Model-Based Clustering of High-Dimensional Data: A review

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Abstract

Model-based clustering is a popular tool which is renowned for its probabilistic foundations and its flexibility. However, high-dimensional data are nowadays more and more frequent and, unfortunately, classical model-based clustering techniques show a disappointing behavior in high-dimensional spaces. This is mainly due to the fact that model-based clustering methods are dramatically over-parametrized in this case. However, high-dimensional spaces have specific characteristics which are useful for clustering and recent techniques exploit those characteristics. After having recalled the bases of model-based clustering, this article will review dimension reduction approaches, regularization-based techniques, parsimonious modeling, subspace clustering methods and clustering methods based on variable selection. Existing softwares for model-based clustering of high-dimensional data will be also reviewed and their practical use will be illustrated on real-world data sets.

Keywords: Model-based clustering, high-dimensional data, dimension reduction, regularization, parsimonious models, subspace clustering, variable selection, softwares, R packages.

1. Introduction

Clustering is a data analysis tool which aims to group data into several homogeneous groups. The clustering problem has been studied for years and usually occurs in applications for which a partition of the data is necessary. In particular, more and more scientific fields require to cluster data in the aim to understand or interpret the studied phenomenon. Earliest approaches were based on heuristic or geometric procedures. They relied on dissimilarity measures between pairs of observations. A popular dissimilarity measure is based on the distance between groups, previously introduced by Ward [97] for hierarchical clustering. In the same way, the k-means algorithm [55] is perhaps the most popular clustering algorithm among the geometric procedures. Clustering was also defined in a probabilistic framework, allowing to formalize the notion of clusters through their probability distribution. One of the main advantages of this probabilistic approach is in the fact that the obtained partition can be interpreted from a statistical point of view. The

first works on finite mixture models were from Wolfe [99], Scott *et al.* [87] and Duda *et al.* [29]. Since then, these models have been extensively studied and, thanks to works such as those of McLachlan *et al.* [62, 64], Banfield & Raftery [5] or Fraley & Raftery [33],[35], model-based clustering has become a popular and reference technique.

Nowadays, the measured observations in many scientific domains are frequently high-dimensional and clustering such data is a challenging problem for model-based methods. Indeed, model-based methods show a disappointing behavior in high-dimensional spaces. They suffer from the well-known *curse of dimensionality* [6] which is mainly due to the fact that model-based clustering methods are over-parametrized in high-dimensional spaces. Furthermore, in several applications, such as mass spectrometry or genomics, the number of available observations is small compared to the number of variables and such a situation increases the problem difficulty. Since the dimension of observed data is usually higher than their intrinsic dimension, it is theoretically possible to reduce the dimension of the original space without loosing any information. For this reason, dimension reduction methods are frequently used in practice to reduce the dimension of the data before the clustering step. Feature extraction methods, such as principal component analysis (PCA), or feature selection methods are very popular. However, dimension reduction usually does not consider the classification task and provide a sub-optimal data representation for the clustering step. Indeed, dimension reduction methods imply an information loss which could have been discriminative.

To avoid the drawbacks of dimension reduction, several approaches have been proposed to allow model-based methods to efficiently cluster high-dimensional data. This work proposes to review the alternatives to dimension reduction for dealing with high-dimensional data in the context of model-based clustering. Earliest approaches include constrained and parsimonious models or regularization. More recently, subspace clustering techniques and variable selection techniques have been proposed to overcome the limitations of previous approaches. Subspace clustering techniques are based on probabilistic versions of the factor analysis model. This modeling allows to cluster the data in low-dimensional subspaces without reducing the dimension. Conversely, variable selection techniques do reduce the dimension of the data but select the variables to retain regarding the clustering task. Both techniques turn out to be very efficient and their practical use will be discussed as well in this article.

This article is organized as follows. Section 2 briefly recalls the bases of mixture modeling and its inference with the EM algorithm. Section 3 introduces the curse of dimensionality in model-based clustering. Approaches based on dimension reduction, regularization and parsimonious models are reviewed in Section 4. Then, Section 5 and 6 present respectively the approaches based on subspace clustering and variable selection. Existing softwares for model-based clustering of high-dimensional data are also reviewed in Section 7 and their practical use is discussed in Section 8. Finally, some concluding remarks are made in Section 9.

2. The mixture model and the EM algorithm

This section first recalls the bases of mixture modeling and its inference with the expectation-maximization (EM) algorithm.

2.1. The mixture model

Let us consider a data set of n observations $\{y_1, \ldots, y_n\} \in \mathbb{R}^p$ that one wants to divide into K homogeneous groups. The aim of clustering is to determine, for each observation y_i, the value of its unobserved label z_i such that $z_i = k$ if the observation y_i belongs to the kth cluster. To do so, model-based clustering [35, 64] considers the overall population as a mixture of the groups and each component of this mixture is modeled through its conditional probability distribution. In this context, the observations $\{y_1, \ldots, y_n\} \in \mathbb{R}^p$ are assumed to be independent realizations of a random vector $Y \in \mathbb{R}^p$ whereas the unobserved labels $\{z_1, ..., z_n\}$ are assumed to be independent realizations of a random variable $Z \in \{1, ..., K\}$. The set of pairs $\{(y_i, z_i)\}_{i=1}^n$ is usually referred to as the complete data set. By denoting by g the probabilistic density function of Y, the finite mixture model is:

$$g(y) = \sum_{k=1}^{K} \pi_k f_k(y), \tag{1}$$

where π_k (with the constraint $\sum_{k=1}^{K} \pi_k = 1$) and f_k respectively represent the mixture proportion and the conditional density function of the kth mixture component. Furthermore, the clusters are often modeled by the same parametric density function in which case the finite mixture model is:

$$g(y) = \sum_{k=1}^{K} \pi_k f(y; \theta_k), \tag{2}$$

where θ_k is the parameter vector for the kth mixture component. For a set of observations $y = \{y_1, ..., y_n\}$, the log-likelihood of this mixture model is then:

$$\ell(\theta; y) = \sum_{i=1}^{n} \log \left(\sum_{k=1}^{K} \pi_k f(y_i; \theta_k) \right). \tag{3}$$

However, the inference of this model cannot be directly done through the maximization of the likelihood since the group labels $\{z_1, ..., z_n\}$ of the observations are unknown. Indeed, due to the exponential number of solutions to explore, the maximization of equation (3) is unfortunately intractable, even for limited numbers of observations and groups. Before introducing the most popular inference algorithm used in this context, let us introduce the complete log-likelihood:

$$\ell_c(\theta; y, z) = \sum_{i=1}^{n} \sum_{k=1}^{K} z_{ik} \log \left(\pi_k f(y_i; \theta_k) \right),$$

where $z_{ik} = 1$ if the ith observation belongs to the kth cluster and $z_{ik} = 0$ otherwise.

2.2. The EM algorithm

Although it is not specifically dedicated to mixture models, the expectation-maximization (EM) algorithm, proposed by Dempster *et al.* [28], is certainly the most popular technique for inferring mixture models. The EM algorithm iteratively maximizes the conditional expectation of the complete log-likelihood:

$$E\left[\ell_c\left(\theta; y, z\right)|\theta^*\right] = \sum_{k=1}^{K}\sum_{i=1}^{n} t_{ik}\log\left(\pi_k f\left(y_i;\theta_k\right)\right),$$

where $t_{ik} = E\left[z = k|y_i, \theta^*\right]$ and θ^* is a given set of the mixture parameters. From an initial solution $\theta^{(0)}$, the EM algorithm alternates two steps: the E-step and the M-step. First, the expectation step (E-step) computes the expectation of the complete log-likelihood $E\left[\ell_c\left(\theta; y, z\right)|\theta^{(q)}\right]$ conditionally to the current value of the parameter set $\theta^{(q)}$. Then, the maximization step (M-step) maximizes $E\left[\ell_c\left(\theta; y, z\right)|\theta^{(q)}\right]$ over θ to provide an update for the parameter set. This algorithm therefore forms a sequence $\left(\theta^{(q)}\right)_{q\geq 1}$ which satisfies, for each $q \geq 1$:

$$\theta^{(q+1)} = \arg\max_{\theta} E\left[\ell_c\left(\theta; y, z\right)|\theta^{(q)}\right].$$

One of the most outstanding properties of the EM algorithm is that it guarantees an improvement of the likelihood function at each iteration. Each update of the parameter set, resulting from an E-step followed by an M-step, is guaranteed to increase the log-likelihood function. In particular, Wu [100] proved that the sequence of $\left(\theta^{(q)}\right)_{q\geq 1}$ converges to a local optimum of the likelihood. For further details on the EM algorithm, the reader may refer to [63].

The two steps of the EM algorithm are iteratively applied until a stopping criterion is satisfied. The stopping criterion may be simply $|\ell(\theta^{(q)}; y) - \ell(\theta^{(q-1)}; y)| < \varepsilon$ where ε is a positive value to provide. It would be also possible to use the Aitken's acceleration criterion [53] which estimates the asymptotic maximum of the likelihood and allows to detect in advance the algorithm convergence. Once the EM algorithm has converged, the partition $\{\hat{z}_1, \ldots, \hat{z}_K\}$ of the data can be deduced from the posterior probabilities $t_{ik} = P(Z = k|y_i, \hat{\theta})$ by using the *maximum a posteriori* (MAP) rule which assigns the observation y_i to the group with the highest posterior probability.

2.3. The Gaussian mixture model

Among the possible probability distributions for the mixture components, the Gaussian distribution is certainly the most used for both theoretical and computational reasons. Let us however notice that several recent works focused on different distributions such as the skew normal [52], asymmetric Laplace [36] or t-distributions [3, 51, 68]. Nevertheless, the density function $f(y;\theta_k)$ is most commonly assumed to be a multivariate Gaussian density $\phi(y;\theta_k)$ parametrized by its mean μ_k and its covariance matrix Σ_k, such that the density

function of Y can be written as:

$$g(y;\theta) = \sum_{k=1}^{K} \pi_k \phi(y;\theta_k), \tag{4}$$

where:

$$\phi(y;\theta_k) = \frac{1}{(2\pi)^{p/2}\left|\Sigma_k\right|^{1/2}} \exp\left(-\frac{1}{2}\left(y-\mu_k\right)^t \Sigma_k^{-1}\left(y-\mu_k\right)\right)$$

is the multivariate Gaussian density with parameter $\theta_k = (\mu_k, \Sigma_k)$. This specific mixture model is usually referred in the literature as the Gaussian mixture model (GMM). In this case, the EM algorithm has the following form, at iteration q:

E-step. This step aims to compute the expectation of the complete log-likelihood conditionally to the current value of the parameter $\theta^{(q-1)}$. In practice, it reduces to the computation of $t_{ik}^{(q)} = E[z_i = k|y_i, \theta^{(q-1)}]$. Let us also recall that $t_{ik}^{(q)}$ is as well the posterior probability $P(z_i = k|y_i, \theta^{(q-1)})$ that the observation y_i belongs to the kth component of the mixture under the current model. Using Bayes' theorem, the posterior probabilities $t_{ik}^{(q)}$, $i = 1, ..., n$, $k = 1, ..., K$, can be expressed as follows:

$$t_{ik}^{(q)} = \frac{\pi_k^{(q-1)} \phi(y_i, \theta_k^{(q-1)})}{\sum_{l=1}^{K} \pi_l^{(q-1)} \phi(y_i|\theta_l^{(q-1)})}, \tag{5}$$

where $\pi_k^{(q-1)}$ and $\theta_k^{(q-1)} = \left\{\mu_k^{(q-1)}, \Sigma_k^{(q-1)}\right\}$ are the parameters of the kth mixture component estimated at the previous iteration.

M-step. This step updates the model parameters by maximizing the conditional expectation of the complete log-likelihood. The maximization of $E\left[\ell_c\left(\theta; y, z\right)|\theta^{(q-1)}\right]$ conduces to an update of the mixture proportions π_k, the means μ_k and the covariance matrices Σ_k as follows, for $k = 1, ..., K$:

$$\hat{\pi}_k^{(q)} = \frac{n_k^{(q)}}{n}, \tag{6}$$

$$\hat{\mu}_k^{(q)} = \frac{1}{n_k^{(q)}} \sum_{i=1}^{n} t_{ik}^{(q)} y_i, \tag{7}$$

$$\hat{\Sigma}_k^{(q)} = \frac{1}{n_k^{(q)}} \sum_{i=1}^{n} t_{ik}^{(q)} \left(y_i - \hat{\mu}_k^{(q)}\right)\left(y_i - \hat{\mu}_k^{(q)}\right)^t, \tag{8}$$

where $n_k^{(q)} = \sum_{i=1}^{n} t_{ik}^{(q)}$.

3. The curse of dimensionality in model-based clustering

Before to present classical and recent methods for high-dimensional data clustering, we focus in this section on the causes of the curse of dimensionality in model-based clustering.

3.1. The origins: the Bellman' sentence

When reading research articles or books related to high-dimensional data, it is very likely to find the term "curse of dimensionality" to refer to all problems caused by the analysis of high-dimensional data. This term was introduced by R. Bellman in the preface of his book [6] promoting dynamic programming. To illustrate the difficulty to work in high-dimensional spaces, Bellman recalled that if one considers a regular grid with step 0.1 on the unit cube in a 10-dimensional space, the grid is made of 10^{10} points. Consequently, the search for the optimum of a given function in this unit cube requires 10^{10} evaluations of this function which was unfordable problem in the 60's (it remains a difficult problem nowadays). Although the term "curse of dimensionality" used by Bellman is of course rather pessimistic, the paragraph of the preface in which the term first appeared is in fact more optimistic:

> *All this* [the problems linked to high dimension] *may be subsumed under the heading « the curse of dimensionality ». Since this is a curse,* [...]*, there is no need to feel discouraged about the possibility of obtaining significant results despite it.*

This paragraph will indeed show that the Bellman's thought was corrected since, at least for clustering, high dimensions have nice properties which do allow to obtain significant results.

