Sparse PLSR by regularized SVD

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A Sparse PLS for Variable Selection when Integrating Omics Data

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R function mixOmics::spls

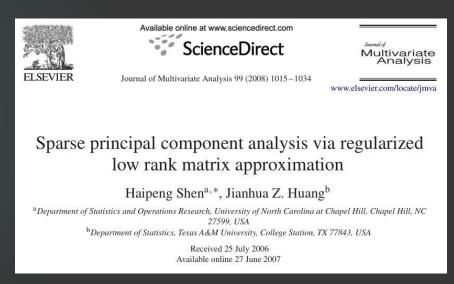
Lê Cao, K.-A., Rohart, F., Gonzalez, I., Dejean, S., Abadi, A.J., Gautier, B., Bartolo, F., Monget, P., Coquery, J., Yao, F., Liquet, B., 2022. mixOmics: Omics Data Integration Project.

https://doi.org/10.18129/B9.bioc.mixOmics

In brief about the method

Use of a regularized (instead of usual)
 SVD in the PLS algorithm





PLS X(n, p), Y(n, q)

• Scores (n, 1)
$$t_X = X w_X$$
 $t_Y = Y w_Y$

• Loading weights w_X (p, 1), w_Y (q, 1)

$$t_X = w_{X,1} x_1 + w_{X,2} x_2 + ... + w_{X,p} x_p$$

$$t_{Y} = w_{Y,1} y_1 + w_{Y,2} y_2 + ... + w_{Y,q} y_q$$

 $\mathbf{w}_{\mathbf{X}}$, $\mathbf{w}_{\mathbf{Y}}$ such as

$$\max \text{cov}^2(t_X, t_Y)$$
 with $||w_X|| = ||w_Y|| = 1$

A usual PLS algorithm

Iterative NIPALS to get $\mathbf{w}_{\mathbf{X}}$ and $\mathbf{w}_{\mathbf{Y}}$:

- 1. Set t_Y
- 2. Repeat until convergence

a)
$$w_X = X' t_Y$$

b)
$$w_x = w_x / norm(w_x)$$

c)
$$w_y = Y' t_x / t_x' t_x$$

d)
$$w_Y = w_Y / norm(w_Y)$$

e)
$$t_Y = Y w_Y$$

$$3. \quad t_X = X w_X$$

But W_X and W_Y can be computed without iteration:

- Let K = Y'X (could consider X'Y)
- SVD of K \Rightarrow U Δ V'

•
$$w_x = V[:, 1]$$

•
$$w_y = U[:, 1]$$

e.g., Höskuldsson 1988 Journal of Chemometrics https://doi.org/10.1002/cem.1180020306

(used in Jchemo: plskern, plsnipals, plscan)

A simple approach to get sparse w_x

<u>Usual PLS</u>

- K = Y'X
- SVD of K \Rightarrow U Δ V'
- $w_X = V[:, 1]$

Sparse PLS

- K = Y'X
- rSVD (S&H 2008) of K \Rightarrow U Δ V'
- $\overline{\bullet} \ \overline{w_X} = V[:, 1]$



This is the idea used by Lê Cao et al.

(authors also compute sparse $w_{\scriptscriptstyle Y}$, not detailed in this presentation)

Summary of the rSVD of Shen & Huang 2008

$$\widehat{X} = u \delta v'$$
 $\|u\| = \|v\| = 1$ 1-rank SVD of a given matrix X

A usual iterative NIPALS algorithm

- 1. Set u
- 2. Repeat until convergence

a)
$$v = X' u$$

b)
$$u = X v / norm(X v)$$

3.
$$v = v / norm(v)$$

Regularization of Shen & Huang

- 1. Set u
- 2. Repeat until convergence
 - a) $v = f_{\lambda}(X' u)$ soft thresholding
 - b) u = X v / norm(X v)
- 3. v = v / norm(v)

