Model-based clustering for conditionally correlated categorical data

Matthieu Marbac, Christophe Biernacki, Vincent Vandewalle

Model-based clustering for conditionally correlated categorical data

Matthieu Marbac*
Inria & DGA

Christophe Biernacki†
University Lille 1 & CNRS & Inria

Vincent Vandewalle‡
EA 2694 University Lille 2 & Inria

January 28, 2014

Abstract

An extension of the latent class model is proposed for clustering categorical data by relaxing the classical "class conditional independence assumption" of variables. In this model, variables are grouped into inter-independent and intra-dependent blocks in order to consider the main intra-class correlations. The dependency between variables grouped inside the same block of a class is taken into account by mixing two extreme distributions, which are respectively the independence and the maximum dependency. In the conditionally correlated data case, this approach is expected to reduce biases involved by the latent class model and to produce a meaningful dependency model with only a few additional parameters. The parameters are estimated by maximum likelihood by means of an EM algorithm while a Gibbs sampler is used for model selection in order to overcome the computational intractability of the combinatorial problems involved by the block structure search. Two applications on medical and biological data sets bring out the proposed model interest. Its results strengthen the idea that the proposed model is meaningful and that biases induced by the conditional independence assumption of the latent class model are reduced.

Keywords: Categorical data; Clustering; Correlation; Expectation-Maximization algorithm; Gibbs sampler; Mixture model; Model selection.

*Matthieu Marbac is Ph.D student at Inria Lille and DGA (Email: matthieu.marbac-lourdelle@inria.fr)

†Christophe Biernacki is Professor at University Lille 1, CNRS and Inria Lille (Email: Christophe.Biernacki@math.univ-lille1.fr)

‡Vincent Vandewalle is Associate Professor at University Lille 2, EA 2694 and Inria Lille (Email: vincent.vandewalle@univ-lille2.fr)

1 Introduction

Nowadays practitioners are often facing very large data sets, which are difficult to analyze directly. In this context, clustering (Jajuga *et al.* , 2002) is an important tool which provides a partition among individuals. Other approaches even simultaneously cluster both individuals and variables (Govaert & Nadif, 2003). Furthermore, with the increasing number of variables at hand, the risk of observing correlated descriptors, even within the same class, is often high. In view of these difficulties, the practitioner can choose between two approaches. The first one is to perform a selection among the observed variables (Maugis *et al.* , 2009) in order to extract uncorrelated data, thereby losing some potentially crucial information. The second approach consists of applying a method for modeling the conditional dependencies on the whole set of variables.

Clustering methods can be split into two kinds of approaches: the geometrical ones based on the distances between individuals and the probabilistic ones which model the data generation process. If the methods of the first kind are generally faster than the methods of the second kind, they are often quite sensitive to the choice of distance between individuals. Furthermore, as the probabilistic tools are not available for these approaches, difficult questions, like selecting the number of clusters cannot be addressed rigorously. For categorical data, geometrical approaches either define a metric in the initial variables space like the *k-means* (Huang *et al.* , 2005), either compute their metric on the axes of the multiple correspondence analysis (Chavent *et al.* , 2010; Guinot *et al.* , 2001).

Lots of geometrical approaches can be also interpreted in a probabilistic way. Thus, for the continuous data, the classical *k-means* algorithm can be identified as an homoscedastic Gaussian mixture model (Banfield & Raftery, 1993; Celeux & Govaert, 1995) with equal proportions. For the categorical variables, Celeux & Govaert (1991) show that the CEM algorithm (McLachlan & Krishnan, 1997), applied to a classical latent class model, maximizes a classical information criteria close to a χ^2 metric. Other links between both approaches are described in Govaert (2010), Chapter 9. Let us now introduce our proposal for this problem.

In the categorical case, the *latent class model* also known as naive Bayes belongs to the folklore (Goodman, 1974; Celeux & Govaert, 1991). In this article, we refer to this model as the conditional independence model (further denoted by CIM). Classes are explicitly described by the probability

of each modality for each variable under the conditional independence assumption. The sparsity of the model implied by this assumption, is a great advantage since it restricts the curse of dimensionality. CIM was observed to obtain quite good results in practice (Hand & Yu, 2001) in different areas like in behavioral science (Reboussin *et al.* , 2006) and in medicine (Strauss *et al.* , 2006). However, CIM may suffer from severe biases when the data are intra-class correlated. For instance, an application presented by Van Hattum & Hoijtink (2009) shows that CIM over-estimates the number of clusters when the conditional independence assumption is violated. For a long time, people have tried to relax the conditional independence assumption by modeling conditional interactions between variables using an additive model (Harper, 1972). The main drawback of this approach is that the number of parameters to estimate becomes huge and estimation turns out to be intractable.

Some other methods take into account the intra-class correlation as *mixtures of Bayesian networks* (Cheng & Greiner, 1999). Conditionally on each class, a directed acyclic graph is built with a set of nodes representing each variable. However, if no constraint is added, the network's estimation is also quite complex. By constraining the network to be a tree, the model selection and the parameter's estimation can be easily performed. Moreover the correlation model enjoys great flexibility. The extension of the dependency tree of Chow & Liu (1968) was done by Friedman *et al.* (1997) for the supervised classification and by Meila & Jordan (2001) for the clustering. However the main problem of these models is that they require too often an intractable number of parameters.

When covariates are available, the conditional dependencies between the categorical ones can be modeled by a logistic function (Formann, 1992; Reboussin *et al.* , 2008). By assuming that these covariates are unobserved, the *multilevel latent class model* (Vermunt, 2003, 2007) naturally incorporates the intra-class dependencies. This model has connections with the approach of Qu *et al.* (1996) where the intra-class dependencies are modeled by a latent continuous variable with a probit function. The *hybrid model* (Muthén, 2008) in which, for each class, a factor analysis model is fitted to either all categorical variables or to those categorical variables having dependencies is a more general approach. Recently, Gollini & Murphy (2013) have proposed the *mixture model of latent traits analyzers* which assume that the distribution of the categorical variables depends on both a categorical latent variable (the class) and many continuous latent traits variables. The

parameter's estimation is also a difficult point which is solved via a variational approach. If all these models consider the intra-class dependencies, their main drawback is that these dependencies have to be interpreted among relations with a latent variable. Thus, pertinent interpretation can be difficult.

The log-linear models (Agresti, 2002; Bock, 1986) were originally proposed to model the individual's log-probability by selecting interactions between variables. Thus, the most general mixture model is the *log-linear mixture model* as it is able to incorporate many forms of interactions. It has been used since Hagenaars (1988) and may be before. Espeland & Handelman (1989) used it to cluster radiographic cross-diagnostics and Van Hattum & Hoijtink (2009) in a market segmentation problem. However this model family is huge and the model selection is a real challenge. In the literature, authors often require ahead of time the modeled interactions. Another option is to perform a deterministic search like the *forward* method which is sub-optimal. Furthermore, the number of parameters to estimate increases with the conditional modalities interactions, thus implying potential over-fitting and more difficult interpretation. The latent class model (CIM) can be seen as a particular log-linear mixture model, where interactions are discarded. Our aim is to present a version of the log-linear mixture model which takes into account the interactions of order one or more while keeping the number of unknown parameters to a reasonable amount.

We propose to extend the classical latent class model (CIM) for categorical data, by a new latent class model which relaxes the variable's conditional independence assumption. We refer to the proposed model as the *conditionally correlated model* (denoted by CMM). This model is a parsimonious version of the log-linear mixture model, and thus benefits from its interpretative power. Furthermore, we propose a Bayesian approach to automatically perform model selection.

The CCM model groups the variables into conditionally independent blocks given the class. The main intra-class dependencies are thus underlined by the variable's repartition into these blocks. This approach, allowing to model the main conditional interactions, was first proposed by Jorgensen & Hunt (1996) in order to cluster continuous and categorical data. For CMM, each block follows a particular dependency distribution which is a bi-component mixture of an *independence* and a *maximal dependency* distribution according to the Cramer's V criterion. This specific distribution of the blocks allows to summarize the variables conditional dependencies with only one parameter: the maximum dependency distribution proportion. Thus, the model underlines

the main conditional dependencies and their strength.

The proposed model can be interpreted as a parsimonious version of a two-level log-linear model. The first level corresponds to group in the same block the variables which are conditionally dependent, so it defines the variable's interactions. The strength of the correlation is reflected by the proportion of the distribution of maximum dependency compared to that of the independence distribution. The second level of sparsity is induced by the small fraction of the parameters of the maximum dependency distribution of the block. As for all log-linear mixture models, the selection of the pertinent interactions is a combinatorial problem. We propose to perform this model selection via a Gibbs sampler in order to overcome the enumeration of all the models. Thus, this general approach could also select the interactions of a log-linear mixture model.

This paper is organized as follows. Section 2 reviews the latent class model's principles. Section 3 presents the new mixture model taking into account the intra-class correlations. Section 4 is devoted to parameter's estimation in the case where the number of classes and the blocks of variables are supposed to be known. Section 5 presents a Gibbs algorithm for avoiding combinatorial difficulties inherent to block selection. Section 6 presents results on simulated data. Section 7 firstly displays a comparison between two main model-based clustering approaches and our proposition on a classical medical data set and secondly presents another application on a larger real data set. A tutorial of the R package `Clustericat`[1] performing the model selection and the estimation of the parameters of CMM is given with the first application (see Appendix A). A conclusion is given in Section 8.

2 Classical models

2.1 Latent class model: intra-class independence of variables

Observations to be classified are described with d discrete variables $\boldsymbol{x} = (\boldsymbol{x}^1, \ldots, \boldsymbol{x}^d)$ defined on the probabilistic space $\mathcal{X}$. Each variable j has m_j response levels with $m_j \geq 2$ and is written $\boldsymbol{x}^j = (x^{j1}, \ldots, x^{jm_j})$ where $x^{jh} = 1$ if the variable j takes the modality h and $x^{jh} = 0$ otherwise. In the standard latent class model (CIM), the variables are assumed to be *conditionally independent*

[1]The R package `Clustericat` is available on Rforge website at the following url: *https://r-forge.r-project.org/R/?group_id=1803*

knowing the latent cluster. Furthermore data are supposed to be drawn independently from a mixture of g multivariate multinomial distributions with probability distribution function (pdf):

$$p(\boldsymbol{x};\boldsymbol{\theta}) = \sum_{k=1}^{g} \pi_k \mathring{p}(\boldsymbol{x};\boldsymbol{\alpha}_k) \qquad \text{with} \qquad \mathring{p}(\boldsymbol{x};\boldsymbol{\alpha}_k) = \prod_{j=1}^{d}\prod_{h=1}^{m_j} (\alpha_k^{jh})^{x^{jh}}, \tag{1}$$

with $\boldsymbol{\theta} = (\pi_1, \ldots, \pi_g, \boldsymbol{\alpha}_1, \ldots, \boldsymbol{\alpha}_g)$, π_k being the proportion of the component k in the mixture where $\pi_k > 0$ and $\sum_{k=1}^{g} \pi_k = 1$, and $\boldsymbol{\alpha}_k = (\alpha_k^{jh}; j = 1, \ldots, d; h = 1, \ldots, m_j)$ where α_k^{jh} denotes the probability that the variable j has level h if the object is in cluster k and satisfies the two following constraints: $\alpha_k^{jh} > 0$ and $\sum_{h=1}^{m_j} \alpha_k^{jh} = 1$.

