# PLSR-DA with unbalanced data

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# Clément Grelet

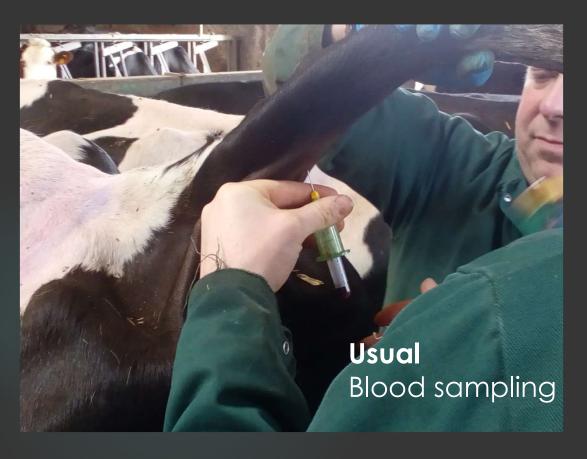
CRA-W Gembloux

Quality and authentication of agricultural products Unit



- → BHB (beta-hydroxybutyrate) dataset
  - Biomarker of ketosis in milking cows

#### BHB concentration in blood



#### 2 classes

Low ≤1.2 mmolg/L

High >1.2 mmol/L ⇒ Disease

#### Possible alternative?

MIR spectrometry

on milk samples

#### European BHB consortium

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### 64 herds N = 4,220 milk samples

Milk samples have been analyzed with 34 spectrometers, in particular FT2, FT6000, FT+, and FT7 (Foss, Hillerød, Denmark), and standard lactoscopes FT-MIR automatic (Delta Instruments, Drachten, the Netherlands).

The MIR spectra from the different instruments were standardized to be merged into a

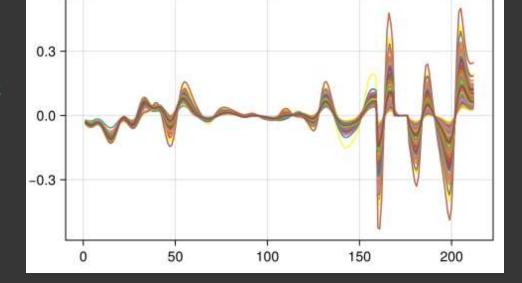
common dataset

#### C. Grellet

The selected spectral area consisted of 212 wavelengths

- 968.1 1,577.5 cm<sup>-1</sup>
- 1,731.8 1,762.6 cm<sup>-1</sup>
- 1,781.9 1,808.9 cm<sup>-1</sup>
- $2.831.0 2.966.0 \text{ cm}^{-1}$

to exclude areas not reproducible between instruments.



The spectra were pretreated by a first derivative

# N = 4,220 samples

	BHI	В		
	Low	High		
Training (3/4)	2,939	256	48 herds	
Test (1/4)	953	72	16 herds	
		~7-8%		
		Unbalanced classes		

# Theoretical aspects

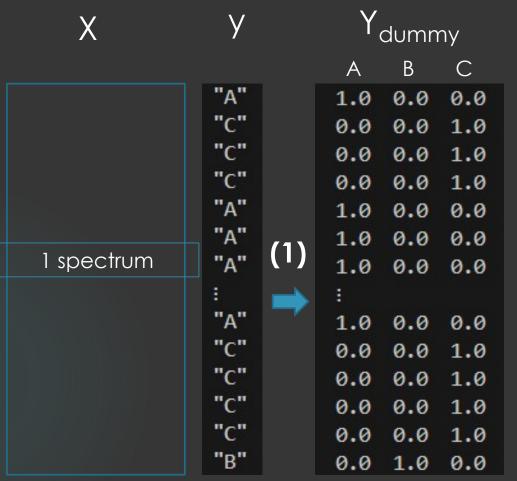
Usual PLSDA (simpler)

