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Abstract

Standard discriminant analysis supposes that both the training sample and the test sample are issued from the same population. When these samples arise from populations differing from their descriptive parameters, a generalization of discriminant analysis consists in adapting the classification rule related to the training population to another rule related to the test population, by estimating a link between both populations. This paper extends an existing work available in a multinormal context to the case of binary data. To raise the major challenge which consists in defining a link between the two binary populations, it is supposed that binary data result from the discretization of latent Gaussian data. Estimation method and robustness study are presented, and two applications in a biological context illustrate this work.

keywords Biological application; Discriminant analysis; EM algorithm; Latent class model; Stochastic link.

1 Introduction

Let consider a first (training) sample of individuals described by explanatory variables, for which a partition in groups or classes is known. Let consider also a

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new sample of individuals (test sample), drawn from the same population than the training sample. Discriminant analysis consists in estimating an allocation rule from the training sample in order to class individuals of the test sample (see McLachlan [1992] for a survey).
Since works of Fisher [1936], who introduced a linear discriminant rule between two groups, numerous evolutions have been proposed. All of them concern the nature of the discriminant rule: Parametric quadratic rule (see for example Tomassone et al. [1988]), semi parametric rule (as logistic discrimination Anderson [1972]) or non parametric rule (Fix and Hodges [1951], Friedman and Stuetzle [1981], Hand [1982], Silverman [1986]).
An alternative evolution, introduced by Van Franeker and Ter Brack [1993] and developed further by Biernacki et al. [2002], considers the case in which the training sample does not arise necessary from the same population than the test sample. Biernacki *et al.* define several models of *generalized discriminant analysis* in a multinormal context, and experiment them in a biological situation, in which both populations consist of birds from the same species, but from different geographical origins. The difference between the training and the test populations was the geographical range in this application, but it could be also temporal considerations or other. However in many domains (insurance, medicine, biology, *etc*.) a large number of applications deals with binary data as well. Consequently the goal of this paper is to extend generalized discriminant analysis, established in a multinormal context, to the case of binary data.
The paper is organized as follows. The next section presents the data and the latent class model for both training and test populations. Section 3 makes the assumption that these binary data are discretized latent continuous variables in which the order information is lost. This hypothesis is the key to establish a general stochastic link between both populations, from which many meaningful parsimonious models are declined. Thereafter in Section 4, estimating the parameters of these models is performed by invoking the maximum likelihood method and the EM algorithm. Then, a robustness study is carried out in Section 5 involving both theoretical and experimental (simulated data) arguments. In Section 6, two applications in a biological context illustrate realistic situations where the proposed generalized discriminant analysis outperforms standard discriminant analysis and clustering. Finally, the last section concludes this paper by discussing possible extensions of the present work.

2 The data and the latent class model

Data consist in two samples: The first sample S, labelled and issued from the training population P, and the second sample $\tilde{S}$, unlabelled and issued from the

test population $\tilde{P}$. A fundamental assumption of the present work is that populations P and $\tilde{P}$ may be different.
The training sample S is composed by n pairs $(x_1, z_1), \ldots, (x_n, z_n)$, where x_i is the binary explanatory vector for the ith object with $x_i = (x_{i1}, \ldots, x_{id})^T \in \{0,1\}^d$ and where $z_i = (z_{i1}, \ldots, z_{iK})^T$ is the group membership with z_{ik} equal to 1 if the ith object belongs to the kth group and equal to 0 if not ($i = 1, \ldots, n$, $k = 1, \ldots, K$). The number of binary explanatory variables and the number of groups are respectively denoted by d and K. Each pair (x_i, z_i) is assumed to be an independent realization of the random vector (X_1, Z_1) with distribution:

$$X_{1j_{|Z_{1k}=1}} \sim \mathcal{B}(\alpha_{kj}) \quad \text{for all } j = 1, \ldots, d \quad \text{and} \quad Z_1 \sim \mathcal{M}(1, p_1, \ldots, p_K) \quad (1)$$

where $\mathcal{B}(\alpha_{kj})$ is the Bernoulli distribution of parameter α_{kj} ($0 < \alpha_{kj} < 1$), and $\mathcal{M}(1, p_1, \ldots, p_K)$ defined the one order multinomial distribution of parameters $p_1, \ldots, p_K$ ($0 < p_k < 1$, $\sum_{k=1}^{K} p_k = 1$). Moreover, using the latent class model assumption that explanatory variables are conditionally independent (Celeux and Govaert [1991], Everitt [1984]), the probability function of X_1 conditionally to the group membership is:

$$f_k(x_{11}, \ldots, x_{1d}) = \prod_{j=1}^{d} {\alpha_{kj}}^{x_{1j}} (1 - \alpha_{kj})^{1 - x_{1j}}. \quad (2)$$

Similarly, the test sample $\tilde{S}$ is composed by $\tilde{n}$ pairs $(\tilde{x}_1, \tilde{z}_1), \ldots, (\tilde{x}_{\tilde{n}}, \tilde{z}_{\tilde{n}})$, where the d variables are the same as in the training sample, but where the $\tilde{z}_i$ are unknown. These pairs are assumed to be independent realizations of $(\tilde{X}_1, \tilde{Z}_1)$ with distribution:

$$\tilde{X}_{1j_{|\tilde{Z}_{1k}=1}} \sim \mathcal{B}(\tilde{\alpha}_{kj}) \quad \text{for all } j = 1, \ldots, d \quad \text{and} \quad \tilde{Z}_1 \sim \mathcal{M}(1, \tilde{p}_1, \ldots, \tilde{p}_K). \quad (3)$$

The explanatory variables $\tilde{X}_{1j}$, for $j = 1, \ldots, d$, are also assumed to be conditionally independent. Basically, the distribution of $(\tilde{X}_1, \tilde{Z}_1)$ differs from this one of (X_1, Z_1) only by the values of the parameters α_{kj} and p_k.
Our goal is to estimate the unknown labels $\tilde{z}_1, \ldots, \tilde{z}_{\tilde{n}}$ by using information from both training and test samples. The challenge is then to find a link between the populations P and $\tilde{P}$.

Remark The use of the terminology "test" for the sample $\tilde{S}$ (and the population $\tilde{P}$) is abusive because this sample is used to determine the discrimination rule. Nevertheless, this terminology is adopted in order to facilitate the link with the usual discrimination methods.

3 Relationship between test and training populations

3.1 Formalizing the link between populations

In a multinormal context, a linear stochastic relationship between P and $\tilde{P}$ is not only justified (with very few assumptions that we will recall further) but also intuitive (Biernacki et al. [2002]). In the binary context, since such an intuitive relationship seems more difficult to exhibit spontaneously, an additional assumption is stated: The binary variables are supposed resulting from the discretization of latent Gaussian variables. For example, if a binary variable is a purchase of a product by a customer, it is assumed that the customer gives a score to the product, and buys it only if this score is greater than a given threshold. This assumption is not new in statistics: See for example Thurstone [1927], who used this idea in his comparative judgment model to choose between two stimuli, or also Everitt [1988], who proposed a classification algorithm for binary, categorical and continuous data.

Thus, the explanatory variables $X_{1j_{|Z_{1k}=1}}$ of Bernoulli distribution $\mathcal{B}(\alpha_{kj})$ are assumed to arise from the discretization of latent continuous variables $Y_{1j_{|Z_{1k}=1}}$ in the following manner:

$$X_{1j_{|Z_{1k}=1}} = \begin{cases} 0 & \text{if } \lambda_j Y_{1j_{|Z_{1k}=1}} < \lambda_j s_j \\ 1 & \text{if } \lambda_j Y_{1j_{|Z_{1k}=1}} \geq \lambda_j s_j \end{cases} \qquad \text{for } j = 1, \ldots, d, \tag{4}$$

where $s_j \in \mathbb{R}$ is the discretization threshold, and $\lambda_j \in \{-1, 1\}$ is introduced to avoid choosing to which value of X_{1j}, 0 or 1, corresponds a positive value of Y_{1j}, and then to avoid binary variables to inherit from the natural order induced by continuous variables.

Moreover, the joint distribution of $Y_{1_{|Z_{1k}=1}} = (Y_{11_{|Z_{1k}=1}}, \ldots, Y_{1d_{|Z_{1k}=1}})^T$ is assumed to be multivariate normal with marginal distributions $\mathcal{N}(\mu_{kj}, \sigma_{kj}^2)$ and such that the obtained discretized variables $X_{1j_{|Z_{1k}=1}}$ ($j = 1, \ldots, d$) are independent in order to retrieve the conditional independence assumption on the binary variables. It should be noted that the conditional independence of the latent Gaussian variables $Y_{1j_{|Z_{1k}=1}}$ ($j = 1, \ldots, d$) is a particular situation which conduces to the conditional independence of the binary variables, but it is probably not the only one situation.

From (1) and (4) the following relationship between α_{kj}, λ_j, μ_{kj} and σ_{kj} can be derived:

$$\alpha_{kj} = p(X_{1j_{|Z_{1k}=1}} = 1) = 1 - \Phi\big(\lambda_j \frac{s_j - \mu_{kj}}{\sigma_{kj}}\big) \tag{5}$$

where Φ is the $\mathcal{N}(0, 1)$ cumulative density function.