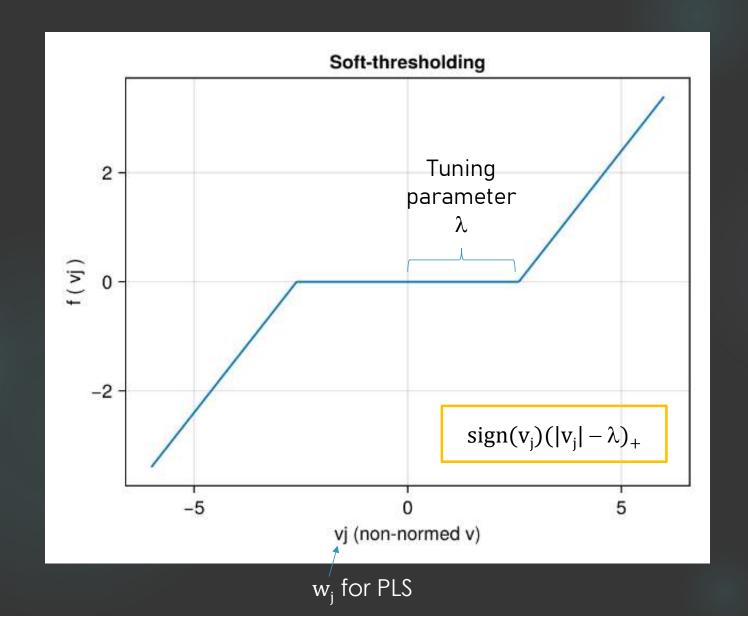
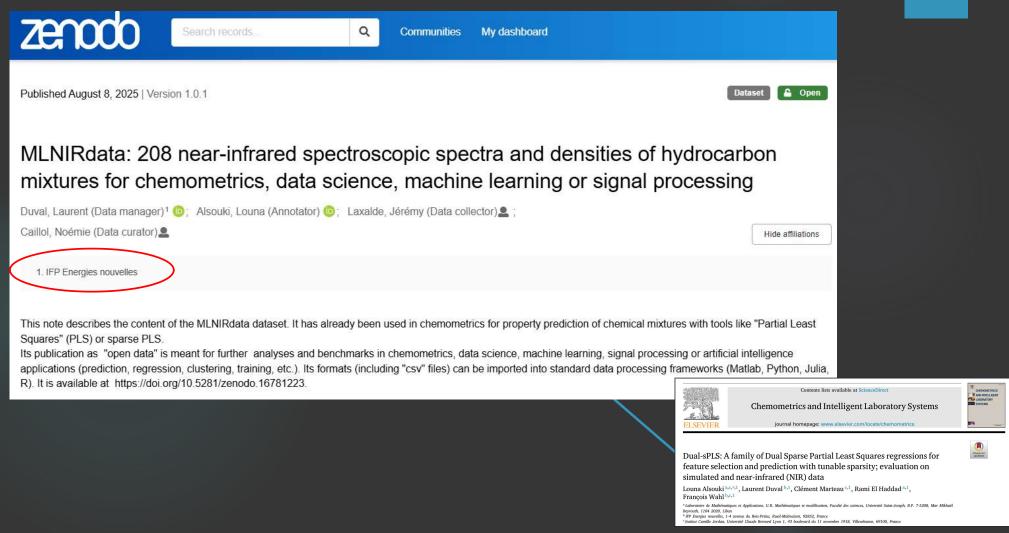


Illustration: MLNIR dataset



All the analyses in this presentation: done with Jchemo.jl https://github.com/mlesnoff/Jchemo.jl

In particular,

function splsr

- Sames results as mixOmics::spls but
 - a) Sparsity only on w_x (predictive approach)
 - b) Nipals PLS algorithm replaced by the **"improved kernel** algorithm #1" of Dayal & McGegor 1997 ⇒ faster



