

Zapping through software for the statistical analysis of spectroscopic data

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Workshop dedicato alla
Chemometria Applicata alla
Spettroscopia NMR

06/13/2012

Contents

- Fee-paying software
- Open-source web-based tools
- Command line tools
- muma



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- Fee-paying software
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Free-paying software (I)

- PLS-Toolbox
- CAMO
- AMIX
- SIMCA-P

- User-friendly graphic interface
- Prompt maintenance
(Updates, custom service, etc)
- Cost



Shared features

- Spectra/Data pre-processing
- Data exploration
- Multivariate analysis/modeling
- Graphical outputs/interpretation



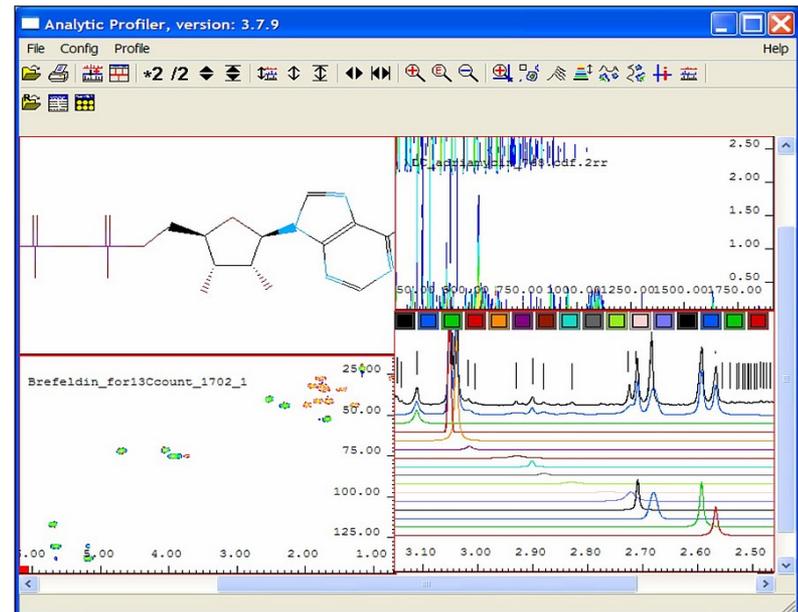
PLS-Toolbox

- Fee: Academic - \$695/\$395
Industrial - \$2195/1395
- With MatLab or Solo
- Possibility to build your own script
- Friendly Pipe-line
- Interactive plots