3.2. The curse of dimensionality in model-based clustering

In the context of model-based clustering, the curse of dimensionality takes a particular form. Indeed, model-based clustering methods require the estimation of a number of parameters which directly depends on the dimension of the observed space. If we consider the classical Gaussian mixture model for instance, the total number of parameters to estimate is equal to:

$$\nu = (K-1) + Kp + Kp(p-1)/2,$$

where $(K-1)$, Kp and $Kp(p-1)/2$ are respectively the numbers of free parameters for the proportions, the means and the covariance matrices. It turns out that the number of parameters to estimate is therefore a quadratic function of p in the case of the Gaussian mixture model and a large number of observations will be necessary to correctly estimate those model parameters. Furthermore, a more serious problem occurs in the EM algorithm when computing the posterior probabilities $t_{ik} = E[Z = k|y_i, \theta]$ which depend, in the GMM context, on the quantity $H_k(x) = -2\log(\pi_k \phi(x; \mu_k, \Sigma_k))$. Indeed, the computation of H_k, which can be rewritten as:

$$H_k(x) \quad = \quad (x-\mu_k)^t \Sigma_k^{-1}(x-\mu_k) + \log(\det \Sigma_k) - 2\log(\pi_k) + p\log(2\pi), \tag{9}$$

requires the inversion of the covariance matrices Σ_k, $k = 1, ..., K$. Consequently, if the number of observations n is small compared to ν, the estimated covariance matrices $\hat{\Sigma}_k$ are ill-conditioned and their inversions conduce to unstable classification functions. In the

worst case where $n < p$, the estimated covariance matrices $\hat{\Sigma}_k$ are singular and model-based clustering methods cannot be used at all. Unfortunately, this kind of situation tends to occur more and more frequently in Biology (DNA sequences, genotype analysis) or in computer vision (face recognition) for instance.

The curse of dimensionality has been also exhibited by [80, 81] in the Gaussian case with the estimation point of view. Let us consider the estimation of the normalized trace $\tau(\Sigma) = \text{tr}(\Sigma^{-1})/p$ of the inverse covariance matrix Σ of a multivariate Gaussian distribution $\mathcal{N}(\mu, \Sigma)$. The estimation of τ from a sample of n observations $\{x_1, ..., x_n\}$ conduces to:

$$\tau(\hat{\Sigma}) = \tau(\hat{\Sigma}) = \frac{1}{p}\text{tr}(\hat{\Sigma}^{-1}),$$

and its expectation is:

$$E[\tau(\hat{\Sigma})] = \left(1 - \frac{p}{n-1}\right)^{-1} \tau(\Sigma).$$

Consequently, if the ratio $p/n \to 0$ when $n \to +\infty$, then $E[\tau(\hat{\Sigma})] \to \tau(\Sigma)$. However, if the dimension p is comparable with n, then $E[\tau(\hat{\Sigma})] \to c\tau(\Sigma)$ when $n \to +\infty$, where $c = \lim_{n\to+\infty} p/n$. We refer to [80, 81] for further details on the effect of the dimensionality on classification in the asymptotic framework, *i.e.* p and $n \to +\infty$.

3.3. The blessing of dimensionality in clustering

Hopefully, as expected by Bellman, high-dimensional spaces have specific features which could facilitate their exploration. Several authors, such as [44, 75], have shown that, in the context of clustering, high-dimensional spaces do have useful characteristics which ease the classification of data in those spaces. In particular, Scott and Thompson [88] showed that high-dimensional spaces are mostly empty. The experiment suggested by Huber [47] consists in drawing realizations of a p-dimensional random vector X with uniform probability distribution on the hypersphere of radius 1. The probability that a realization x_i of this experiment belongs to the shell between the hypersphere of radius 0.9 and the unit hypersphere is therefore:

$$\mathbb{P}\left(x_i \in S_{0.9}(p)\right) = 1 - 0.9^p.$$

In particular, the probability that x_i belongs to the shell between the hypersphere of radius 0.9 and the unit hypersphere in a 20-dimensional space is roughly equals to 0.88. Therefore, most of the realizations of the random vector X live near a $p-1$ dimensional subspace and the remaining of the space is mostly empty. This suggests that clustering methods should model the groups in low-dimensional subspaces instead to model them in the whole observation space. Furthermore, it seems reasonable to expect that different groups live in different subspaces and this may be a useful property for discriminating the groups. Subspace clustering methods, presented in Section 6, exploit this specific characteristic of high-dimensional spaces.

4. Earliest approaches

Earliest approaches to deal with the clustering of high-dimensional data can be split into three families: dimension reduction methods, regularization methods and parsimonious methods.

4.1. Dimension reduction

Approaches based on dimension reduction assume that the number p of measured variables is too large and, implicitly, that the data at hand live in a space of lower dimension, let us say $d < p$. Once the data projected in a low-dimensional space, it is then possible to apply the EM algorithm on the projected observations to obtain a partition of the original data.

The most popular linear method used for dimension reduction is certainly principal component analysis (PCA). It was introduced by Pearson [82] who defines PCA as a linear projection that minimizes the average projection cost. Later, Hotelling [46] proposed another definition for PCA which reduces the dimension of the data by keeping as much as possible the variation of the data set. In other words, this method aims to find an orthogonal projection of the data set in a low-dimensional linear subspace, such that the variance of the projected data is maximum. This leads to the classical result where the principal axes $\{u_1, ..., u_d\}$ are the eigenvectors associated with the largest eigenvalues of the empirical covariance matrix S of the data. Several decades after, Tipping and Bishop [91] proposed a probabilistic view of PCA by assuming that the observations are independent realizations of a random variable $Y \in \mathbb{R}^p$ which is linked to a latent variable $X \in \mathbb{R}^d$ through the linear relation:

$$Y = \Lambda^t X + \varepsilon.$$

It is further assume that $X \sim \mathcal{N}(\mu, I_d)$ and $\varepsilon \sim \mathcal{N}(0, \sigma^2 I_p)$, such that the marginal distribution of Y is $\mathcal{N}(\Lambda\mu, \Lambda^t\Lambda + \sigma^2 I_p)$. The estimation of the parameters μ, Λ and b by maximum likelihood conduces in particular to estimate Λ by the eigenvectors associated with the largest eigenvalues of the empirical covariance matrix S of the data.

Factor analysis (FA) is an other way to deal with dimension reduction. This approach is as old as PCA since its origins are relative to Spearman [90] and there is an important literature on this subject too (see for example [12, chap. 12]). The basic idea of factor analysis is to both reduce the dimensionality of the space and to keep the observed covariance structure of the data. It turns out that the probabilistic PCA (PPCA) model is in fact a particular case of the factor analysis model. Indeed, the FA model makes the same assumption as the PPCA model except regarding the distribution of ε which is assumed to be $\mathcal{N}(0, \Psi)$, where Ψ is a diagonal covariance matrix. However, conversely to the PPCA model, the estimation of model parameters by maximum likelihood does not conduce to closed-form estimators.

4.2. Regularization

It is also possible to see the curse of dimensionality in clustering as a numerical problem in the inversion of the covariance matrices Σ_k in Equation (9). From this point of view, a way to tackle the curse of dimensionality is to numerically regularize the estimates of the covariance matrices Σ_k before their inversion. As we will see, most of the regularization techniques have been proposed in the supervised classification framework, but they can be easily used for clustering as well. A simple way to regularize the estimation of Σ_k is to consider a ridge regularization which adds a positive quantity σ_k to the diagonal of the matrix:

$$\tilde{\Sigma}_k = \hat{\Sigma}_k + \sigma_k I_p.$$

Notice that this regularization is often implicitly used in statistical softwares, such as R [93] for performing a linear discriminant analysis (LDA) where, for instance, the `lda()` function spheres the data before analysis. A more general regularization has been proposed by Hastie *et al.* [45]:

$$\tilde{\Sigma}_k = \hat{\Sigma}_k + \sigma_k \Omega,$$

where Ω is a $p \times p$ regularization matrix. This penalization differs from the previous one by the fact that it penalizes also correlations between the predictors. This regularization is used in particular in the supervised classification method penalized discriminant analysis (PDA). Friedman [39] also proposed, for his famous regularized discriminant analysis (RDA), the following regularization:

$$\hat{\Sigma}_k(\lambda, \gamma) = (1-\gamma)\hat{\Sigma}_k(\lambda) + \gamma \left(\frac{\mathrm{tr}(\hat{\Sigma}_k(\lambda))}{p} \right) I_p,$$

where :

$$\hat{\Sigma}_k(\lambda) = \frac{(1-\lambda)(n_k - 1)\hat{\Sigma}_k + \lambda(n-K)\hat{\Sigma}}{(1-\lambda)(n_k-1) + \lambda(n-K)}.$$

Thus, the parameter γ controls the ridge regularization whereas λ controls the contribution of the estimators $\hat{\Sigma}_k$ and $\hat{\Sigma}$, where $\hat{\Sigma}$ estimates the within covariance matrix. Finally, it is also possible to use the Moore–Penrose pseudo-inverse of $\hat{\Sigma}$ in Equation (9) instead of the usual inverse $\hat{\Sigma}^{-1}$. The reader can also refer to [72] which provides a comprehensive overview of regularization techniques in classification.

More recently, with the exponential growth of high-dimensional data and since many areas in statistical analysis require the inversion or the estimation of covariance matrices, several works were focused on the estimation of large covariance matrices. According to the type of variables, different approaches have been developed. On the one hand, approaches have been proposed to deal with variables having a natural ordering such as longitudinal data or time series (see the works of [50] for example). On the other hand, works were focused on variables for which there is no notion of distances, such as gene expression arrays. For such applications, sparsity is therefore necessary: the methods proposed are mainly based on the use of lasso penalties (see [38] in particular) or on thresholding the

Model	Nb. of parameters	$K = 4$ and $p = 100$
Full-GMM	$(K-1) + Kp + Kp(p+1)/2$	20603
Com-GMM	$(K-1) + Kp + p(p+1)/2$	5453
Diag-GMM	$(K-1) + Kp + Kp$	803
Com-Diag-GMM	$(K-1) + Kp + p$	503
Sphe-GMM	$(K-1) + Kp + K$	407
Com-Sphe-GMM	$(K-1) + Kp + 1$	404

TABLE 1: Number of free parameters to estimate for constrained Gaussian models.

covariance matrix [9, 48]. The reader can refer to the introduction of [8] for an overview of existing methods in this field.

4.3. Constrained and parsimonious models

A third way to look at the the curse of dimensionality in clustering is to consider it as a problem of over-parameterized modeling. Indeed, as we discussed before in Section 3.2, the Gaussian model turns out to be highly parameterized which naturally yields inference problems in high-dimensional spaces. Consequently, the use of constrained or parsimonious models is another solution to avoid the curse of dimensionality in model-based clustering.

Constrained Gaussian models. A traditional way to reduce the number of free parameters of Gaussian models is to add constraints on the model through their parameters. Let us recall that the unconstrained Gaussian model (Full-GMM hereafter) is a highly parametrized model and requires the estimation of 20603 parameters when the number of components is $K = 4$ and the number of variables is $p = 100$. A first possible constraint for reducing the number of parameters to estimate is to constraint the K covariance matrices to be the same across all mixture components, *i.e.* $\Sigma_k = \Sigma$, $\forall k$. This model will be denoted to by Com-GMM in the sequel. Notice that this model yields the famous linear discriminant analysis (LDA) [31] method in the supervised classification case. For the sake of comparison, Table 1 lists the most used constrained models which can be obtained from a Gaussian mixture model with K components in a p-dimensional space. The number of free parameters to estimate, given in the central column, can be *decomposed* in the number of parameters to estimate for the proportions $(K-1)$, for the means (Kp) and for the covariance matrices (last terms). As one can see in Table 1, it is also possible to assume that the variables are conditionally independent. Such an assumption implies that the covariance matrices are diagonal, *i.e.* $\Sigma_k = \text{diag}\left(\sigma_{k1}^2, ..., \sigma_{kp}^2\right)$ with $\sigma_{k.}^2 \in \mathbb{R}^+$, and the associated model (Diag-GMM) has a very low number of free parameters. Finally, Sphe-GMM refers to the Gaussian mixture model for which $\Sigma_k = \sigma_k^2 I_p$. Two other intermediate models are presented in Table 1. The Com-Diag-GMM which supposes diagonal common covariances such as $\Sigma_k = \Sigma = \text{diag}\left(\sigma_1^2, \ldots, \sigma_p^2\right)$ or the Com-Sphe-GMM model which assumes that the covariance matrices of each class are equal and spherical such that $\Sigma_k = \Sigma = \sigma^2 I_p$, for $k = 1, ..., K$ and with $\sigma^2 \in \mathbb{R}$. One can see in Table 1 that, whereas the Full-GMM model is a highly parametrized model, the Sphe-GMM and Com-Sphe-GMM models are

Model	Name	Nb. of parameters	$K = 4$ $p = 100$
$[\lambda_k D_k A_k D_k^t]$	VVV	$(K-1) + Kp + Kp(p+1)/2$	20603
$[\lambda D_k A_k D_k^t]$	EVV*	$(K-1) + Kp + Kp(p+1)/2 - (K-1)$	20600
$[\lambda_k D_k A D_k^t]$	VEV	$(K-1) + Kp + Kp(p+1)/2 - (K-1)(p-1)$	20306
$[\lambda D_k A D_k^t]$	EEV	$(K-1) + Kp + Kp(p+1)/2 - (K-1)p$	20303
$[\lambda_k D A_k D^t]$	VVE*	$(K-1) + Kp + p(p+1)/2 + (K-1)p$	5753
$[\lambda D A_k D^t]$	EVE*	$(K-1) + Kp + p(p+1)/2 + (K-1)(p-1)$	5750
$[\lambda_k D A D^t]$	VEE*	$(K-1) + Kp + p(p+1)/2 + (K-1)$	5456
$[\lambda D A D^t]$	EEE	$(K-1) + Kp + p(p+1)/2$	5453
$[\lambda_k B_k]$	VVI	$(K-1) + Kp + Kp$	803
$[\lambda B_k]$	EVI	$(K-1) + Kp + Kp - (K-1)$	800
$[\lambda_k B]$	VEI	$(K-1) + Kp + p + (K-1)$	506
$[\lambda B]$	EEI	$(K-1) + Kp + p$	503
$[\lambda_k \mathbf{I}_p]$	VII	$(K-1) + Kp + K$	407
$[\lambda \mathbf{I}_p]$	EII	$(K-1) + Kp + 1$	404

TABLE 2: Number of free parameters to estimate for parsimonious Gaussian mixture models with K components and p variables. The models flagged with a star are unfortunately not available in the `mclust` software (see Section 8.1).

conversely very parsimonious models. They indeed respectively require the estimation of only 407 and 404 parameters when $K = 4$ and $p = 100$. Those models however make a strong assumption on the independence of the variables which may be unrealistic in several situations. Finally, the Com-GMM model which requires the estimation of an intermediate number of parameters (5453) is known to be a useful model in practical situations. This model is known as well to be efficient for the classification of data sets for which the Gaussian assumption does not hold.