The classical latent class model is much more parsimonious than the saturated log-linear model, which requires $(\prod_j m_j) - 1$ parameters, since it only requires ν_{CIM} parameters with:

$$\nu_{\text{CIM}} = (g-1) + g\sum_{k=1}^{g}(m_j - 1). \tag{2}$$

Its maximum likelihood estimator is easily computed via an EM algorithm (McLachlan & Krishnan, 1997). In the clustering case, the mixture identifiability up to a permutation of the class is generally necessary (McLachlan & Peel, 2000). However, there are mixtures, such as the products of Bernoulli distributions, which are not identifiable but produce good results in applications. In order to relax the stringent concept of identifiability, the notion of generic identifiability was introduced by Allman *et al.* (2009): a model is generically identifiable if it is identifiable except for a subset of the parameter space with Lebesgue measure zero.

2.2 Latent class model extension: intra-class independence of blocks

Despite its simplicity, the latent class model leads to good results in many situations (Hand & Yu, 2001). However, in the case of intra-correlated variables it can lead to severe biases in the partition estimation and also it may overestimate the number of clusters. In order to reduce these biases, a classical extension of the latent class model was introduced by Jorgensen & Hunt (1996) for conditionally correlated mixed data. This model is implemented in the Multimix software (Hunt & Jorgensen, 1999).

It considers that *conditionally* on the class k, variables are grouped into B_k *independent blocks* and each block follows a specific distribution. The repartition in blocks of the vari-

ables determines a partition $\boldsymbol{\sigma}_k = (\boldsymbol{\sigma}_{k1}, \ldots, \boldsymbol{\sigma}_{k\mathrm{B}_k})$ of $\{1, \ldots, d\}$ in B_k disjoint non-empty subsets where $\boldsymbol{\sigma}_{kb}$ represents the subset b of variables in the partition $\boldsymbol{\sigma}_k$. This partition defines $\boldsymbol{x}^{\{kb\}} = \boldsymbol{x}^{\boldsymbol{\sigma}_{kb}} = (\boldsymbol{x}^{\{kb\}j}; j = 1, \ldots, d^{\{kb\}})$ which is the subset of $\boldsymbol{x}$ associated to $\boldsymbol{\sigma}_{kb}$. The integer $d^{\{kb\}} = \mathrm{card}(\boldsymbol{\sigma}_{kb})$ is the number of variables in the block b of the component k and $\boldsymbol{x}^{\{kb\}j} = (x^{\{kb\}jh}; h = 1, \ldots, m_j^{\{kb\}})$ corresponds to the variable j of the block b for the component k with $x^{\{kb\}jh} = 1$ if the individual takes the modality h for the variable $\boldsymbol{x}^{\{kb\}j}$ and $x^{\{kb\}jh} = 0$ otherwise and where $m_j^{\{kb\}}$ represents the modalities number of $\boldsymbol{x}^{\{kb\}j}$. Note that different variables repartitions in blocks are allowed for each component and they are grouped into $\boldsymbol{\sigma} = (\boldsymbol{\sigma}_1, \ldots, \boldsymbol{\sigma}_g)$.

For each component k, each block b follows a specific parametric distribution denoted as $p(\boldsymbol{x}^{\{kb\}}; \boldsymbol{\theta}_{kb})$ where $\boldsymbol{\theta}_{kb}$ are the parameters of this distribution. The model pdf can be written as:

$$p(\boldsymbol{x}; \boldsymbol{\sigma}, \boldsymbol{\theta}) = \sum_{k=1}^{g} \pi_k p(\boldsymbol{x}; \boldsymbol{\sigma}_k, \boldsymbol{\theta}_k) \qquad \text{with} \qquad p(\boldsymbol{x}; \boldsymbol{\sigma}_k, \boldsymbol{\theta}_k) = \prod_{b=1}^{B_k} p(\boldsymbol{x}^{\{kb\}}; \boldsymbol{\theta}_{kb}), \tag{3}$$

where $\boldsymbol{\theta}$ is redefined as $\boldsymbol{\theta} = (\pi_1, \ldots, \pi_g, \boldsymbol{\theta}_1, \ldots, \boldsymbol{\theta}_g)$ with $\boldsymbol{\theta}_k = (\boldsymbol{\theta}_{k1}, \ldots, \boldsymbol{\theta}_{k\mathrm{B}_k})$. Figure 1 is an example of the distribution with conditional independent blocks for a mixture with two components described by five variables. Blank cells indicate that the intra-class correlation is neglected and black cells indicate that this correlation is taken into account. Note that the classical latent class model with conditional independence, would be represented by white cells off the diagonal and black on the latter.

(a) (b)

Figure 1: example of the conditional independent blocks mixture model with $g = 2$ and $d = 5$, (a) $k = 1$, $B_1 = 2$ and $\boldsymbol{\sigma}_1 = (\{1, 2\}, \{3, 4, 5\})$, (b) $k = 2$, $B_2 = 3$ and $\boldsymbol{\sigma}_2 = (\{1, 5\}, \{2, 4\}, \{3\})$.

This approach is very general, since any distribution can be chosen for each block as soon as it

is different from the distribution of independence. The mixture model by conditional independent blocks is a parsimonious version of the log-linear mixture model. Indeed, the distribution of variables in blocks determines which interactions will need to be estimated. Interactions between variables of different blocks will be zero and those between variables of the same block can be modeled by the specific distribution of the block. The limiting case of this model where $\text{B}_k = d$ for each class is equivalent to the latent class model with the conditional independence assumption.

The generic identifiability of mixture model with conditionally independent blocks follows, under specific constraints, from Theorem 4 of Allman *et al.* (2009) by assuming that the distribution of each block is itself identifiable. This proof is given in Appendix A of Marbac *et al.* (2013).

3 Intra-block parsimonious distribution

The goal is now to define a parsimonious distribution for each block that takes into account the correlation between variables. Furthermore, the parameters of the distribution inside block have to be meaningful for the practitioner. In this context, we propose to model the distribution of each block by a mixture of the extreme distributions according to the Cramer's V criterion computed on all the couples of variables. It results in a bi-component mixture between an independence distribution and a maximum dependency distribution which can be easily interpreted by the user. The maximum dependency distribution is introduced first. The resulting conditional correlated model (CCM) is also defined as a block model extension of the latent class model where the distribution inside the block is modeled by this bi-component mixture.

Remark: without loss of generality, the variables are considered as ordered by decreasing number of modalities in each block: $\forall(k,b)\ m_j^{\{kb\}} \geq m_{j+1}^{\{kb\}}$ where $j = 1, \ldots, d^{\{kb\}} - 1$.

3.1 Maximum dependency distribution

The maximum dependency distribution is defined as the "opposite" distribution of independence according to the Cramer's V criterion computed on all the couples of variables since this latter minimizes this criterion while the maximum dependency distribution maximizes it. Under this distribution, the modality knowledge of one variable provides the maximum information on all the subsequent variables. Note that it is a non-reciprocal functional link between variables. Indeed,

if $\boldsymbol{x}^{\{kb\}}$ arises from this distribution, the knowledge of the variable having the largest number of modalities determines exactly the others but not necessarily the other way around. So this distribution defines successive surjections from the space of $x^{\{kb\}j}$ to the space of $x^{\{kb\}j+1}$ with $j = 1, \ldots, d^{\{kb\}} - 1$ (recall that the variables are ordered by decreasing number of modalities in each block). In fact, it is a reciprocal functional link only when $m_j^{\{kb\}} = m_{j+1}^{\{kb\}}$.

Since the first variable determines the other ones, this distribution is defined by a product between the multinomial distribution of the first variable parametrized by $\boldsymbol{\tau}_{kb} = (\tau_{kb}^h; h = 1, \ldots, m_1^{\{kb\}})$ with $\tau_{kb}^h \geq 0$ and $\sum_{h=1}^{m_1^{\{kb\}}} \tau_{kb}^h = 1$, and the product between the conditional distributions defined as specific multinomial distributions. So, if $x^{\{kb\}1h} = 1$, then $\forall j = 2, \ldots, d^{\{kb\}}$, $\boldsymbol{x}^{\{kb\}j}$ follows a multinomial distribution parametrized by $\boldsymbol{\delta}_{kb}^{hj} = (\delta_{kb}^{hjh'}; h' = 1, \ldots, m_j^{\{kb\}})$ with the following constraints defining the successive surjections: $\delta_{kb}^{hjh'} \in \{0, 1\}$, $\sum_{h'=1}^{m_j^{\{kb\}}} \delta_{kb}^{hjh'} = 1$ (multinomial distribution) and $\sum_{h=1}^{m_1^{\{kb\}}} \delta_{kb}^{hjh'} \geq 1$ (surjections).

By denoting $\boldsymbol{\delta}_{kb} = (\boldsymbol{\delta}_{kb}^{hj}; h = 1, \ldots, m_1^{\{kb\}}; j = 2, \ldots, d^{\{kb\}})$, the distribution of maximum dependency distribution is then defined as:

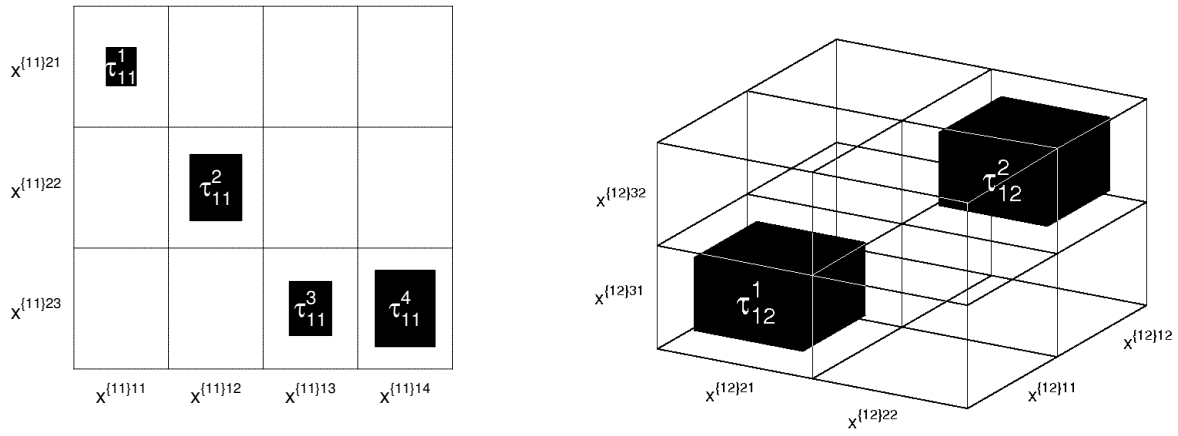
$$\begin{aligned} \acute{p}(\boldsymbol{x}^{\{kb\}}; \boldsymbol{\tau}_{kb}, \boldsymbol{\delta}_{kb}) &= p(\boldsymbol{x}^{\{kb\}1}; \boldsymbol{\tau}_{kb}) \prod_{j=2}^{d^{\{kb\}}} p(\boldsymbol{x}^{\{kb\}j} | \boldsymbol{x}^{\{kb\}1}; \{\boldsymbol{\delta}_{kb}^{hj}\}_{h=1,\ldots,m_1^{\{kb\}}}) \\ &= \prod_{h=1}^{m_1^{\{kb\}}} \left(\tau_{kb}^h \prod_{j=2}^{d^{\{kb\}}} \prod_{h'=1}^{m_j^{\{kb\}}} (\delta_{kb}^{hjh'})^{x^{\{kb\}jh'}} \right)^{x^{\{kb\}1h}}. \end{aligned} \tag{4}$$

Figure 2 shows two examples of the maximum dependency distributions. The probabilities of the joint distribution are represented by the area of dark boxes. Notice that $\boldsymbol{\delta}_{kb}$ defines the position where the probabilities are non zero (location of a dark boxes) and $\boldsymbol{\tau}_{kb}$ defines the probabilities of this non zero cells (area of the dark boxes).