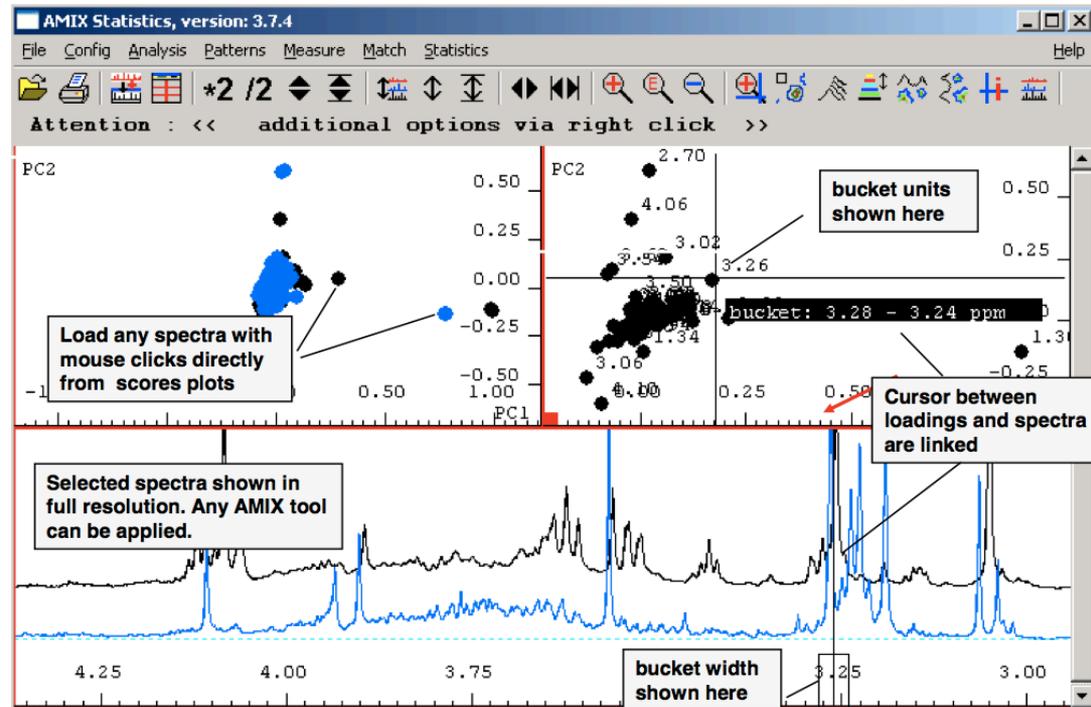
- Pre-processing
 - Noise, Baseline
 - Filtering (OSC)
 - Normalization
 - Centering/Scaling
- Model building
 - Exploration: PCA, Multiway PCA
 - Classification: SIMCA, KNN, PLS-DA, SVM
 - Regression: PLSR, PCR, MLR, ...
- Model validation
 - Cross-validation
- Design of experiment (DoE)

- Spectra management
 - Color, Bucketing
 - Metabolite concentration via deconvolution
 - Baseline correction
 - Line shaping
 - Reference DB (1D,2D,J-res)
- Statistics
 - Pareto/Auto scaling
 - Exploration – PCA
 - Classification – PLS, SIMCA
 - Covariance Analysis (STOCSY)
 - Boxplots of selected variables



- Interaction between statistics and spectra

- Routine analysis automation



- Link with DBs
 - HMDB: - Import spectra
- Query
 - KEGG, BMRB, ChEBI, PubChem

- Fee: ????
- OS: Windows 7, Vista, XP
- Data pre-treatment
- Exploratory data analysis
 - Descriptive (Mean, SD, ..)
 - Univariate (T, F, Contingency)
 - K-means/Hierarchical clustering
 - PCA (SVD or NIPALS) + ROTATION METHODS
 - Multivariate Curve Resolution (MCR)



- Regression
 - PCR, PLSR, OPLS, SVMR
 - L-PLSR
 - “Z” matrix
 - Reduced false positive rate
 - Accuracy
- Classification
 - SIMCA, LDA, SVM
- No extensive model validation
- Design of experiment
- On-line implementation
 - Automation
 - Industrial



SIMCA

- Fee: Academic: €1500
Industrial: €8000
- OS: Windows 7, Vista, XP
- Data visualization
 - Friendly GUI
 - Comprehensive data import and management
 - Spectrum plot from dataset
- Pre-processing
 - Derivatives, MSC/SNV, de-noising, etc
 - Wavelet denoising/compression
 - Variable and Block scaling



- Modeling

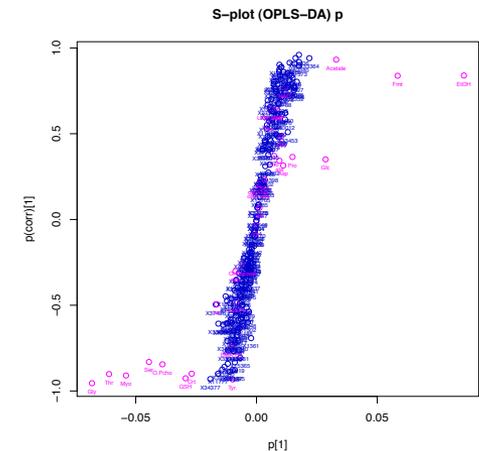
- Overview: PCA
- Regression and Discriminant: PLS, OPLS, O2PLS
- Cluster analysis with PLS tree