As for the variable X_{1j}, the binary variable $\tilde{X}_{1j}$ is also assumed to arise from the

discretization of a latent Gaussian variable $\tilde{Y}_{1j}$ with distribution $\mathcal{N}(\tilde{\mu}_{kj}, \tilde{\sigma}^2_{kj})$. The equations are the same than (4) and (5), by changing α_{kj} into $\tilde{\alpha}_{kj}$, μ_{kj} into $\tilde{\mu}_{kj}$ and σ_{kj} into $\tilde{\sigma}_{kj}$. The thresholds $\tilde{s}_j$ are naturally supposed to be equal to s_j ($\tilde{s}_j = s_j$) since, with the previous example, it is equivalent to assume that customers of both populations buy the product if the score is greater than the same threshold. In the same spirit $\tilde{\lambda}_j$ is supposed to be equal to λ_j, so the rule of purchase – lower or higher than the threshold – is the same for both populations.
In a Gaussian context, Biernacki et al. [2002] showed that the only possible stochastic relationship between the latent continuous variable $Y_{1_{|Z_{1k}=1}}$ of P and $\tilde{Y}_{1_{|\tilde{Z}_{1k}=1}}$ of $\tilde{P}$ is linear when the two following plausible hypotheses are assumed: (i) The transformation between P and $\tilde{P}$ is $\mathcal{C}^1$ and (ii) the jth component $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ of $\tilde{Y}_{1_{|\tilde{Z}_{1k}=1}}$ only depends on the jth component $Y_{1j_{|Z_{1k}=1}}$ of $Y_{1_{|Z_{1k}=1}}$. More precisely, this relationship is expressed by

$$\tilde{Y}_{1_{|\tilde{Z}_{1k}=1}} \sim A_k Y_{1_{|Z_{1k}=1}} + b_k, \tag{6}$$

where A_k is a diagonal matrix of $\mathbb{R}^{d\times d}$ containing the elements a_{kj} and b_k is a vector of $\mathbb{R}^d$ containing the elements b_{kj} ($1 \leq k \leq K$, $1 \leq j \leq d$).
By using (6) the following relationship between the parameters $\tilde{\alpha}_{kj}$ and α_{kj} can be obtained (see details in Appendix A):

$$\tilde{\alpha}_{kj} = \Phi\Big(\delta_{kj}\ \Phi^{-1}(\alpha_{kj}) + \lambda_j \gamma_{kj}\Big), \tag{7}$$

where $\delta_{kj} \in \mathbb{R}^+ \setminus \{0\}$, $\lambda_j \in \{-1, 1\}$ and $\gamma_{kj} \in \mathbb{R}$. Let notice that this relationship corresponds to a linear link between the *probit* functions of both α_{kj} and $\tilde{\alpha}_{kj}$. Conditionally to the fact that α_{kj} are known (they will be estimated in practice), estimation of the Kd continuous parameters $\tilde{\alpha}_{kj}$ is thus obtained from the estimated parameters of the link between P and $\tilde{P}$ (plug-in method): δ_{kj}, γ_{kj} and λ_j. Note that the choice of the discretization thresholds s_j does not have any importance. It implies that the number of free continuous parameters is $2Kd$ and it means that the model is overparameterized. It could be expected since the underlying Gaussian model is by far more complex (in number of parameters) than the Bernoulli model. Consequently there is a need to reduce the number of free continuous parameters in (7). Thus some sub-models are defined by imposing constraints on the transformation between both populations P and $\tilde{P}$.

3.2 Models of constraints on the stochastic link

The parameters δ_{kj} ($1 \leq k \leq K$ and $1 \leq j \leq d$) will be successively constrained to be equal to 1 (denoted by 1), to be class- and dimension-independent (δ), to be

only class-dependent (δ_k) or only dimension-dependent (δ_j). In the same way, γ_{kj} can be constrained with easy understood notations to be equal to 0, γ, γ_k or γ_j. Then, 16 models are defined; They are summarized in (Table 1) where an *ad-hoc* notation is also given. For instance, the notation $[1\,0]$ means that $\delta_{kj} = 1$ and $\gamma_{kj} = 0$, and corresponds to the usual discriminant analysis model.

For these 16 models, an additional assumption on the group proportions is taken into account: They are conserved or not from P to $\tilde{P}$. In the following, $[p_k\,1\,0]$ denotes the model $[1\,0]$ with equal proportions whereas $[\tilde{p}_k\,1\,0]$ denotes this model with free proportions. The number of constrained models is thus growing to 32. (Table 2) gives the number of (continuous) parameters to be estimated for these models. If the mixing proportions are different between P and $\tilde{P}$, $K-1$ must be added to these numbers.

Finally, to automatically choose among the 32 generalized discriminant models, the BIC criterion (*Bayesian Information Criterion*, Schwarz [1978]) can be employed. It is defined by:

$$\text{BIC} = -2l(\hat{\theta}) + \nu \log(\tilde{n}),$$

where $\theta = (\tilde{p}_k, \delta_{kj}, \lambda_j, \gamma_{kj})$ for $1 \leq k \leq K$ and $1 \leq j \leq d$, $l(\hat{\theta})$ is the maximum log-likelihood corresponding to the estimation $\hat{\theta}$ of θ, and ν is the number of free continuous parameters associated to the given model. The model leading to the smallest BIC value is then retained.
Before estimating the parameter θ by the maximum likelihood method, there is a need to discuss identifiability of each parametrization.

3.3 Model identifiability

Some of the constrained models previously defined can be non-identifiable, and the aim of this section is to clarify these problems. The model identifiability arises at two levels: Identifiability of the model parameters when α_{kj} is transformed into $\tilde{\alpha}_{kj}$, and identifiability of the transformation which ensures that α_{kj} can be only transformed into $\tilde{\alpha}_{kj}$ and not into $\tilde{\alpha}_{k'j}$ (with $k' \neq k$). We call respectively them *intra-group* and *inter-group* identifiability.

3.3.1 Intra-group identifiability

Firstly, the identifiability of the couple (λ_j, γ_{kj}) in different constrained model situations is reaching as follows:

- models involving $\gamma_{kj} = 0$ or $\gamma_{kj} = \gamma_j$: By setting for instance $\lambda_j = +1$ ($j = 1, \ldots, d$),

- models involving $\gamma_{kj} = \gamma$ or $\gamma_{kj} = \gamma_k$: By setting for instance $\lambda_1 = +1$.

By this way, the product $\lambda_j \gamma_{kj}$ is allways identifiable and obviously all these constraints on λ_j have no impact on the estimation of the product $\lambda_j \gamma_{kj}$, as the reader can easily convince himself.
Secondly, the identifiability of the couple of parameters $(\delta_{kj}, \gamma_{kj})$ conditionally to λ_j is discussed. Equation (7) leads to

$$\Phi^{-1}(\tilde{\alpha}_{kj}) = \delta_{kj}\ \Phi^{-1}(\alpha_{kj}) + \lambda_j \gamma_{kj} \tag{8}$$

which can be expressed as the following linear system

$$\tilde{\Phi} = \Phi_\lambda \times u_{\delta,\gamma}$$

where $\tilde{\Phi} = (\Phi^{-1}(\tilde{\alpha}_{11}), \ldots, \Phi^{-1}(\tilde{\alpha}_{kj}), \ldots, \Phi^{-1}(\tilde{\alpha}_{Kd}))^T \in \mathbb{R}^{Kd}$ and Φ_λ and $u_{\delta,\gamma}$ are respectively a matrix and a vector, with dimension depending on the model at hand, representing the values of $\Phi^{-1}(\alpha_{kj})$ and λ_j for Φ_λ, and the values of δ_{kj} and γ_{kj} for $u_{\delta,\gamma}$.
Identifiability is obtained if and only if the matrix Φ_λ is of full rank. It is easily noticed (see the example below) that Φ_λ is not of full rank only for very particular values of α_{kj} (typically $\alpha_{kj} = \frac{1}{2}$ for some k, j for instance). Moreover these theoretical non-identifiable situations lead seldom to practical non-identifiable situations since an estimator $\hat{\alpha}_{kj}$ is used instead of the unknown true value α_{kj}. To be definitively convinced of this fact, the reader can have an early look at the robustness study (Section 5) where simulations involve a theoretically non-identifiable model (all $\alpha_{1j} = \frac{1}{2}$) but where practical identifiability is observed.

Example with model $[p_k\, \delta_k\, \gamma_k]$ for intra-group identifiability In this situation, $\Phi_\lambda = [MN]$ is a $(Kd \times 2K)$-matrix formed by two matrix blocks $M = (M_{lk})_{\substack{1 \le k \le K \\ 1 \le l \le Kd}}$ and $N = (N_{lk})_{\substack{1 \le k \le K \\ 1 \le l \le Kd}}$ defined by

$$\begin{cases} M_{lk} = \Phi^{-1}(\alpha_{k\, l-(k-1)d}) \mathbb{1}_{\{1+(k-1)d \le l \le kd\}} \\ N_{lk} = \lambda_{k\, l-(k-1)d} \mathbb{1}_{\{1+(k-1)d \le l \le kd\}} \end{cases}$$

and $u_{\lambda,\gamma} = (\delta_1, \ldots, \delta_K, \gamma_1, \ldots, \gamma_K)^T$ is a $(2K)$-vector. See Appendix B for a developed version of Φ_λ.
Φ_λ is not of full rank ($\min(Kd, 2K)$) if and only if

- Possibility 1: there exists $k \in \{1, \ldots, K\}$ such that $\alpha_{kj} = \frac{1}{2}$ for all $j \in \{1, \ldots, d\}$,
- Possibility 2: there exists $k_1, \ldots, k_\tau \in \{1, \ldots, K\}$, $k_1, \ldots, k_\tau$ being all different, with $\tau > 0$ satisfying $d(K - \tau) < 2K$, such that for all $j, j' \in \{1, \ldots, d\}$, for all $k \in \{k_1, \ldots, k_\tau\}$, $\lambda_j \Phi^{-1}(\alpha_{kj}) = \lambda_{j'} \Phi^{-1}(\alpha_{kj'})$.