A sufficient condition of identifiability is to impose $\forall h \ \tau_{kb}^h > 0$. This distribution has very limited interest because it is so unrealistic that it can almost never be used alone. We will see in the next section how to use it in a more efficient way.

3.2 A new block distribution: mixture of two extreme distributions

It is proposed to model the distribution of each block by a bi-components mixture between an *independence* distribution and a *maximum dependency* distribution. For block b of component k,



(a) (b)

Figure 2: Two examples of the maximum dependency distributions for the first component of the mixture illustrated by Figure 1(a). (a) The first block is displayed with $m^{\{11\}1} = 4$, $m^{\{11\}2} = 3$, $\delta_{11}^{h1h} = 1$ for $h = 1, 2, 3$, $\delta_{11}^{413} = 1$ and $\boldsymbol{\tau}_{11} = (0.1, 0.3, 0.2, 0.4)$; (b) The second block is displayed with $m^{\{12\}1} = m^{\{12\}2} = m^{\{12\}3} = 2$, $\delta_{12}^{hjh'} = 1$ iff $(h = h')$ and $\boldsymbol{\tau}_{12} = (0.5, 0.5)$.

the block distribution is modeled by:

$$p(\boldsymbol{x}^{\{kb\}}; \boldsymbol{\theta}_{kb}) = (1 - \rho_{kb})\mathring{p}(\boldsymbol{x}^{\{kb\}}; \boldsymbol{\alpha}_{kb}) + \rho_{kb}\acute{p}(\boldsymbol{x}^{\{kb\}}; \boldsymbol{\tau}_{kb}, \boldsymbol{\delta}_{kb}), \tag{5}$$

where $\boldsymbol{\theta}_{kb} = (\rho_{kb}, \boldsymbol{\alpha}_{kb}, \boldsymbol{\tau}_{kb}, \boldsymbol{\delta}_{kb})$, ρ_{kb} being the proportion of the maximum dependency distribution in this mixture with $0 \leq \rho_{kb} \leq 1$. The proposed model requires little additional parameters compared with the conditional independence model. In addition, it is easily interpretable as explained in the next paragraph. Note that the limiting case where $\rho_{kb} = 0$ defines the block distribution by the independence one. In this particular case, the parameters of the maximum dependency distribution are no longer defined.

Under this distribution, the maximum dependency distribution proportion reflects the deviation from independence under the assumption that the other allowed distribution is the maximum dependency distribution. The parameter ρ_{kb} gives an indicator of the *inter-variables correlation* of the block. It is not here a pairwise dependency among variables but a dependency between all variables of the block. Furthermore, it stays bounded when the number of variables is larger than two while the Cramer's V is non upper-bounded in this case. The *intra-variables dependen-*

cies between the variables are defined by $\boldsymbol{\delta}_{kb}$. The strength of these dependencies is explained by $\boldsymbol{\tau}_{kb}$ since it gives the *weight of the over-represented modalities crossing* compared with the independence distribution.

We interpreted before the distribution with independent blocks as a parsimonious version of the log-linear mixture model because it determines the interactions to be modeled. By choosing the proposed distribution for blocks, a second level of parsimony is added. Indeed, among the interactions allowed by this distribution with independent blocks, only those corresponding to the maximum dependency distribution will be modeled. Other interactions are considered as null.

Properties:

- The CCM, stays parsimonious compared with CIM since, for each block with at least two variables, the additional parameters number depends only on the modalities number of the first variable of the block and not on the number of variables into the block. By using ν_{CIM} defined in Equation (2), the number of parameters of CCM is denoted ν_{CCM} by:

$$\nu_{\text{CCM}} = \nu_{\text{CIM}} + \sum_{\{(k,b)|d^{\{kb\}}>1\}} m_1^{\{kb\}}. \tag{6}$$

- The proposed distribution is identifiable under the condition that the block is composed by at least three variables ($d^{\{kb\}} > 2$) or that the modalities number of the last variable of the block is more than two ($m_2^{\{kb\}} > 2$). This result is demonstrated in Appendix B of Marbac *et al.* (2013). The parameter ρ_{kb} is a new indicator allowing to measure the correlation between variables, not limited to correlation between couples of variables. In the case where the identifiability conditions could not be met, we distinguish two cases. If $d^{\{kb\}} = 1$, then the block b contains only one variable, the proposed model is reduced to model a multinomial distribution, $\rho_{kb} = 0$ and the maximum dependency distribution is not defined. If $d^{\{kb\}} = 2$ and $m_2^{\{kb\}} = 2$ then a new constraint is added. In order to have the most meaningful parameters, the chosen value of ρ_{kb} is the largest value maximizing the log-likelihood. This additional constraint does not falsify the definition of ρ_{kb} as an indicator of the dependency strength between the variables of the same block. Furthermore, this constraint is natural since blocks with the biggest dependencies are wanted. Note that ρ_{kb} seems to be correlated with the Cramer's V. An example is given in Section 3 of Marbac *et al.* (2013).

4 Estimation of the parameters

For a fixed model $(g, \boldsymbol{\sigma})$, the parameters have to be estimated. Since the proposed distribution CCM has two latent variables (the classes membership and the intra-block distributions membership), two algorithms derived from the EM algorithm are performed for the estimation of the associated continuous parameters. The combinatorial problems arising from the consideration of the discrete parameters are avoided by using a Metropolis-Hastings algorithm.

4.1 Global GEM algorithm

The whole data set consisting of n independent and identically distributed individuals is denoted by $\mathbf{x} = (\boldsymbol{x}_1, \dots \boldsymbol{x}_n)$ where $\boldsymbol{x}_i \in \mathcal{X}$. The objective is to obtain the maximum log-likelihood estimator $\hat{\boldsymbol{\theta}}$ defined as (g is now implicit in each expression):

$$\hat{\boldsymbol{\theta}} = \text{argmax}_{\boldsymbol{\theta}} L(\boldsymbol{\theta}; \mathbf{x}, \boldsymbol{\sigma}) \quad \text{with} \quad L(\boldsymbol{\theta}; \mathbf{x}, \boldsymbol{\sigma}) = \sum_{i=1}^{n} \ln \Big(p(\boldsymbol{x}_i; \boldsymbol{\sigma}, \boldsymbol{\theta}) \Big). \tag{7}$$

The search of maximum likelihood estimates for mixture models leads to solve equations having no analytical solutions. For the mixture models, the assignments of the individuals to the classes can be considered as missing data. This is why the tool generally used is the Expectation-Maximization algorithm (denoted EM algorithm) and its extensions (Dempster *et al.* , 1977; McLachlan & Krishnan, 1997). Denoting the unknown indicator vectors of the g clusters by $\mathbf{z} = (z_{ik}; i = 1, \dots, n; k = 1, \dots, g)$ where $z_{ik} = 1$ if $\boldsymbol{x}_i$ arises from cluster k, $z_{ik} = 0$ otherwise, the mixture model distribution corresponds to the marginal distribution of the random variable $\mathbf{X}$ obtained from the couple distribution of the random variables $(\mathbf{X}, \mathbf{Z})$. In order to maximize the log-likelihood, the EM algorithm uses the complete-data log-likelihood which is defined as:

$$L_{\text{c}}(\boldsymbol{\theta}; \mathbf{x}, \mathbf{z}, \boldsymbol{\sigma}) = \sum_{i=1}^{n} \sum_{k=1}^{g} z_{ik} \ln \Big(\pi_k p(\boldsymbol{x}_i; \boldsymbol{\sigma}_k, \boldsymbol{\theta}_k) \Big). \tag{8}$$

The EM algorithm is an iterative algorithm which alternates between two steps: the computation of the complete-data log-likelihood conditional expectation (E step) and its maximization (M step). Many algorithms are derived from the EM algorithm and among them the Generalized EM algorithm (GEM) is of interest for us. It works on the same principle as the EM algorithm but the maximization step is replaced by a GM step where the proposed parameters increase the

expectation of the complete-data log-likelihood according to its previous value without necessarily maximizing it.

We prefer to use the GEM algorithm, since the maximization step in the EM algorithm requires to estimate the continuous parameters for too many possible values of the discrete parameters in order to warrant the maximization of the complete-data log-likelihood expectation. Indeed, exhaustive enumeration for estimating the discrete parameters is generally impossible when a block contains variables with many modalities and/or many variables, as detailed now. If $S(a, b)$ is the number of possible surjections from a set of cardinal a into a set of cardinal b, then $\boldsymbol{\delta}_{kb}$ is defined in the discrete space of dimension $\prod_{j=1}^{d^{\{kb\}}-1} S(m_j^{\{kb\}}, m_{j+1}^{\{kb\}})$. For example, a block with three variables and $m^{\{kb\}} = (5, 4, 3)$ implies 51 840 possibilities for $\boldsymbol{\delta}_{kb}$. Thus, a stochastic approach is proposed in Section 4.2 to overcome this problem. Then, the estimation of the continuous parameters conditionally on the discrete parameters is performed via the classical EM algorithm presented in Section 4.3 since their estimation cannot be obtained in closed form. At the iteration (r), the steps of the global GEM can be written as:

- $\mathbf{E_{global}}$ **step:** $z_{ik}^{(r)} = \frac{\pi_k^{(r)} p(\boldsymbol{x}_i; \boldsymbol{\sigma}_k, \boldsymbol{\theta}_k^{(r)})}{\sum_{k'=1}^{g} \pi_{k'}^{(r)} p(\boldsymbol{x}_i; \boldsymbol{\sigma}_{k'}, \boldsymbol{\theta}_{k'}^{(r)})}$,
- $\mathbf{GM_{global}}$ **step:** $\pi_k^{(r+1)} = \frac{n_k^{(r)}}{n}$ where $n_k^{(r)} = \sum_{i=1}^{n} z_{ik}^{(r)}$ and $\forall (k, b)$ $\boldsymbol{\theta}_{kb}^{(r+1)}$ is updated under the constraint that the conditional expectation of complete-data log-likelihood increases (see Sections 4.2 and 4.3).

Initialization of the algorithm: since this algorithm is performed in an stochastic algorithm used for the model selection (see Section 5) and since this latter has an influence on the GEM initialization, this point will be detailed in Section 5.2.

Stopping criterion: the GEM algorithm is stopped after $r_{\max}$ iterations and we fix $\hat{\boldsymbol{\theta}} = \boldsymbol{\theta}^{(r_{\max})}$.

