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A Comparison of Methods for Analysing Logistic Regression Models with both Clinical and Genomic Variables

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INTRODUCTION

- An active field in today medical research : prediction from high-dimensional genomic data
 - Number of samples relatively small compared to the number of covariates
 - Collinear measurements
- ⇒ Use of reduction dimension methods
 - Traditional approach : Principal Component Regression (PCR) [10]
 - Most useful : Partial Least Square (PLS) [6]
- Most of this studies included clinical data in addition to genomic data
 - However most of the proposed prediction methods used only genomic data
 - Recent studies consider situations combining both type of covariates improving predictions
 - Development of Clinico-genomic models
 - For survival prediction with Cox model's [3], for classification of patients [2]
- ⇒ Few of them used dimension reduction or applied dimension reduction only to the high-dimensional genomic variables
- Recently, prediction method have been proposed to combine both type of covariates [7]
 - Developed only in regression Gaussian context
 - * Method based on combination of PLS and ordinary least square (OLS) ⇒ LS-PLS
 - ⇒ More information from the experiment
 - ⇒ Lower variance in the parameter estimates
- Adaptation to logistic regression model
 - Not relevant to combine both type of variables without reduction dimension
 - An alternative → compress the information from genomic data into new few components before modelling
 - * Partial Least Squares (PLS) adapted to logistic regression [11, 9, 4, 1]

OBJECTIVES

- To adapt LS-PLS to combine clinical and genomic variables for logistic regression model
- To perform a comparison by simulation of the performance of these approaches

LS-PLS FOR LOGISTIC REGRESSION

Linear Logistic Discrimination

- Y : binary response variable $\{0, 1\}^n$
- D : matrix of clinical variables of size $n \times q$
- X : design matrix for expression levels of the p genes for the n microarray samples
 - * $X = (x_{ij}), 1 \leq i \leq n, 1 \leq j \leq p$
- General statistical model
 - * The conditional expectation of y_i given $D_{i\cdot}$, given by $\pi_i = P(y_i = 1 | D_{i\cdot} = d_i)$
 - * Related to linear predictor $\eta_i = [1; d_i] \gamma$
 - with $\gamma \in \mathbb{R}^{q+1}$ and the non-linear relation $\pi_i = h(\eta_i)$
 - where $h(\eta_i) = 1/(1 + \exp(-\eta_i))$
- Estimation of γ by maximum likelihood (ML) estimation method
- Use of Iteratively Reweighted Least Squares (IRLS) algorithm [5]

$$z^{(t)} = \tilde{D} \gamma^{(t)} + [W(\gamma^{(t)})^{(t)}]^{-1} (y - \pi^{(t)}), \quad (1)$$

$$\gamma^{(t+1)} \leftarrow \text{weighted regression by } W(\gamma^{(t)})^{(t)} \text{ of } z^{(t)} \text{ on } \tilde{D} \quad (2)$$

where $\tilde{D} = [1_n D]$, $1_n = (1, \dots, 1)^T$
 $W(\gamma^{(t)})$ the diagonal $n \times n$ matrix with entries $W_{i,i}(\gamma) = \pi_k(1 - \pi_k)$.

LS-PLS in Gaussian context [7]

- Iterative procedure
 1. Perform ordinary least squares regression of Y on (\tilde{D}) and estimate the regression coefficients β and calculate residuals.
 2. Perform PLS regression of the residuals on centred X and combine the design (\tilde{D})
 3. Perform OLS regression on the combined matrix design (\tilde{D}) and the score T to predict Y .
 4. Calculate the predicted \hat{y} based on (\tilde{D}) and calculate new residuals.
 5. Repeat steps 2 to 4 until convergence.
- ⇒ Method denoted LS-PLS(y, D, X, κ) where κ the PLS component number