3.3.2 Inter-group identifiability

This non-identifiability problem means that one group of the population P can be transformed into more than one group of the population $\tilde{P}$. It cannot happen if the group proportions p_k in P are all different (it is likely in practice) and if simultaneously all the constrained models are with fixed proportions between populations (models $[p_k\,.\,]$). But if these proportions conditions are not verified, the non-identifiability problem is the following: For fixed k_1 and k_2 ($k_1, k_2 \in \{1, ..., K\}$, $k_1 \neq k_2$) and for fixed j ($j \in \{1, \ldots, d\}$) there exists two sets of parameters $(\delta_{k_1 j}, \lambda_j, \gamma_{k_1 j}) \neq (\delta'_{k_1 j}, \lambda'_j, \gamma'_{k_1 j})$ which transform respectively $\alpha_{k_1 j}$ into $\tilde{\alpha}_{k_1 j}$ and $\tilde{\alpha}_{k_2 j}$. In fact, if the group k_1 of P is transformed into the group k_2 of $\tilde{P}$ (instead of the group k_1 of $\tilde{P}$) then necessarily the group k_2 of P is not transformed into the group k_2 of $\tilde{P}$, but into a group $k_3 \neq k_2$ of $\tilde{P}$; The simplest solution is $k_3 = k_1$ but it is not certain if $K > 2$.
Thus, the identifiability problem can be rewritten equivalently: There exists $k_2 \neq k_1$ and $k_3 \neq k_2$ such that, for any j and $(\delta_{k_1 j}, \lambda_j, \gamma_{k_1 j})$, $(\delta_{k_2 j}, \lambda_j, \gamma_{k_2 j})$ such that

$$\Phi^{-1}(\tilde{\alpha}_{k_1 j}) = \delta_{k_1 j}\ \Phi^{-1}(\alpha_{k_1 j}) + \lambda_j \gamma_{k_1 j} \tag{9}$$
$$\Phi^{-1}(\tilde{\alpha}_{k_2 j}) = \delta_{k_2 j}\ \Phi^{-1}(\alpha_{k_2 j}) + \lambda_j \gamma_{k_2 j}, \tag{10}$$

there exists $(\delta'_{k_1 j}, \lambda'_j, \gamma'_{k_1 j}) \neq (\delta_{k_1 j}, \lambda_j, \gamma_{k_1 j})$ and $(\delta'_{k_2 j}, \lambda'_j, \gamma'_{k_2 j}) \neq (\delta_{k_2 j}, \lambda_j, \gamma_{k_2 j})$ such that

$$\Phi^{-1}(\tilde{\alpha}_{k_2 j}) = \delta'_{k_1 j}\ \Phi^{-1}(\alpha_{k_1 j}) + \lambda'_j \gamma'_{k_1 j} \tag{11}$$
$$\Phi^{-1}(\tilde{\alpha}_{k_3 j}) = \delta'_{k_2 j}\ \Phi^{-1}(\alpha_{k_2 j}) + \lambda'_j \gamma'_{k_2 j}. \tag{12}$$

It follows from (9) and (11) that

$$\Phi^{-1}(\tilde{\alpha}_{k_2 j}) = \frac{\delta'_{k_1 j}}{\delta_{k_1 j}} \Phi^{-1}(\tilde{\alpha}_{k_1 j}) - \lambda_j \frac{\gamma_{k_1 j}}{\delta_{k_1 j}} \delta'_{k_1 j} + \lambda'_j \gamma'_{k_1 j} \tag{13}$$

and similarly from (10) and (12)

$$\Phi^{-1}(\tilde{\alpha}_{k_3 j}) = \frac{\delta'_{k_2 j}}{\delta_{k_2 j}} \Phi^{-1}(\tilde{\alpha}_{k_2 j}) - \lambda_j \frac{\gamma_{k_2 j}}{\delta_{k_2 j}} \delta'_{k_2 j} + \lambda'_j \gamma'_{k_2 j}. \tag{14}$$

Equations (13) and (14) lead to the following linear system

$$\tilde{\Phi}^{(k_2, k_3)} = \Phi^{(k_1, k_2)}_{\delta, \gamma, \lambda, \lambda'} \times u^{(k_1, k_2)}_{\delta', \gamma'} \tag{15}$$

where $\tilde{\Phi}^{(k_2, k_3)} = (\Phi^{-1}(\tilde{\alpha}_{k_2 1}), \ldots, \Phi^{-1}(\tilde{\alpha}_{k_2 d}), \Phi^{-1}(\tilde{\alpha}_{k_3 1}), \ldots, \Phi^{-1}(\tilde{\alpha}_{k_3 d}))' \in \mathbb{R}^{2d}$ and $\Phi^{(k_1, k_2)}_{\delta, \gamma, \lambda, \lambda'}$ and $u^{(k_1, k_2)}_{\delta', \gamma'}$ are respectively a matrix and a vector, with dimension depending on the model at hand, representing values of $\Phi^{-1}(\tilde{\alpha}_{k_1 j})$, $\Phi^{-1}(\tilde{\alpha}_{k_2 j})$,

$\delta_{k_1 j}$, $\delta_{k_2 j}$, $\gamma_{k_1 j}$, $\gamma_{k_2 j}$, λ_j, λ'_j for $\Phi^{(k_1,k_2)}_{\delta,\gamma,\lambda,\lambda'}$ and values of $\delta'_{k_1 j}$, $\delta'_{k_2 j}$, $\gamma'_{k_1 j}$, $\gamma'_{k_2 j}$ for $u^{(k_1,k_2)}_{\delta',\gamma'}$.
Conditionally to the values of λ'_j, the problem is identifiable if no solution exists to System (15) or, in other words, if the number of linearly independent lines of $\Phi^{(k_1,k_2)}_{\delta,\gamma,\lambda,\lambda'}$ is no less than the number of free parameters in $u^{(k_1,k_2)}_{\delta',\gamma'}$. The number of lines of $\Phi^{(k_1,k_2)}_{\delta,\gamma,\lambda,\lambda'}$ is equal to $2d$ and in most cases of interest these lines are independent for any values λ'_j. See for instance the following example with the model $[\tilde{p}_k\, \delta_k\, \gamma_k]$ for a discussion on this subject. The number of free parameters of $u^{(k_1,k_2)}_{\delta',\gamma'}$ corresponds to the values in (Table 2) by artificially fixing $K = 2$ in this table. Except for model $[\tilde{p}_k\, \delta_j\, \gamma_j]$ the maximum number of free parameters is equal to $\max(4, d+2)$. Thus, a sufficient condition of inter-group identifiability is that $2d > \max(4, d+2)$. Since $d > 2$ usually for binary data, all models are identifiable except the model $[\tilde{p}_k\, \delta_j\, \gamma_j]$ since the number of free parameters is $2d$. Although this model is non-identifiable, it can nevertheless be used by bearing in mind that a label switching may occur from P to $\tilde{P}$.

Remark Only a single switch between 2 classes ((k_1, k_2) of P becomes (k_2, k_1) of $\tilde{P}$) may occur with the model $[\tilde{p}_k\, \delta_j\, \gamma_j]$. Indeed in case of a switch between more than 2 classes, for instances (k_1, k_2, k_3) of P become (k_2, k_3, k_1) of $\tilde{P}$ or (k_1, k_2, k_3, k_4) of P becomes (k_2, k_1, k_4, k_3) of $\tilde{P}$, the number of equations reaches at least $3d$ for $2d$ free parameters: The model $[\tilde{p}_k\, \delta_j\, \gamma_j]$ is then identifiable.

Example with model $[\tilde{p}_k\, \delta_k\, \gamma_k]$ for inter-group identifiability. In this situation $\Phi^{(k_1,k_2)}_{\delta,\gamma,\lambda,\lambda'} = [MN]$ is a $(2d \times 4)$-matrix formed by two matrix blocks $M = (M_{ls})_{\substack{1\le s\le 2\\ 1\le l\le 2d}}$ and $N = (N_{ls})_{\substack{1\le s\le 2\\ 1\le l\le 2d}}$ defined by

$$\begin{cases} M_{ls} = \left(\frac{1}{\delta_{k_s l}}\Phi^{-1}(\tilde{\alpha}_{k_s l}) - \lambda_l \frac{\gamma_{k_s l}}{\delta_{k_s l}}\right) \mathbb{1}_{\{1+(s-1)d \le l \le sd\}} \\ N_{ls} = \lambda'_{l-(s-1)d} \mathbb{1}_{\{1+(s-1)d \le l \le sd\}} \end{cases}$$

and $u^{(k_1,k_2)}_{\delta',\gamma'} = (\delta'_{k_1}, \delta'_{k_2}, \gamma'_{k_1}, \gamma'_{k_2})$. Refer to Appendix B for a developed version of $\Phi^{(k_1,k_2)}_{\delta,\gamma,\lambda,\lambda'}$.
The reader can easily convince himself that the $2d$ lines are generally linearly independent in practice. For instance, the simulation involved in the robustness study (Section 5) consider this model and none identifiability problem is encountered (the classification error rates are always strictly lower than 50% and thus none label switching has been obtained).

