$$

where $\mathbf{A} = [\mathbf{a}_1 \cdots \mathbf{a}_i \cdots \mathbf{a}_n]$ with $\mathbf{a}_i \in \mathbb{R}^K$ represents the coefficients of the representation of $\mathbf{x}_i$ over $\mathbf{D}$ and $\|\mathbf{A}\|_1 = \sum\limits_{i=1}^{n} \|\mathbf{a}_i\|_1$ a term promoting sparsity of each decomposition.

5.2 Discriminative dictionary

Let $\{(\mathbf{x}_i, y_i) \in \mathbb{R}^d \times \mathcal{Y}\}_{i=1}^n$ where $\mathcal{Y} = \{1, \cdots, C\}$ is the label set. A method introduced in this context is dictionary learning with structured incoherence [69]. It attempts to learn a dictionary per class while enforcing incoherence in order to make dictionaries from different class as different as possible. The resulting optimization problem is:

$$\begin{cases} \min\limits_{\substack{\{\mathbf{D}_c\}_{c=1}^C \in \mathbb{R}^{d\times K} \\ \{\mathbf{A}_c\}_{c=1}^C \in \mathbb{R}^{K\times n}}} \sum_{c=1}^C \left\{ \|\mathbf{X}_c - \mathbf{D}_c\mathbf{A}_c\|_F^2 + \lambda \|\mathbf{A}_c\|_1 \right\} + \eta \sum\limits_{c=1}^{C} \sum_{\substack{j=1 \\ j\neq c}}^C \left\|\mathbf{D}_c^T\mathbf{D}_j\right\|_F^2 \\ \text{s.t} \quad \left\|\mathbf{d}_k^c\right\|_2^2 \leq 1 \quad \forall k = 1, \cdots, K \quad \forall c = 1, \cdots, C \end{cases} \tag{22}$$

where $\mathbf{X}_c$, $\mathbf{D}_c$ and $\mathbf{A}_c$ respectively correspond to the data from class c, the corresponding learned dictionary and the coefficients of representing $\mathbf{X}_c$ over $\mathbf{D}_c$. The first term in (22) represents the classical dictionary learning expression; the second term promotes orthogonality of learned $\mathbf{D}_c$ hence inducing their incoherence.

5.3 Discriminative coefficients

The most prominent method in the context of discriminative coefficients is the supervised dictionary method introduced in [62]. They incorporated a classification cost based on the logistic loss function:

$$\begin{cases} \min\limits_{\substack{\mathbf{D}\in\mathbb{R}^{d\times K} \\ \mathbf{A}\in\mathbb{R}^{K\times n} \\ \mathbf{w}\in\mathbb{R}^K \\ b\in\mathbb{R}}} \sum\limits_{i=1}^{n} (L(y_i f(\mathbf{x}_i, \mathbf{a}_i, \mathbf{w})) + \lambda_0 \|\mathbf{x}_i - \mathbf{D}\mathbf{a}_i\|_2^2 + \lambda_1 \|\mathbf{a}_i\|_1 + \lambda_2 \|\mathbf{w}\|_2^2 \\ \text{s.t} \quad \|\mathbf{d}_k\|_2^2 \leq 1 \quad \forall k = 1, \cdots, K \end{cases} \tag{23}$$

where L represents the logistic loss function (Section 6.2) and $f(\mathbf{x}, \mathbf{a}, \mathbf{w}) = \mathbf{w}^T\mathbf{a} + b$ is a linear classification function depending on the learned decomposition coefficients $\mathbf{a}$ for the sample $\mathbf{x}$.

6 Classification

Classification methods can be broadly organized in two main groups: generative and discriminative approaches. The Generative classifiers learn a model of the joint probability $p(\mathbf{x}, y)$, of the inputs $\mathbf{x}$ and the label y, and make their predictions using Bayes rule to calculate $p(y|\mathbf{x})$, and then picking the most likely label y [11]. Discriminative classifiers model the posterior $p(y|\mathbf{x})$ directly, or learn a direct map from inputs $\mathbf{x}$ to the class label. There are several compelling reasons for using discriminative rather than generative classifiers, one of which, succinctly articulated by [97] is that ”one should solve the classification problem directly and never solve a more general problem as an intermediate step such as modeling $p(\mathbf{x}|y)$”. Indeed leaving aside computational issues and other matters, the prevailing consensus seems to be that discriminative classifiers are efficient alternatives to generative approaches. Indeed, the discriminative methods require few parameters to be determined ; they are not prone to a mis-specification of the joint distribution $p(\mathbf{x}, y)$.

