

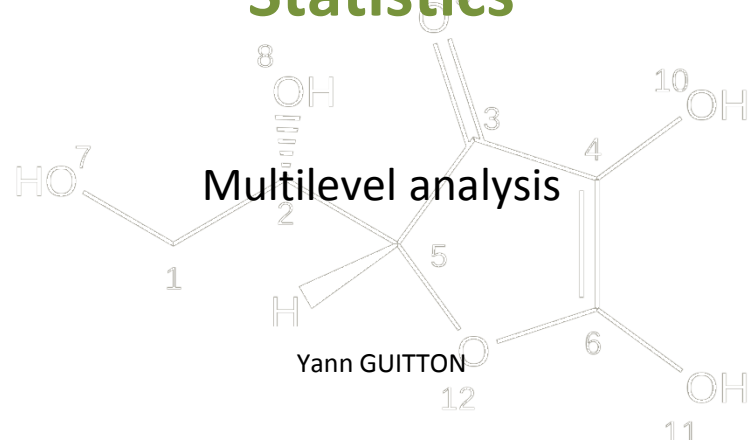


# 4 Wm

Workflow4metabolomics

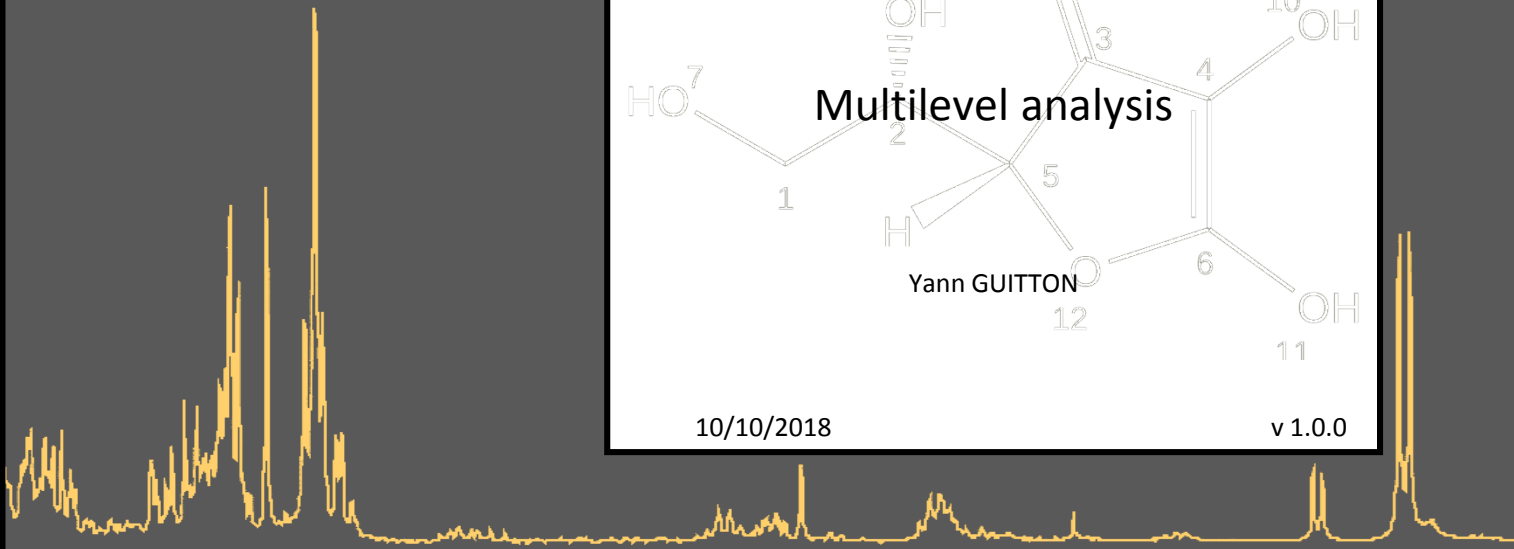


## Statistics



10/10/2018

v 1.0.0



# Multilevel Design

How to transform your dataMatrix



# How to use Multilevel and Why

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## Experimental Design with:

- Repeated measurement on same subjects
  - Treatment (Before vs After)

Problem : inter-individual biological variability can be really high, sometime higher than the expected studied biological effect.