4 Parameter estimation

In this section, only the situation where proportions are unknown is presented, the contrary case being immediate.

4.1 The three estimation steps

Generalized discriminant analysis needs three estimation steps. The first step consists in estimating parameters p_k and α_{kj} ($1 \leq k \leq K$ and $1 \leq j \leq d$) of population P from the training sample S. Since S is a labelled sample, the maximum likelihood estimate is simply given by (Everitt [1984], Celeux and Govaert [1991]):

$$\hat{p}_k = \frac{1}{n}\sum_{i=1}^{n} z_{ik} \qquad \text{and} \qquad \hat{\alpha}_{kj} = \frac{1}{n}\sum_{i=1}^{n} x_{ij} z_{ik}.$$

The second step consists in estimating parameters $\tilde{p}_k$ and $\tilde{\alpha}_{kj}$ ($1 \leq k \leq K$ and $1 \leq j \leq d$) of the Bernoulli mixture by using $\hat{p}_k$, $\hat{\alpha}_{kj}$ ($1 \leq k \leq K$ and $1 \leq j \leq d$) and $\hat{\theta}$. For estimating $\tilde{\alpha}_{kj}$, the parameters δ_{kj}, γ_{kj} and λ_j of the link between P and $\tilde{P}$ are to be estimated, and then an estimate of $\tilde{\alpha}_{kj}$ is deduced by Equation (7) by plug-in. This step is described below.
Finally, the third step consists in estimating the group membership of the individuals from the test sample $\tilde{S}$, by maximum *a posteriori*.

4.2 Estimation of the link parameters

For the second step above, maximum likelihood estimation can be efficiently based on the EM algorithm (Dempster et al. [1977]). The likelihood is given by:

$$L(\theta) = \prod_{i=1}^{\tilde{n}} \sum_{k=1}^{K} \tilde{p}_k \prod_{j=1}^{d} \tilde{\alpha}_{kj}^{\tilde{x}_{ij}} (1 - \tilde{\alpha}_{kj})^{1-\tilde{x}_{ij}}.$$

The completed log-likelihood is given by:

$$l_c(\theta; \tilde{\mathbf{z}}_1, \ldots, \tilde{\mathbf{z}}_{\tilde{n}}) = \sum_{i=1}^{\tilde{n}} \sum_{k=1}^{K} \tilde{z}_{ik} \log \left(\tilde{p}_k \prod_{j=1}^{d} \tilde{\alpha}_{kj}^{\tilde{x}_{ij}} (1 - \tilde{\alpha}_{kj})^{(1-\tilde{x}_{ij})} \right).$$

The E step From a current value $\theta^{(q)}$ of the parameter θ, the E step of the EM algorithm consists in computing the conditional expectation of the completed log-likelihood:

$$\begin{aligned}\mathcal{Q}(\theta;\theta^{(q)}) &= E_{\theta^{(q)}}[l_c(\theta;\tilde{\mathbf{Z}}_1,\ldots,\tilde{\mathbf{Z}}_{\tilde{n}})|\tilde{\mathbf{x}}_1,\ldots,\tilde{\mathbf{x}}_{\tilde{n}}] \\ &= \sum_{i=1}^{\tilde{n}}\sum_{k=1}^{K} t_{ik}^{(q)}\Big\{\log(\tilde{p}_k)+\sum_{j=1}^{d}\log\Big(\tilde{\alpha}_{kj}{}^{\tilde{x}_{ij}}(1-\tilde{\alpha}_{kj})^{1-\tilde{x}_{ij}}\Big)\Big\}\end{aligned}$$

where

$$t_{ik}^{(q)} = p(\tilde{Z}_{ik}=1|\tilde{\mathbf{x}}_1,\ldots,\tilde{\mathbf{x}}_{\tilde{n}};\theta^{(q)}) = \frac{\tilde{p}_k^{(q)}\prod_{j=1}^{d}(\tilde{\alpha}_{kj}^{(q)})^{\tilde{x}_{ij}}(1-\tilde{\alpha}_{kj}^{(q)})^{(1-\tilde{x}_{ij})}}{\sum_{\kappa=1}^{K}\tilde{p}_\kappa^{(q)}\prod_{j=1}^{d}(\tilde{\alpha}_{\kappa j}^{(q)})^{\tilde{x}_{ij}}(1-\tilde{\alpha}_{\kappa j}^{(q)})^{(1-\tilde{x}_{ij})}}$$

is the conditional probability that the individual i belongs to the group k.

The M step The M step of the EM algorithm consists in choosing the value $\theta^{(q+1)}$ which maximizes the conditional expectation $\mathcal{Q}$ computed at the E step:

$$\theta^{(q+1)} = \underset{\theta\in\Theta}{\operatorname{argmax}}\,\mathcal{Q}(\theta;\theta^{(q)}) \tag{16}$$

where Θ is a parameter space depending on the model at hand. The M step is described for each component of $\theta = \{\tilde{p}_k, \delta_{kj}, \lambda_j, \gamma_{kj}\}$.
For proportions, the maximum is:

$$\tilde{p}_k^{(q+1)} = \frac{1}{\tilde{n}}\sum_{i=1}^{\tilde{n}} t_{ik}^{(q)}.$$

The parameters δ_{kj} and γ_{kj} are never considered because the full generalized discriminant analysis model is overparameterized. Thus, only the constrained models are to be estimated. For this, it is proved in Appendix C that $\mathcal{Q}$ is a strictly concave function of δ_k, δ_j, δ, γ_k, γ_j and γ. Thus, the maximisation of $\mathcal{Q}(\theta;\theta^{(q)})$ is computed by an alternated iterative algorithm which consists in a succession, parameter component per parameter component, of simplex algorithms if the optimisation is unconstrained ($\gamma_k, \gamma_j \in \mathbb{R}$). If the optimisation is constrained ($\delta_k, \delta_j > 0$), the same algorithm is used but if the optimisation conduces to a negative result, the value 0 is retained (in this case the EM algorithm is used on its generalized form: GEM, Dempster et al. [1977]). The starting point of the alternated algorithm is

$\theta^{(q)}$, and this one of the EM algorithm $\theta^{(0)}$ is the point which correpond to $P = \tilde{P}$. For the discrete parameters λ_j, if the dimension d is not too high, the maximization is carried out by computing $\mathcal{Q}(\theta; \theta^{(q)})$ for all possible values of these discrete parameters. For high dimension, a relaxation method can be used, which consists to assume that λ_j is not a binary parameter in $\{-1, 1\}$ but a continuous one in $[-1, 1]$, named λ_j^* (see Wolsey [1998] for instance). Optimization is thus performed on this continuous parameter, with the previous alternated algorithm since $\mathcal{Q}$ is a strictly concave function of λ_j (Appendix C), and the solution $\lambda_j^{*(q+1)}$ is then discretized to obtain a binary solution $\lambda_j^{(q+1)}$ as follows: $\lambda_j^{(q+1)} = \text{sgn}(\lambda_j^{*(q+1)})$, where sgn denotes the sign function. This relaxation method is not used in the experiments of this paper but see Jacques [2005] for some examples of use.

5 Robustness study

Generalized discriminant analysis for binary data essentially relies on three kinds of assumptions:

1. Assumption on the binary data: Inside a population (P or $\tilde{P}$) the binary variables are conditionally independent;

2. Assumption on the link between binary and continuous variables inside a population (P or $\tilde{P}$): The binary variables arise from the discretization of a multivariate Gaussian distribution preserving the conditional independence for binary variables;

3. Assumption on the link between continuous variables of both populations P and $\tilde{P}$: They are exactly the assumption of generalized discriminant analysis for Gaussian data.

Only the second assumption is in the depth of this work, the two other ones arising from a context different from generalized discriminant analysis for binary data. In Assumption 2, continuous variables preserving conditional independence for binary variables (inside a population) seems weak since it is similar to this one of Assumption 1; The robustness against this hypothesis will be nevertheless illustrated by both the practical robustness study (Section 5.2) and also by the first biological application (Section 6.1). Finally, the main assumption of the present work is that binary variables arise from the discretization of Gaussian variables.
In this section, we first prove that the Gaussian hypothesis can be weakened into a new assumption and, then, some experiments illustrate and evaluate the robustness of the methodology when this weakened assumption is itself violated.