- Model validation

- Cross validation (random/custom)
- Permutation test
- CV ANOVA, CV scores

- Graphics

- Model summary/diagnostics (Hotelling's T2, DModX, ..)
- VIP
- Calibration diagnostics
- Contribution plots
- Observation/Variable plots
- Y-related profiles for OPLS and O2PLS



- 2D, 3D scatter, line, column, time series
- Wavelet structure
- Auto/Cross correlation
- Including/Removing data

INTERACTIVE

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MetaboAnalyst

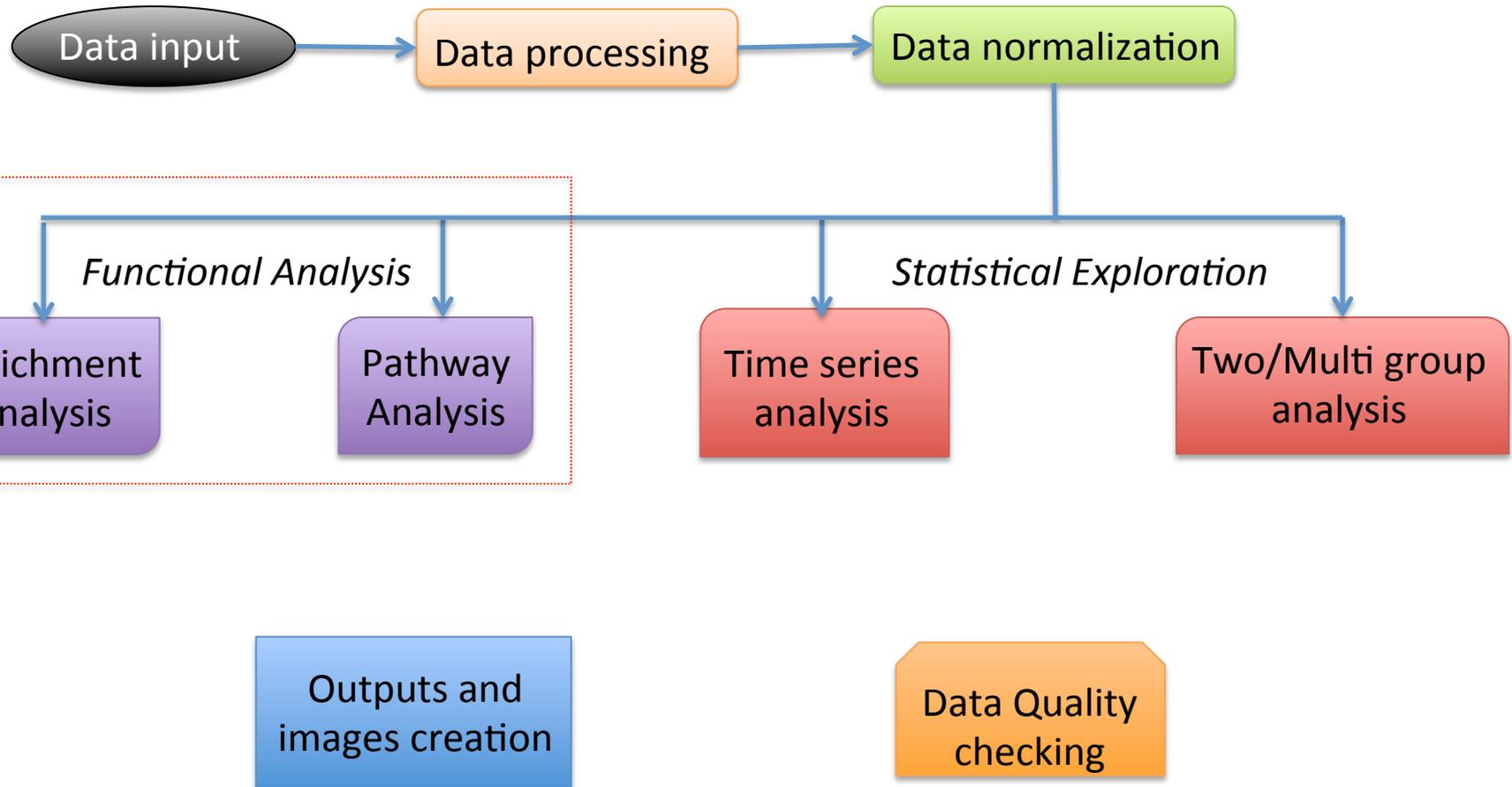
- First release: 2009
- Update 2.0: March 2012
- Metabolomic-specific data processing and statistical analysis
- Potentiated server
- FAQs section and tutorials
- Downloadable for local installation