4.2 Details of the $\mathbf{GM_{global}}$ step of the GEM

The maximization of the expected complete-data log-likelihood is done by optimizing its terms for each (k, b). Thus, the determination of $\boldsymbol{\theta}_{kb}^{(r+1)}$ is performed independently to the parameters of the other blocks. A Metropolis-Hastings algorithm (Robert & Casella, 2004) is also performed, for each (k, b), to avoid the combinatorial problems induced by the detection of the discrete

parameters $\boldsymbol{\delta}_{kb}$. It performs a random walk over the discrete parameters space and computes the maximum likelihood estimators of continuous parameters $(\rho_{kb}, \boldsymbol{\alpha}_{kb}, \boldsymbol{\tau}_{kb})$ associated with them. This stochastic algorithm allows to find the estimator maximizing the expected complete-data log-likelihood of the block b for the component k:

$$\underset{\boldsymbol{\theta}_{kb}}{\operatorname{argmax}} \sum_{i=1}^{n} z_{ik}^{(r)} \ln p(\boldsymbol{x}_i^{\{kb\}}; \boldsymbol{\theta}_{kb}). \tag{9}$$

At each iteration (s) of this Metropolis-Hastings algorithm, a discrete parameter denoted by $\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})}$ is sampled with a uniform distribution in a neighborhood of $\boldsymbol{\delta}_{kb}^{(r,s)}$ denoted as $\Delta(\boldsymbol{\delta}_{kb}^{(r,s)})$. Then the continuous parameters $(\rho_{kb}^{(r,s+\frac{1}{2})}, \boldsymbol{\alpha}_{kb}^{(r,s+\frac{1}{2})}, \boldsymbol{\tau}_{kb}^{(r,s+\frac{1}{2})})$ are computed, conditionally on the value of $\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})}$, in order to maximize the expected complete-data log-likelihood of the block b for the component k:

$$\sum_{i=1}^{n} z_{ik}^{(r)} \ln p(\boldsymbol{x}_i^{\{kb\}}; \rho_{kb}, \boldsymbol{\alpha}_{kb}, \boldsymbol{\tau}_{kb}, \boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})}). \tag{10}$$

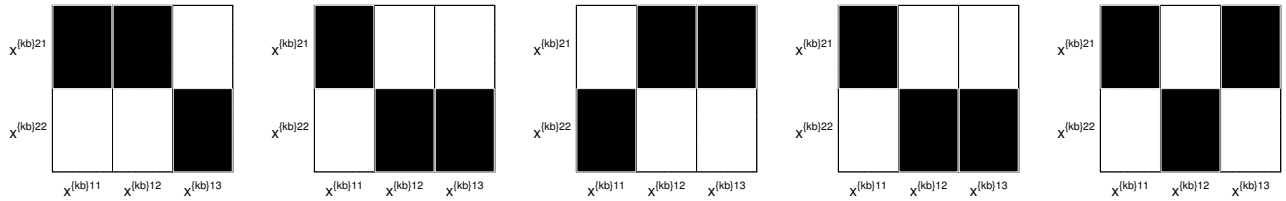
The candidate parameters are now denoted by $\boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})} = (\rho_{kb}^{(r,s+\frac{1}{2})}, \boldsymbol{\alpha}_{kb}^{(r,s+\frac{1}{2})}, \boldsymbol{\tau}_{kb}^{(r,s+\frac{1}{2})}, \boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})})$. The whole block parameters $\boldsymbol{\theta}_{kb}^{(r,s+1)}$ of the next step are then defined as $\boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})}$ with the acceptance probability $\mu^{(r,s+1)}$ and $\boldsymbol{\theta}_{kb}^{(r,s)}$ otherwise, where:

$$\mu^{(r,s+1)} = \min \left\{ \frac{\prod_{i=1}^{n} p(\boldsymbol{x}_i^{\{kb\}}; \boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})})^{z_{ik}^{(r)}} |\Delta(\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})})|}{\prod_{i=1}^{n} p(\boldsymbol{x}_i^{\{kb\}}; \boldsymbol{\theta}_{kb}^{(r,s)})^{z_{ik}^{(r)}} |\Delta(\boldsymbol{\delta}_{kb}^{(r,s)})|}, 1 \right\}, \tag{11}$$

$|\Delta(\boldsymbol{\delta}_{kb}^{(r,s)})|$ denoting the cardinal of $\Delta(\boldsymbol{\delta}_{kb}^{(r,s)})$. Thus, at the iteration (s), the algorithm performs the three following steps:

- **Stochastic step on $\boldsymbol{\delta}_{kb}$:** generate $\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})}$ with a uniform distribution among the elements of $\Delta(\boldsymbol{\delta}_{kb}^{(r,s)})$,
- **Maximization step on the continuous parameters ($\mathbf{M}_{\boldsymbol{\theta}}$ step):** compute the continuous parameters of $\boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})}$ (see Section 4.3),
- **Stochastic step on $\boldsymbol{\theta}_{kb}$:** sample $\boldsymbol{\theta}_{kb}^{(r,s+1)} = \begin{cases} \boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})} & \text{with probability } \mu^{(r,s+1)} \\ \boldsymbol{\theta}_{kb}^{(r,s)} & \text{otherwise.} \end{cases}$

The neighborhood $\Delta(\boldsymbol{\delta}_{kb}^{(r,s)})$ is defined as the set of the parameters where at most two surjections are different from that of $\boldsymbol{\delta}_{kb}^{(r,s)}$. Figure 3 illustrates this definition.



(a) (b.1) (b.2) (b.3) (b.4)

Figure 3: Example of $\Delta(\boldsymbol{\delta}_{kb})$ with $d^{\{kb\}} = 2$ and $\boldsymbol{m}^{\{kb\}} = (3, 2)$. For the row h' and the column h, a black cell indicates that $\delta_{kb}^{h2h'} = 1$ and a white cell that $\delta_{kb}^{h2h'} = 0$: (a) $\boldsymbol{\delta}_{kb}$; (b.1), (b.2), (b.3), (b.4) are the elements of $\Delta(\boldsymbol{\delta}_{kb})$.

Initialization of the algorithm: the initialization of the algorithm is done by $\boldsymbol{\theta}_{kb}^{(r+1,0)} = \boldsymbol{\theta}_{kb}^{(r)}$.

Stopping criterion: this algorithm is stopped after a number of iterations $s_{\max}$. The parameter $\boldsymbol{\theta}_{kb}^{(r+1)} = \boldsymbol{\theta}_{kb}^{(r+1,\tilde{s})}$ is returned with $\tilde{s} = \underset{s}{\operatorname{argmax}} \sum_{i=1}^{n} z_{ik}^{(r)} \ln p(\boldsymbol{x}_i^{\{kb\}}; \boldsymbol{\theta}_{kb}^{(r,s)})$. Thus, the proposed initialization ensures the growing of the likelihood at each iteration of the GEM algorithm.

Remark: when the space of possible $\boldsymbol{\delta}_{kb}$'s is small (for example when the block groups a small number of binary variables), an exhaustive approach obtains the same results as the proposed algorithm with less computation time. Thus, the retained approach (exhaustive or stochastic) depends on the number of variables and modalities.

4.3 Details of the $\mathrm{M}_{\boldsymbol{\theta}}$ step of the $\mathrm{GM}_{\mathbf{global}}$ step

As there is a second level of mixing, another EM algorithm can be performed for the continuous parameters $(\rho_{kb}, \boldsymbol{\alpha}_{kb}, \boldsymbol{\tau}_{kb})$ estimation by introducing other unknown vectors corresponding to the indicator of the blocks distributions conditionally on $\mathbf{z}$. These vectors are written as $\mathbf{y} = (\mathbf{y}^{\{kb\}}; k = 1, \ldots, g; b = 1, \ldots, \mathrm{B}_k)$ with $\mathbf{y}^{\{kb\}} = (y_1^{\{kb\}}, ..., y_n^{\{kb\}})$ where $y_i^{\{kb\}} = 1$ if $\boldsymbol{x}_i^{\{kb\}}$ arises from the *maximum dependency* distribution for the block b of the cluster k and $y_i^{\{kb\}} = 0$ if $\boldsymbol{x}_i^{\{kb\}}$ arises from the *independence* distribution for the block b of the cluster k. The whole mixture model distribution corresponds to the marginal distribution of the random variable $\mathbf{X}$ obtained from the triplet distribution of the random variables $(\mathbf{X}, \mathbf{Y}, \mathbf{Z})$. Since the blocks are independent

conditionally on $\mathbf{Z}$, the *full* complete-data log-likelihood (both in $\mathbf{Y}$ and $\mathbf{Z}$) is defined as:

$$L_{\mathrm{c}}^{\mathrm{full}}(\boldsymbol{\theta};\mathbf{x},\mathbf{y},\mathbf{z},\boldsymbol{\sigma}) = \sum_{i=1}^{n}\sum_{k=1}^{g} z_{ik}\Big(\ln\pi_k + \sum_{b=1}^{B_k}\big((1-y_i^{\{kb\}})\ln(1-\rho_{kb}) + (1-y_i^{\{kb\}})\ln\mathring{p}(\boldsymbol{x}_i^{\{kb\}};\boldsymbol{\alpha}_{kb}) + y_i^{\{kb\}}\ln\rho_{kb} + y_i^{\{kb\}}\ln\acute{p}(\boldsymbol{x}_i^{\{kb\}};\boldsymbol{\tau}_{kb},\boldsymbol{\delta}_{kb})\big)\Big). \quad (12)$$

At the iteration (t), the local EM algorithm estimates the continuous parameters of the block b, with fixed values of $\mathbf{z}^{(r)}$ and $\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})}$, by the following two steps:

- **$\mathbf{E}_{\mathbf{local}}$ step:** $y_i^{\{kb\}(r,s+\frac{1}{2},t)} = \frac{\rho_{kb}^{(r,s+\frac{1}{2},t)}\acute{p}(\boldsymbol{x}_i^{\{kb\}};\boldsymbol{\tau}_{kb}^{(r,s+\frac{1}{2},t)},\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})})}{p(\boldsymbol{x}_i^{\{kb\}};\rho_{kb}^{(r,s+\frac{1}{2},t)},\boldsymbol{\alpha}_{kb}^{(r,s+\frac{1}{2},t)},\boldsymbol{\tau}_{kb}^{(r,s+\frac{1}{2},t)},\boldsymbol{\delta}_{kb}^{(r,s+\frac{1}{2})})}$,
- **$\mathbf{M}_{\mathbf{local}}$ step:** $\rho_{kb}^{(r,s+\frac{1}{2},t+1)} = \frac{n_{kb}^{(r,s+\frac{1}{2},t)}}{n_k^{(r)}}$, $\tau_{kb}^{(r,s+\frac{1}{2},t+1)} = \frac{\sum_{i=1}^{n} z_{ik}^{(r)} y_i^{\{kb\}(r,s+\frac{1}{2},t)} x_i^{\{kb\}1h}}{n_{kb}^{(r,s+\frac{1}{2},t)}}$,
  $\alpha_{kb}^{(r,s+\frac{1}{2},t+1)} = \frac{\sum_{i=1}^{n} z_{ik}^{(r)}(1-y_i^{\{kb\}(r,s+\frac{1}{2},t)})x_i^{\{kb\}jh}}{n_k^{(r)}-n_{kb}^{(r,s+\frac{1}{2},t)}}$, where $n_{kb}^{(r,s+\frac{1}{2},t)} = \sum_{i=1}^{n} z_{ik}^{(r)} y_i^{\{kb\}(r,s+\frac{1}{2},t)}$.