5.1 Theoretical robustness study for the Gaussian assumption

Under the hypothesis that the link between the latent variables of both populations P and $\tilde{P}$ is linear, the assumption of normality of the latent variables $Y_{1j_{|Z_{1k}=1}}$ and $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ is in fact not necessary, and sufficient conditions are the following:

$$\left\{ \begin{array}{l} F_{Y_{1j_{|Z_{1k}=1}}}(s_j) = \Phi(\frac{s_j-\mu_{kj}}{\sigma_{kj}}) \\ F_{Y_{1j_{|Z_{1k}=1}}}(\frac{s_j-b_{kj}}{a_{kj}}) = \Phi(\frac{s_j-a_{kj}\mu_{kj}-b_{kj}}{a_{kj}\sigma_{kj}}), \end{array} \right. \tag{17}$$

where $F_{Y_{1j_{|Z_{1k}=1}}}$ denotes the conditional cumulative density function of variable $Y_{1j_{|Z_{1k}=1}}$ and μ_{kj}, σ_{kj} its mean and its standard deviation respectively.
Effectively, by using these two relationships, it is possible to write:

$$\alpha_{kj} = p(X_{1j_{|Z_{1k}=1}} = 1) = \left\{ \begin{array}{ll} 1 - F_{Y_{1j_{|Z_{1k}=1}}}(s_j) & \text{if } \lambda_j = 1 \\ F_{Y_{1j_{|Z_{1k}=1}}}(s_j) & \text{if } \lambda_j = -1 \end{array} \right. = 1 - \Phi\big(\lambda_j \frac{s_j - \mu_{kj}}{\sigma_{kj}}\big)$$

and also

$$\begin{aligned} \tilde{\alpha}_{kj} &= p(\tilde{X}_{1j_{|Z_{1k}=1}} = 1) = \left\{ \begin{array}{ll} 1 - F_{\tilde{Y}_{1j_{|Z_{1k}=1}}}(s_j) & \text{if } \lambda_j = 1 \\ F_{\tilde{Y}_{1j_{|Z_{1k}=1}}}(s_j) & \text{if } \lambda_j = -1 \end{array} \right. \\ &= \left\{ \begin{array}{ll} 1 - F_{Y_{1j_{|Z_{1k}=1}}}(\frac{s_j-b_{kj}}{a_{kj}}) & \text{if } \lambda_j = 1 \\ F_{Y_{1j_{|Z_{1k}=1}}}(\frac{s_j-b_{kj}}{a_{kj}}) & \text{if } \lambda_j = -1 \end{array} \right. = 1 - \Phi\big(\lambda_j \frac{s_j - a_{kj}\mu_{kj} - b_{kj}}{a_{kj}\sigma_{kj}}\big). \end{aligned}$$

The values of α_{kj} and $\tilde{\alpha}_{kj}$ are the same than in the situation where $Y_{1j_{|Z_{1k}=1}}$ and $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ were Gaussian, and consequently Relationship (7) is still right.

5.2 Practical robustness study for both Gaussian and conditional independence assumptions

To illustrate the robustness against both Condition (17) and conditional independence for binary variables after discretization, let consider the following example: For all $1 \leq j \leq 5$, $X_{1j_{|Z_{1k}=1}}$ (respectively $\tilde{X}_{1j_{|\tilde{Z}_{1k}=1}}$) is the binary discretization (with the threshold $s_j = s$) of $Y_{1j_{|Z_{1k}=1}}$ (resp. $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$), where $Y_{1j_{|Z_{1k}=1}}$ (resp. $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$) is a mixture of two Gaussians $\pi\mathcal{N}(\mu_{k1}, {\sigma_{k1}}^2) + \underline{\pi}\mathcal{N}(\underline{\mu}_{k1}, {\underline{\sigma}_{k1}}^2)$ (resp. $\tilde{\pi}\mathcal{N}(\tilde{\mu}_{k1}, \tilde{\sigma}^2_{k1}) + \underline{\tilde{\pi}}\mathcal{N}(\underline{\tilde{\mu}}_{k1}, \underline{\tilde{\sigma}}^2_{k1})$) for all $1 \leq k \leq 2$ ($\pi + \underline{\pi} = 1$ and $\tilde{\pi} + \underline{\tilde{\pi}} = 1$).
The mixture density distribution of $Y_{1j_{|Z_{1k}=1}}$ and $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ (for fixed j and k), and the Gaussian corresponding density (with the same moments than $Y_{1j_{|Z_{1k}=1}}$ and $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$) are presented in (Figure 1).

Table 1: Generalized discriminant analysis models.

δ_{kj} \ γ_{kj}	0	γ	γ_k	γ_j
1	$[1\,0]$	$[1\,\gamma]$	$[1\,\gamma_k]$	$[1\,\gamma_j]$
δ	$[\delta\,0]$	$[\delta\,\gamma]$	$[\delta\,\gamma_k]$	$[\delta\,\gamma_j]$
δ_k	$[\delta_k\,0]$	$[\delta_k\,\gamma]$	$[\delta_k\,\gamma_k]$	$[\delta_k\,\gamma_j]$
δ_j	$[\delta_j\,0]$	$[\delta_j\,\gamma]$	$[\delta_j\,\gamma_k]$	$[\delta_j\,\gamma_j]$

Table 2: Number of continuous parameters (param.) to be estimated for the constrained models.

model	$[p_k\,1\,0]$	$[p_k\,1\,\gamma]$	$[p_k\,1\,\gamma_k]$	$[p_k\,1\,\gamma_j]$	$[p_k\,\delta\,0]$	$[p_k\,\delta\,\gamma]$	$[p_k\,\delta\,\gamma_k]$	$[p_k\,\delta\,\gamma_j]$
param.	0	1	K	d	1	2	$K+1$	$d+1$
model	$[p_k\,\delta_k\,0]$	$[p_k\,\delta_k\,\gamma]$	$[p_k\,\delta_k\,\gamma_k]$	$[p_k\,\delta_k\,\gamma_j]$	$[p_k\,\delta_j\,0]$	$[p_k\,\delta_j\,\gamma]$	$[p_k\,\delta_j\,\gamma_k]$	$[p_k\,\delta_j\,\gamma_j]$
param.	K	$K+1$	$2K$	$K+d$	d	$d+1$	$K+d$	$2d$

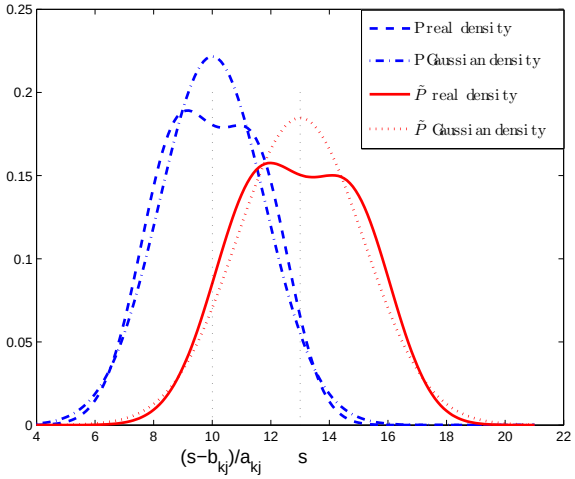


Figure 1: Density distribution of $Y_{1j_{|Z_{1k}=1}}$ and $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ for the robustness study.

The values of the discretization threshold, of the transformation parameters between P and $\tilde{P}$ (a_{kj} and b_{kj}) and of the first and of the second moments of $Y_{1j_{|Z_{1k}=1}}$ and $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ (μ_{kj}, ${\sigma_{kj}}^2$, $\tilde{\mu}_{kj}$ and $\tilde{\sigma}^2_{kj}$) are arbitrary chosen: $s = 13$; $a_{kj} = 1.2$ and $b_{kj} = 1$ for $1 \leq k \leq 2$ and $1 \leq j \leq 5$; $(\mu_{1j}, \mu_{2j}) = (10, 13)$ and $(\sigma_{1j}, \sigma_{2j}) = (1.8, 1.7)$ for $1 \leq j \leq 5$.
Now, let choose the parameters of the mixture density of $Y^j_{|Z^k=1}$ with respect to the following constraints, for $0 \leq \epsilon \leq 1$:

$$\begin{cases} F_{Y_{1j_{|Z_{1k}=1}}}(s_j) = \Phi(\frac{s_j-\mu_{kj}}{\sigma_{kj}}) + (1 - \Phi(\frac{s_j-\mu_{kj}}{\sigma_{kj}})) \times \epsilon \\ F_{Y_{1j_{|Z_{1k}=1}}}(\frac{s_j-b_{kj}}{a_{kj}}) = \Phi(\frac{s_j-a_{kj}\mu_{kj}-b_{kj}}{a_{kj}\sigma_{kj}}) + (1 - \Phi(\frac{s_j-a_{kj}\mu_{kj}-b_{kj}}{a_{kj}\sigma_{kj}})) \times \epsilon. \end{cases} \tag{18}$$

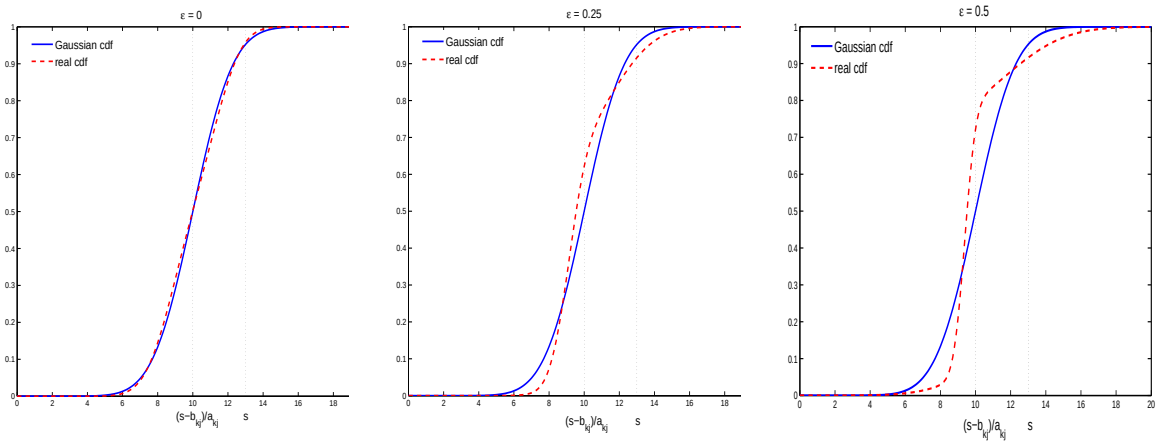
When $\epsilon = 0$, these constraints correspond to (17), and the greater is ϵ, the less (17) are respected. (Figure 2) illustrates the cumulative density function of the latent variables for different values of ϵ.