Parsimonious Gaussian models. In a similar spirit than constrained models, Banfield & Raftery [5] and Celeux & Govaert [24] proposed, almost simultaneously, a parameterization of the Gaussian mixture model which yields a family of parsimonious models. To this end, they parametrize the covariance matrices from their eigenvalue decomposition:

$$\Sigma_k = \lambda_k D_k A_k D_k^t,$$

where D_k is the matrix of eigenvectors which determines the orientation of the cluster, A_k is a diagonal matrix proportional to the eigenvalues which explains its shape, and λ_k is a scalar which controls its volume. This model is referred to by the $[\lambda_k D_k A_k D_k^t]$ model in [24] and to by VVV in [5]. By constraining the parameters λ_k, D_k and A_k within and across the groups, 14 different parsimonious models can be enumerated. This family of 14 models are listed in Table 2 in which the first column stands for the model names used by Celeux & Govaert and the second one corresponds to the nomenclature used by Raftery & Fraley. First of all, we can observe that this family of models can be divided in three levels of parsimony, as shown in Table 1. Among the 14 models, 4 models are highly parametrized as the Full-GMM model, 4 models have an intermediate level of parsimony as the Com-GMM model and, finally, 6 models are very parsimonious and are in the same order as the Diag-

GMM and Sphe-GMM models. Besides, this reformulation of the covariance matrices can be viewed as a generalization of the constrained models, presented previously. For example, the Com-GMM model is equivalent to the model $[\lambda DAD^t]$. The model proposed by [76], which uses the equal shape ($\lambda_k = \lambda, \forall k$) and equal volume ($A_k = A, \forall k$), turns out to be equivalent to the model $[\lambda D_k A D_k^t]$. It is worth to notice that the work of Celeux & Govaert widens the family of parsimonious models since they add unusual models which allow different volumes for the clusters such as the $[\lambda_k DAD^t]$, $[\lambda_k DA_k D^t]$ and $[\lambda_k D_k A D_k^t]$ models. Furthermore, by assuming that the covariance matrix Σ_k are diagonal matrices, Celeux & Govaert proposed a new parametrization $\Sigma_k = \lambda_k B_k$ where $|B_k| = 1$. Such a parametrization leads to 4 additional models listed at the bottom of Table 2. Finally, by considering the spherical shape, it leads to 2 other models: the $[\lambda_k \mathbf{I}_p]$ and $[\lambda \mathbf{I}_p]$ models. The reader can refer to [24] for more details on these models.

4.4. Discussion on classical approaches and related works

Firstly, regarding the dimension reduction solution, we would like to caution the reader that reducing the dimension without taking into consideration the clustering goal may be dangerous. Indeed, such a dimension reduction may yield a loss of information which could have been useful for discriminating the groups. In particular, when PCA is used for reducing the data dimensionality, only the components associated with the largest eigenvalues are kept. Such a practice is disproved mathematically and practically by Chang [26] who shows that the first components do not necessary contain more discriminative information than the others. In addition, reducing the dimension of the data may not be a good idea since, as discussed in Section 3, it is easier to discriminate groups in high-dimensional spaces than in lower dimensional spaces, assuming that one can build a good classifier in high-dimensional spaces. With this point of view, subspace clustering methods are good alternatives to dimension reduction approaches. The solution based on regularization does not have the same drawbacks than dimension reduction and can be used with less fear. However, all regularization techniques require the tuning of a parameter which is difficult to tune in the unsupervised context, although this can be done easily in the supervised context using cross validation. Finally, the solution which introduces parsimony in the models is clearly a better solution in the context of model-based clustering since it proposes a trade-off between the perfect modeling and what one can correctly estimate in practice. We will see in the next sections that recent solutions for high-dimensional clustering are partially based on the idea of parsimonious modeling.

5. Subspace clustering methods

Conversely to previous solutions, subspace clustering methods exploit the "empty space" phenomenon to ease the discrimination between groups of points. To do so, they model the data in low-dimensional subspaces and introduce some restrictions while keeping all dimensions. Subspace clustering methods can be split into two categories: heuristic and model-based methods. Heuristic methods use algorithms to search for subspaces of

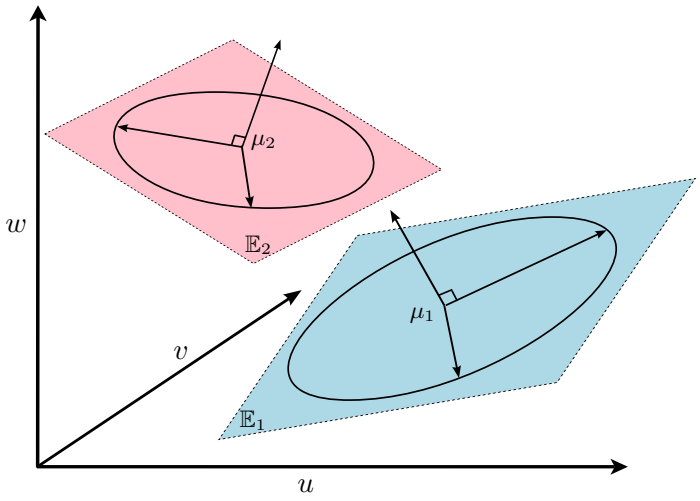
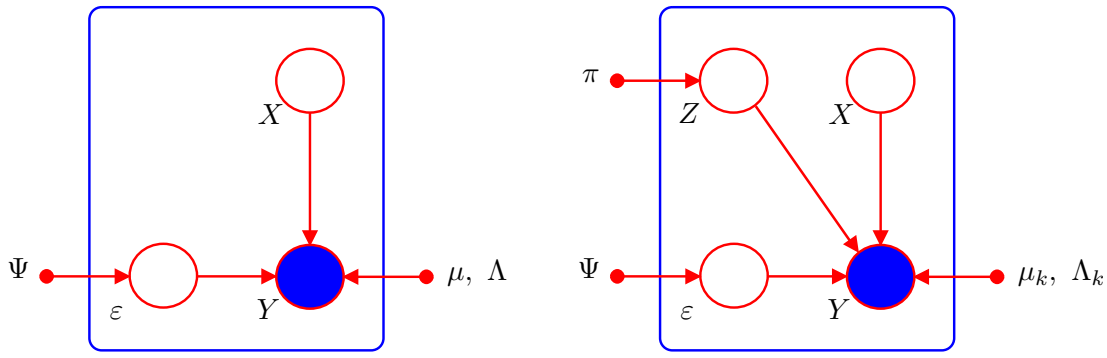


Figure 1: Illustration of the modeling of subspace clustering methods in the case of two groups (illustration from [20]).



(a) FA model (b) G-MFA model.

FIGURE 2: Graphical summary of factor analysis (FA) model (a) and mixture of factor analyzers (G-MFA) model of Ghahramani and Hinton (b).

high density within the original space. The Clique algorithm [1] is one of the heuristic algorithms and remains a reference in this family of methods. A review on heuristic methods is given by [79]. On the other hand, model-based subspace clustering methods are mostly related to the factor analysis [84] model which assumes that the observation space is linked to a latent space through a linear relationship. Figure 1 illustrates the typical modeling of subspace clustering methods.

5.1. Mixture of factor analyzers (MFA)

Mixture of factor analyzers (MFA) [43, 65] may be considered at the earliest subspace clustering method which both clusters the data and reduces locally the dimensionality of each cluster. The MFA model differs from the FA model by the fact that it allows to have different local factor models, in different regions of the input space, whereas the

standard FA assumes a common factor model. The MFA model was firstly introduced by Ghahramani & Hinton [43], and then extended by McLachlan *et al.* [65]. In this first paragraph, the original work of Ghahramani & Hinton on MFA is introduced before to develop the work of Baek & McLachlan on this subject and other recent works [4, 74, 103, 104]. To make a distinction between both approaches, we will refer to the model of Ghahramani & Hinton by G-MFA and to the model of McLachlan *et al.* by M-MFA.

The G-MFA model is an extension of the factor analysis model to a mixture of K factor analyzers. Let $\{y_1, \ldots, y_n\}$ be independent observed realizations of a random vector $Y \in \mathbb{R}^p$. Let us also consider that Y can be expressed from an unobserved random vector $X \in \mathbb{R}^d$, named the factor and described in a lower dimensional space of dimension $d < p$. Moreover, the unobserved labels $\{z_1, \ldots, z_n\}$ are assumed to be independent unobserved realizations of a random vector $Z \in \{1, \ldots, K\}$ where $z_i = k$ indicates that y_i is generated by the kth factor analyzer. The relationship between these two spaces is finally assumed, conditionally to Z, to be linear:

$$Y_{|Z=k} = \Lambda_k X + \mu_k + \varepsilon, \tag{10}$$

where Λ_k is a $p \times d$ matrix and $\mu_k \in \mathbb{R}^p$ is the mean vector of the kth factor analyzer. Moreover $\varepsilon \in \mathbb{R}^p$ is assumed to be a centered Gaussian noise term with a diagonal covariance matrix Ψ, common to all factors:

$$\varepsilon \sim \mathcal{N}(0, \Psi). \tag{11}$$

Besides, as in the FA model, the factor $X \in \mathbb{R}^d$ is assumed to be distributed according to a Gaussian density function such as $X \sim \mathcal{N}(0, \mathbf{I}_d)$. This implies that the conditional distribution of Y is also Gaussian:

$$Y|X, Z = k \sim \mathcal{N}(\Lambda_k X + \mu_k, \Psi). \tag{12}$$

The marginal density of Y is thus a Gaussian mixture model such as $f(y) = \sum_{k=1}^{K} \pi_k \phi(y|\theta_k)$, where π_k stands for the mixture proportion and $\theta_k = \{\mu_k, \Lambda_k \Lambda_k^t + \Psi\}$. Figures 2a and 2b summarize respectively the FA and G-MFA models. The complexity of the G-MFA model can be computed according to the number of parameters to estimate. Since the G-MFA model is in a Gaussian mixture model of K components, there are $(K-1)$ parameters for the proportions and Kp for the means. Moreover, $Kd(p-(d-1)/2)+p$ parameters are required to estimate the component covariance matrices, since the covariances matrices are defined in a factor representation such as $S_k = \Lambda_k \Lambda_k^t + \Psi$. The model complexity is then $\gamma_{G-MFA} = (K-1) + Kp + Kd(p-(d-1)/2) + p$ and, by considering the practical case where $p = 100$, $K = 4$ and $d = 3$, then 1691 parameters have to be estimated for this G-MFA model.

This approach, introduced by Ghahramani & Hinton, was generalized a few years later by McLachlan *et al.* [65] who removed in particular the constraint on the variance of the noise. Therefore, the conditional distribution of the noise term becomes $\varepsilon|Z = k \sim \mathcal{N}(0, \Psi_k)$ where Ψ_k stands for the diagonal covariance matrix of the cluster k. The new

Model name	Cov. structure	Nb. of parameters	$K=4, d=3$ $p=100$
M-MFA	$S_k = \Lambda_k \Lambda_k^t + \Psi_k$	$(K-1) + Kp + Kd[p-(d-1)/2] + Kp$	1991
G-MFA	$S_k = \Lambda_k \Lambda_k^t + \Psi$	$(K-1) + Kp + Kd[p-(d-1)/2] + p$	1691
MCFA	$S_k = A\Omega_k A^t + \Psi$	$(K-1) + Kd + p + d[p-(d+1)/2] + Kd(d+1)/2$	433
HFMA	$S_k = V\Omega_k V^t + \Psi$	$(K-1) + (K-1)d + p + d[p-(d-1)/2] + (K-1)d(d+1)/2$	427
MCUFSA	$S_k = A\Delta_k A^t + \lambda \mathbf{I}_p$	$(K-1) + Kd + 1 + d[p-(d+1)/2] + Kd$	322

A is defined such as $A^t A = \mathbf{I}_d$, V such as $V\Psi^{-1}V^t$ is diagonal with decreasing order and Δ_k is a diagonal matrix.

TABLE 3: Nomenclature of the MFA models developed by Ghahramani and Hinton (G-MFA), MacLachlan *et al.* (M-MFA), and several MCFA models with their corresponding covariance structure.

conditional distribution of Y is then: $Y|X, Z=k \sim \mathcal{N}(\Lambda_k X + \mu_k, \Psi_k)$. In this case, since there are K covariance matrices of noise to compute in comparison to the G-MFA model, the model complexity increases and takes the following expression for the M-MFA model: $\gamma_{M-MFA} = (K-1) + Kp + Kd(p-(d-1)/2) + Kp$.

Regarding the model inference, Ghahramani & Hinton proposed in [43] an exact EM algorithm for their G-MFA model. In the case of the M-MFA model, McLachlan *et al.* [65] proposed to make use of the alternating expectation-conditional maximization (AECM) [71] for parameter estimation.

5.2. Extensions of the MFA model

More recently, McLachlan & Baek [4] provided an alternative approach which aims to lower the complexity of the MFA model by proposing a more parsimonious modeling. To that end, they re-parametrized the mixture model with restrictions on the means, such as $\mu_k = A\rho_k$, where A is a $p \times d$ orthonormal matrix ($A^t A = \mathbf{I}_d$) and ρ_k is a d-dimensional vector, and on the covariance matrix $S_k = A\Omega_k A^t + \Psi$, where Ω_k is a $d \times d$ positive definite symmetric matrix and Ψ a diagonal $p \times p$ matrix. This model is referred to by the mixture of factor analyzers with common factor loadings (MCFA) by its authors, as the matrix A is common to the factors. According to the MCFA assumptions, there are only Kd means parameters to estimate instead of Kp in the MFA model. Moreover, since the matrix A is constrained to have orthonormal columns and to be common to all classes, then only $pd - d(d+1)/2$ loadings are required to estimates it. Finally, according to the restriction on the matrices Ω_k, the number of parameters to estimate for these K matrices is $Kd(d+1)/2$. Consequently, the complexity of the MCFA model is: $\gamma_{MCFA} = (K-1) + Kd + p + (pd - d(d+1)/2)) + Kd(d+1)/2$ and, for our recurrent practical case, this complexity is equal to 433 which is much more parsimonious than the previous MFA models. Besides, this MCFA approach is a special case of the MFA model but has the main advantage to allow the data to be displayed in a common low-dimensional plot.