Conjecture: during our numerous experiments, we empirically noticed that the log-likelihood function of the mixture between the independence and the maximum dependency distributions had a unique optimum. We conjecture that this function has indeed a unique maximum.

Initialization of the algorithm: the previous conjecture allows to perform only one initialization of the EM algorithm fixed to: $(\rho_{kb}^{(r,s+\frac{1}{2},0)}, \boldsymbol{\alpha}_{kb}^{(r,s+\frac{1}{2},0)}, \boldsymbol{\tau}_{kb}^{(r,s+\frac{1}{2},0)}) = (\rho_{kb}^{(r,s)}, \boldsymbol{\alpha}_{kb}^{(r,s)}, \boldsymbol{\tau}_{kb}^{(r,s)})$.

Stopping criterion: this algorithm is stopped after a number of iterations denoted by $t_{\max}$ and returns the value of block parameters $\boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})}$ defined as $\boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2})} = \boldsymbol{\theta}_{kb}^{(r,s+\frac{1}{2},t_{\max})}$.

Remark: in the specific case where $\boldsymbol{\delta}_{kb}$ are known for each (k,b), the estimation of all the continuous parameters could be performed by a unique EM algorithm where, at the iteration (r), the E step would compute both $\mathbf{z}^{(r)}$ and $\mathbf{y}^{(r)}$ while the M step would estimate all the parameters maximizing the expectation of the *full* complete-data log-likelihood.

5 Model selection

5.1 Gibbs algorithm for exploring the space of models

Since the number of components g determines the dimension of $\boldsymbol{\sigma}$, the model construction is done in two steps: firstly, the selection of the number of components and, secondly, the determination of the variable repartition per blocks for each component. In a Bayesian context, the best model $(\hat{g}, \hat{\boldsymbol{\sigma}})$ is defined as (Robert, 2005):

$$(\hat{g}, \hat{\boldsymbol{\sigma}}) = \underset{g,\boldsymbol{\sigma}}{\operatorname{argmax}}\ p(g, \boldsymbol{\sigma}|\mathbf{x}). \tag{13}$$

Thus, by considering that $p(g) = \frac{1}{g_{\max}}$ if $g \leq g_{\max}$ and 0 otherwise, where $g_{\max}$ is the maximum number of classes allowed by the user, and by assuming that $p(\boldsymbol{\sigma}|g)$ follows a uniform distribution, the best model is also defined as:

$$(\hat{g}, \hat{\boldsymbol{\sigma}}) = \underset{g}{\operatorname{argmax}} \left[\underset{\boldsymbol{\sigma}}{\operatorname{argmax}}\ p(\mathbf{x}|g, \boldsymbol{\sigma})\right]. \tag{14}$$

To find $(\hat{g}, \hat{\boldsymbol{\sigma}})$, a Gibbs algorithm is used for estimating $\operatorname{argmax}_{\boldsymbol{\sigma}}\ p(\mathbf{x}|g, \boldsymbol{\sigma})$, for each value of $g \in \{1, \ldots, g_{max}\}$, to avoid the combinatorial problem involved by the detection of the block structure of variables. A reversible jump method could be used (Richardson & Green, 1997), however this approach is rarely performed with mixed parameters (continuous and discrete). Indeed, in such a case, it is difficult to define a mapping between the parameters space of two models. So, we propose to use an easier Gibbs sampler-type having $p(\boldsymbol{\sigma}|\mathbf{x}, g)$ as stationary distribution. It alternates between two steps: the generation of a stochastic neighborhood $\Sigma^{[q]}$ conditionally on the current model $\boldsymbol{\sigma}^{[q]}$ by a proposal distribution and the generation of a new pattern $\boldsymbol{\sigma}^{[q+1]}$ included in $\Sigma^{[q]}$ with a probability proportional to its posterior probability. At the iteration $[q]$, it is written as:

- **Neighborhood step:** generate a stochastic neighborhood $\Sigma^{[q]}$ by a proposal distribution given below conditionally on the current model $\boldsymbol{\sigma}^{[q]}$,
- **Pattern step:** $\boldsymbol{\sigma}^{[q+1]} \sim p(\boldsymbol{\sigma}|\mathbf{x}, g, \Sigma^{[q]})$ with $p(\boldsymbol{\sigma}|\mathbf{x}, g, \Sigma^{[q]}) = \begin{cases} \frac{p(\mathbf{x}|g,\boldsymbol{\sigma})}{\sum_{\boldsymbol{\sigma'} \in \Sigma^{[q]}} p(\mathbf{x}|g,\boldsymbol{\sigma'})} & \text{if } \boldsymbol{\sigma} \in \Sigma^{[q]} \\ 0 & \text{otherwise.} \end{cases}$

A possible deterministic neighborhood of $\boldsymbol{\sigma}^{[q]}$ could be defined as the set of models where, at most one variable is affected, for one component, in another block (possibly creating a new block):

$\left\{\boldsymbol{\sigma} : \exists!(k,b,j)\ j \in \boldsymbol{\sigma}_{kb}^{[q]} \text{ and } j \notin \boldsymbol{\sigma}_{kb}\right\} \cup \left\{\boldsymbol{\sigma}^{[q]}\right\}$. However, this deterministic neighborhood can be very large, this is why a proposal distribution allows to reduce it to a stochastic neighborhood $\Sigma^{[q]}$ by reducing the number of (k,b) where $\boldsymbol{\sigma}_{kb}$ could be different to $\boldsymbol{\sigma}_{kb}^{[q]}$. Thus, one component $k^{[q]}$ is randomly sampled in $\{1,\ldots,g\}$ then one block $b_{from}^{[q]}$ is randomly sampled in $\{1,\ldots,B_{k^{[q]}}^{[q]}\}$. Another block $b^{[q]}$ is randomly sampled in $\{1,\ldots,B_{k^{[q]}}^{[q]}\} \setminus b_{from}^{[q]}$ and the set $b_{to}^{[q]} = \{b^{[q]}, B_{k^{[q]}}^{[q]} + 1\}$ is built. The stochastic neighborhood $\Sigma^{[q]}$ is then defined as:

$$\Sigma^{[q]} = \left\{\boldsymbol{\sigma} : \exists!(k,b,j)\ j \in \boldsymbol{\sigma}_{kb}^{[q]},\ j \notin \boldsymbol{\sigma}_{kb} \text{ and } j \in \boldsymbol{\sigma}_{kb'} \text{ with } k = k^{[q]},\ b = b_{\text{from}}^{[q]},\ b' \in b_{\text{to}}^{[q]}\right\} \cup \left\{\boldsymbol{\sigma}^{[q]}\right\}. \quad (15)$$

We denote the elements of $\Sigma^{[q]}$ as $\boldsymbol{\sigma}^{[q+\varepsilon(e)]}$ where $\varepsilon(e) = \frac{e}{|\Sigma^{[q]}|+1}$ and $e = 1,\ldots,|\Sigma^{[q]}|$. Figure 4 shows an illustration of this definition.

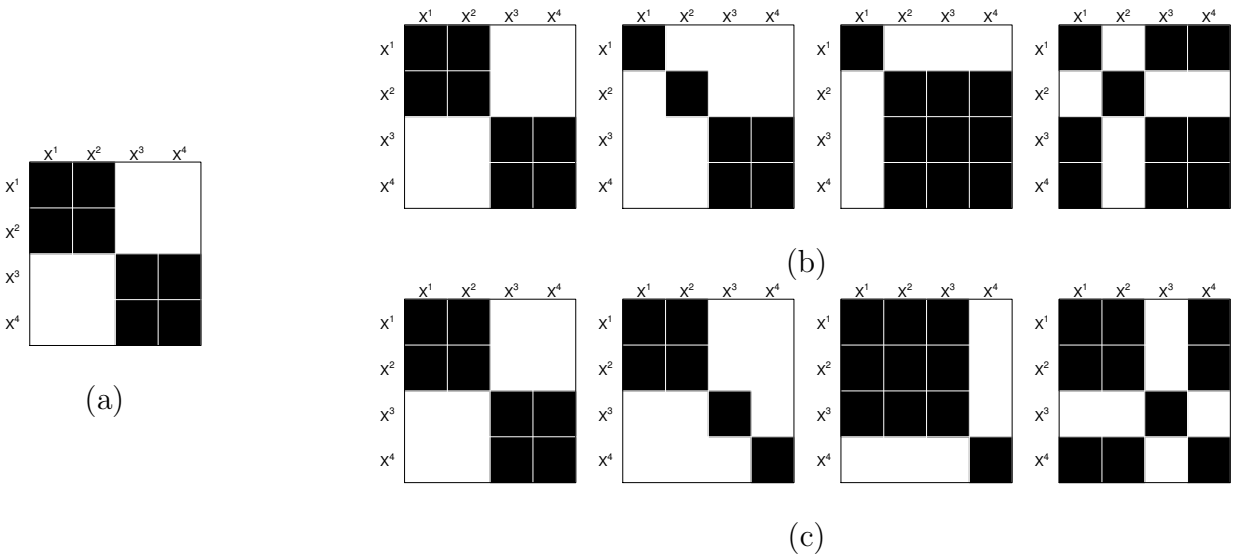


Figure 4: Example of the support of $\Sigma^{[q]}$ in a case of four variables. If the variable of the row j and the variable of the column j' are in the same block then the cell (j,j') is painted in black. This cell is painted in white otherwise. (a) Graphical representation of $\boldsymbol{\sigma}_k^{[q]} = (\{1,2\},\{3,4\})$; (b) Elements of $\Sigma^{[q]}$ if $b_{from}^{[q]} = 1$; (c) Elements of $\Sigma^{[q]}$ if $b_{from}^{[q]} = 2$.

At the generation pattern step, the previous algorithm needs the value of $p(\mathbf{x}|g,\boldsymbol{\sigma})\ \forall \boldsymbol{\sigma} \in \Sigma^{[q]}$. By using the BIC approximation (Schwarz, 1978; Lebarbier & Mary-Huard, 2006), this probability is approximated by:

$$\ln p(\mathbf{x}|g,\boldsymbol{\sigma}) \simeq L(\hat{\boldsymbol{\theta}};\mathbf{x},g,\boldsymbol{\sigma}) - \frac{\nu_{\text{CCM}}}{2}\log(n), \quad (16)$$

$\hat{\boldsymbol{\theta}}$ being the maximum likelihood estimator obtained by the GEM algorithm previously described in Section 4. Thus, at the iteration $[q]$, for each $e = 1,\ldots,|\Sigma^{[q]}|$, the estimator $\hat{\boldsymbol{\theta}}^{[q+\varepsilon(e)]}$ associated

to the element $\boldsymbol{\sigma}^{[q+\varepsilon(e)]}$ is computed by the GEM algorithm.

Initialization: whatever the initial value selected for $\boldsymbol{\sigma}^{[0]}$, the algorithm converges to the same value of $\boldsymbol{\sigma}$. However, this convergence can be very slow when the initialization is poor. Since blocks consist of the most correlated variables, a Hierarchical Ascendant Classification (HAC) is used on the matrix of Cramer's V distances on the couples of variables. The partition produced by the HAC minimizing the block number without blocks consisting of more than four variables are chosen for each $\boldsymbol{\sigma}_k^{[0]}$. The variables number of a block is limited to four, for the initialization, because very few blocks having more than four variables were exhibited during our experiments. Obviously, the Gibbs algorithm can then violate this initial constraint if necessary.