Some extensions for logistic regression

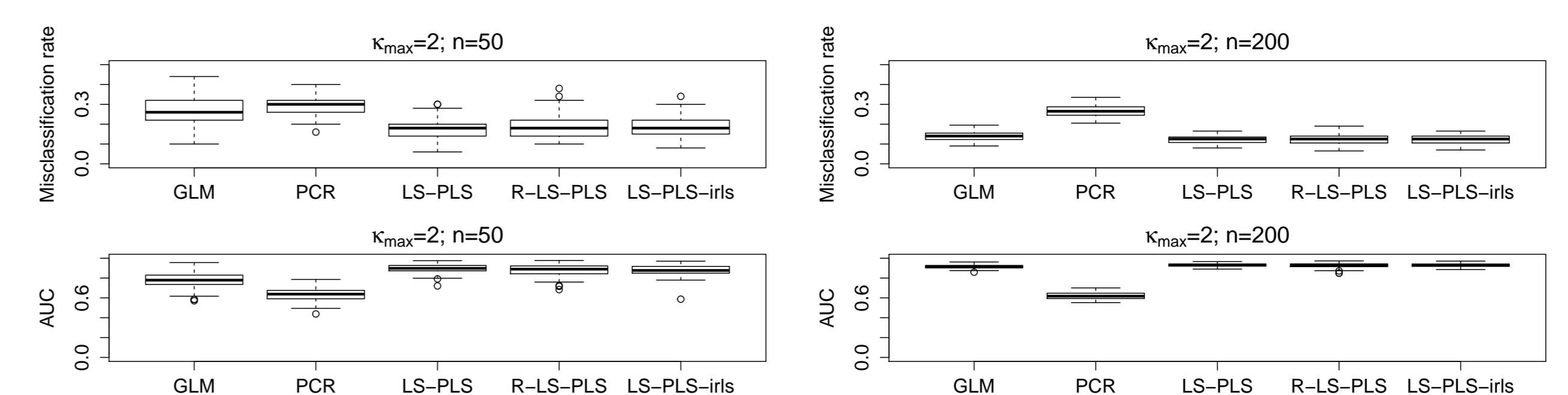
- NGUYEN and ROCKE's APPROACH [11]
 - * Extension of PLS to logistic regression substituting X by a $n \times \kappa$ matrix T
 - Columns of which are the first κ PLS-scores given by PLS regression of y on X
 - Estimation of the parameter with ML with IRLS(y, T).
 - ⇒ Replace PLS by LS-PLS
 - ⇒ κ obtained by cross-validation
 - ⇒ Method denoted **LS-PLS**.
- MARX's APPROACH [9]
 - * Estimation of the parameter γ with ML using IRLS(y, T) algorithm
 - * Where T defined by IRPLS, an algorithm that extends PLS to generalized linear models
 - * Matrix T collects the first κ components "at convergence" of IRPLS
 - ⇒ Replace PLS by LS-PLS to adopt this approach for LS-PLS
 - ⇒ κ obtained by cross-validation
 - ⇒ Method denoted **LS-PLS-irls**.
- RIDGE PARTIAL LEAST SQUARES APPROACH [4]
 - * Replace binary by a pseudo-response variable $z^{\text{inf}} \leftarrow$ linear relationship with the covariates
 - At convergence of IRLS algorithm : $z^{\text{inf}} = X \hat{\gamma}^R + \varepsilon$
 - $\hat{\gamma}^R$: the true value of the parameter
 - ε a centered vector of covariance matrix $(W^{\text{inf}})^{-1}$.
 - * When $n \ll p \rightarrow$ Regularisation methods as Ridge Penalty with λ the shrinkage parameter [8]
 - * Extension with LS-PLS
 - ⇒ Method called **R-LS-PLS**
 - ⇒ R-LS-PLS depends on two parameters : λ and κ obtained by cross-validation.
- BASTIEN's APPROACH [1]
 - * Not developed at the moment