FREE

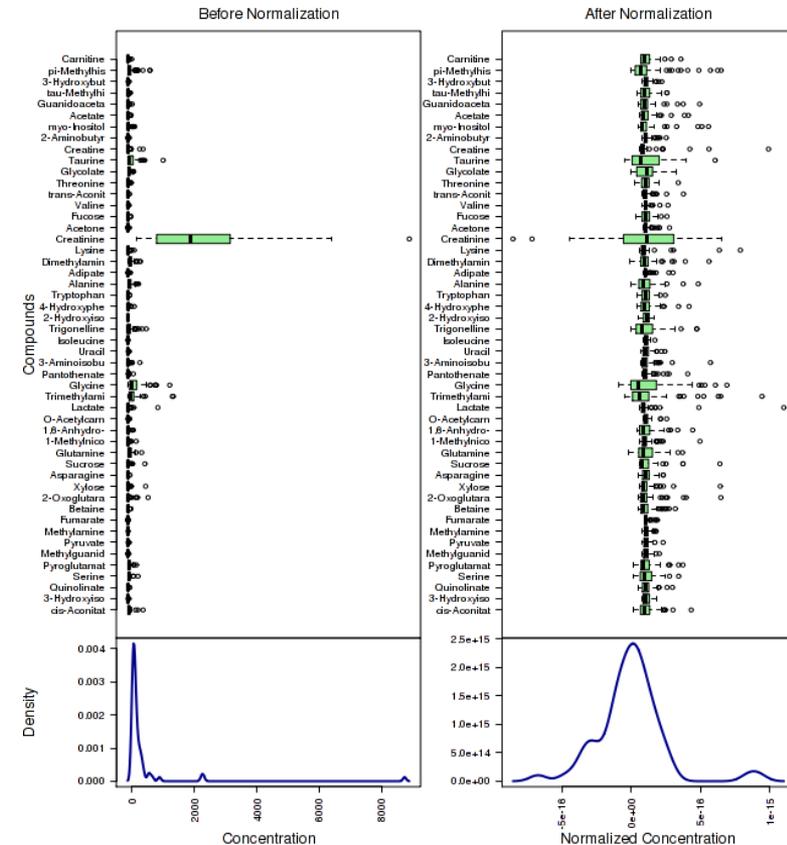
MetaboAnalyst - Overview

MetaboAnalyst 2.0
-- a comprehensive



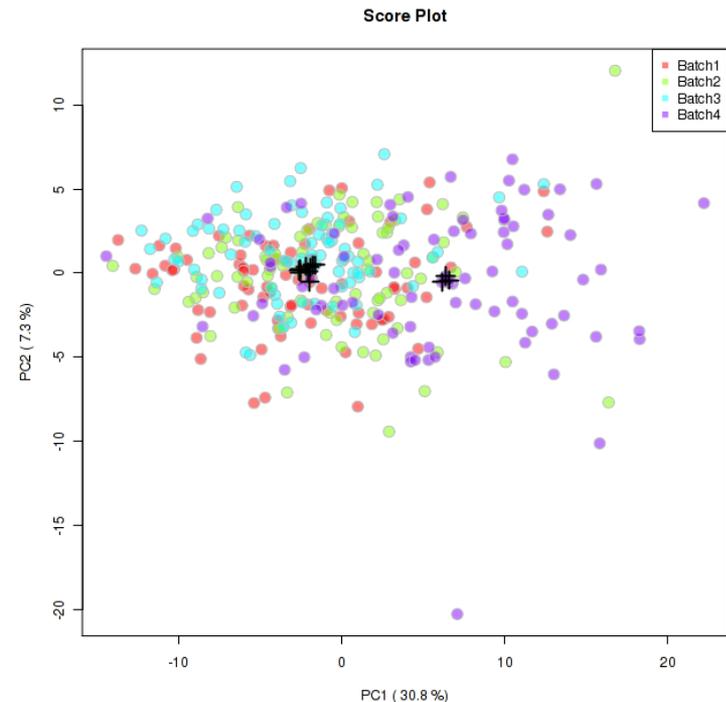
Processing and normalization

- Data Filtering
 - Remove low-quality data points
 - Low-value threshold
 - Low-variance (noise)
- Data Editing
 - Exclude/Include
- Use standard names of compounds
 - Link to web databases
- Normalization
 - 11 different procedures