MLNIR dataset available at: https://zenodo.org/records/16783068

N = 208 hydrocarbon samples. For each sample, a near-infrared spectrum (intensities measured at given wavelenghts in cm-1) and a density value are provided. The dataset contains:

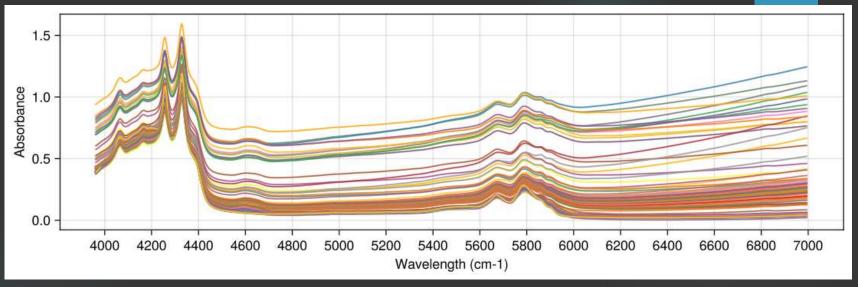
- X: Raw NIR data
- Xp: NIR data after preprocessing (SNV + 2nd derivative Savitzky-Golay)
- y: Density normalized to [0, 1] (response to predict)

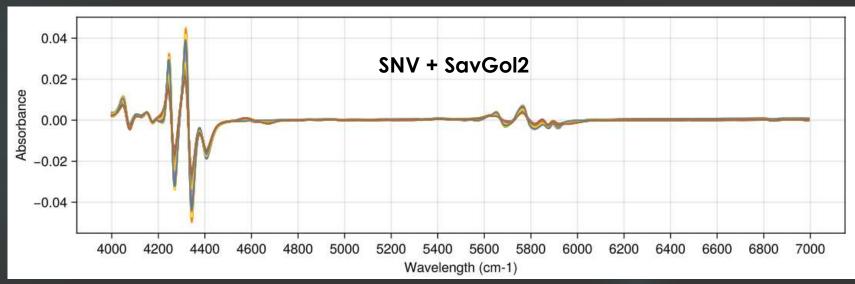
Available (JLD2) at: https://github.com/mlesnoff/JchemoData.jl?tab=readme-ov-file#mnist20pcts

MLNIR data

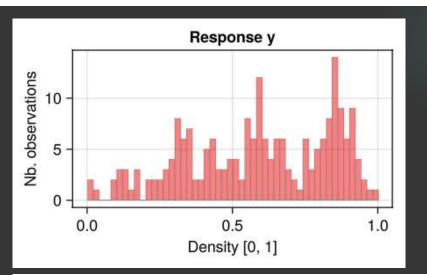
with pre-selection of range 4000-7000 cm-1

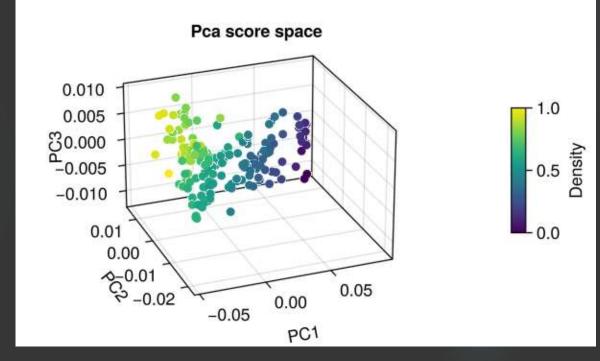
1556 variables (wavelengths)