The MCFA approach is also a generalization of the works of Yoshida *et al.* [103, 104] since they constrained the covariance of the noise term to be spherical ($\Psi = \lambda \mathbf{I}_p$) and the component-covariance matrices of the factors to be diagonal ($\Omega_k = \Delta_k = \text{diag}(\sigma_{k1}^2, \ldots, \sigma_{kd}^2)$). This approach, called mixtures of common uncorrelated factor spherical-error analyzers

Model name	Cov. structure	Nb. of parameters	$K=4, d=3$ $p=100$
UUUU - UUU	$S_k = \Lambda_k \Lambda_k^t + \Psi_k$	$(K-1) + Kp + Kd[p-(d-1)/2] + Kp$	1991
UUCU -	$S_k = \Lambda_k \Lambda_k^t + \omega_k \Delta_k$	$(K-1) + Kp + Kd[p-(d-1)/2] + [1 + K(p-1)]$	1988
UCUU -	$S_k = \Lambda_k \Lambda_k^t + \omega_k \Delta$	$(K-1) + Kp + Kd[p-(d-1)/2] + [K + (p-1)]$	1694
UCCU - UCU	$S_k = \Lambda_k \Lambda_k^t + \Psi$	$(K-1) + Kp + Kd[p-(d-1)/2] + p$	1691
UCUC - UUC	$S_k = \Lambda_k \Lambda_k^t + \psi_k \mathbf{I}_p$	$(K-1) + Kp + Kd[p-(d-1)/2] + K$	1595
UCCC - UCC	$S_k = \Lambda_k \Lambda_k^t + \psi \mathbf{I}_p$	$(K-1) + Kp + Kd[p-(d-1)/2] + 1$	1592
CUUU - CUU	$S_k = \Lambda \Lambda^t + \Psi_k$	$(K-1) + Kp + d[p-(d-1)/2] + Kp$	1100
CUCU -	$S_k = \Lambda \Lambda^t + \omega \Delta_k$	$(K-1) + Kp + d[p-(d-1)/2] + [1 + K(p-1)]$	1097
CCUU -	$S_k = \Lambda \Lambda^t + \omega_k \Delta$	$(K-1) + Kp + d[p-(d-1)/2] + [K + (p-1)]$	803
CCCU - CCU	$S_k = \Lambda \Lambda^t + \Psi$	$(K-1) + Kp + d[p-(d-1)/2] + p$	800
CCUC - CUC	$S_k = \Lambda \Lambda^t + \psi_k \mathbf{I}_p$	$(K-1) + Kp + d[p-(d-1)/2] + K$	704
CCCC - CCC	$S_k = \Lambda \Lambda^t + \psi \mathbf{I}_p$	$(K-1) + Kp + d[p-(d-1)/2] + 1$	701

where $\omega_k \in \mathbb{R}^+$and $|\Delta_k| = 1$.

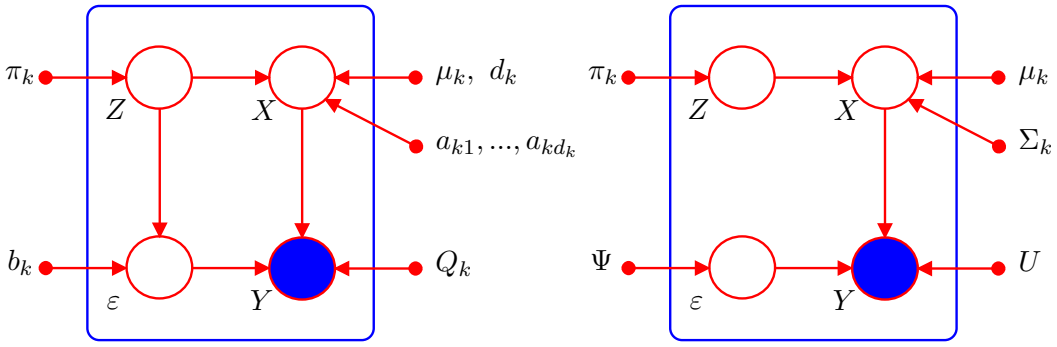
TABLE 4: Nomenclature of the members of the PGMM and EPGMM families and the corresponding covariance structure.

(MCUFSA), is therefore more parsimonious than MCFA according to the additional assumptions done on the parameters of the MFA model. Finally, Montanari & Viroli [74] presented an approach called heteroscedastic mixture factor model (HMFA) which is very similar to the model described in MCFA. Their model differs from the MCFA approach only on the definition of the common loadings matrix A which does not need to have orthonormal columns. However, to obtain a unique solution for the matrix A, Montanari & Viroli added restrictions on this matrix such as $A^t \Psi^{-1} A$ is diagonal with elements in decreasing order. The links and differences between all these MCFA models are summarized in Table 3 which presents both the covariance structure and the model complexity of each approach.

The inference of both the MCFA and MCUFSA models is done using the AECM algorithm whereas a simple EM algorithm is used for the HMFA model.

5.3. Mixture of parsimonious Gaussian mixture models (PGMM)

A general framework for the MFA model was also proposed by McNicholas & Murphy [69] which, in particular, includes the previous works of Ghahramani and Hinton and of McLachlan *et al.*[65]. By considering the previous framework, defined by Equations (10) and (12), McNicholas & Murphy [70] proposed a family of models known as the expanded parsimonious Gaussian mixture model (EPGMM) family. They decline 12 EPGMM models by either constraining the terms of the covariance matrix to be equal or not, considering an isotropic variance for the noise term, or re-parametrizing the factor analysis covariance structure. The nomenclature of both PGMM and EPGMM is given by Table 4 in which the covariance structure of each model is detailed as well. In particular, the terminology of the PGMM family is as follows: the first letter refers to the loading matrix which is constrained to be common between groups (C..) or not (U..), the second term indicates whether the noise variance is common between factors (.C.) or not (.U.), and the last term refers to the covariance structure which can be either isotropic (..C) or not (..U). Thus,



(a) HD-GMM model (b) DLM model

FIGURE 3: Graphical representations of the HD-GMM model $[a_{kj}b_kQ_kd_k]$ (a) and of the $\text{DLM}_{[\Sigma_k\beta]}$ model (b).

the CCC model refers to a model with common factors ($\Lambda_k = \Lambda$, $\forall k \in \{1, \ldots, K\}$) and a common and isotropic noise variance ($\Psi_k = \psi\mathbf{I}_p$). In the terminology of the EPGMM family, the structure of the noise covariance matrix is described as follows: Δ_k can be common (.C..) or not (.U..), $\omega_k = \omega\ \forall k \in \{1, \ldots, K\}$ (..C.) or not (..U.) and finally $\Delta_k = \mathbf{I}_p$ (...C) or not (...U). The table also gives the maximum number of free parameters to estimate according to K, p and d for the 12 models. Once again, this number of free parameters to estimate can be decomposed in the number of parameters to estimate for the proportions $(K-1)$, for the means (Kp) and for the covariance matrices (last terms).

According to this family of 12 models, the previous approaches developed by [4, 43, 65, 69, 92] then become submodels of the EPGMM approach. For example, by constraining only the noise variance to be isotropic on each class ($\Psi_k = \sigma_k^2\mathbf{I}_p$), which by the way corresponds to the UUC and UUUC models, it produces the famous mixture of prababilistic PCA (Mixt-PPCA) of Tipping & Bishop [92]. In the same way, by considering the covariance structure of the UCU and UCCU models such that $\Psi_k = \Psi$ and Λ_k, then we obtain the mixture of factor analyzers model developed by Ghahramani & Hinton. The UUUU model is as well equivalent to the MFA model proposed by McLachlan *et al.* in [65]. Finally, by parameterizing the covariance structure as $\Psi_k = \omega_k\Delta_k$, where Δ_k is a diagonal matrix and $|\Delta_k| = 1$, McNicholas & Murphy proposed 4 additional models to their previous work [69].

In the case of the EPGMM models, McNicholas & Murphy [70] proposed for the model inference to make use of the AECM algorithm to speed up the convergence. It is worth to notice that the AECM could be used for inferring most of the MFA-based models.

5.4. Mixture of high-dimensional Gaussian mixture models (HD-GMM)

In a slightly different context, Bouveyron *et al.* [20, 21] proposed a family of 28 parsimonious and flexible Gaussian models to deal with high-dimensional data. Conversely to

the previous approaches, this family of GMM was directly proposed in both supervised and unsupervised classification contexts. In order to ease the designation of this family, we propose to refer to these Gaussian models for high-dimensional data by the acronym HD-GMM. Bouveyron *et al.* [20] proposed to constraint the GMM model through the eigen-decomposition of the covariance matrix Σ_k of the kth group:

$$\Sigma_k = Q_k \Lambda_k Q_k^t,$$

where Q_k is a $p \times p$ orthogonal matrix which contains the eigenvectors of Σ_k and Λ_k is a $p \times p$ diagonal matrix containing the associated eigenvalues (sorted in decreasing order). The key idea of the work of Bouveyron *et al.* is to reparametrize the matrix Λ_k, such as Σ_k has only $d_k + 1$ different eigenvalues:

$$\Lambda_k = \text{diag}\left(a_{k1}, \ldots, a_{kd_k}, b_k, \ldots, b_k\right),$$

where the d_k first values $a_{k1}, \ldots, a_{kd_k}$ parametrize the variance in the group-specific subspace and the $p - d_k$ last terms, the b_k's model the variance of the noise and $d_k < p$. With this parametrization, these parsimonious models assume that, conditionally to the groups, the noise variance of each cluster k is isotropic and is contained in a subspace which is orthogonal to the subspace of the kth group. Following the classical parsimony strategy, the authors proposed a family of parsimonious models from a very general model, the model $[a_{kj} b_k Q_k d_k]$, to very simple models. Table 5 lists the 16 HD-GMM models with closed-form estimators and reports their complexity for comparison purposes. Once again, the first quantity $(K-1) + Kp$ stands for the number of parameters for the means and the mixture proportions of K clusters. Then, there are $\sum_{k=1}^{K} d_k[p(d_k+1)/2]$ loadings to estimate for the K orientation matrices Q_k. Finally, the last terms represent the number of free parameters for the covariance matrices in the latent and in the noise subspaces of K clusters and their intrinsic dimension.

Such an approach can be viewed in two different ways: on the one hand, these models enable to regularize the models in high-dimension. In particular, by constraining d_k such that $d_k = p - 1$ for $k = 1, ..., K$, the proposed approach can be viewed as a generalization of the works of [24, 35]. Indeed, the model $[a_{kj} b_k Q_k (p-1)]$ is equivalent to the Full-GMM model or the $[\lambda_k D_k A_k D_k]$ model in [24]. In the same manner, the model $[a_{kj} b_k Q (p-1)]$ is equivalent to the Diag-GMM and the $[a_j b Q (p-1)]$ is also the Com-Diag-GMM. On the other hand, this approach can also be viewed as an extension of the mixture of principal component analyzer (Mixt-PPCA) model [92] since it relaxes the equality assumption on d_k made in [92] and the model $[a_{kj} b_k Q_k d]$ is therefore equivalent to the Mixt-PPCA model.

In the case of the 16 HD-GMM models listed in Table 5, the inference can be done easily using the EM algorithm since update formula for mixture parameters are closed-form. We refer to [20] regarding the inference of the other 13 models which require an iterative M step. Finally, the estimation of the intrinsic dimensions d_k, $k = 1, ..., K$, relies on the scree test of Cattell [23] which looks for a break in the eigenvalue scree of the

Model name	Nb. of parameters	$p = 100$ $K = 4$, $d = 3$
$[a_{kj}b_kQ_kd_k]$	$(K-1) + Kp + \sum_{k=1}^{K} d_k[p-(d_k+1)/2] + \sum_{k=1}^{K} d_k + 2K$	1599
$[a_{kj}bQ_kd_k]$	$(K-1) + Kp + \sum_{k=1}^{K} d_k[p-(d_k+1)/2] + \sum_{k=1}^{K} d_k + 1 + K$	1596
$[a_kb_kQ_kd_k]$	$(K-1) + Kp + \sum_{k=1}^{K} d_k[p-(d_k+1)/2] + 3K$	1591
$[ab_kQ_kd_k]$	$(K-1) + Kp + \sum_{k=1}^{K} d_k[p-(d_k+1)/2] + 1 + 2K$	1588
$[a_kbQ_kd_k]$	$(K-1) + Kp + \sum_{k=1}^{K} d_k[p-(d_k+1)/2] + 1 + 2K$	1588
$[abQ_kd_k]$	$(K-1) + Kp + \sum_{k=1}^{K} d_k[p-(d_k+1)/2] + 2 + K$	1585
$[a_{kj}b_kQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + Kd + K + 1$	1596
$[a_jb_kQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + d + K + 1$	1587
$[a_{kj}bQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + Kd + 2$	1593
$[a_jbQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + d + 2$	1584
$[a_kb_kQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + 2K + 1$	1588
$[ab_kQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + K + 2$	1585
$[a_kbQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + K + 2$	1585
$[abQ_kd]$	$(K-1) + Kp + Kd[p-(d+1)/2] + 3$	1582
$[a_jbQd]$	$(K-1) + Kp + d[p-(d+1)/2] + d + 2$	702
$[abQd]$	$(K-1) + Kp + d[p-(d+1)/2] + 3$	700

TABLE 5: Nomenclature for the members of the Hd-GMM family and the number of parameters to estimate. For the numerical example, the intrinsic dimension of the clusters has been fixed to $d_k = \bar{d} = 3$, $\forall k = 1, \ldots, K$.

empirical covariance matrix of each group. Let us finally notice that Bouveyron *et al.* [19] have demonstrated the surprising result that the maximum likelihood estimator of the intrinsic dimensions d_k is asymptotically consistent in the case of the model $[a_kb_kQ_kd_k]$.

5.5. The discriminative latent mixture (DLM) models

Recently, Bouveyron & Brunet [17] proposed a family of mixture models which fit the data into a common and discriminative subspace. This mixture model, called the discriminative latent mixture (DLM) model, differs from the FA-based models in the fact that the latent subspace is common to all groups and is assumed to be the most discriminative subspace of dimension d. This latter feature of the DLM model makes it significantly different from the other FA-based models. Indeed, roughly speaking, the FA-based models choose the latent subspace(s) maximizing the projected variance whereas the DLM model chooses the latent subspace which maximizes the separation between the groups.