SIMULATION STUDY - A "STANDARD" EXAMPLE

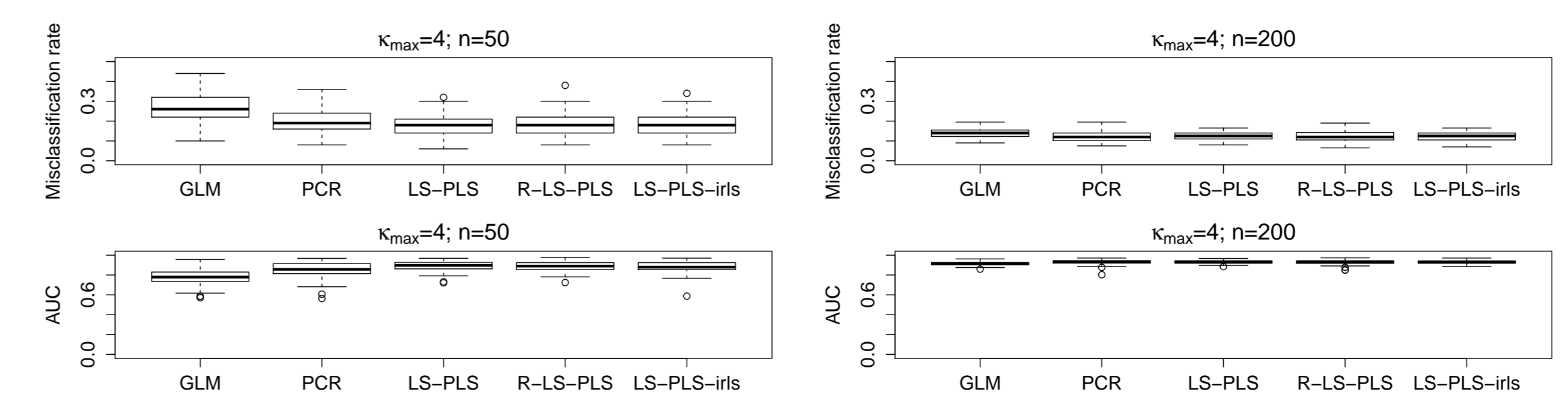
Methods

- Simulation framework (R software)
 - * Simulation of 100 data sets of size n (learning set=100 and test set = 100)
 - * Statistical model
 - For an individual i ($i = 1, \dots, n$), $y_i \sim \mathcal{B}(\pi_i)$
 - $\beta_X = \{\{0\}^8, \{2\}^8\}$ and $\beta_D = \{0.5\}^4$ ($p = 16$ and $q = 4$)
 - X such as $X = (X^1, X^2, X^3, X^4)$ where $X^k \sim N(0_4, \Sigma_X^k)$ with $\Sigma_{i,j}^k = c^k \rho^{|i-j|}$ with $k = 1, \dots, 4$, $i = 1, \dots, 4$, $j = 1, \dots, 4$ where $c^1 = 8$, $c^2 = 4$, $c^3 = 2$, $c^4 = 1$ and $\rho = 0.9999$
 - $D \sim N(0_q, \Sigma_D)$ with $\Sigma_D = \rho^{|i-j|}$ with $i = 1, \dots, q$ and $j = 1, \dots, q$ and $\rho = 0.5$
- Comparison of the different prediction methods to analyse both X and D matrices :
 - * **1) GLM 2) PCR on X then GLM on $[DX_{PCR}]$ 3) LS-PLS 4) LS-PLS-irls 5) R-LS-PLS**
 - * Choice for hyperparameters :
 - κ (for all approaches) obtained by cross-validation over a grid 1 to κ_{\max} (for $\kappa_{\max} = 2, 4, 8$)
 - λ (for R-LS-PLS) obtained by cross-validation
 - * $n = 50, 200$
 - * Criterion of comparison
 - Computation of AUC and Missclassification rate error for each method

Results



- No optimal conditions for PCR → Poor performance especially when n increase
- Similar compartment for GLM only when $n=50$
- ⇒ Relevance of method using reduction
- Closed distribution of Missclassification rate and AUC for new approaches and GLM when $n = 200$



- Slightly poor performance of GLM when $n = 50$
- ⇒ Correct and closed distribution of missclassification rate and AUC when n and κ increase
- ⇒ Relevance of all the approaches as well as PCR

CONCLUSION

- Comparison by simulation of prediction methods developed for logistic regression model to analyse both clinical and genomic data based on LS-PLS approach
 - Poor performance of GLM compared to other approaches especially n small
 - Similar relevance for proposed extensions of LS-PLS and PCR with ideal number of components
 - ⇒ Interest of reduction even if reasonable case of "high dimensional" case
 - ⇒ Need of extensive simulations to explore high-dimensional situations
- Some applications of these approaches to real data without relevant results
 - ⇒ Need further exploration
- Extension of LS-PLS approach to survival prediction model Cox' models

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