Response y
Hydrocarbon density

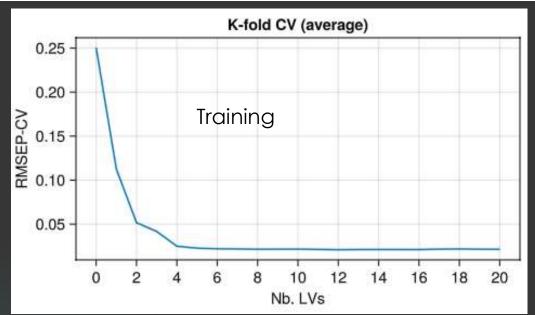


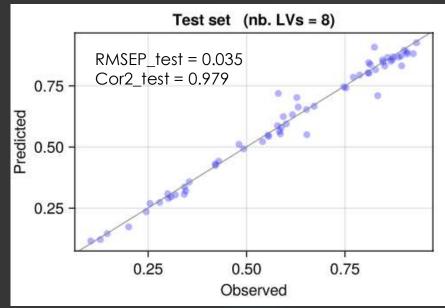


Model calibration and validation

```
Total n = 208 obs. 
 Train n = 146 \Rightarrow Replicated K-fold CV K = 3, nrep = 30 test n = 62 30% by random sampling
```

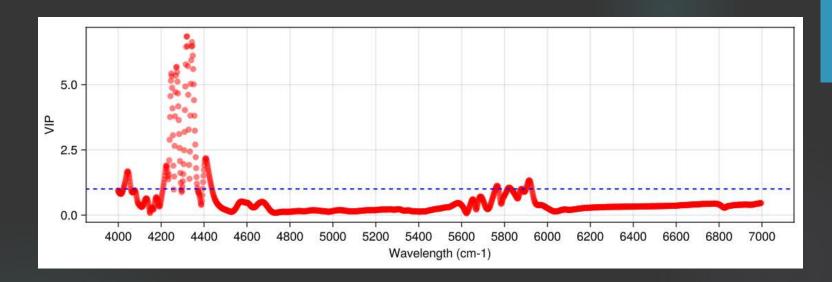
PLSR

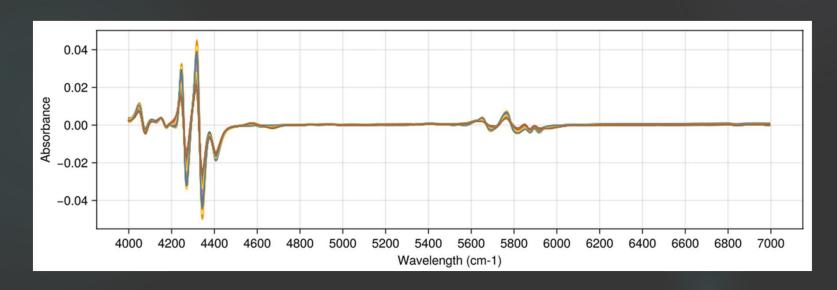




VIPs

PLS 8 LVs

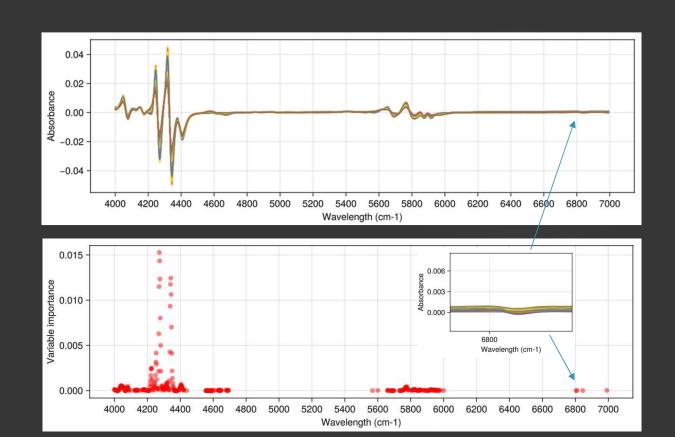




Alternative to VIPs (very simple and efficient):