Let suppose $\{(\mathbf{x}_i, y_i)\}_{i=1}^n \in \mathcal{X} \times \mathcal{Y}$ where each sample $(\mathbf{x}, y)$ is drawn from an unknown joint distribution $\mathbb{P}(X, Y)$. The goal of classification is to find a decision function $f : \mathcal{X} \rightarrow \mathbb{R}$ capable to predict the correctly the label y' of a given observation $\mathbf{x}'$.

6.1 Regularized risk minimization

Learning a decision function could be based on a fixed structure such as k nearest neighbors, or by expressing the learning as an optimization problem. For this sake, a loss function L which measures the error between the predicted and real label is defined. Usually one seeks this function equals to 0 if the real and predicted labels are similar and greater than 0 otherwise. Theoretically, the best possible decision function is the one which minimizes the expected prediction error:

$$R(f) = \mathbb{E}[L(Y, f(X))] = \int_{\mathcal{X}\times\mathcal{Y}} L(y, f(\mathbf{x}))\mathbb{P}(\mathbf{x}, y)\, \mathrm{d}y\mathrm{d}\mathbf{x} \tag{24}$$

Unfortunately, in practice $R(f)$ can not be minimized since the distribution $\mathbb{P}(X, Y)$ is unknown. However, an approximation called empirical risk, can be computed by averaging the loss function on the training set:

$$\hat{R}(f) = \frac{1}{n}\sum_{i=1}^{n} L(y_i, f(\mathbf{x}_i)) \tag{25}$$

Minimizing $\hat{R}(f)$ with respect to f does not guarantee to obtain a function with good generalization properties (as overfitting can occur). Indeed, the minimization of empirical risk suffers from a lack of generalization and stability. Furthermore it has been demonstrated that the generalization and stability are linked, a stable problem implies generalization and vice versa [13, 63, 71]. To make the problem stable, a regularization term $\Omega(.)$ is added leading to the minimization of the structural risk [27, 97]. Usually one addresses the regularized empirical risk minimization:

$$\min_f \frac{1}{n}\sum_{i=1}^{n} L(y_i, f(\mathbf{x}_i)) + \lambda\Omega(f) \tag{26}$$

The first term is the classical empirical risk and the second is similar to the one introduced in (15) to (19). We refer the reader to [61] to have a broad overview of the usual regularizers.

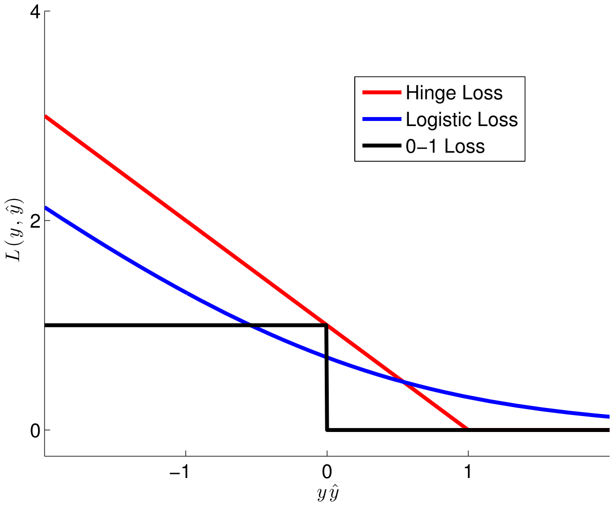

Fig. 5 Visualization of the loss functions

6.2 Loss function

There are numerous loss functions $L(y, \hat{y})$ measuring the error of prediction $\hat{y}$ of y. A large part of binary classification methods are based on learning a function capable to predict the class label using the sign of the predicted value. In this case the quantity used in the loss function is the product $y\hat{y}$. In the following we review a few most common loss functions shown in Fig. 5.