Let us nevertheless start with a FA-like modeling. Let $Y \in \mathbb{R}^p$ be the observed random vector and let $Z \in \{1, \ldots, K\}$ be once again the unobserved random variable to predict. The DLM model then assumes that Y is linked to a latent random vector $X \in \mathbb{E}$ through a linear relationship of the form $Y = UX + \varepsilon$, where $\mathbb{E} \subset \mathbb{R}^p$ is assumed to be the most discriminative subspace of dimension $d \leq K-1$ such that $\mathbf{0} \in \mathbb{E}$, $K < p$, U is a $p \times d$ orthonormal matrix common to the K groups and satisfying $U^tU = \mathbf{I}_d$, and $\varepsilon \sim \mathcal{N}(0, \Psi)$ models the non discriminative information. Besides, within the latent space and conditionally to $Z = k$, X is assumed to be distributed as $X|Z = k \sim \mathcal{N}(\mu_k, \Sigma_k)$ where $\mu_k \in \mathbb{R}^d$ and $\Sigma_k \in \mathbb{R}^{d \times d}$ are respectively the mean vector and the covariance matrix

Model	Nb. of parameters	$p = 100$ and $K = 4$
$\text{DLM}_{[\Sigma_k\beta_k]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K^2(K-1)/2+K$	337
$\text{DLM}_{[\Sigma_k\beta]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K^2(K-1)/2+1$	334
$\text{DLM}_{[\Sigma\beta_k]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K(K-1)/2+K$	319
$\text{DLM}_{[\Sigma\beta]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K(K-1)/2+1$	316
$\text{DLM}_{[\alpha_{kj}\beta_k]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K^2$	325
$\text{DLM}_{[\alpha_{kj}\beta]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K(K-1)+1$	322
$\text{DLM}_{[\alpha_k\beta_k]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+2K$	317
$\text{DLM}_{[\alpha_k\beta]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K+1$	314
$\text{DLM}_{[\alpha_j\beta_k]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+(K-1)+K$	316
$\text{DLM}_{[\alpha_j\beta]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+(K-1)+1$	313
$\text{DLM}_{[\alpha\beta_k]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+K+1$	314
$\text{DLM}_{[\alpha\beta]}$	$(K-1)+K(K-1)+(K-1)(p-K/2)+2$	311

TABLE 6: Number of free parameters to estimate when $d = K-1$ for the DLM models and some classical models (see text for details).

of the kth group. Given these distribution assumptions, the marginal distribution of Y is once again a mixture of Gaussians, *i.e.* $g(y) = \sum_{k=1}^{K} \pi_k \phi(y; m_k, S_k)$, where $m_k = U\mu_k$ and $S_k = U\Sigma_k U^t + \Psi$. Let $W = [U, V]$ be the $p \times p$ matrix such that $W^tW = WW^t = \mathbf{I}_p$ and V is an orthogonal complement of U. Finally, the noise covariance matrix Ψ is assumed to satisfy the conditions $V\Psi V^t = \beta\mathbf{I}_{p-d}$ and $U\Psi U^t = \mathbf{0}_d$, such that $\Delta_k = W^t S_k W$ is block-diagonal:

$$\Delta_k = \text{diag}\left(\Sigma_k, \beta I_{p-d}\right)$$

These last conditions imply that the discriminative and the non-discriminative subspaces are orthogonal, which suggests in practice that all the relevant clustering information remains in the latent subspace.

This model is referred to by $\text{DLM}_{[\Sigma_k\beta]}$ in [17]. Following the classical strategy, several other models can be obtained from the $\text{DLM}_{[\Sigma_k\beta]}$ model by relaxing or adding constraints on model parameters. Firstly, it is possible to consider a more general case than the $\text{DLM}_{[\Sigma_k\beta]}$ by relaxing the constraint on the variance term of the non discriminative information. Assuming that $\varepsilon|Z = k \sim \mathcal{N}(0, \Psi_k)$ yields the $\text{DLM}_{[\Sigma_k\beta_k]}$ model which can be useful in some practical cases. From this extended model, 10 parsimonious models can be obtained by constraining the parameters Σ_k and β_k to be common between and within the groups. The list of the 12 different DLM models is given by Table 6 which also provides the number of free parameters to estimate. As we can see, the DLM family yields very parsimonious models and allows, in the same time, to fit into various situations. In particular, the complexity of the $\text{DLM}_{[\Sigma_k\beta_k]}$ model mainly depends on the number of clusters K since the dimensionality of the discriminative subspace is such that $d \leq K-1$. Let us finally notice that a model similar to the $\text{DLM}_{[\alpha\beta]}$ model has been considered in [85].

Conversely to most of the MFA-based models, the inference of the DLM models cannot be directly done using the EM algorithm because of the specific features of its latent subspace. To overcome this problem, an estimation procedure, called the Fisher-EM al-

gorithm, is also proposed in [17] for estimating both the discriminative subspace and the parameters of the mixture model. This algorithm is based on the EM algorithm from which an additional step is introduced, between the E and the M-step. This additional step, named F-step, aims to compute the projection matrix U whose columns span the discriminative latent space. This step estimates at iteration q, the orientation matrix $U^{(q)}$ of the discriminative latent space by maximizing the Fisher's criterion [31, 40] under orthonormality constraints and conditionally to the posterior probabilities:

$$\begin{aligned} \hat{U}^{(q)} &= \max_{U} \quad \text{trace}\left((U^t S U)^{-1} U^t S_B^{(q)} U\right), \\ &\quad \text{w.r.t.} \quad U^t U = \mathbf{I}_d, \end{aligned} \tag{13}$$

where S stands for the empirical covariance matrix and $S_B^{(q)}$, defined as follows:

$$S_B^{(q)} = \frac{1}{n} \sum_{k=1}^{K} n_k^{(q)} (m_k^{(q)} - \bar{y})(m_k^{(q)} - \bar{y})^t, \tag{14}$$

denotes the soft between covariance matrix with $n_k^{(q)} = \sum_{i=1}^{n} t_{ik}$, $m_k^{(q)} = 1/n_k^{(q)} \sum_{i=1}^{n} t_{ik}^{(q)} y_i$ and $\bar{y} = 1/n \sum_{i=1}^{n} y_i$. This optimization problem is solved in [17] using the concept of orthonormal discriminant vector developed by [32] through a Gram-Schmidt procedure. Such a process enables to fit a discriminative and low-dimensional subspace conditionally to the current soft partition of the data while providing orthonormal discriminative axes. In addition, according to the rank of the matrix $S_B^{(q)}$, the dimensionality of the discriminative space d is strictly bounded by the number of clusters K and can be set to $K-1$ in practice. Two additional procedures are proposed in [15] for the estimation of the latent subspace orientation. The convergence properties of the Fisher-EM algorithm were also studied in [18] from both the theoretical and the practical points of view.

5.6. Discussion on subspace clustering methods and related works

The subspace clustering methods which have been presented in this section belong to a huge family of Gaussian mixture models and several links exist between these approaches. Indeed, in the last paragraph, we saw that some constrained HD-GMM models are equivalent to traditional parsimonious models such that Com-Diag-GMM or Diag-GMM and consequently to the models proposed by Raftery & Fraley or by Celeux & Govaert. Besides, it also appears that the model $[a_{kj} b_k Q_k d]$ is equivalent to the Mixt-PPCA model. In the same manner, few models which belong to the EPGMM family of [70] are also included in the HD-GMM family (and *vice-versa*). In particular, the UCUC model of [70] corresponds to the HD-GMM model $[a_{kj} b_k Q_k d]$. Moreover, the EPGMM family proposed by McNicholas & Murphy includes individual works on MFA such as the works of Ghahramani [43], Tipping and Bishop [92], McLachlan [65], McNicholas and Murphy [70] and Baek *et al.*[4]. Let us highlight that the hypothesis of HD-GMM models are more restrictive than the MFA models since, for example, the subspace of each class is spanned by orthogonal vectors, whereas it is not a necessary condition in MFA, even if such a situation

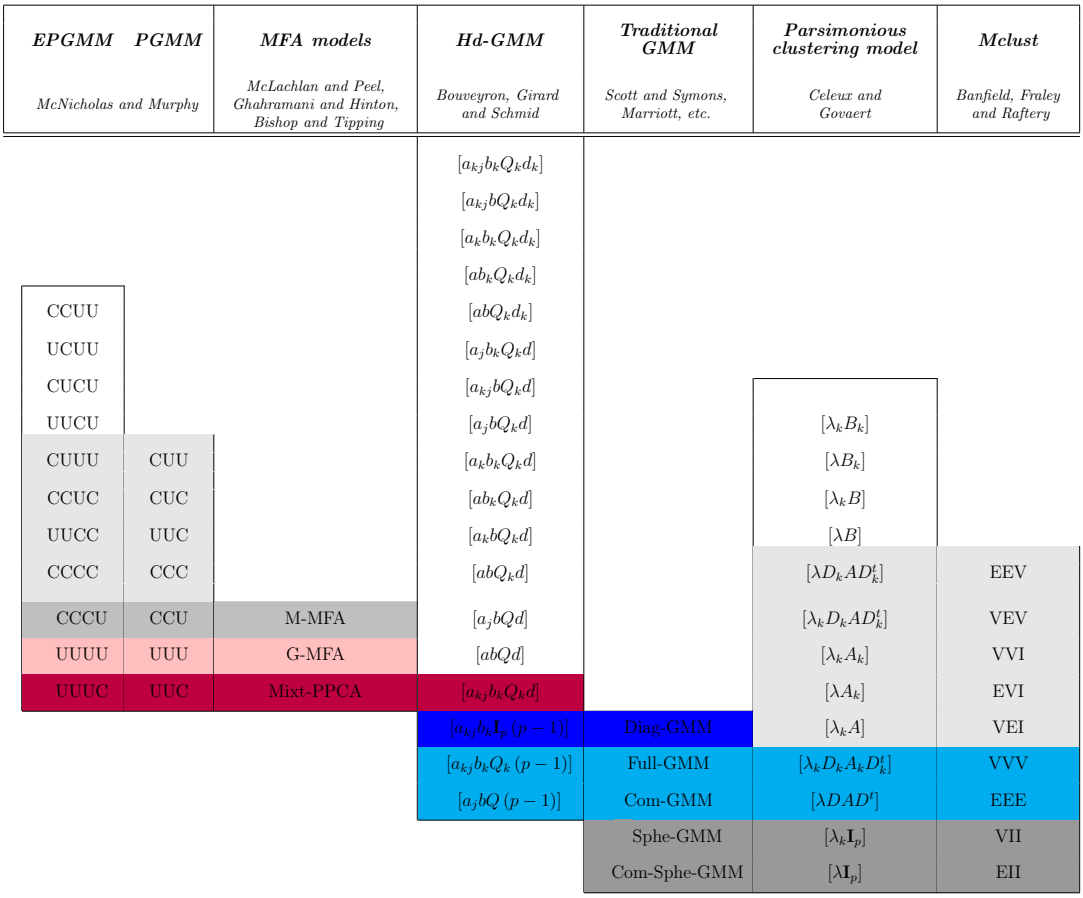


FIGURE 4: Links between MFA-bsed models for subspace clustering and some parsimonious models.

can occur sometimes as in the case of the model UCUC (CUC). The links between the different families of parsimonious models are presented in Figure 4. However, it is worth noting that, despite their efficiency to cluster high-dimensional data, these probabilistic methods based on subspace clustering present several limitations. Indeed, since most models assume that each cluster lives in a specific subspace, the visualization of the clustering results is not easy. Only the MCFA, MCUFSA, HMFA and DLM, for which the latent subspace is assumed to be common, can provide low-dimensional plots of the clustered data.

Among the related works, we may cite the robust versions [2, 66] of the MFA models which relies on t-distributions and the GMMDR technique [89] which iteratively looks for the subspace containing the most relevant information for clustering. Let us finally notice that some subspace clustering methods have been modified for performing variable selection through ℓ_1 penalization. We will discuss in the next section the sparse extensions of the HMFA and DLM models.

6. Variable selection for clustering

Conversely to the approaches of the previous section, several recent works have been interested to simultaneously cluster data and reduce their dimensionality by selecting relevant variables for the clustering task. A common assumption to these works is that the true underlying clusters are assumed to differ only with respect to some of the original features. The clustering task aims therefore to group the data on a subset of relevant features. This presents two practical advantages: clustering results should be improved by removing non informative features and the interpretation of the obtained clusters should be eased by the meaning of retained variables. In the literature, variable selection for clustering is handled in two different ways.

On the one hand, some authors such as [49, 54, 57, 83] tackle the problem of variable selection for model-based clustering within a Bayesian framework. In particular, the determination of the role of each variable is recast as a model selection problem. On the other hand, penalized clustering criteria have also been proposed to deal with the problem of variable selection in clustering. In the Gaussian mixture model context, several works, such as [78, 96, 101, 105] in particular, introduced a penalty term in the log-likelihood function in order to yield sparsity in the features.

6.1. Variable selection as a model selection problem

The underlying idea of the works of Law *et al.* [49], Raftery and Dean [83] and Maugis *et al.* [57] is to find the variables which are relevant for the clustering task. The determination of the role of each variable is in particular apprehended in [57, 83] as a model selection problem in the GMM context. In particular, Raftery & Dean and Maugis *et al.* consider a collection of parsimonious and interpretable models, developed by Banfield & Raftery [5] and Celeux & Govaert [24], based on a specific decomposition of the mixture component variance matrix (see Section 4 for more details).

In the Raftery & Dean's approach, the authors define two different sets of variables: $\mathcal{S}$ which denotes the set of relevant variables and $\mathcal{S}_c$ which is the set containing the irrelevant variables. An interesting aspect of their approach is that they do not assume that the irrelevant variables are independent of the clustering variables conversely to Law *et al.* [49]. In particular, they define the irrelevant variables as those which are independent of the clustering but which remain dependent of the set of relevant variables according to a linear relationship. The models in competition are compared with the integrated log-likelihood *via* a BIC approximation. Thus, the selected model maximizes the following quantity:

$$\left(\hat{K}, \hat{m}, \hat{\mathcal{S}}\right) = \arg \max_{(K,m,r,\ell,V)} \left\{ \mathrm{BIC}_{\mathrm{clust}}(\mathbf{y}^{\mathcal{S}}|\mathrm{K}, \mathrm{m}) + \mathrm{BIC}_{\mathrm{reg}}(\mathbf{y}^{\mathcal{S}_c}|\mathbf{y}^{\mathcal{S}}) \right\}, \tag{15}$$

where K is the number of clusters and $m \in \mathcal{M}$ is a model which belongs to the family of parsimonious models available in the `mclust` [34] software. Note that the quantity to be maximized in expression (15), can be decomposed into two parts: the first term corresponds

to the Gaussian mixture model of K components on the subset of relevant variables $\mathcal{S}$, whereas the second one is relative to the regression of irrelevant variables in $\mathcal{S}_c$ on the set of all clustering variables in $\mathcal{S}$. However, the dependence assumption which defines the irrelevant set of variables according to all the relevant ones remains debatable. Indeed, on the one hand, considering only the case where the irrelevant variables are independent on both the clustering and the relevant partition, as it was considered in the work of Law *et al.* [49], seems to be unrealistic. On the other hand, considering that all the irrelevant variables depends on the relevant variables by a linear relationship seems to be as well a strong hypothesis which may be not valid in certain practical cases. An other limitation of the Raftery & Dean's procedure is linked to their variable selection algorithm. Indeed, they proposed in [83] a forward-stepwise algorithm which considers only few variables at the beginning and which prevents from taking into account the block interactions between variables.