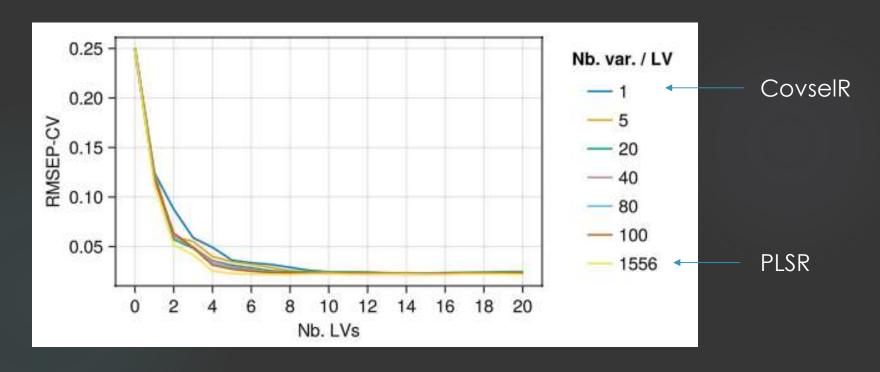
Variable importance by permutation

- Successively for each variable:
 - a) Obs. are randomly permuted
 - b) The model (here PLSR 8 LVs) is fitted on Xtrain and used to predict Xtest
 - c) Rmsep_test (or other indicator) is computed and compared to the original without permutation
- Grouped-approaches are very easy to implement (simultaneous permutation of sets of variables)
- Better than Interval-PLS

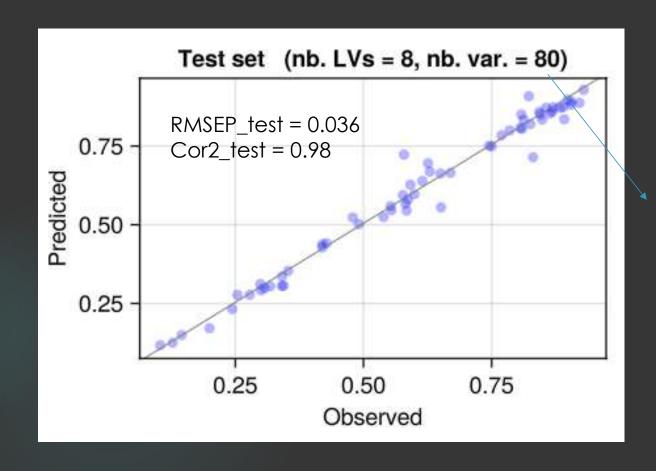


Sparse PLSR

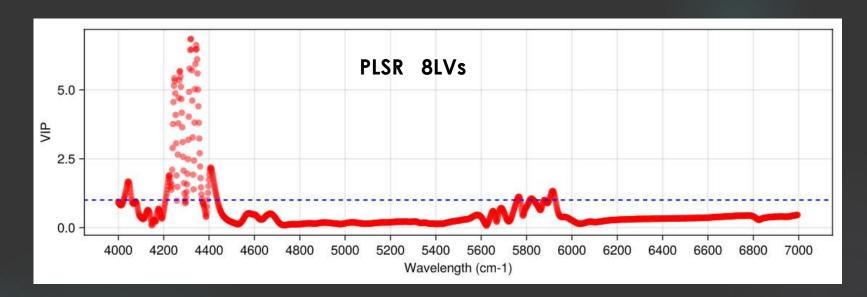
 \Rightarrow CV to tune the nb. LVs and the nb. variables that are selected for each LV

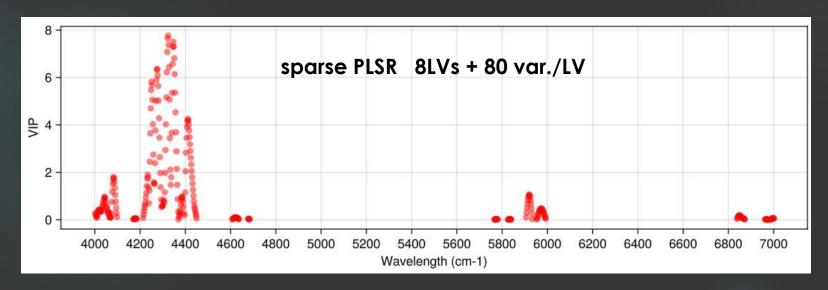


In this example, the same nb. variables are selected for all the LVs, but this can be relaxed