 - Diagnostic plots aiding the choice..



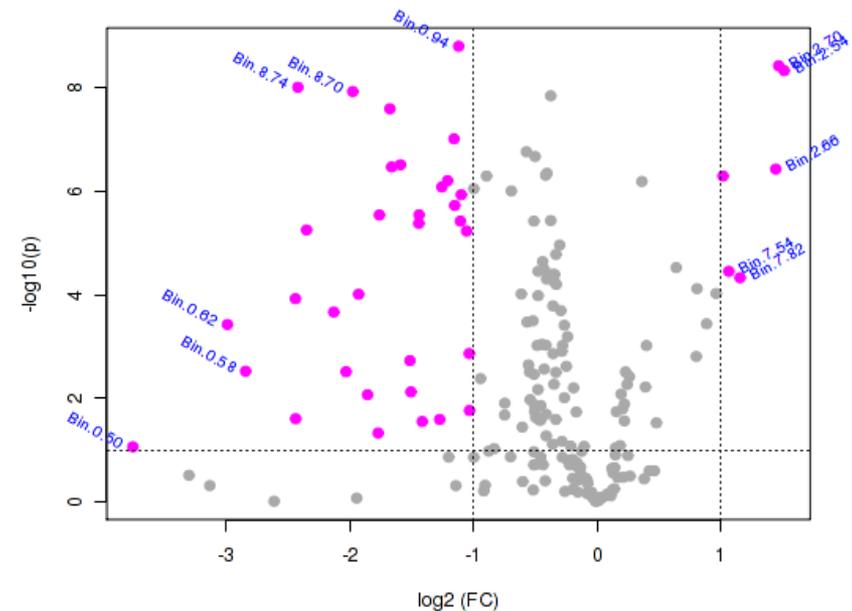
Data quality checking

- Pair-wise comparison of 2 measurements
 - Consistency of 2 protocols/instruments/platforms ...
- Temporal drift
 - Variations related to long-period analyses
- Batch effect
 - Batch systemic variation
 - Uni/Multi-variate methods
- Reference concentration ranges
 - Link with databases
 - Only for human