To overcome these limitations, Maugis *et al.* [25, 57, 58] relax such restrictions and propose a more general variable role modeling. They define two subsets of variables: on the one hand, the relevant ones, which are grouped in $\mathcal{S}$ and, on the other hand, its complementary $\mathcal{S}_c$, which is formed by the irrelevant variables. Maugis *et al.* consider two types of behaviors among these irrelevant variables: a subset $\mathcal{U}$ of irrelevant variables which can be explained by a linear regression from a subset $\mathcal{R}$ of the clustering variables and a subset $\mathcal{W}$ of irrelevant variables which are totally independent of all relevant variables. Such a variable partition allows to both consider the approaches developed by Law *et al.* [49] and by Raftery & Dean [83]. It is referred to by the model collection SRUW. From this characterization, the authors also recast the variable selection problem into a model selection problem through an approximation of the integrated log-likelihood. Then the selected model satisfies:

$$\left(\hat{K}, \hat{m}, \hat{r}, \hat{h}, V\right) = \arg \max_{(K,m,r,h,V)} \left\{ \mathrm{BIC}_{\mathrm{clust}}(\mathbf{y}^{\mathcal{S}}|\mathrm{K},\mathrm{m}) + \mathrm{BIC}_{\mathrm{reg}}(\mathbf{y}^{\mathcal{U}}|\mathrm{r},\mathbf{y}^{\mathcal{R}}) + \mathrm{BIC}_{\mathrm{ind}}(\mathbf{y}^{\mathcal{W}}|\mathrm{h}) \right\}, \tag{16}$$

where $V = (\mathcal{S}, \mathcal{R}, \mathcal{U}, \mathcal{W})$ stands for the variable partition. The first term of this expression, called $\mathrm{BIC}_{\mathrm{clust}}$, corresponds to the BIC criterion [86] for a Gaussian mixture of K components on the relevant subset of variables $\mathcal{S}$. The model m belongs here to a collection of 28 parsimonious models which are available in the Mixmod software [11] and include the GMM family introduced by Celeux & Govaert [24]. The second term denoted by $\mathrm{BIC}_{\mathrm{reg}}$, is linked to the BIC criterion for a linear regression of the irrelevant variables $\mathcal{U}$ on a subset of clustering variables $\mathcal{R}$. Note that the index r stands for the structure of the covariance matrix which can be assumed to be spherical, diagonal or non-constraint. Finally, the last term depicts the BIC criterion for a Gaussian density on the variable subset $\mathcal{W}$ independent of the clustering variables. This Gaussian marginal distribution is characterized by a variance matrix σ which is constrained to be either diagonal or spherical and is specified by the index h in the expression (16).

The identifiability of the SRUW model and the consistency of their variable selection problem has been studied in [57]. Regarding the implementation, they propose an algorithm based on a backward-stepwise selection. It implies that all the variables are considered at the beginning of the procedure and only a block of variables is either included or excluded of the clustering relevant set of features at each iteration. Such an approach enables them to take into account variable block interactions, if they exist. Then a second algorithm is executed to select both the model and the number of components for the mixture model.

6.2. Variable selection by likelihood penalization

An other way to combine variable selection and clustering is to penalize the clustering criteria in order to yield sparsity in the features. This technique has been used, in particular, by penalizing the log-likelihood function to optimize. A general form for the penalized log-likelihood function is:

$$\mathcal{L}_{\mathrm{p}}(\theta) = \ell(\theta) - \mathrm{p}_\lambda(\theta) \tag{17}$$

where $\ell(\theta)$ stands for the log-likelihood function and $\mathrm{p}_\lambda(\theta)$ is the penalty function. In GMM context, Pan & Shen [78] proposed a penalized log-likelihood criterion by assuming a Gaussian mixture model with common diagonal covariance matrices, meaning that $\forall k \in \{1, \ldots, K\}$, $\Sigma_k = \Sigma = \mathrm{diag}(\sigma_1^2, \ldots, \sigma_j^2, \ldots, \sigma_p^2)$ where $\sigma_j^2 \in \mathbb{R}$. The penalty function is focused on the means of K clusters ($m_{1k}, \ldots, m_{pk}$, $\forall k \in \{1, \ldots, K\}$) and has the following form:

$$\mathrm{p}_\lambda(\theta) = \lambda_1 \sum_{k=1}^{K} \sum_{j=1}^{p} |m_{kj}|\,, \tag{18}$$

where m_{kj} denotes the mean of the jth variable in the component k and λ_1 an hyper-parameter which stands for the desired level of sparsity. Thus, since the observations are standardized, if the means of a variable j on each component are equal *i.e.* $m_{1j} = \cdots = m_{Kj} = 0$, then this variable is irrelevant and can be removed from the clustering variables. Therefore, a variable selection is realized when some m_{kj}'s can be shrunken toward 0. This situation occurs for an ℓ_1 penalty term large enough. In the same spirit, Wang & Zhou [96] proposed two other penalty terms. The first one is based on ℓ_∞-norm:

$$\mathrm{p}_\lambda(\theta) = \lambda_\infty \sum_{j=1}^{p} \max_{k \in \{1,\ldots,K\}} |m_{kj}|\,, \tag{19}$$

which has the advantage to incorporate group information. Thus, this penalty tends to shrink all the m_{kj}'s toward 0 as soon as the jth variable is non informative. However, such a penalty tends to shrink the m_{kj}'s in the same magnitude and thus does no take into account the situation where a variable is different from 0 on only one component. To that end, Wang & Zhou proposed a second penalty function based on hierarchical penalties. These three penalized log-likelihood functions have been developed with the restriction of the diagonal common covariance matrix of each cluster in the mixture model. Xie *et al.* [101] extended the model of Pan & Shen [78] by relaxing the equality constraint on the

covariance matrices. Indeed, they proposed an approach dealing with the case of cluster-specific diagonal covariance matrices ($\forall k \in \{1, \ldots, K\}$, $S_k = \text{diag}(\sigma_{k1}^2, \ldots, \sigma_{kp}^2)$) leading to the following penalty function:

$$\text{p}_\lambda(\theta) = \lambda_1 \sum_{k=1}^{K} \sum_{j=1}^{p} |m_{kj}| + \lambda_2 \sum_{k=1}^{K} \sum_{j=1}^{p} \left| \sigma_{kj}^2 - 1 \right|. \tag{20}$$

In this case, a second regularized term is added and holds on the variance of the variable j of the kth component σ_{kj}^2 which can be shrunk towards 0. As previously, the hyper-parameters λ_1 and λ_2 are selected through a modified BIC criterion, which takes into account the level of sparsity in the model complexity term. Finally, Zhan *et al.* [105] recently proposed a penalization in the case of Com-GMM model ($S_k = S$, $\forall k \in \{1, \ldots K\}$):

$$\text{p}_\lambda(\theta) = \lambda_1 \sum_{k=1}^{K} \sum_{j=1}^{p} |m_{kj}| + \lambda_2 \sum_{\ell=1}^{p} \sum_{j=1}^{p} |C_{j\ell}|,$$

where $\{C_{j\ell}\}_{j,\ell=1}^{p}$ are the elements of the inverse covariance matrix S^{-1}. In the same work, Zhan *et al.* also proposed an estimation procedure to deal with the $n < p$ case.

6.3. Variable selection by penalization of the loadings

An alternative approach for selecting the relevant variables through penalization is to directly apply the lasso penalty on the loading matrix of a MFA-based model. This has been achieved in particular in [16, 41, 102]. In the case of the MFA model, Galimberti *et al.* [41] introduced an ℓ_1-penalty on the factor loadings in the log-likelihood function such as:

$$\text{p}_\lambda(\theta) = \lambda_2 \sum_{\ell=1}^{d} \sum_{j=1}^{p} |b_{\ell j}| \tag{21}$$

where $b_{\ell j}$ stands for the factor loadings. In a very recent work, Xie *et al.* [102] proposed a penalized MFA approach from the model introduced by Gharamani & Hinton where the covariance matrix of the noise term is diagonal and common to all factors. The penalty function has the following form:

$$\text{p}_\lambda(\theta) = \lambda_1 \sum_{k=1}^{K} \sum_{j=1}^{p} |m_{kj}| + \lambda_2 \sum_{k=1}^{K} \sum_{j=1}^{p} b_{kj}^2, \tag{22}$$

where b_{kj} stands for the factor loading of the kth factor. As in the previous approaches, the first term based on the ℓ_1-norm is used to shrink the means m_{kj} to be exactly equal to 0 while the second term serves as a grouped variable penalty. Indeed, this last penalty aims to shrink the estimates of factor loadings b_{kj} which are close to 0 to be exactly equal to 0. Consequently, if a variable has a common mean equal to 0, a common variance on each factor across the clusters and is independent with all other cluster such as $b_{kj} = 0$ $\forall k$, then this variable is irrelevant and does not contribute in the clustering task.

In the context of Fisher-EM, the direct penalization of the loading matrix U makes particularly sense since it is not estimated by likelihood maximization. The matrix U

is indeed estimated in the F-step of the Fisher-EM algorithm by maximizing the Fisher criterion conditionally to the current partition of the data. To achieve the penalization of U, two solutions are proposed in [16]. The first solution is a two stage approach which first estimate U, at each iteration, with the F-step and then looks for its best sparse approximation as follows:

$$\min_U \left\| X^{(q)t} - Y^t U \right\|_F^2 + \lambda \sum_{j=1}^{d} \|u_j\|_1 ,$$

where u_j is the jth column vector of U, $X^{(q)} = \hat{U}^{(q)t} Y$ and $\| \|_F$ refers to the Frobenius norm. The solution of this penalized regression problem can be computed through the LARS algorithm [30]. The second solution directly recasts the maximization of the Fisher criterion as a regression problem and provides a sparse loading matrix by solving the lasso problem associated to this regression problem. Let us define, conditionally to the posterior probabilities $t_{ik}^{(q)}$, the matrices $H_W^{(q)} = \frac{1}{\sqrt{n}} \left[Y - \sum_{k=1}^K t_{1k}^{(q)} m_k^{(q)}, \ldots, Y - \sum_{k=1}^K t_{nk}^{(q)} m_k^{(q)} \right] \in \mathbb{R}^{p \times n}$ and $H_B^{(q)} = \frac{1}{\sqrt{n}} \left[\sqrt{n_1^{(q)}}(m_1^{(q)} - \bar{y}), \ldots, \sqrt{n_K^{(q)}}(m_K^{(q)} - \bar{y}) \right] \in \mathbb{R}^{p \times K}$, where $n_k^{(q)} = \sum_{i=1}^n t_{ik}^{(q)}$ and $m_k^{(q)} = \frac{1}{n} \sum_{i=1}^n t_{ik}^{(q)} y_i$. According to these definitions, the matrices $H_W^{(q)}$ and $H_B^{(q)}$ satisfy $H_W^{(q)} H_W^{(q)t} = S_W^{(q)}$ and $H_B^{(q)} H_B^{(q)t} = S_B^{(q)}$where $S_W^{(q)}$ and $S_B^{(q)}$ are respectively the soft within and between covariance matrices computed at iteration q. Then, the best sparse approximation of the solution of the Fisher criterion is the solution $\hat{B}^{(q)}$ of the following penalized regression problem:

$$\begin{aligned} &\min_{A,B} \sum_{k=1}^{K} \left\| R_W^{(q)-t} H_{B,k}^{(q)} - AB^t H_{B,k}^{(q)} \right\|_F^2 + \rho \sum_{j=1}^{d} \beta_j^t S_W^{(q)} \beta_j + \lambda \sum_{j=1}^{d} |\beta_j|_1 , \\ &\text{w.r.t. } A^t A = \mathbf{I}_d, \end{aligned}$$

where $A = [\alpha_1, \ldots, \alpha_d] \in \mathbb{R}^{p \times d}$, $B = [\beta_1, \ldots, \beta_d] \in \mathbb{R}^{p \times d}$, $R_W^{(q)} \in \mathbb{R}^{p \times p}$ is a upper triangular matrix resulting from the Cholesky decomposition of $S_W^{(q)}$, *i.e.* $S_W^{(q)} = R_W^{(q)t} R_W^{(q)}$, $H_{B,k}^{(q)}$ is the kth column of $H_B^{(q)}$ and $\rho > 0$. However, solving this lasso problem is not direct in this case and requires the use of an iterative algorithm. Regarding the implementation details, it is proposed in [16] to initialize the sparseFEM algorithm with the result of the Fisher-EM algorithm and to determine the value of λ by model selection through a modified BIC criterion.

6.4. Discussion on variable selection methods and related works

As we have seen, two main approaches are nowadays used for achieving variable selection in the context of model-based clustering. On the one hand, the approaches based on model selection present the clear advantage of being fully automatic since they automatically select the number of variables to retain. Their current implementations, based on forward-backward strategies, can however prevent their application to very high-dimensional data. On the other hand, the approaches based on lasso-type penalizations are usually fast and work well even on very high-dimensional data. However, the selection

of the sparsity parameter λ is still an open issue. Solutions on model selection criteria are indeed relatively unstable and require further studies.

Among the related works, we shall cite the recent work of Witten & Tibshirani [98], even though it is actually not a model-based approach. They proposed a general non-probabilistic framework for variable selection in clustering, based on a penalized criterion which governs both variable selection and clustering. Several clustering methods can be reformulated from such a criterion and Witten & Tibshirani apply in particular their criterion to the k-means and hierarchical clustering methods. Let us also notice that a recent work of Galimberti & Soffritti [42] proposes an intermediate solution between parsimonious modeling and variable selection by constraining the group covariance matrices to be block-diagonal.