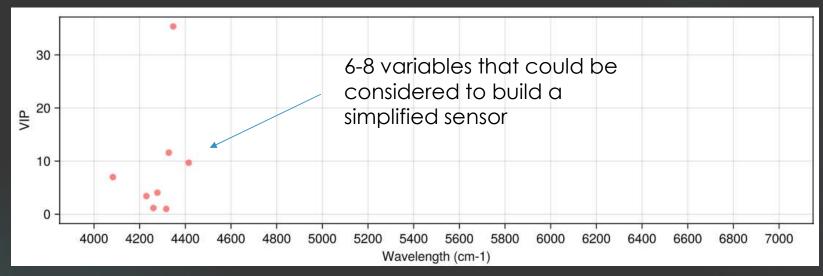


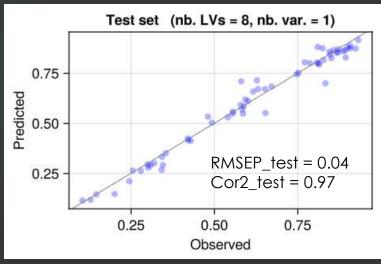
⇒ Total nb. selected variables = 256 (over 1556)





With only 1 variable selected / LV (CovSeIR)

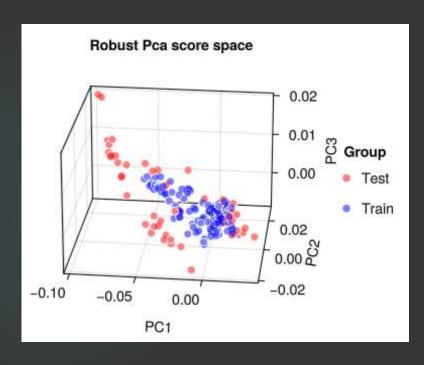


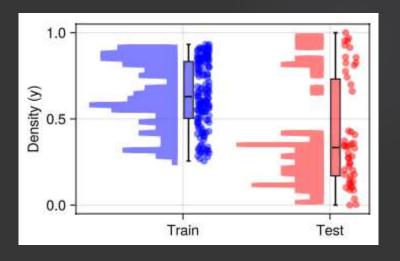


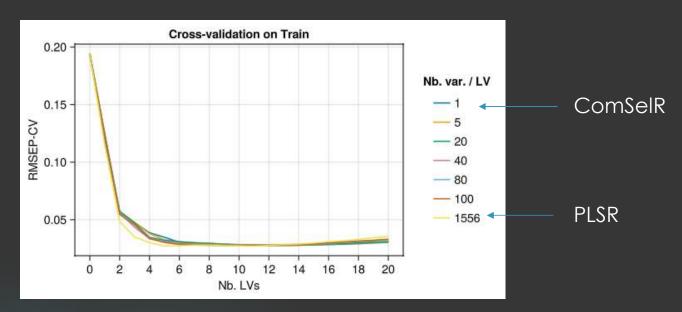
And what about predictive robustness?

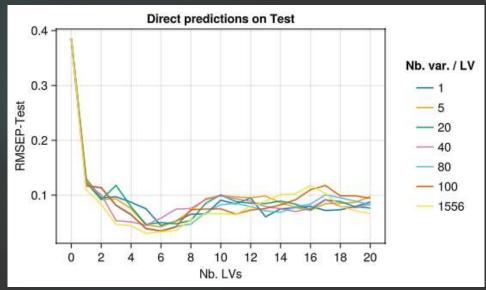
New split Train/Test

• Test (n = 50): Mainly in extrapolation









sparse PLSR 8LVs 80 var. / LV