Stopping criterion: the algorithm is stopped when $q_{\max}$ successive iterations have not discovered a better model.

5.2 Consequences of the Gibbs algorithm on the GEM algorithm

Initialization of the GEM algorithm: at the iteration $[q]$ of the Gibbs algorithm, the GEM algorithm estimates $\hat{\boldsymbol{\theta}}^{[q+\varepsilon(e)]}$ associated to the model $\boldsymbol{\sigma}^{[q+\varepsilon(e)]}$ for $e = 1, \ldots, |\Sigma^{[q]}|$. Since these models are close to $\boldsymbol{\sigma}^{[q]}$, their maximum likelihood estimators should be closed to $\hat{\boldsymbol{\theta}}^{[q]}$. The GEM algorithm initialization is also done by the value of $\hat{\boldsymbol{\theta}}^{[q]}$ for the not modified blocks. Thus, $\boldsymbol{\theta}_{kb}^{[q+\varepsilon(e)](0)} = \hat{\boldsymbol{\theta}}_{kb}^{[q]}$ if the blocks are not modified ($\boldsymbol{\sigma}_{kb}^{[q+\varepsilon(e)]} = \boldsymbol{\sigma}_{kb}^{[q]}$). For the other blocks, the continuous parameters are randomly sampled. For those blocks, in order to avoid the combinatorial problems, we use a sequential method to initialize $\boldsymbol{\delta}_{kb}^{[q+\varepsilon(e)](0)}$: the surjections from $\boldsymbol{x}^{\{kb\}1}$ to $\boldsymbol{x}^{\{kb\}j}$ are sampled, according to $\mathbf{x}$ and to the continuous parameters previously sampled $(\rho_{kb}^{[q+\varepsilon(e)](0)}, \boldsymbol{\alpha}_{kb}^{[q+\varepsilon(e)](0)}, \boldsymbol{\tau}_{kb}^{[q+\varepsilon(e)](0)})$, for each $j = 2, \ldots, d^{\{kb\}}$ as follows:

$$\boldsymbol{\delta}_{kb}^{\cdot j[q+\varepsilon(e)](0)} \propto \prod_{i=1}^{n} p(x_i^{\{kb\}1}, x_i^{\{kb\}j}; \rho_{kb}^{[q+\varepsilon(e)](0)}, \boldsymbol{\alpha}_{kb}^{1[q+\varepsilon(e)](0)}, \boldsymbol{\alpha}_{kb}^{j[q+\varepsilon(e)](0)}, \boldsymbol{\tau}_{kb}^{[q+\varepsilon(e)](0)}, \boldsymbol{\delta}_{kb}^{\cdot j})^{z_{ik}^{[q]}}, \tag{17}$$

where $\boldsymbol{\delta}_{kb}^{\cdot j[q+\varepsilon(e)]} = (\boldsymbol{\delta}_{kb}^{hj[q+\varepsilon(e)]}; h = 1, \ldots, m_1^{\{kb\}})$ and where $z_{ik}^{[q]} = E\big[Z_{ik} | \boldsymbol{x}_i, \boldsymbol{\theta}^{[q]}\big]$.

Remark about $r_{\max}$: as said in Section 4.1, the algorithm is stopped after a fixed number of iterations $r_{\max}$. If the algorithm is stopped before its convergence, the proposed initialization

limits the problems. Indeed, if the model has a high *a posteriori* probability, it will stay in the neighborhood $\Sigma^{[q]}$ during some successive iterations, so its log-likelihood will increase.

6 Simulations

Table 1 presents the adjustment parameters values used for all the simulations.

Algorithms	Gibbs	GEM	Metropolis-Hastings	EM
Criteria	$q_{\max} = 20 \times d$	$r_{\max} = 10$	$s_{\max} = 1$	$t_{\max} = 5$

Table 1: Values of the different stopping criteria.

As these algorithms are interlocked, the iterations number of the most internal algorithms are small. Since the number of possible models increases with d, we propose to fix: $q_{\max} = 20 \times d$. When the best model is selected by the Gibbs algorithm, this latter will stay in this model during lots of iterations so the Metropolis-Hastings and the EM algorithm are performed lots of times. Thus, it is not necessary to have a large iterations number as stopping criterion.

6.1 Study of the algorithm for the $\boldsymbol{\delta}_{kb}$ estimation

In this section, we illustrate the performance of the Metropolis-Hastings algorithm used for the $\boldsymbol{\delta}_{kb}$ estimation (see Section 4.2) and the relevance of its initialization (see Equation (17)). Since this algorithm is interlocked in the Gibbs and in the GEM algorithm, we need it to converge quickly. It is shown in the following simulations that the algorithm stays relevant up to six modalities per variables and up to six variables per block. These conditions hold in most situations.

Samples of size 200 described by variables having the same modalities number are generated by a mixture between an independence distribution and a maximum dependency distribution. The parameter's estimation is also performed by the Metropolis-Hastings algorithm, described in Section 4.2, since only one class is generated. The discrete parameters initializations are performed according to Equation (17) with $z_{i1} = 1$ for $i = 1, \ldots, 200$.

Figure 5 shows the box-plots of the iterations number needed by the Metropolis-Hastings algorithm for finding the true links between modalities maximizing the likelihood[2].

[2]In fact, the algorithm is stopped as soon as it finds a discrete estimator involving a likelihood higher than or

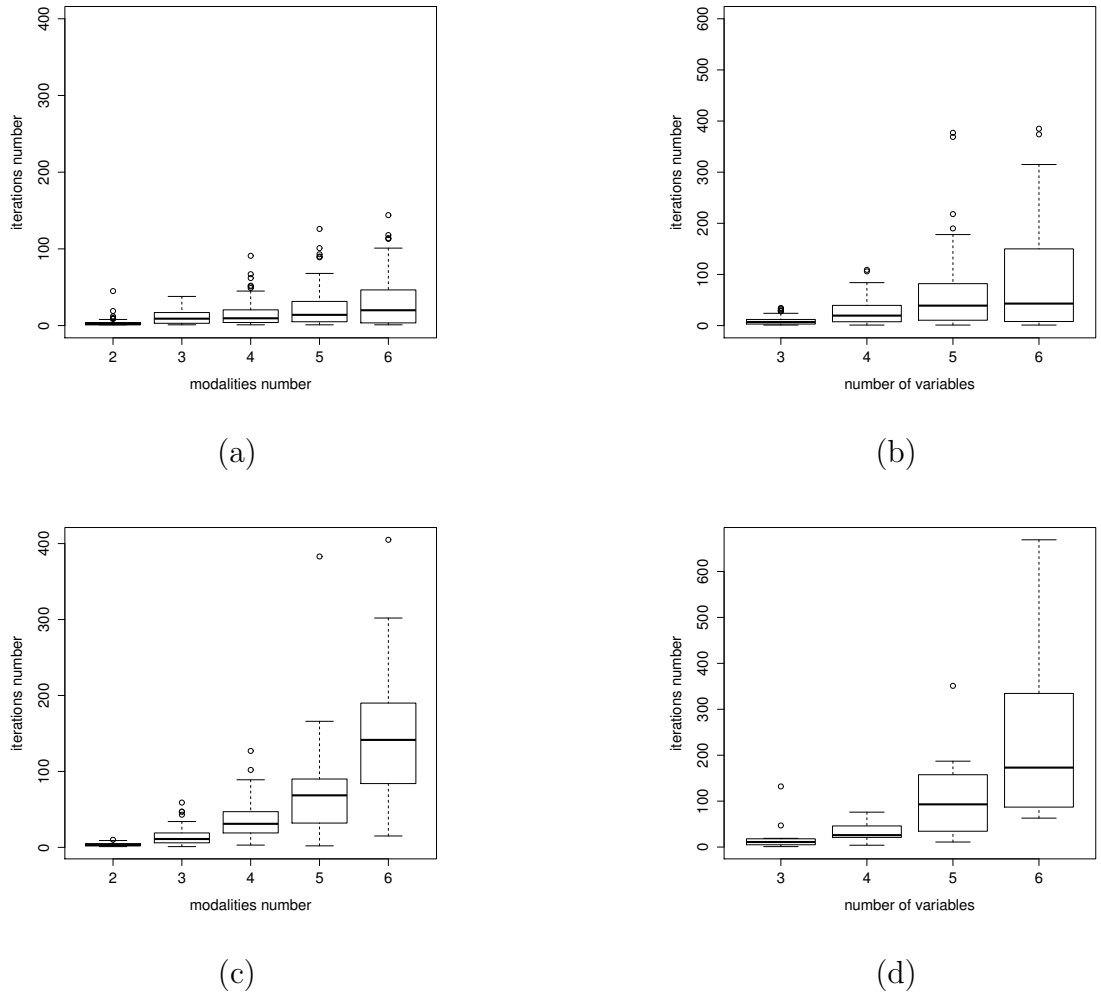


Figure 5: Box-plots of the iterations number needed by the Metropolis-Hastings algorithm for finding the best links between modalities, according to the modalities number when datasets are simulated with a proportion of maximum dependency distribution equal to 0.5. (a) Three variables with the proposed initialization; (b) Three modalities per variables with the proposed initialization; (c) Three variables with a random initialization; (d) Three modalities per variables with a random initialization.

According to these simulations, one observes that the results of this algorithm are good thanks to its initialization which allows to significantly reduce the number of iterations needed in order to find the maximum likelihood estimators.

equal to the likelihood obtained with the true discrete parameters used for the simulation.

6.2 Study of the algorithm for model selection

In order to illustrate the efficiency of the algorithm for the model selection (and also the included estimation process), we want to study the evolution of the Kullback-Leibler divergence according to the number of variables and to the size of the data set. Thus, 100 samples are generated for many situations according to the CCM with two components. Note that the parameter u is introduced for controlling the overlapping of classes: when it is close to one their overlapping (Bayes error) is close to one. These parameters fix the error rate to 0.10 for each studied situation:

$$\boldsymbol{\sigma}_{kb} = (d/b, 1 + d/b) \quad \rho_{kb} = 0.6(1-u) \quad \boldsymbol{\tau}_{kb} = (0.60, 0.20, 0.20),$$

$$\delta_{1b}^{h2h'} = 1 \text{ iff } h = h' \quad \delta_{1b}^{122} = \delta_{1b}^{223} = \delta_{1b}^{321} = 1 \quad \boldsymbol{\alpha}_{1b}^{j} = (0.20, 0.20, 0.60),$$

$$\boldsymbol{\alpha}_{2b}^{1} = \boldsymbol{\alpha}_{1b}^{1}(1-u) + (0.075, 0.850, 0.075)u \quad \text{and} \quad \boldsymbol{\alpha}_{2b}^{2} = \boldsymbol{\alpha}_{1b}^{2}(1-u) + (0.850, 0.075, 0.075)u.$$

Table 2 shows the mean and the standard deviation of the Kullback-Leibler divergence between the parameters used for the dataset generation and the estimated parameters according to the number of variables. When n increases, the Kullback-Leibler divergence converges to zero. It confirms the good behavior of the proposed algorithm.