7. Softwares for model-based clustering

This paragraph aims to list the existing softwares which provide model-based clustering methods for high-dimensional data.

7.1. Sofwares with parsimonious models

A first and basic function for the Matlab software, called `emgm` [73], allows to fit data with a Gaussian mixture model, without allowing to impose any restrictions on the covariance matrices. The `statlearn` toolbox [13] for Matlab contains conversely many supervised and unsupervised learning algorithms among which several model-based methods for clustering. For the R software, the reference package `mclust` [34] allows to fit a mixture of Gaussians with different volumes and shapes of the group covariance matrices. The modeling choices can be controlled by the user (see next paragraph) or chosen according to the BIC criterion. An EM algorithm fits the parameters of the considered model and allows agglomerative hierarchical clustering based on maximum likelihood. In order to deal with large data sets, the package `pmclust` [27], available for the `R` software, performs a parallel version of the EM algorithm for mixtures of Gaussians and this allows to fit ultra large data. The standalone `EMMIX` software [60, 67] provides a robust approach based on t-distributions and on the ECM algorithm [68]. With this t-mixture model-based approach, the normal distribution for each component in the mixture is embedded in a wider class of elliptically symmetric distributions. The MIXMOD [11] software, written in C++ and with interfaces with the Matlab, Scilab and R softwares, is a general tool for model-based supervised and unsupervised classification. The main asset of this software remains in the fact that it deals with both quantitative and qualitative data. To that end, different models are proposed: 14 parsimonious Gaussian models are available for quantitative data and 5 multinomial mixture models can be used for qualitative data. This software allows as well to deal with high-dimensional data. Moreover, likelihood maximization can be done using the CEM or SEM algorithms in addition to the traditional EM algorithm. The model and the number of clusters can be chosen by different criteria according to the required task: the BIC, ICL [10] and NEC [14] criteria can be used for clustering and the cross-validation

is also available in the supervised classification context. Finally, an `R` version of MIXMOD has been released recently and the package is called `Rmixmod`.

7.2. Subspace clustering methods

Different softwares and R packages provide subspace clustering methods in the Gaussian mixture model context. Firstly, the package `HDclassif` [7] for the R software provides routines for model-based clustering and classification of high-dimensional data. In particular, the `hddc` function implements the subspace clustering method of [20]. Among the 28 original HD-GMM models, 14 models can be used in the function: 12 models with group-specific orientation matrices and 2 models with common covariance matrices (see Table 5). The `hddc` function allows to choose the most appropriate model for the data at hand according to the BIC criterion and, for each group, the intrinsic dimension is chosen according the Cattell scree-test or BIC. The EM algorithm is used for fitting the model parameters. Let us notice that `HDclassif` provides also the `hdda` function for executing a discriminant analysis on high-dimensional data. Both classifiers are also available in the MIXMOD software. Amongst the mixture of factor analyzers, the `R` package `pgmm` [69, 70] provides an implementation of model-based clustering and model-based classification using several parsimonious Gaussian mixture models. The Fortran `EMMIX-MFA` software [59] implements the mixture of factor analyzers [65]. The software allows the user to choose the number of factor analyzers to fit and the shape of covariance matrices to use. Finally, the `mfma` function [95] for the R software extends and combines the mixture of factor analyzers [65] and the factor mixture analyzers [74]. More precisely, it provides a unified class of dimensionally reduced mixture models and offers an interesting tool for modeling non-Gaussian latent variables.

Some of these subspace clustering approaches model the data in a low and common subspace which allows the data to be displayed in a low-dimensional plot. The `mcfa` function [61] for R, which implements the method of [4], is one of them. It enables model-based density estimation to be undertaken for high-dimensional data, where the number of observations is not very large relative to their dimension. Still for the R software, the `hmfa` function [94] implements the approach proposed in [74], also based on the mixture of factor analyzers. Finally, the `FisherEM` package for the R software implements the eponymous algorithm [17] and provides an efficient tool to model and cluster the data at hand in a discriminative and low-dimensional latent subspace.

7.3. Variable selection and clustering in a GMM context

The `clustvarsel` package for the R software implements the approach proposed by [83]. The package allows the user to simultaneously partition the data in the GMM context and select the relevant variables using an approximate Bayes factor. The C++ software `selvarclust` [56] implements the extension proposed by [57, 58] which embeds the Raftery & Dean's approach. This software allows to cluster data where individuals are described by quantitative block variables. It returns a data clustering and the variable partition. A sparse version of the FisherEM algorithm is also available in `FisherEM` package

for R. Performing a selection of discriminative variables within the FisherEM algorithm is made possible by the use of the option `method='sparse'` in the `fem` function. Finally, the `R` package `bclust` [77] is useful for clustering high-dimensional continuous data. The package uses a parametric spike-and-slab Bayesian model to down-weight the effect of noise variables and to quantify the importance of each variable in agglomerative clustering. Unlike `HDclassif`, the `bclust` package implements a Bayesian approach to the clustering, with priors for model parameters and for the allocation of subjects to groups. The model and its priors are chosen so that the marginal posterior is analytically tractable, providing a fast algorithm.

8. Numerical experiments

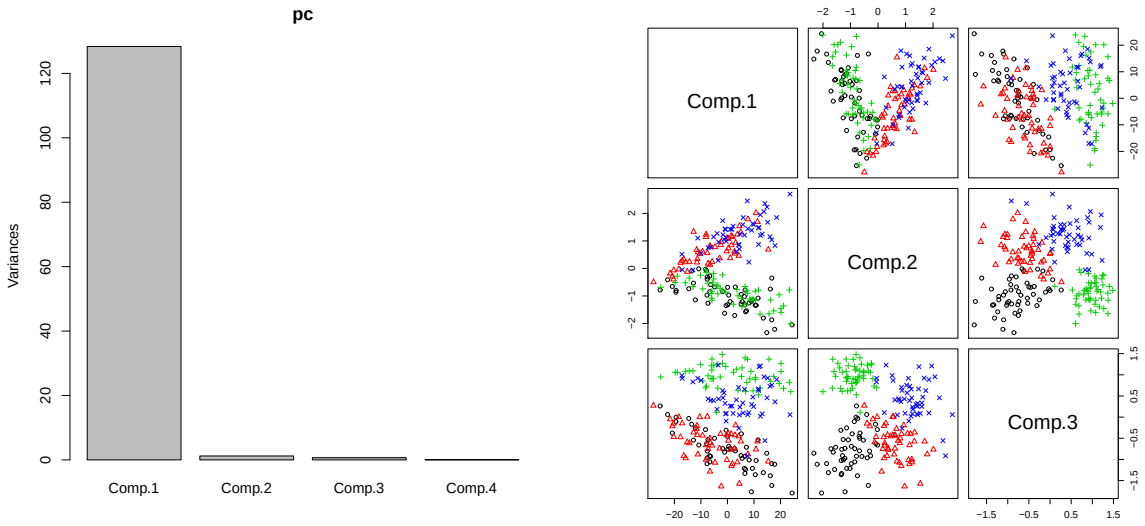
This section now considers some specific R packages and data sets in order to illustrate the practical use of model-based clustering techniques on high-dimensional data.

8.1. Why it is important not to reduce the dimension before the clustering ?

Before to move further, we would like to convince the reader that reducing the data dimension without taking into account the clustering goal conduces to suboptimal results. Indeed, as we discussed earlier, the disconnection between the dimension reduction and the clustering steps can lead to a loss of information which could have been discriminative for the clustering. Such a problem is illustrated in this paragraph on the Crabs data set [22] because, even though it is not high-dimensional, it is known to be difficult to cluster and allows nice visualizations. The data consist in 200 Leptograpsus variegatus crabs, collected at Fremantle, Australia. Each individual is described by 5 morphological measurements: frontal lobe size, rear with, carapace length and width, and finally body depth. The data set is made of 4 groups of 50 crabs each, grouped together according to their color (blue or orange) and their sex (female or male). The main difficulty in clustering these data comes from the existing linear correlation between the 5 variables which implies a "size effect" when a PCA is executed. Therefore, if a PCA is run without any special care, then the clustering task can lead to poor results. Let us first illustrate such a remark by running in first a PCA on the Crabs data set before clustering the data using the `mclust` package for R.

```
library(MASS)
data(crabs)
lbl <- rep(1:4,each=50)
pc <- princomp(crabs[,5:8])
plot(pc)                    # produce the scree plot
X <- as.matrix(crabs[,5:8]) %*% pc$loadings

library(mclust)
res <- Mclust(X[,1:2],G=4)
```



(a) (b)

FIGURE 5: Scree plot obtained by executing a PCA on the Crabs'data set (a) and scatterplots of projected data in the 3 first principal components (b).

The scree plot is presented on Figure 5a and shows that the 2 first principal components seem to be sufficient to represent the data. Indeed, almost 99% of the total variance is explained by the 2 first principal axes. However, the quality of the partition obtained by running `Mclust` on the 2 first principal components is disappointing since almost 51% of the data are misclassified with regard to the true partition. In particular, as we can observe in Table 7a, only 2 different groups can be distinguished in this case and the gender is not taking into account. This can be explained by the task of dimension reduction and the size effect. We then switched the 1st principal component with the third one since, as one can observe in Figure 5b, the 2nd and 3rd principal components appear to be discriminant for the 4 groups.

```
res <- Mclust(X[,2:3],G=4)
```

The resulted partition is now clearly better since the correct classification rate reaches 82% of agreement with the know partition for this data set. In particular, the orange males (OM) and females (OF) form now 2 distinct groups but we have still a mixture of genders for the blue crabs. This is illustrated in Table 7b. The dimension reduction task done independently of the clustering task is in fact prejudicial. Let us now use a subspace clustering method which allows to simultaneously reduce the dimension and find a partition of data. The clustering of the Crabs data set is done with the `pgmmEM` function from the `pgmm` package (all the default settings are kept):

```
library(pgmm)
res <- pgmmEM(crabs[,5:8],Gmin=4,Gmax=4)
```

	label			
cluster	BM	BF	OM	OF
1	26	16	7	5
2	23	30	2	2
3	0	4	41	42
4	1	0	0	1

(a) Mclust executed on the 2 first pc.

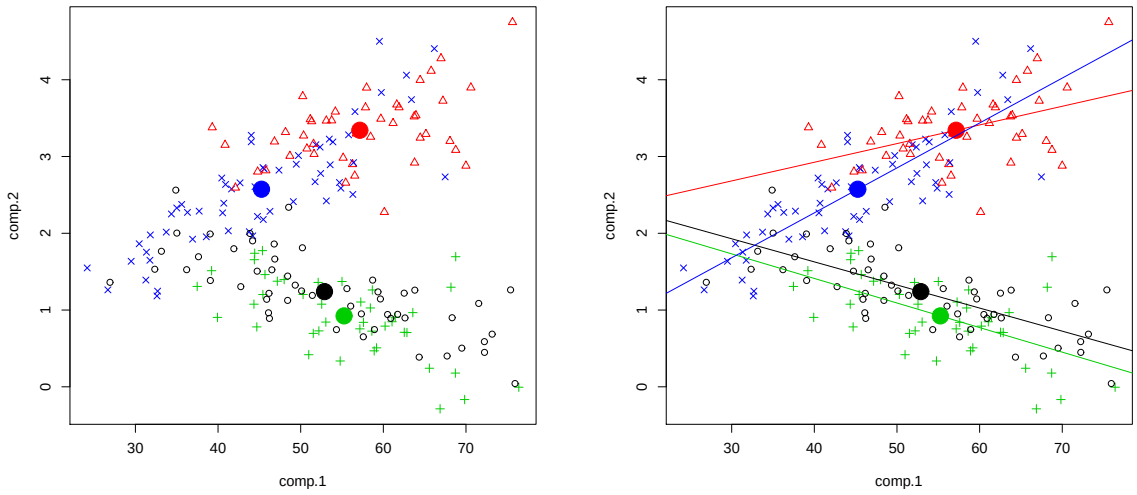
	label			
cluster	BM	BF	OM	OF
1	27	0	0	0
2	23	50	1	9
3	0	0	49	3
4	0	0	0	38

(b) Mclust executed on the pc2 and pc3.

	label			
cluster	BM	BF	OM	OF
1	49	4	0	0
2	0	43	0	2
3	1	0	41	0
4	0	3	9	48

(c) PGMM

TABLE 7: Contingency tables for the Mclust and PGMM for the crabs data set.



(a) (b)

FIGURE 6: Clustering of the Crabs data set with the pgmmEM function and visualization on the 2 first principal axes. The segments represent the groups subspaces while the dots are the means.

```
UCC model with q = 1 and G = 4
The BIC for this model is -2589.95.
```

The quality of the resulted partition is once again really improved and only 9.5% of Crabs are now misclassified: while the orange females (OF) and blue males (BM) are now almost totally well classified, the orange males (OM) still overlap with the orange females (OF), as resumed in Table 7c. As the estimated dimension of the intrinsic subspace of each class is estimated by the `pgmmEM` function to be equal to 1, it allows an easy representation of the group subspaces using line segments. Figure 6a shows these group subspaces as line segments with the projection of the clustered data on the 2 first principal components.

This practical example has therefore make the demonstration that, when groups are localized in different subspaces, a global dimension reduction is not adapted for the clustering task. A efficient way to overcome such a problem is to use subspace clustering methods which model and cluster the data in group-specific low-dimensional subspaces.

8.2. Subspace clustering methods with group-specific subspaces

We now consider subspace clustering methods with group-specific subspaces. In this experiment, the `HDclassif` and `PGMM` packages are used to cluster the Diagnostic Wisconsin Breast Cancer data set coming from the UCI repository [37]. This data set consists of 30 quantitative features which are computed from a digitized image of a fine needle aspirate of a breast mass. They describe characteristics of the cell nuclei present in the image. The number of instances is 569 whose are divided on two groups of nuclei: 357 are benign and 212 are malignant. Of course the class label is not used for the clustering task but, for both methods, the number of clusters have been fixed to 2 and the BIC criterion is used for selecting the model and the intrinsic dimension of each group.

```
library(HDclassif)
res1 <- hddc(as.matrix(Y),K=K,model="ALL",d='BIC')
  SELECTED: model AKJBKQKD with 2 clusters, BIC=16579.28.
res1$d
  Intrinsic dimensions of the classes:
        1  2
  dim: 11 11

library(pgmm)
res2 <- pgmmEM(Y,Gmin=2,Gmax=2)
  Based on k-means starting values, the best model (BIC) for the range of
factors and components used is a CUU model with q = 2 and G = 2. The BIC for
this model is 23779.74.
```

The model selected by `hddc` is the $[a_{kj}b_kQ_kd]$ model, which is formally equivalent to the Mixt-PPCA model, with all intrinsic dimensions equal to 11. Table 8a shows the contingency table which allows to compare the known partition for the data with the one returned by the `hddc` function. One can observed that in this case the two groups are well-identified. Regarding the PGMM approach, the model selected by the BIC criterion is the CUU model. This choice of model implies that the loading matrix is common to the groups but the error variance remains different. Let us notice that this model is much more parsimonious than the one chosen by `hddc` since the intrinsic dimension for both groups is equal to 2 here. Consequently, the complexity of the CUU model is 180 whereas the one of the $[a_{kj}b_kQ_kd]$ model reaches 614 parameters to estimate. The counterpart of such a parsimony is perhaps a little degradation of the quality of the partition obtained by the PGMM approach on this data set, as we can observe in Table 8b.