The sample size is set to 70, the experiments are repeated 20 times and the mean error rate is presented on (Figure 3) for different strategies: Generalized discriminant analysis (GDA) with model $[\tilde{p}_k\, \delta_k\, \gamma_k]$, standard discriminant analysis and clustering. Moreover, the optimal error rate is also given. GDA outperforms usual methods when ϵ is moderate ($\epsilon < 0.22$), and for higher ϵ, the assumed model of generalized discriminant analysis is too incorrect and then the clustering becomes better.

6 Comparison of methods on biological data

6.1 Discretized continuous data

The first motivations for which generalized discriminant analysis was developed are biological applications (Biernacki et al. [2002], Van Franeker and Ter Brack [1993]), in which the aim was to predict sex of birds from biometrical variables. Very powerful results have been obtained with multinormal assumptions.
The species of birds considered in the present application is Cory's Shearwater *Calanectris diomedea* (Thibault et al. [1997]). Two subspecies can be identified: *borealis* which lives in the Atlantic islands (the Azores, Canaries, etc.) and *diomedea* which lives in the Mediterranean islands (Balearics, Corsica, etc.).
A sample of *Borealis* ($n = 206$, 45% females) was measured using skins in several National Museums. Five morphological variables were measured: Culmen (bill length), tarsus, wings and tail lengths, and culmen depth. Similarly, a sample of *diomedea* ($n = 38$, 58% females) was measured using the same set of variables. In this example, two groups are present, males and females, and all the birds are of known sex (from dissection). (Figure 4) illustrates differences between the two subspecies *borealis* and *diomedea*, for two biometrical variables.



$\epsilon = 0$ $\epsilon = 0.25$ $\epsilon = 0.5$

Figure 2: Cumulative density function of the latent variables for different values of ϵ.

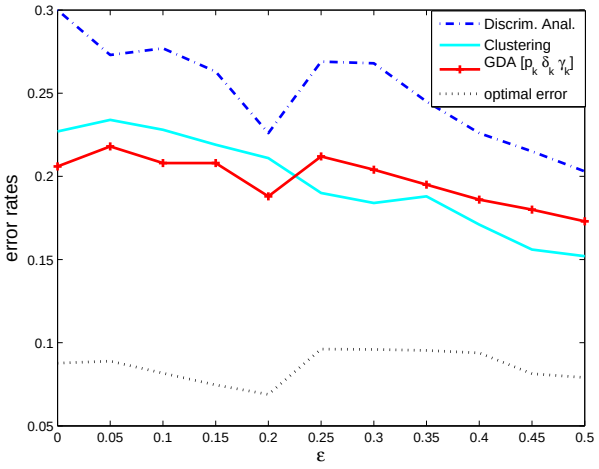


Figure 3: Classification error rate for usual discriminant analysis, generalized discriminant analysis (GDA) and clustering compared to the optimal error rate for different values of ϵ.

To provide an application of the present work, the continuous biometrical variables are discretized into binary data. As it can be shown on (Figure 4), discretization must be carried out carefully, and particularly for the choice of the discretization threshold. Effectively, if this threshold is fixed at the mean of the biometrical variables for one subspecies, all the values for the other subspecies will be on the same side of this discretization threshold. Consequently, the threshold is chosen such that there is a maximum of individuals in each side of the discretization threshold. (Table 3) presents values of retained discretization thresholds for the five biometrical variables and (Table 4) displays frequency of each couple (subspecies, sex) for two binarized biometrical variables.

The subspecies *borealis* is selected as the training population and the subspecies *diomedea* as the test population. The 32 generalized discriminant analysis models, standard discriminant analysis ($[p_k\, 1\, 0]$) and clustering are applied on these data. The classification error rate and the value of the BIC criterion are given in (Table 5).

If the results are compared according to the error rate, generalized discriminant analysis with the model $[p_k\, \delta_j\, \gamma_j]$ is the best method, with error 15.78%. This error is lower than that obtained by standard discriminant analysis (42.1%) and by clustering (23.68%). By using the BIC criterion, which leads to select the model $[\tilde{p}_k\, \delta\, \gamma]$, the error rate ($21.05\%$) is still the best with generalized discriminant analysis.

This application illustrates the interest of generalized discriminant analysis with respect to standard discriminant analysis or clustering. Effectively, by adapting the classification rule issued from the training population to the test population, generalized discrimination analysis gives lower classification error rates than by applying directly the rule issued from the training population (standard discriminant analysis), or by omitting the training population and applying directly clustering on the test population.

It is interesting to remark that the assumption which supposes that binary data are issued from the discretization of Gaussian variables (biometrical variables) is relatively realistic in this application. Nevertheless, there exists a strong correlation between the five biometrical variables, which violates the assumption that discretized variables are independent.

6.2 Real binary data

The second application considers sea birds from the species *puffins* (Bretagnolle(2006), personnal communication). Two groups of subspecies are considered: The first one is composed of subspecies living in Pacific Islands – *subalaris* (Galapagos Island), *polynesial*, *dichrous* (Enderbury and Palau Islands) and *gunax* – and the second one is composed of subspecies living in Atlantic Islands – *boydi* (Cap

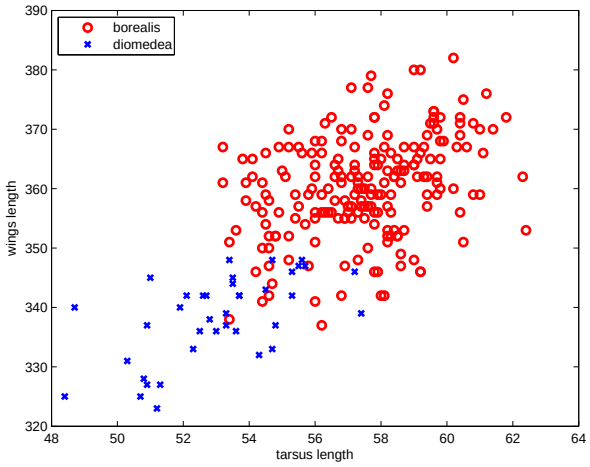


Figure 4: Wings and tarsus lengths for *diomedea* and *borealis*.

Table 3: Chosen discretization thresholds for the five biometrical variables for the two subspecies *diomedea* and *borealis*.

	culmen depth	culmen	tarsus	wing length	tail length
discret. threshold (mm)	14.35	51.50	54.45	342.50	28.40

Table 4: Binary wings and tarsus lengths for *diomedea* and *borealis*.

			wings			
			0		1	
			borealis	*diomedea*	*borealis*	*diomedea*
tarsus	0	male	108	6	2	3
		female	76	1	4	1
	1	male	3	3	0	4
		female	11	1	2	19

Verde Islands). The difference between populations is here the geographical range (Pacific *vs.* Atlantic Islands). A sample of Pacific birds ($n = 171$) was measured using skins in several National Museums. Four variables are mesured on these birds: Coller, stripe and piping (absence or presence for these three variables) and under-caudal (self couloured or not). Similarly, a sample of Atlantic birds ($n = 19$) was measured using the same set of variables. Like in the previous example, two groups are present (males and females) and all the birds are of known sex. Pacific birds are selected as the training population and Atlantic ones as the test population. According to the biologist Vincent Bretagnolle (CEBC-CNRS), the morphological variables which are used in this application are not very discriminative, and then one can not expect better than an error around $40 - 45\%$.
The 32 generalized discriminant analysis models – among which discriminant analysis ($[p_k\, 1\, 0]$) – are applied on these data, and the results are presented in (Table 6). Clustering is also applied, and the obtained error rate is 49.05%.

As in the previous study, generalized discriminant analysis is more efficient than standard discriminant analysis and clustering to classify birds according to their sex, and moreover the BIC criterion leads to choose the model with the smallest error rate. The relatively poor classification results (the minimal error rate is 43%) confirm the assumption of the biologist.