= PLSR-DA

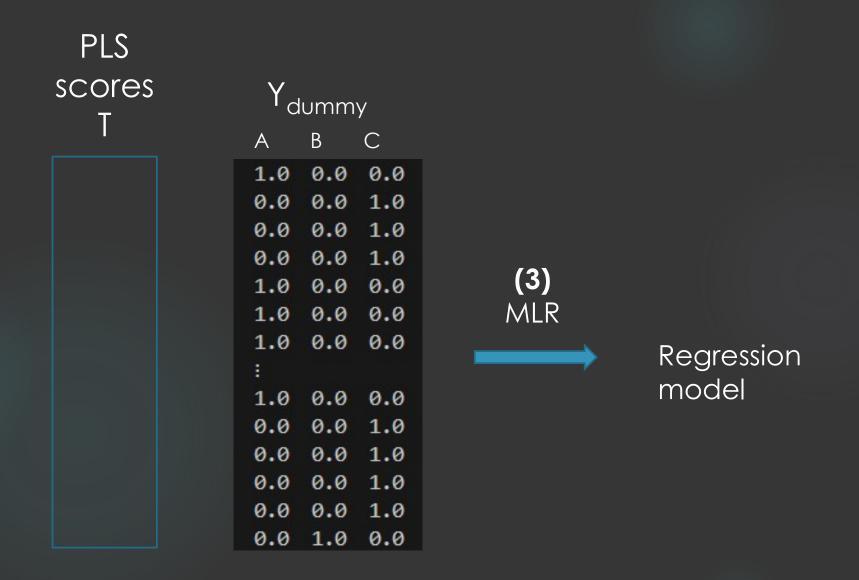
= PLS-MLR-DA

Other methods not considered here

- PLS-LDA
- PLS-QDAPLS-KDEDA
- etc.







$$(2) + (3) = PLSR2 \{ X, Y_{dummy} \}$$

# **Prediction**



 $\hat{y}_{new}$ 

	Α	В	С		
Fitted PLSR2	0.468518	0.316516	0.214966		Α
model	0.420873	0.277312	0.301815		Α
{X, Ydummy }  Xnew	0.285408	0.429812	0.28478		В
	0.378064	0.405632	0.216304		В
	0.301464	0.337026	0.361509		С
	0.322369	0.381457	0.296174		•••
	0.443234	0.266208	0.290558		
	1				

• (2): PLS2 { X , Y<sub>dummy</sub>} 
$$\rightarrow$$
 T  
• (3): MLR { T , Y<sub>dummy</sub>}  $\rightarrow$   $\hat{y}$ 

Bias if classes unbalanced

Dominant class is favored in the predictions

# Simple approach to decrease the bias

Weighting the PLS

<u>Usual PLSR</u> <u>V</u>

Weighted PLSR

Means

1'X

1' D X

Covariances

T'y

T' Dy

MLR  $\hat{\beta}$ 

 $(T'T)^{-1}T'y$ 

(T' D T)-1T D' y

$$\mathbf{D} = \begin{bmatrix} \mathbf{w}_1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \mathbf{w}_n \end{bmatrix}$$

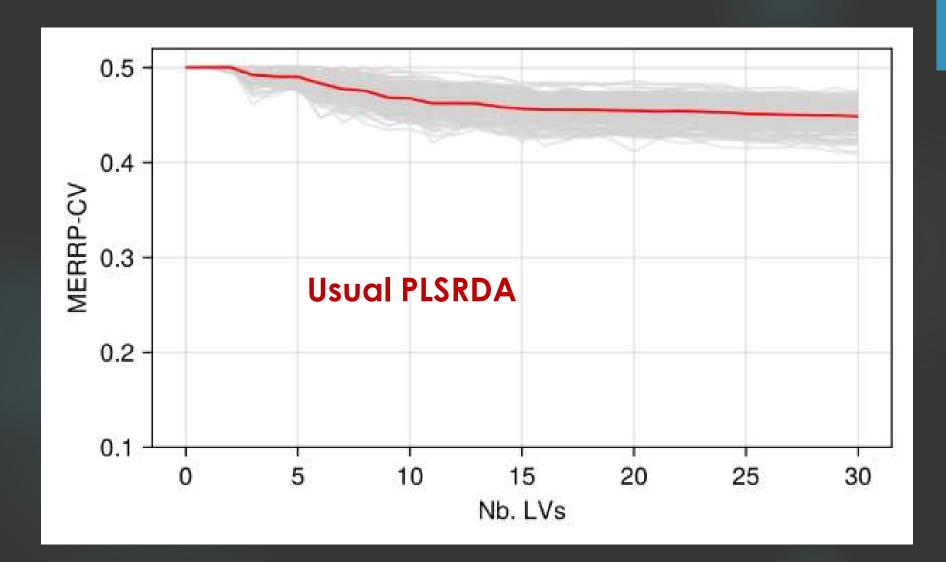
# BHB dataset

		ВН	ВНВ	
		Low	High	
Replicated K-Fold CV  K = 3, nrep = 50	Training (3/4)	2,939	256	
Generalization error	<b>Test</b> (1/4)	953	72	