$d \setminus n$	100	200	400	800
4	**0.77** (*1.34*)	**0.26** (*0.26*)	**0.15** (*0.05*)	**0.12** (*0.05*)
6	**1.22** (*1.77*)	**0.27** (*0.14*)	**0.09** (*0.07*)	**0.05** (*0.05*)
8	**1.72** (*2.50*)	**0.41** (*0.20*)	**0.09** (*0.05*)	**0.05** (*0.03*)
10	**1.73** (*4.06*)	**0.52** (*0.14*)	**0.10** (*0.03*)	**0.04** (*0.03*)

Table 2: **mean** (*standard deviation*) of the Kullback-Leibler divergence.

7 Application

7.1 Dentistry clustering

The Handelman's dentistry data (Handelman *et al.* , 1986) display the evaluation of 3869 dental x-rays (sound or carious) that may show incipient caries performed by five dentists. This data set

was clustered by several models in the past. It is suggested that there are two main classes: the sound teeth and the carious ones.

According to the BIC criterion, data are split into three classes by CIM. Furthermore, dependencies are observed between the variables into classes since the Cramer's V computed per class is not close to zero. Thus, Espeland & Handelman (1989) apply a log-linear mixture model to fit the data. The authors fix the model, so some assumptions are added to better fit the data. More precisely, they consider a mixture with four components. The first two ones take into account the interactions between the dentists 3 and 4. The last two components are specific since their allow only one modality interaction, when all the diagnosis are respectively carious and sound. Note that these assumptions are require by the above authors due to their realistic nature. Indeed, this model fits the data better than CIM. On the other hand, its interpretation needs the analysis of four classes.

As the last two classes seem artificial, Qu *et al.* (1996) prefer to use the random effects models in a latent class analysis with two classes. They assume that the conditional dependencies can be modeled by a single continuous latent variable which varies among the individuals. According to the authors, one class represents the sound teeth and the other represents the carious ones, while the random effect represents all the patient specific unrecorded characteristics of the x-ray images. Their model does not need the two additional artificial classes. Thus their interpretation is easier.

We now display the results of the proposed model CCM estimated with the R package `Clustericat` (the code is presented in Appendix A). The BIC criterion selects two classes with a value of -7473. It claims that CMM better fits the data than the model of Qu *et al.* (1996) since their BIC criterion value is -7487. The BIC criterion values for CIM and CMM are displayed in Table 3. We indicate the computing time (in second), obtained with a processor Intel Core i5-3320M, to estimate CMM where 20 MCMC chains were started with a stopping rules $q_{\max} = 100$ while CIM needs less than 0.1 sec with the R package RMixmod (Lebret *et al.* , 2012).

We note that CMM obtains better values for the BIC criterion than CIM when $g = 1, 2$. When the number of classes is larger ($g \geq 3$) the best model of CMM assumes the conditional independence between variables.

The BIC criterion selects two classes for CMM and this is coherent with a clustering of the teeth between the sound and the carious ones. Furthermore, the two main characteristics of the model

	g	1	2	3	4
CIM	BIC	-8766	-7511	**-7481**	-7503
CCM	BIC	-7743	**-7473**	-7481	-7503
	time (sec)	1.7	4.9	6.1	7.7

Table 3: BIC criterion values for the CIM and the CMM according to different classes numbers for the dentistry data set. For each model, the best results according to the BIC criterion are in bold. Computing time in second is indicates for CMM where 20 MCMC chains was started with a stopping rules $q_{\max} = 500$.

fixed by Espeland & Handelman (1989) are automatically detected by the model: importance of the two modalities crossings where all the dentists have the same diagnosis and a dependency between the diagnosis of the dentists 3 and 4. Thus, the estimated model is coherent with the imposed model of Espeland & Handelman (1989) while no information was given *a priori*.

The fitted model can be interpreted as:

- the majority class ($\pi_1 = 0.86$) mainly gathers the sound teeth. There is a strong dependency between the five dentists ($\boldsymbol{\sigma}_1 = (\{1, 2, 3, 4, 5\})$ and $\rho_{11} = 0.35$). The dependency structure of the maximum dependency distribution indicates an over contribution of both modality interactions where the five dentists have the same diagnosis, especially when they claim that the teeth is sound ($\tau_{11}^{\text{all\_sound}} = 0.93$ and $\tau_{11}^{\text{all\_carious}} = 0.07$).

- the minority class ($\pi_2 = 0.14$) groups principally the carious teeth. There is a dependency between the dentists 3 and 4 while the diagnosis of the other ones are independent given the class ($\boldsymbol{\sigma}_2 = (\{3, 4\}, \{1, 2, 5\})$, $\rho_{21} = 0.31$ and $\rho_{22} = 0$).

Figure 6 helps the interpretation of the clusters for the CCM with two components (best model according to the BIC criterion). On ordinates, the estimated classes are represented with respect to their proportions in decreasing order. Their corresponding area depends on their proportion. The cumulated proportions are indicated on the left side. On abscissae, three indications are given. The first one is the inter-variables correlations (ρ_{kb}) for all the blocks of the class ordered by their strength of correlation (in decreasing order). The second one is the intra-variables correlations ($\boldsymbol{\tau}_{kb}$) for each block drawn according to their strength dependencies (in decreasing order). The

third is the variables repartition per blocks. A black cell indicates that the variable is assigned to the block and a white cell indicates that, conditionally on this class, the variable is independent to the variables of this block. For example, this figure shows that the first class has a proportion of 0.86 and that all the variables are assigned into the same block.

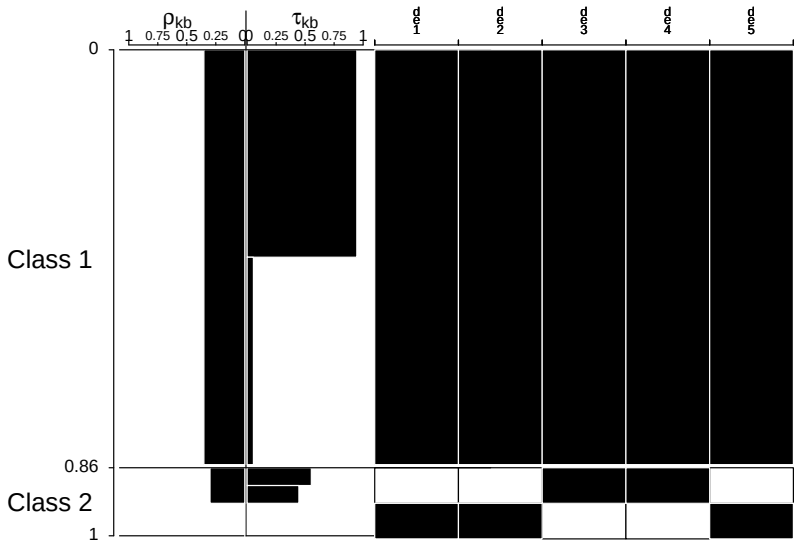


Figure 6: Summary of the best CCM according to BIC for the dentists data set.

7.2 Calves clustering

In this section, the results obtained by the CCM are compared to those obtained for the CIM by the RMixmod software (Lebret *et al.* , 2012). The "Genes Diffusion" company has collected information from the French breeders in order to cluster calves. The 4270 studied calves are described by nine variables of behavior (aptitude for sucking *Apt*, behavior of the mother just before the calving *Iso*) and health related (treatment against omphalite *TOC*, respiratory disease *TRC* and diarrhea *TDC*, umbilicus disinfection *Dis*, umbilicus emptying *Emp*, mother preventive treatment against respiratory disease *TRM* and diarrhea *TDM*).

Table 4 displays the BIC criterion values and the number of parameters for the CIM and CCM models. Furthermore, the computing time in minutes (obtained with a processor Intel Core i5-3320M) to estimate CCM by starting 20 MCMC chains with a stopping criterion of $q_{\max} = 180$ while CIM needs 3 sec with the R package RMixmod (Lebret *et al.* , 2012).

	g	1	2	3	4	5	6	7	8
CIM	BIC	-28589	-26859	-26526	-26333	-26238	-26235	-26226	**-26185**
	ν_{CIM}	17	35	53	71	89	107	125	**143**
CCM	BIC	-26653	-26289	-26173	-26038	**-26025**	-26059	-26045	-26058
	ν_{CCM}	24	48	80	89	**112**	131	148	163
	time (min)	0.97	3.32	6.16	6.56	**10.03**	11.76	12.31	14.92

Table 4: Results for the CIM and the CMM according to different class numbers. For both models, first row corresponds to the BIC criterion values and the second row indicates the continuous parameter number. For each model, the best results according to the BIC criterion are in bold. Computing time for the CCM estimation is given in minutes.

For the CIM, the BIC criterion selects a high number of classes, since it selected eight classes. The interpretation of the clusters is also difficult and we can assume that the estimator's quality is very bad. Figure 7 helps the interpretation for the CCM with five components (best model according to the BIC criterion). Its interpretation is the same as the interpretation of Figure 6. For example, this figure shows that the first class has a proportion of 0.29 and it is composed of four blocks. The most correlated block of the first class has $\rho_{kb} \simeq 0.80$ and the strength of the biggest modalities link is close to 0.85 too. This block consists of the variables *TDC* and *TRM*. Here is now a possible interpretation of Class 1 (note that the others classes are also meaningful; see details in Marbac *et al.* (2013)):

- **General:** this class has a proportion equal to 0.29 and consists of three blocks of dependency and one block of independence.
- **Block 1:** there is a strong correlation (ρ_{11}) between the variables diarrhea treatment of the calve and mother preventive treatment against respiratory disease, especially between the modality no treatment against the calve diarrhea and the absence of preventive treatment against respiratory disease of its mother ($\boldsymbol{\tau}_{11}$ and $\boldsymbol{\delta}_{11}$).
- **Block 2:** there is a strong correlation (ρ_{12}) between the variables treatment against respiratory illness of the calve and mother preventive treatment against diarrhea, especially between the modality preventive treatment against respiratory illness of the calve and the presence of diarrhea preventive treatment of its mother ($\boldsymbol{\tau}_{12}$ and $\boldsymbol{\delta}_{12}$).

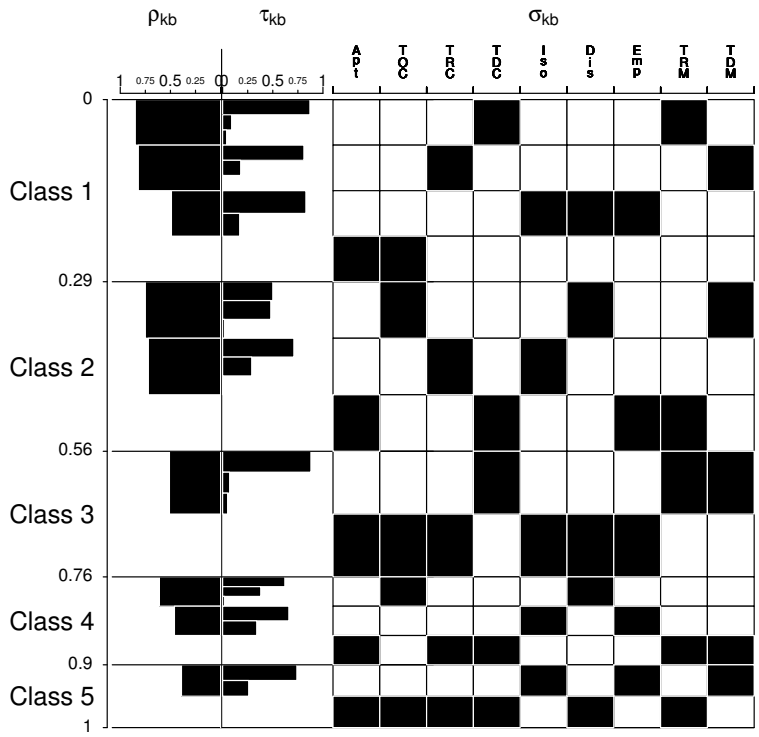


Figure 7: Summary of the best CCM according to BIC for the calves data set.