7 Conclusion

Generalized discriminant analysis extends standard discriminant analysis by allowing training and test samples to arise from different but stochastically linked populations. Our contribution consists to adapt precursor works in a multinormal context to the case of binary data.
Applications in a biological context illustrates this work. A classification of birds according to their sex is provided by using generalized discriminant analysis, and this classification is better than those obtained by discriminant analysis or by clustering.
Perspectives for this work are numerous. Firstly, the parameters of both populations P and $\tilde{P}$ are estimated successively: α_{kj} and p_k are estimated in a first step and after $\tilde{\alpha}_{kj}$ and $\tilde{p}_k$ are deduced from these estimation and from those of the link parameters. It should be very (computationally) usefull to consider a joint estimation of this four parameters.
Secondly, the link between the two populations was defined by using Gaussian cumulative density function. Although it seemed initially difficult to find this link, a simple link involving the probit function was obtained. It was not easy to imagine it, but it is meaningful afterwards. It would be interesting to try other types of cumulative density functions; Obviously theoretical reasons will have to be devel-

Table 5: Classification error rates (%) and value of the BIC criterion for test population *diomedea* with training population *borealis*.

model	$[p_k\, 1\, 0]$	$[p_k\, 1\, \gamma]$	$[p_k\, 1\, \gamma_k]$	$[p_k\, 1\, \gamma_j]$	$[p_k\, \delta\, 0]$	$[p_k\, \delta\, \gamma]$	$[p_k\, \delta\, \gamma_k]$	$[p_k\, \delta\, \gamma_j]$
error	42.1	23.68	15.78	18.42	57.89	23.68	15.78	18.42
BIC	648	216	218	225	263	214	218	214
model	$[p_k\, \delta_k\, 0]$	$[p_k\, \delta_k\, \gamma]$	$[p_k\, \delta_k\, \gamma_k]$	$[p_k\, \delta_k\, \gamma_j]$	$[p_k\, \delta_j\, 0]$	$[p_k\, \delta_j\, \gamma]$	$[p_k\, \delta_j\, \gamma_k]$	$[p_k\, \delta_j\, \gamma_j]$
error	57.89	15.78	18.42	18.42	57.89	18.42	18.42	**15.78**
BIC	270	1219	216	220	281	214	220	228
model	$[\tilde{p}_k\, 1\, 0]$	$[\tilde{p}_k\, 1\, \gamma]$	$[\tilde{p}_k\, 1\, \gamma_k]$	$[\tilde{p}_k\, 1\, \gamma_j]$	$[\tilde{p}_k\, \delta\, 0]$	$[\tilde{p}_k\, \delta\, \gamma]$	$[\tilde{p}_k\, \delta\, \gamma_k]$	$[\tilde{p}_k\, \delta\, \gamma_j]$
error	42.1	26.31	23.68	21.05	42.1	21.05	23.68	21.05
BIC	595	215	215	226	267	**213**	215	215
model	$[\tilde{p}_k\, \delta_k\, 0]$	$[\tilde{p}_k\, \delta_k\, \gamma]$	$[\tilde{p}_k\, \delta_k\, \gamma_k]$	$[\tilde{p}_k\, \delta_k\, \gamma_j]$	$[\tilde{p}_k\, \delta_j\, 0]$	$[\tilde{p}_k\, \delta_j\, \gamma]$	$[\tilde{p}_k\, \delta_j\, \gamma_k]$	$[\tilde{p}_k\, \delta_j\, \gamma_j]$
error	42.1	23.68	21.05	21.05	42.1	21.05	21.05	23.68
BIC	274	217	217	222	285	215	222	225

Table 6: Classification error rates (%) and value of the BIC criterion for test population of Atlantic birds with training on Pacific birds population.

model	$[p_k\, 1\, 0]$	$[p_k\, 1\, \gamma]$	$[p_k\, 1\, \gamma_k]$	$[p_k\, 1\, \gamma_j]$	$[p_k\, \delta\, 0]$	$[p_k\, \delta\, \gamma]$	$[p_k\, \delta\, \gamma_k]$	$[p_k\, \delta\, \gamma_j]$
error	50.94	**43.39**	45.28	43.39	50.94	43.39	45.28	45.28
BIC	212	**209**	216	224	212	209	216	224
model	$[p_k\, \delta_k\, 0]$	$[p_k\, \delta_k\, \gamma]$	$[p_k\, \delta_k\, \gamma_k]$	$[p_k\, \delta_k\, \gamma_j]$	$[p_k\, \delta_j\, 0]$	$[p_k\, \delta_j\, \gamma]$	$[p_k\, \delta_j\, \gamma_k]$	$[p_k\, \delta_j\, \gamma_j]$
error	45.28	45.28	52.83	45.28	45.28	52.83	50.94	50.94
BIC	210	210	215	226	225	224	227	239
model	$[\tilde{p}_k\, 1\, 0]$	$[\tilde{p}_k\, 1\, \gamma]$	$[\tilde{p}_k\, 1\, \gamma_k]$	$[\tilde{p}_k\, 1\, \gamma_j]$	$[\tilde{p}_k\, \delta\, 0]$	$[\tilde{p}_k\, \delta\, \gamma]$	$[\tilde{p}_k\, \delta\, \gamma_k]$	$[\tilde{p}_k\, \delta\, \gamma_j]$
error	45.28	50.94	50.94	45.28	45.28	50.94	50.94	45.28
BIC	213	213	220	228	213	213	220	228
model	$[\tilde{p}_k\, \delta_k\, 0]$	$[\tilde{p}_k\, \delta_k\, \gamma]$	$[\tilde{p}_k\, \delta_k\, \gamma_k]$	$[\tilde{p}_k\, \delta_k\, \gamma_j]$	$[\tilde{p}_k\, \delta_j\, 0]$	$[\tilde{p}_k\, \delta_j\, \gamma]$	$[\tilde{p}_k\, \delta_j\, \gamma_k]$	$[\tilde{p}_k\, \delta_j\, \gamma_j]$
error	45.28	45.28	47.16	45.28	45.28	52.83	45.28	52.83
BIC	214	213	213	229	228	227	224	243

oped and practical tests will have to be carried out.
Thirdly, with this contribution generalized discriminant analysis is now developed for continuous data and for binary data. To allow to analyse a large number of practical cases, it is important to study the case of categorical variables (*i.e.* much than two modalities), and thereafter the case of mixed variables (binary, categorical and continuous together). Everitt's works (Everitt [1988]), which defined a classification algorithm for mixed variables, can be helpful for this topics.
Finally, it would be also interesting to extend other classical discriminant method like non-parametric discrimination or semi-parametric discrimination. See Biernacki and Beninel [2005] for logistic regression.

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A Proof of the relation between test and training populations

From (6) it follows that $\tilde{Y}_{1j_{|\tilde{Z}_{1k}=1}}$ is Gaussian with mean $\tilde{\mu}_{kj} = a_{kj}\mu_{kj} + b_{kj}$ and with standard deviation $\tilde{\sigma}_{kj} = |a_{kj}|\sigma_{kj}$. However, this transformation is non-identifiable: There exists more than one couple (A_k, b_k) which satisfies Relationship (6). To solve this problem, we assume then than all the a_{kj} are non negative ($a_{kj} \geq 0$).
It is possible to derived from Equation (5):

$$\lambda_j \frac{s_j}{\sigma_{kj}} = -\Phi^{-1}(\alpha_{kj}) + \lambda_j \frac{\mu_{kj}}{\sigma_{kj}},$$

and then, using expressions of $\tilde{\mu}_{kj}$ and $\tilde{\sigma}_{kj}$ just given above:

$$\begin{aligned} \tilde{\alpha}_{kj} &= 1 - \Phi\left(\lambda_j \frac{s_j - \tilde{\mu}_{kj}}{\tilde{\sigma}_{kj}}\right) = 1 - \Phi\left(\frac{1}{a_{kj}} \frac{\lambda_j s_j}{\sigma_{kj}} - \lambda_j \frac{a_{kj}\mu_{kj} + b_{kj}}{a_{kj}\sigma_{kj}}\right) \quad (19) \\ &= \Phi\left(\frac{\Phi^{-1}(\alpha_{kj})}{a_{kj}} + \lambda_j \frac{a_{kj}\mu_{kj} + b_{kj} - \mu_{kj}}{a_{kj}\sigma_{kj}}\right). \quad (20) \end{aligned}$$

Alternatively, it is also possible to write from (5) again:

$$\lambda_j \frac{\mu_{kj}}{\sigma_{kj}} = \Phi^{-1}(\alpha_{kj}) + \lambda_j \frac{s_j}{\sigma_{kj}},$$

and thus, following the same process than in (19),

$$\begin{aligned} \tilde{\alpha}_{kj} &= 1 - \Phi\left(\lambda_j \frac{s_j - \tilde{\mu}_{kj}}{\tilde{\sigma}_{kj}}\right) = 1 - \Phi\left(-\lambda_j \frac{\mu_{kj}}{\sigma_{kj}} + \lambda_j \frac{s_j - b_{kj}}{a_{kj}\sigma_{kj}}\right) \quad (21) \\ &= \Phi\left(\Phi^{-1}(\alpha_{kj}) + \lambda_j \frac{a_{kj}s_j + b_{kj} - s_j}{a_{kj}\sigma_{kj}}\right). \quad (22) \end{aligned}$$

Of course, Equations (19) and (21) are equivalent but the first one will be retained since Parametrization (19) will be more convenient for proposing later numerous parsimonious models of constraints on the link. Consequently, the following relationship between α_{kj} and $\tilde{\alpha}_{kj}$ is obtained:

$$\tilde{\alpha}_{kj} = \Phi\Big(\delta_{kj}\ \Phi^{-1}(\alpha_{kj}) + \lambda_j \gamma_{kj}\Big),$$

where $\delta_{kj} \in \mathbb{R}^+ \setminus \{0\}$, $\lambda_j \in \{-1, 1\}$ and $\gamma_{kj} \in \mathbb{R}$.