8.2.1. Subspace clustering methods with common subspaces

Several subspace clustering approaches model the data in a low-dimensional and common subspace. This allows in particular the clustered data to be displayed on a low-dimensional plot. In this experiment, we aim to compare the different visualizations of

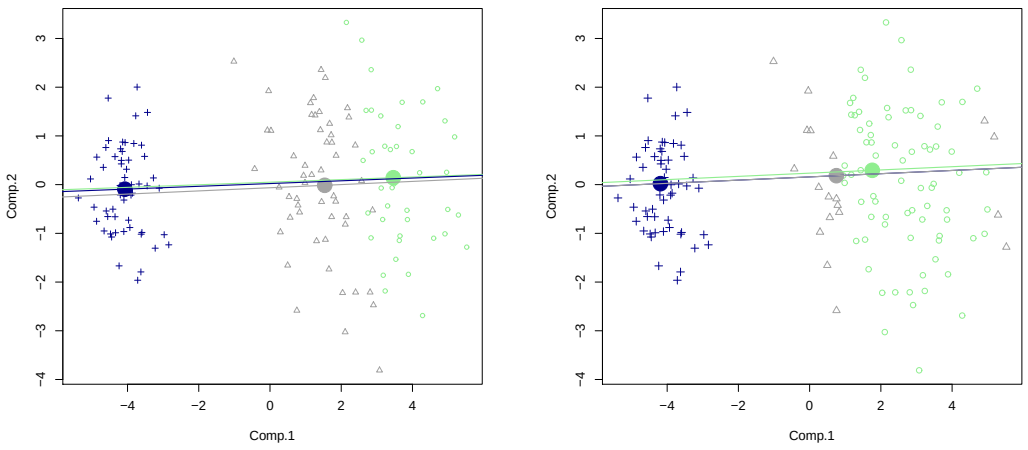
	label	
cluster	Malign	Benign
1	172	16
2	40	341

(a) HDDC

	label	
cluster	Malign	Benign
1	145	52
2	67	305

(b) PGMM

TABLE 8: Contingency tables for the HDDC and PGMM algorithms for the subset of the breast cancer data.



(a) MCFA (b) HMFA

FIGURE 7: Projection of the clustered chironomus data in the 2 first principal components of PCA. The fitted subspace is represented by parallel lines centered on the means of each cluster for the MCFA and HMFA approaches.

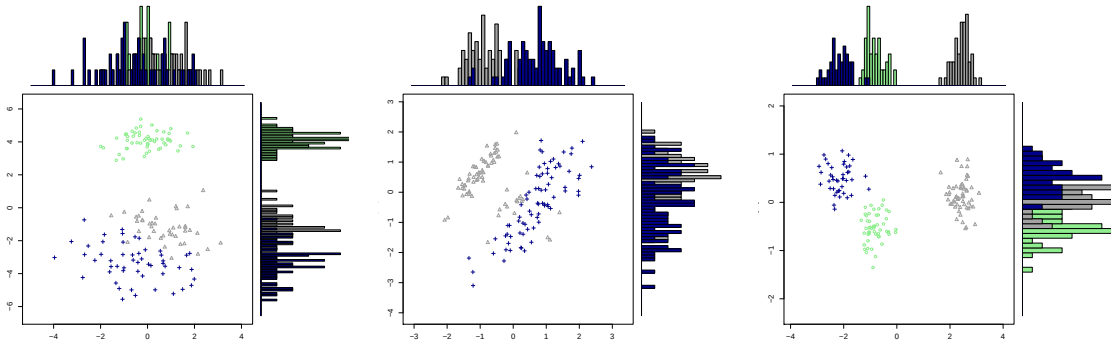
the clustered data obtained with 3 subspace clustering methods: MCFA, HMFA and FisherEM. We use for this experiment the chironomus data set which is made of 148 larvae belonging to 3 different species: *cloacalis*, *frommeri* and *staegeri*. For each larva, 17 characters of the larval head capsule have been measured. A detailed description of this data set can be found in [74]. In first, for each method, the default settings have been used. In particular, the FisherEM algorithm fixes itself the intrinsic dimension of the discriminative subspace to $d = K - 1$. For the MCFA and HMFA approaches, the number of factor analyzers is determined using the BIC criterion.

```
library(FisherEM)
res1 = fem(scale(Y),3,model='all')
  The best model is: AkjBk and the BIC is: 59.33106

library(mcfa)
resultat = pairlist()
bic = rep(NA,6)
for (i in 1:6){resultat[[i]] <- mcfa(scale(Y),g=3,q=i,maxinit=5)
for (i in 1:6){bic[i]<-resultat[[i]]$BICval}
max_bic = max(bic,na.rm=T)
for(i in 1:6){ if(max_bic==bic[i]) {res2=resultat[[i]]
for(i in 1:6){ if(max_bic==bic[i]) {q = i} }
   The number of factor analyzers is: 1 and the BIC value is: 4694.725

source(L1mfa.r)
resultat = pairlist()
bic = rep(NA,6)
for (i in 1:6){resultat[[i]] <- L1mfa.em(scale(Y),K,i)
for (i in 1:6){bic[i]<-resultat[[i]]$bic}
max_bic = max(bic,na.rm=T)
for(i in 1:6){ if(max_bic==bic[i]) {res3=resultat[[i]]
for(i in 1:6){ if(max_bic==bic[i]) {q = i} }
   The number of factor analyzers is: 1 and the BIC value is: 4698.284
```

The first results shows that, except for the FisherEM algorithm for which the discriminative space is 2-dimensional, the BIC criterion selects only one factor analyzer for both MCFA and HMFA approaches. In order to visualize the fitted subspaces of 1 dimension, we have projected the data in the 2 first principal components of PCA for the MCFA and HMFA approaches. They are represented by a straight line in Figures 7a and 7b. As we can observe, 2 of the 3 groups seem to be difficult to separate linearly. This difficulty is illustrated with HMFA which merges 2 groups. This might be explained by the fact that only one factor analyzer is not sufficient to discriminate 3 groups.



(a) MCFA (b) HMFA (c) FisherEM

FIGURE 8: Projection of the clustered chironomus data in the 2-dimensional subspaces fitted by MCFA, HMFA and FisherEM.

In order to compare the representation of clustered data in the latent spaces fitted by MCFA, HMFA and FisherEM, let us now set the number q of factor analyzers to 2 for MCFA and HMFA.

```
# MCFA
res_mcfa <- mcfa(scale(Y),g=3,q=2,maxinit=5)
    The number of factor analyzers is: 2 and the BIC value is: 4338.437

# HMFA
res_HMFA <- L1mfa.em(scale(Y),k=3,r=2)
    The number of factor analyzers is: 2 and the BIC value is: 4350.784
```

Figures 8a, 8b and 8c plot the clustered data in their 2-dimensional subspace, respectively fitted by MCFA, HMFA and FisherEM. Group-conditional histograms are also displayed on the right and top sides of the figures. One can observe that FisherEM provides a visualization of the clustered data which clearly differs from the one of MCFA and HMFA. Indeed, FisherEM looks for a subspace which best discriminate the groups. Conversely, the subspaces built by MCFA and HMFA are such that the variance of the projected data is maximum.

8.3. Variable selection through penalized approaches

We focus now on variable selection for clustering with penalized approaches. We consider here the USPS358 data set which is a subset of the USPS data set from the UCI repository. The original data set is made of 7291 images divided in 10 classes corresponding to handwritten digits from 0 to 9. Each digit is a 16×16 gray level image represented as a 256-dimensional vector. For this experiment, we extracted a subset of the data ($n = 1756$) corresponding to the digits 3, 5 and 8 which are the most difficult to discriminate. Figure 9 shows a subset of images from the USPS358 data set and Figures 10a–10d show the group means and the global mean of the data. As we can observe on these images, there are 3

FIGURE 9: Samples from the usps358 data set.

different kinds of variables (pixels here): the irrelevant variables which are never used, the non-discriminative variables which are used by all groups, and finally the relevant pixels which allow the discrimination of the 3 groups. In this experiment, the variable selection task remains therefore to select a subset of pixels allowing the discrimination between the numbers 3, 5 and 8. The sparse version of the FisherEM algorithm is used for such a task with all the default settings.

```
library(FisherEM)
res = fem(Y,3,method='sparse')
  The level of sparsity is: 0.2 with a penalized bic: 2997.332
```

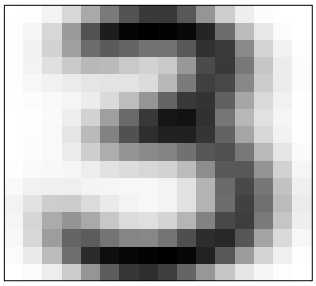
Figure 10e shows the absolute values of the loadings of the two discriminative axes estimated by sparseFEM. The weights assigned by sparseFEM to each feature are represented by gray levels: lighter is the pixel, weaker is the absolute value of the loadings. We can observe in Figure 10e that the subset of selected pixels is small compared to the average number of pixels used to draw the digits 3, 5 and 8. Only 15 pixels are selected by sparseFEM among the 256 original ones. Furthermore, the selected pixels appear to be relevant since, for instance, the darker pixel on the bottom right corner of Figure 10e discriminates the digit 8 from the digits 3 and 5.

8.4. Variable selection as a model selection problem

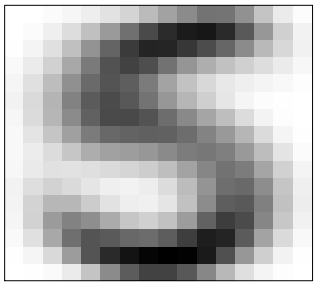
Finally, another way to combine variable selection and clustering is to consider variable selection as a model selection problem in the mixture model context. We consider here the `clustvarsel` [83] and `selvarclust` [58] algorithms and applied them on the zoo data set coming from the UCI repository. This data set is made of 7 families of 101 animals characterized by 16 attributes. For the `clustvarsel` algorithm, a package for the R software is available:

```
library(clustvarsel)
res <- clustvarsel(Y,G=7)
colnames(res$sel.var)
  The variables selected are: 2 9 13
result <- Mclust(res$sel.var,1:3)
```

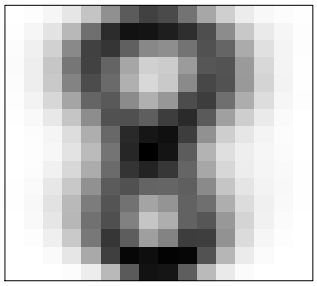
The variables 2, 9 and 13 are selected and the resulting partition on these 3 variables for the zoo data set is resumed by Table 9a. We can observe that 4 among 7 known groups are correctly recognized. For the `selvarclust` algorithm, we used the C++ code



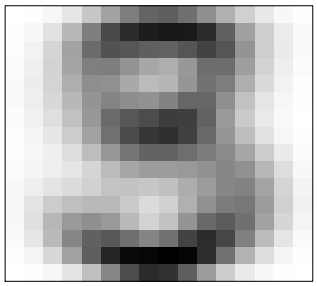
(a) Group mean of digit 3



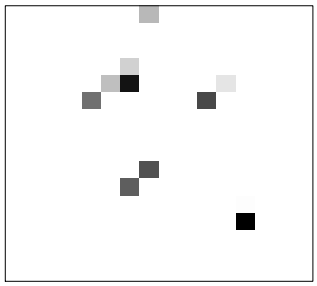
(b) Group mean of digit 5



(c) Group mean of digit 8



(d) Overall mean of the data set



(e) Variable selection by sparseFEM

FIGURE 10: Pixels averaging on the 1756 images (a) and discriminative pixels selected by the sparseFEM algorithm (b).

	label						
cluster	1	2	3	4	5	6	7
1	8	0	0	0	0	0	3
2	0	31	0	2	0	4	1
3	0	0	20	0	0	0	0
4	0	0	0	0	0	0	4
5	0	3	0	3	13	0	0
6	0	0	0	0	0	0	2
7	0	7	0	0	0	0	0

(a) Clustvarsel

	label						
cluster	1	2	3	4	5	6	7
1	8	0	0	0	0	0	3
2	0	41	0	0	0	0	0
3	0	0	20	0	0	0	0
4	-	-	-	-	-	-	-
5	0	0	0	0	13	0	0
6	0	0	0	4	0	4	0
7	0	0	0	1	0	0	7

(b) SelvarClust

TABLE 9: Contingency tables for the `clustvarsel` and `selvarclust` algorithms for the zoo data.

developed by C. Maugis [56] with all the default settings. The obtained results are the following:

```
Number of clusters K = 7
Relevant clustering variables = 2 4 9 10 12
Relevant variables required for the regression = 2 4 9 12
Irrelevant redundant variables = 1 3 5 6 7 8 11 13 14 16
Irrelevant independent variables = 15
Criterion value = 350.109
```

and the provided partition is given in Table 9b. The algorithm selects 5 relevant clustering variables among which 2 are in common with the `clustvarsel` algorithm. Even though the `selvarclust` algorithm found a partition with 6 groups instead of 7, nevertheless the quality of the partition is improved compared to `clustvarsel`. More particularly, we can observe in Table 9b that 5 groups are well recognized.

9. Conclusion

This article has therefore presented a review of existing solutions for model-based clustering of high-dimensional data. We hope that the reader is now convinced that it is better to use parsimonious models, subspace clustering methods or variable selection methods designed for clustering instead of preprocessing the data with dimension reduction. The short software review and the few practical examples may also help the practitioner in applying recent model-based techniques to his own data.

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