- **Block 3:** there exists another strong link between the behavior of the mother, the emptying of the umbilical and its disinfection ($\boldsymbol{\tau}_{13}$ and $\boldsymbol{\delta}_{13}$).
- **Block 4:** this block is characterized by absence of preventive treatment against omphalite and have 50% of the calves infected by this illness ($\boldsymbol{\alpha}_{14}$).

8 Conclusion

By using the block extension of the latent class model, a new mixture model is proposed for clustering categorical data by taking into account the intra-class correlation. The block distribution is defined as a mixture between an independent distribution and a maximum dependency distribution. This specific distribution, which stays parsimonious, is compared to the full latent class model and allows different levels of interpretation. The blocks of variables detect the conditional dependency between variables and its strength is reflected by the proportion of maximum dependency distribution. The parameters of this distribution reflect the links and its strength between

modalities.

The parameter's estimation and the model selection are simultaneously performed via a Gibbs sample-type algorithm. It allows to reduce the combinatorial problems of the block structure detection and the links between modalities search for the estimation of the maximum dependency distribution. The results are good when the number of modalities is small for each variable. For more than six modalities, the detection of other links meets some persistent difficulties. So the algorithm can be slow in this case. The proposed approach to estimate the block structure is not adapted for data sets with lots of variables. A deterministic but sub-optimal solution could be used to perform a forward algorithm.

The R package *Clustericat* allows to cluster categorical data sets by using CMM. This package is available on Rforge at the following url *https://r-forge.r-project.org/R/?group_id=1803*.

The proposed model can be easily extended to the case of ordinal data. For this, some additional constraints on the dependency structure of each distribution of maximum dependency need to be added.

Acknowledgments: The authors are grateful to Genes Diffusion company for the provision of the data set and especially its members: Amélie Vallée, Julie Hamon and Claude Grenier. We are grateful to Parmeet Bhatia, engineer in Modal Team, and Stphane Chrétien for their precious valued. This work was financed by DGA and Inria.

References

Agresti, A. 2002. *Categorical data analysis*. Vol. 359. John Wiley and Sons.

Allman, E.S., Matias, C., & Rhodes, J.A. 2009. Identifiability of parameters in latent structure models with many observed variables. *The Annals of Statistics*, **37**(6A), 3099–3132.

Banfield, J.D., & Raftery, A.E. 1993. Model-based Gaussian and non-Gaussian clustering. *Biometrics*, 803–821.

Bock, H.H. 1986. Loglinear models and entropy clustering methods for qualitative data. *Classification as a tool of research. North Holland, Amsterdam*, 19–26.

Celeux, G., & Govaert, G. 1991. Clustering criteria for discrete data and latent class models. *Journal of classification*, **8**(2), 157–176.

Celeux, G., & Govaert, G. 1995. Gaussian parsimonious clustering models. *Pattern Recognition*, **28**(5), 781–793.

Chavent, M., Kuentz, V., & Saracco, J. 2010. A partitioning method for the clustering of categorical variables. *Pages 91–99 of: Classification as a Tool for Research*. Springer.

Cheng, J., & Greiner, R. 1999. Comparing Bayesian network classifiers. *Pages 101–108 of: Proceedings of the Fifteenth conference on Uncertainty in artificial intelligence*. Morgan Kaufmann Publishers Inc.

Chow, C., & Liu, C. 1968. Approximating discrete probability distributions with dependence trees. *Information Theory, IEEE Transactions on*, **14**(3), 462–467.

Dempster, A.P., Laird, N.M., & Rubin, D.B. 1977. Maximum likelihood from incomplete data via the EM algorithm. *Journal of the Royal Statistical Society. Series B (Methodological)*, 1–38.

Espeland, M.A., & Handelman, S.L. 1989. Using Latent Class Models to Characterize and Assess Relative Error in Discrete Measurements. *Biometrics*, **45**(2), pp. 587–599.

Formann, A.K. 1992. Linear logistic latent class analysis for polytomous data. *Journal of the American Statistical Association*, **87**(418), 476–486.

Friedman, N., Geiger, D., & Goldszmidt, M. 1997. Bayesian network classifiers. *Machine learning*, **29**(2), 131–163.

Gollini, I., & Murphy, T.B. 2013. Mixture of latent trait analyzers for model-based clustering of categorical data. *Statistics and Computing*, 1–20.

Goodman, L.A. 1974. Exploratory latent structure analysis using both identifiable and unidentifiable models. *Biometrika*, **61**(2), 215–231.

Govaert, G. 2010. *Data analysis*. Vol. 136. Wiley. com.

Govaert, G., & Nadif, M. 2003. Clustering with block mixture models. *Pattern Recognition*, **36**(2), 463–473.

Guinot, C., Latreille, J., Malvy, D., Preziosi, P., Galan, P., Hercberg, S., & Tenenhaus, M. 2001. Use of multiple correspondence analysis and cluster analysis to study dietary behaviour: food consumption questionnaire in the SU. VI. MAX. cohort. *European journal of epidemiology*, **17**(6), 505–516.

Hagenaars, J.A. 1988. Latent structure models with direct effects between indicators local dependence models. *Sociological Methods & Research*, **16**(3), 379–405.

Hand, D.J., & Yu, K. 2001. Idiot's BayesNot So Stupid after All? *International Statistical Review*, **69**(3), 385–398.

Handelman, S.L., Leverett, D.H., Espeland, M.A., & Curzon, J.A. 1986. Clinical radiographic evaluation of sealed carious and sound tooth surfaces. *The Journal of the American Dental Association*, **113**(5), 751–754.

Harper, D. 1972. Local dependence latent structure models. *Psychometrika*, **37**(1), 53–59.

Huang, J.Z., Ng, M.K., Rong, H., & Li, Z. 2005. Automated variable weighting in k-means type clustering. *Pattern Analysis and Machine Intelligence, IEEE Transactions on*, **27**(5), 657–668.

Hunt, L., & Jorgensen, M. 1999. Theory & Methods: Mixture model clustering using the MULTIMIX program. *Australian & New Zealand Journal of Statistics*, **41**(2), 154–171.

Jajuga, K., Sokołowski, A., & Bock, H.H. 2002. *Classification, clustering and data analysis: recent advances and applications*. Springer Verlag.

Jorgensen, M., & Hunt, L. 1996. Mixture model clustering of data sets with categorical and continuous variables. *Pages 375–384 of: Proceedings of the Conference ISIS*, vol. 96.

Lebarbier, E., & Mary-Huard, T. 2006. Une introduction au critre BIC : fondements thoriques et interprtation. *Journal de la SFdS*, **147**(1), 39–57.

Lebret, R., Iovleff, S., Langrognet, F., Biernacki, C., Celeux, G., & Govaert, G. 2012. Rmixmod: The R Package of the Model-Based Unsupervised, Supervised and Semi-Supervised Classification Mixmod Library. *preprint submitted*.

Marbac, M., Biernacki, C., & Vandewalle, V. 2013. *Model-based clustering for conditionally correlated categorical data*. Rapport de recherche RR-8232. INRIA.

Maugis, C., Celeux, G., & Martin-Magniette, M-L. 2009. Variable selection in model-based clustering: A general variable role modeling. *Computational Statistics & Data Analysis*, **53**(11), 3872–3882.

McLachlan, G.J., & Krishnan, T. 1997. *The EM algorithm*. Wiley-Interscience, New York: Wiley Series in Probability and Statistics: Applied Probability and Statistics.

McLachlan, G.J., & Peel, D. 2000. *Finite mixutre models*. Wiley-Interscience, New York: Wiley Series in Probability and Statistics: Applied Probability and Statistics.

Meila, M., & Jordan, M.I. 2001. Learning with mixtures of trees. *The Journal of Machine Learning Research*, **1**, 1–48.

Muthén, B. 2008. Latent variable hybrids: Overview of old and new models. *Advances in latent variable mixture models*, **1**, 1–24.

Qu, Y., Tan, M., & Kutner, M.H. 1996. Random Effects Models in Latent Class Analysis for Evaluating Accuracy of Diagnostic Tests. *Biometrics*, **52**(3), pp. 797–810.

Reboussin, B.A., Song, E.Y., Shrestha, A., Lohman, K.K., & Wolfson, M. 2006. A latent class analysis of underage problem drinking: Evidence from a community sample of 16–20 year olds. *Drug and alcohol dependence*, **83**(3), 199–209.

Reboussin, B.A., Ip, E.H., & Wolfson, M. 2008. Locally dependent latent class models with covariates: an application to under-age drinking in the USA. *Journal of the Royal Statistical Society: Series A (Statistics in Society)*, **171**(4), 877–897.

Richardson, S., & Green, P.J. 1997. On Bayesian analysis of mixtures with an unknown number of components (with discussion). *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **59**(4), 731–792.

Robert, C.P. 2005. *Le choix bayesien: principes et pratique*. Springer France Editions.

Robert, C.P., & Casella, G. 2004. *Monte Carlo statistical methods*. Springer Verlag.

Schwarz, G. 1978. Estimating the dimension of a model. *Annals of Statistics*, **6**, 461–464.

Strauss, S.M., Rindskopf, D.M., Astone-Twerell, J.M., Des Jarlais, D.C., & Hagan, H. 2006. Using latent class analysis to identify patterns of hepatitis C service provision in drug-free treatment programs in the US. *Drug and alcohol dependence*, **83**(1), 15–24.

Van Hattum, P., & Hoijtink, H. 2009. Market Segmentation Using Brand Strategy Research: Bayesian Inference with Respect to Mixtures of Log-Linear Models. *Journal of Classification*, **26**(3), 297–328.

Vermunt, J.K. 2003. Multilevel latent class models. *Sociological methodology*, **33**(1), 213–239.

Vermunt, J.K. 2007. Multilevel mixture item response theory models: an application in education testing. *Proceedings of the 56th session of the International Statistical Institute. Lisbon, Portugal*, 22–28.

A Dentistry clustering with the R package `Clustericat`

The R package `Clustericat` is available on Rforge website at the following url: *https://r-forge.r-project.org/R/?group_id=1803*. This section presents the code used to cluster the dentistry data set.

```
# Loading of the data set
> data("dentist")

# to define the parameters of the algorithm performing the estimation
# here 25 MCMC are performed with a stopping criterion equals to
# 200 successive iterations having not found a better model
> st <- strategycat(dentist, nb_init=25, stop_criterion=200)

# estimation of the model for a class number equal to 2.
# for the data set with five binary variables (modal)
> res <- clustercat(dentist, 2, modal=rep(2,5), st)
```

presentation of the best model

> `summary(res)`

presentation of the parameters of the conditional dependencies for the best model

> `summary_dependencies(res)`

a plot summarizing the best model like Figure 6

> `plot(res)`