Experimental design; « cross-over » every individual is it own control

Variability is separated in 2 parts taking into account repeated measurments on each individuals

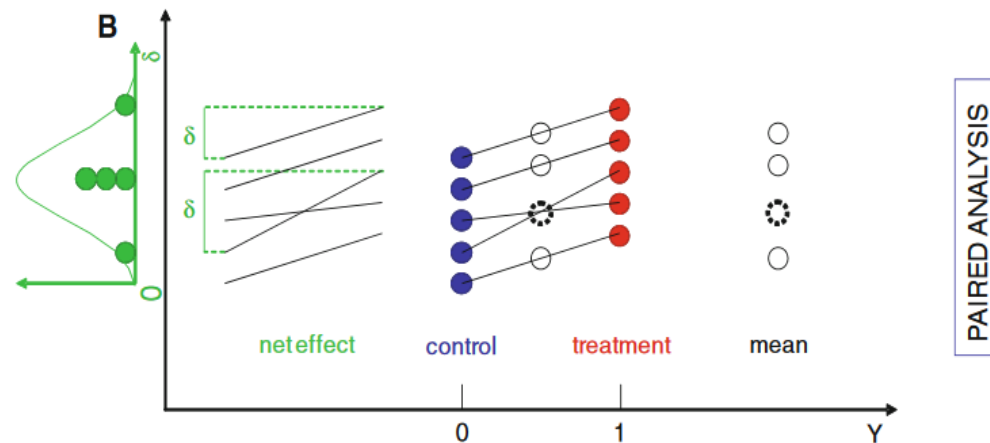
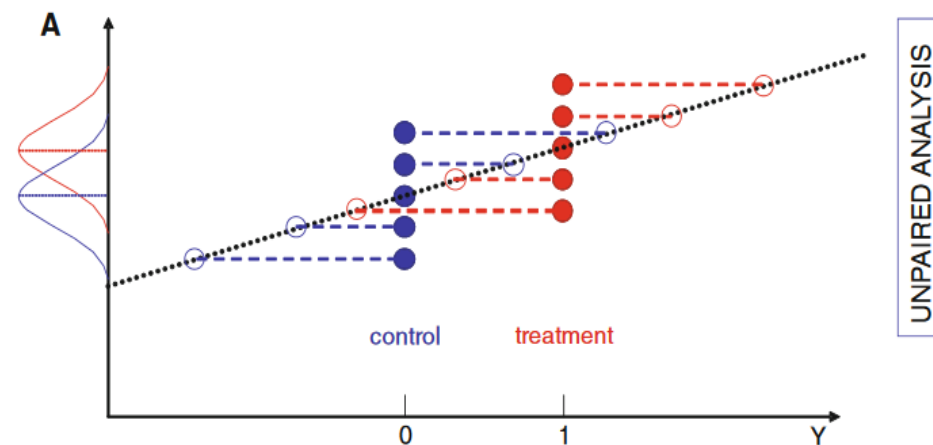
Data pairing= no independance  
Not taken into account in usal Multivariates statistics



# How to use Multilevel and Why

## Experimental Design with:

- Repeated measurement on same subjects
- Treatment (Before vs After)



Westerhuis, Johan A., Ewoud J. J. van Velzen, Huub C. J. Hoefsloot, and Age K. Smilde. 2010. 'Multivariate Paired Data Analysis: Multilevel PLSDA versus OPLSDA'. *Metabolomics* 6 (1): 119–28. doi:10.1007/s11306-009-0185-z.