B Developed version of the linear system matrices for intra-group and inter-group identifiability example

The linear system matrices Φ_λ are for the intra-group identifiability example:

$$\Phi_\lambda = \begin{pmatrix}
\Phi^{-1}(\alpha_{11}) & 0 & \dots & 0 & \lambda_1 & 0 & \dots & 0 \\
\vdots & & & & & \vdots & & \\
\Phi^{-1}(\alpha_{1d}) & 0 & \dots & 0 & \lambda_1 & 0 & \dots & 0 \\
0 & \dots 0 & \Phi^{-1}(\alpha_{k1}) & 0 \dots 0 & 0 & \dots 0 & \lambda_1 & 0 \dots 0 \\
\vdots & & & & & \vdots & & \\
0 & \dots 0 & \Phi^{-1}(\alpha_{kd}) & 0 \dots 0 & 0 & \dots 0 & \lambda_d & 0 \dots 0 \\
0 & \dots & 0 & \Phi^{-1}(\alpha_{K1}) & 0 & \dots & 0 & \lambda_1 \\
\vdots & & & & & \vdots & & \\
0 & \dots & 0 & \Phi^{-1}(\alpha_{Kd}) & 0 & \dots & 0 & \lambda_d
\end{pmatrix}$$

and for the inter-group identifiability example:

$$\Phi^{(k_1,k_2)}_{\delta,\gamma,\lambda,\lambda'} = \begin{pmatrix}
\frac{1}{\delta_{k_1 1}}\Phi^{-1}(\tilde{\alpha}_{k_1 1}) - \lambda_1\frac{\gamma_{k_1 1}}{\delta_{k_1 1}} & 0 & \lambda'_1 & 0 \\
\vdots & & & \\
\frac{1}{\delta_{k_1 d}}\Phi^{-1}(\tilde{\alpha}_{k_1 d}) - \lambda_d\frac{\gamma_{k_1 d}}{\delta_{k_1 d}} & 0 & \lambda'_d & 0 \\
0 & \frac{1}{\delta_{k_2 1}}\Phi^{-1}(\tilde{\alpha}_{k_2 1}) - \lambda_1\frac{\gamma_{k_2 1}}{\delta_{k_2 1}} & 0 & \lambda'_1 \\
\vdots & & & \\
0 & \frac{1}{\delta_{k_2 d}}\Phi^{-1}(\tilde{\alpha}_{k_2 d}) - \lambda_d\frac{\gamma_{k_2 d}}{\delta_{k_2 d}} & 0 & \lambda'_d
\end{pmatrix}$$

C Proof of the concavity of the function $\mathcal{Q}(\theta, \theta^{(q)})$

The aim of this appendix is to prove that $\mathcal{Q}(\theta, \theta^{(q)})$ is a strictly concave function of γ_k, γ_j and γ, and also of δ_k, δ_j, δ and λ_j. The fundamental key of the proof is to study first concavity of $\mathcal{Q}(\theta, \theta^{(q)})$ for γ_{kj}.
Let $\mathcal{Q}(\gamma_{kj})$ be the function $\mathcal{Q}(\theta, \theta^{(q)})$ with parameters $\tilde{p}_k, \delta_{kj}, \lambda_j$ and $\theta^{(q)}$ fixed, and let prove that $\mathcal{Q}(\gamma_{kj})$ is strictly concave:

$$\mathcal{Q}(\gamma_{kj}) = \sum_{i=1}^{\tilde{n}}\sum_{k=1}^{K} t_{ik}\Big\{\log(\tilde{p}_k) + \sum_{j=1}^{d}\tilde{x}_{ij}\log\Big(\Phi(\zeta_{kj})\Big) + \sum_{j=1}^{d}(1-\tilde{x}_{ij})\log\Big(1-\Phi(\zeta_{kj})\Big)\Big\}$$

with $\zeta_{kj} = \delta_{kj}\Phi^{-1}(\alpha_{kj}) + \lambda_j\gamma_{kj}$.
The derivative of the function $\mathcal{Q}(\gamma_{kj})$ is:

$$\frac{\partial \mathcal{Q}(\gamma_{kj})}{\partial \gamma_{kj}} = \sum_{i=1}^{\tilde{n}}\sum_{k=1}^{K} t_{ik} \sum_{j=1}^{d} \Big\{ \tilde{x}_{ij}\lambda_j \frac{\phi(\zeta_{kj})}{\Phi(\zeta_{kj})} + (1-\tilde{x}_{ij})\lambda_j \frac{-\phi(\zeta_{kj})}{1-\Phi(\zeta_{kj})} \Big\},$$

where ϕ is the probability density function of $\mathcal{N}(0,1)$.
Using that $\frac{\partial \phi(bx+a)}{\partial x} = -b(bx+a)\phi(bx+a)$ with $a, b \in \mathbb{R}$, the second derivative is:

$$\begin{aligned}\frac{\partial^2 \mathcal{Q}(\gamma_{kj})}{\partial \gamma_{kj}^2} = \sum_{i=1}^{\tilde{n}}\sum_{k=1}^{K} t_{ik} \sum_{j=1}^{d} \lambda_j \Big\{ \tilde{x}_{ij} \frac{-\lambda_j\zeta_{kj}\phi(\zeta_{kj})\Phi(\zeta_{kj}) - \lambda_j\phi(\zeta_{kj})^2}{[\Phi(\zeta_{kj})]^2} \\ + (1-\tilde{x}_{ij}) \frac{\lambda_j\zeta_{kj}\phi(\zeta_{kj})(1-\Phi(\zeta_{kj})) - \lambda_j\phi(\zeta_{kj})^2}{[1-\Phi(\zeta_{kj})]^2} \Big\},\end{aligned}$$

that can be rewritten:

$$\begin{aligned}\frac{\partial^2 \mathcal{Q}(\gamma_{kj})}{\partial \gamma_{kj}^2} = -\sum_{i=1}^{\tilde{n}}\sum_{k=1}^{K} t_{ik} \sum_{j=1}^{d} \lambda_j^2\phi(\zeta_{kj}) \Big\{ \frac{\tilde{x}_{ij}}{[\Phi(\zeta_{kj})]^2} \overbrace{(\zeta_{kj}\Phi(\zeta_{kj}) + \phi(\zeta_{kj}))}^{g_1(\zeta_{kj})} \\ + \frac{(1-\tilde{x}_{ij})}{[1-\Phi(\zeta_{kj})]^2} \overbrace{(\zeta_{kj}(\phi(\zeta_{kj})-1) + \phi(\zeta_{kj}))}^{g_2(\zeta_{kj})} \Big\}. \qquad (23)\end{aligned}$$

To prove that $\mathcal{Q}$ is strictly concave, it is sufficient to prove that both functions g_1 and g_2 are strictly positive:

- for all $x \in \mathbb{R}$: $g_1(x) = x\Phi(x) + \phi(x) > 0$, because $\lim_{x\to-\infty} g_1(x) = 0$ and g_1 is strictly increasing since $g_1'(x) = \Phi(x) + x\phi(x) - x\phi(x) = \Phi(x) > 0$,
- for all $x \in \mathbb{R}$: $g_2(x) = x\Phi(x) - x + \phi(x) > 0$, because $\lim_{x\to+\infty} g_2(x) = 0$ and g_2 is strictly decreasing since $g_2'(x) = \Phi(x) - 1 + x\phi(x) - x\phi(x) = \Phi(x) - 1 < 0$.

Thus $\frac{\partial^2 \mathcal{Q}(\gamma_{kj})}{\partial \gamma_{kj}^2} < 0$ and $\mathcal{Q}(\gamma_{kj})$ is strictly concave. □
If $\mathcal{Q}$ is no longer function of γ_{kj} but now of γ_k (respectively of γ_j, of γ) the expression of the second derivative is the same than (23) by removing the sum on j (resp. on k, on (k,j)), and thus $\mathcal{Q}$ is still strictly concave.
Let consider now the function $\mathcal{Q}(\delta_{kj})$ with the above convention ($\tilde{p}_k, \gamma_{kj}, \lambda_j$ and $\theta^{(q)}$ fixed). Same type of calculus leads to:

$$\frac{\partial^2 \mathcal{Q}(\delta_{kj})}{\partial \delta_{kj}^2} = -\sum_{i=1}^{\tilde{n}}\sum_{k=1}^{K} t_{ik} \sum_{j=1}^{d} \Big(\Phi^{-1}(\alpha_{kj})\Big)^2 \phi(\zeta_{kj}) \Big\{ \frac{\tilde{x}_{ij}}{[\Phi(\zeta_{kj})]^2} g_1(\zeta_{kj}) + \frac{(1-\tilde{x}_{ij})}{[1-\Phi(\zeta_{kj})]^2} g_2(\zeta_{kj}) \Big\},$$

and thus $\mathcal{Q}(\delta_{kj})$ is strictly concave. By using the above arguments, it arises immediately that $\mathcal{Q}(\delta_k)$, $\mathcal{Q}(\delta_j)$, $\mathcal{Q}(\delta)$ are also strictly concave. □
Let finally consider the function $\mathcal{Q}(\lambda_j)$. The second derivative is:

$$\frac{\partial^2 \mathcal{Q}(\lambda_j)}{\partial \lambda_j^2} = -\sum_{i=1}^{\tilde{n}} \sum_{k=1}^{K} t_{ik} \sum_{j=1}^{d} \gamma_{kj}^2 \phi(\zeta_{kj}) \Big\{ \frac{\tilde{x}_{ij}}{[\Phi(\zeta_{kj})]^2} g_1(\zeta_{kj}) + \frac{(1-\tilde{x}_{ij})}{[1-\Phi(\zeta_{kj})]^2} g_2(\zeta_{kj}) \Big\},$$

and $\mathcal{Q}(\lambda_j)$ is strictly concave. □