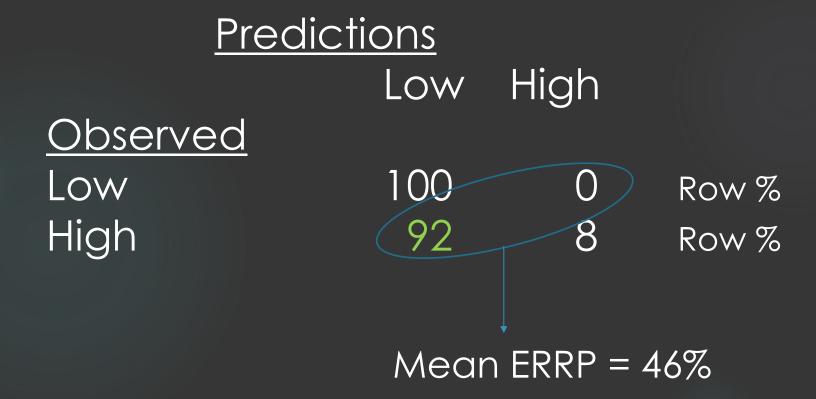
# When validation / test sets are unbalanced

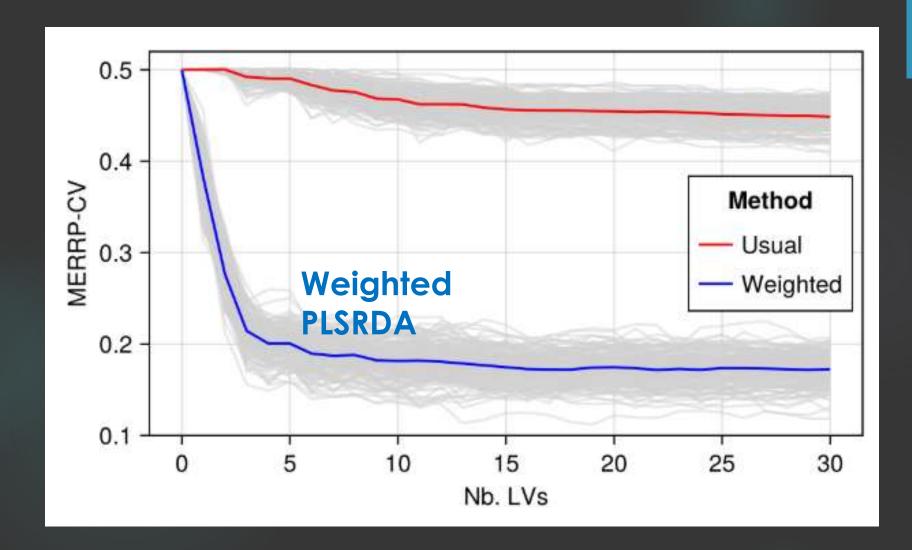
$$Mean \, ERRP = \frac{\sum_{i=1}^{G} ERR_i}{G}$$

Nb. classes



# Test set results Usual PLSRDA with 15 LVs





# Test set results Weighted PLSDA with 15 LVs

# **Predictions**

Observed

Low High Low High

Mean ERRP = 16%

### **Conclusions**

- PLSRDA: simple, very fast (can manage very large DB)
  - But only recommended when few classes (2-3)
  - And highly biased when unbalanced classes
- Easy solutions to remove the bias
  - Weighting: very performant (should be the default)
  - Sub-sampling the classes to balance the training (but loss of information)
- Other PLSDA methods (e.g. probabilistic) less sensitive but can also be weighted
- Weighted PLSRDA in practice, see next slides

# Jchemo.jl

Chemometrics and machine learning on high-dimensional data with Julia







```
model = plsrda(nlv = 20, prior = :unif)
```

```
fit! (model, Xtrain, ytrain)
pred = predict(model, Xtest).pred
```



## Also possible with package rchemo

Brandolini-Bunlon M. et al.

https://cran.r-project.org/web/packages/rchemo

(But: a weight vector has to be specified manually before the model fitting)

# Thank you!