6.2.1 The 0-1 loss

It returns 0 if the class is well predicted and 1 otherwise. This cost is non differentiable and non-convex. Furthermore, the complexity of the resulting optimization problem is combinatorial which makes it very difficult to use in practice. It is given by:

$$L(y, \hat{y}) = (1 - sgn(y\hat{y}))/2 \tag{27}$$

6.2.2 The hinge loss

It is the cost used in the Support Vector Machines (SVM). Unlike the previous loss function, this cost is not necessarily equal to 0 when the class is well predicted. Hinge loss is equal to 0 only if $y\hat{y}$ is greater than 1, which means in other terms that $\hat{y}$ is predicted with some margin.

The hinge function is convex, however it needs a regularization term to make the problem strictly convex and ensure the uniqueness of the solution [86]. Its expression is:

$$L(y, \hat{y}) = \max(0, 1 - y\hat{y}) \tag{28}$$

6.2.3 The logistic loss

It permits to learn probabilistic classifiers; the decision could be made based on the estimation of class conditional probability. In the binary classification case with $\mathcal{Y} = \{-1, 1\}$ this probability is:

$$\hat{P}(Y = y|X = \mathbf{x}) = \frac{1}{1 + \exp(-yf(\mathbf{x}))} \tag{29}$$

The logistic loss has the particularity to be strictly convex with value equals to 0 when $y\hat{y} = \infty$; it is given by:

$$L(y, f(x)) = \log(1 + \exp(-yf(x)) \tag{30}$$

7 Discussions

Obtaining good recognition performances relies mainly on finding suitable feature representations where observations from different classes are well separated. For the latter, huge efforts have been devoted to find adequate feature spaces which could offer these properties. Several approaches have been introduced, such as dimensionality reduction, feature selection and decomposition learning.

Dimensionality reduction is a common preprocessing step for classification. Learning a classifier on low-dimensional space is fast (despite learning the dimensionality reduction itself may be costly). Furthermore, dimensionality reduction can help learn a better classifier, particularly when the data do have an intrinsic low-dimensional structure at small scale since dimensionality reduction has a regularizing effect that can help avoid overfitting. This can be explained by the ability of dimensionality reduction to attenuate the impact of noise that perturbs the samples along the manifold.

The majority of supervised dimensionality reduction techniques usually encourage to learn a mapping $\mathbf{F}$ to push apart inputs having different labels. For classification, once the data is mapped into the low-dimensional space, a classifier g is learned on the pairs $(\mathbf{F}(\mathbf{x}_i), y_i)$. This clearly shows that $\mathbf{F}$ and g are separately learned and this gives an insight to jointly learn them for improved performances [8, 102].

From our point of view, despite the positive points of dimensionality reduction and feature selection techniques, we believe that the methods based on learning feature representations such as dictionary learning are more able to represent the data for classification purpose, since they have more flexibility to model the problem while introducing classification in the formalized problem and sparsity to avoid the overfitting.

We shall notice that a growing and intensive body of research, with the goal of end-to-end recognition system from feature extraction, representation and classification, is displayed by Deep Learning [9, 52]. The involved approaches proceed by giving raw signal as input features and by stacking more than the usual two neural layers. Each low level layer encodes specific properties of the signals as primitives that are gradually combined by successive higher level layers in order to produce representative and hopefully discriminative representations of the signals.

Among the deep learning models we can cite: i) Convolutional Neural Networks (CNN) [51], suited to represent invariance property; ii) Deep Boltzman Machine (DBM) [84] that can provide a generative model of the data; and iii) (Bidirectional) Long-Short Term Memory (BLSTM) [33] adapted for a recurrent representation, taking into account the temporal nature of the data. To be effective deep models require a huge amount of data, due to their complex structure coupled with their computing power to exhibit striking performances. When one lacks training data (as in the case of most of biometric applications), the conventional techniques provide valuable alternatives.

8 Conclusion

The performance of the biometric recognition systems strongly dependents on learning a proper suitable feature representation space where samples from different classes are well presented and separated. In this paper, we have presented a comprehensive study of the existing state-of-the-art feature representation techniques. This was carried out by introducing simple and clear taxonomies as well as well as simple and effective explanation of the prominent techniques. This is intended to guide the neophyte and provide researchers with state-of-the-art approaches in order to help advance the research topic in biometrics.

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