# How to use Multilevel and Why

Without data correction

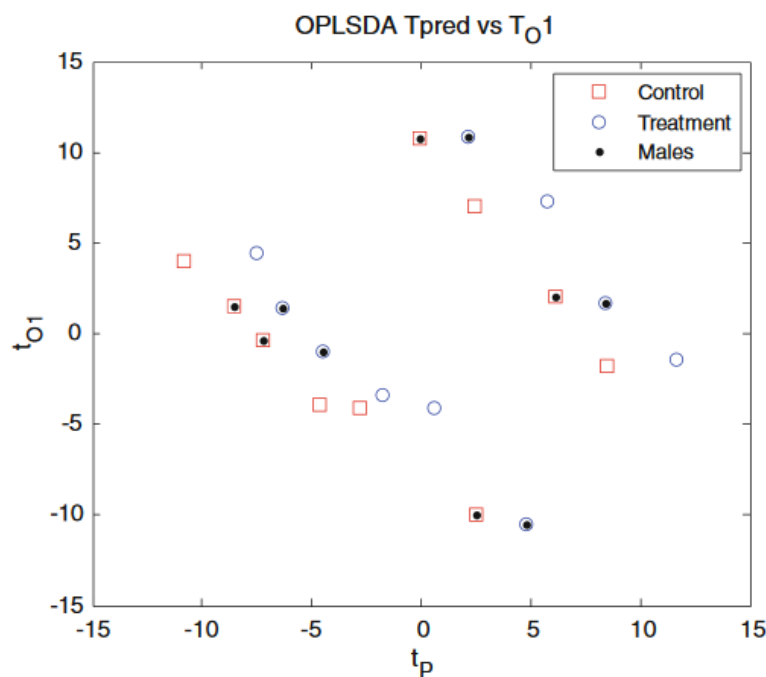


Fig. 2 Double cross validated OPLSDA score plot of simulated data.

With data correction

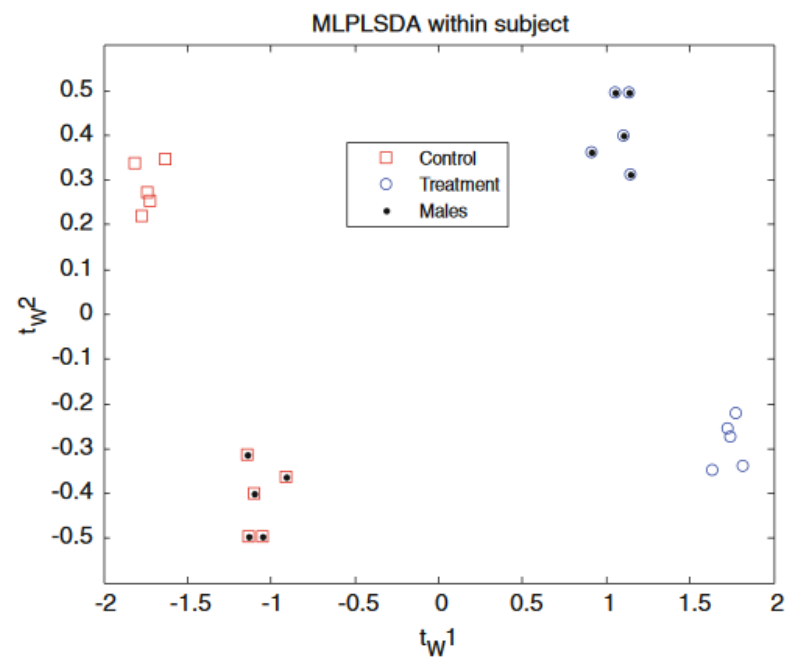


Fig. 3 The multilevel PLSDA scores ( $t_{w1}$ ,  $t_{w2}$ ) of the within subject

Westerhuis, Johan A., Ewoud J. J. van Velzen, Huub C. J. Hoefsloot, and Age K. Smilde. 2010. 'Multivariate Paired Data Analysis: Multilevel PLSDA versus OPLSDA'. *Metabolomics* 6 (1): 119–28. doi:10.1007/s11306-009-0185-z.

# How to use Multilevel and Why

## Normalisation

Normalization Normalization of (preprocessed) spectra

Multilevel Data transformation: Within matrix decomposition for repeated measurements (cross-over design) with mixOmics package

Determine batch correction to choose between linear, lowess and loess methods

Batch correction Corrects intensities for signal drift and batch-effects

Transformation Transforms the dataMatrix intensity values

**Multilevel** Data transformation: Within matrix decomposition for repeated measurements (cross-over design) with mixOmics Options

package (Galaxy Version 0.5.0)

### Data matrix file

18: dataMatrix.tsv

variable x sample, decimal: '.', missing: NA, mode: numerical, sep: tabular

### Sample metadata file

18: dataMatrix.tsv

sample x metadata, decimal: '.', missing: NA, mode: character and numerical, sep: tabular

### Repeated measurement label (Individual IDs, ...)

Indicate the column name of the sample table to be used as repeated measurement factor

### Select number of levels1

### Level name (as in sampleMetadata)

Indicate the column name of the sample table to be used as factor

### Add transformation to dataMatrix before withinVariation

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The multilevel function will first decompose the within from the between variance in the data sets X (**dataMatrix.tsv**) via the internal functions mixOmics withinVariation(). Once the within variance is calculated, we can run the classical multivariate approaches, such as PCA, PLS-DA and PLS on the within- subject deviation.

# references

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<http://mixomics.org/>