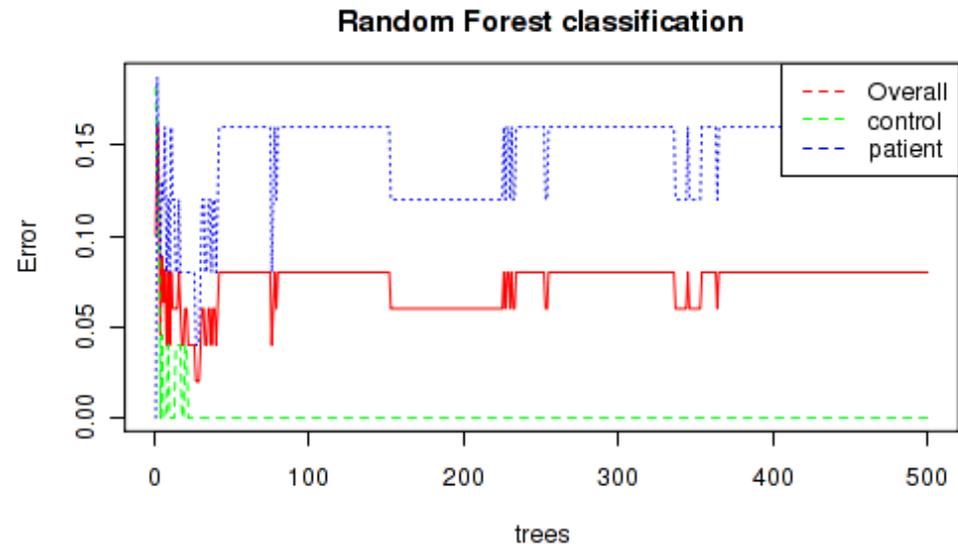
Important compounds identification

- Differential expression
 - Univariate methods
 - T test/ANOVA
 - Multiple test correction (FDR or Bonferroni)
- Co-expression analysis
 - Correlation heatmaps (STOCSY)
 - 1D and 2D
 - Euclidean distances, Pearson/Spearman correlations
- Pattern search
 - Template matching method
 - (Supervised-like)



1 Classification and 2 way

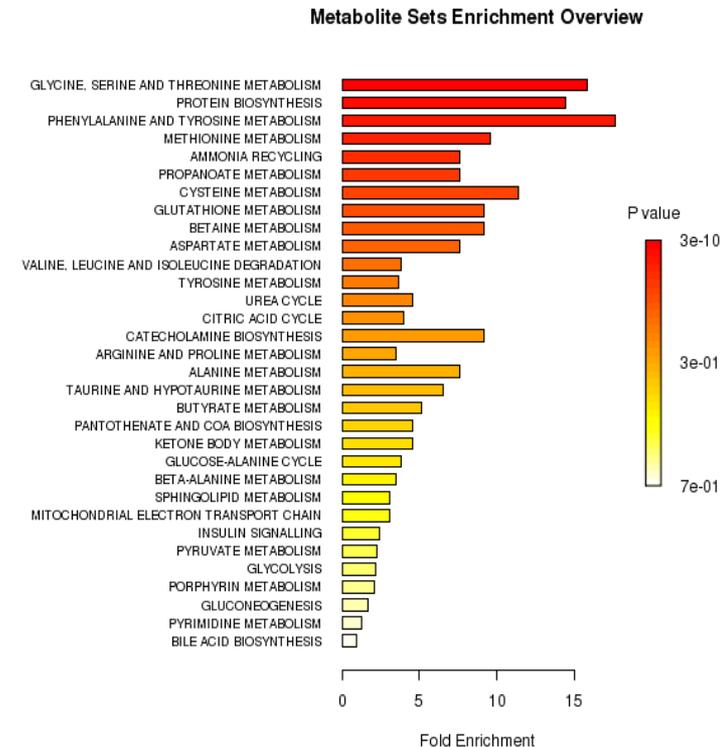
- Chemometrics
 - PCA, PLS-DA
- Machine learning
 - Hierarchical/
K-means clustering
 - Self Organizing
Maps (SOMs)
 - SUPERVISED:
SVM, Random Forest
- Time course/2 factors Analysis
 - Clustering for 2-way data
 - Within/Between subject ANOVA
 - Multivariate time course with Bayes approach



1 Functional Interpretation

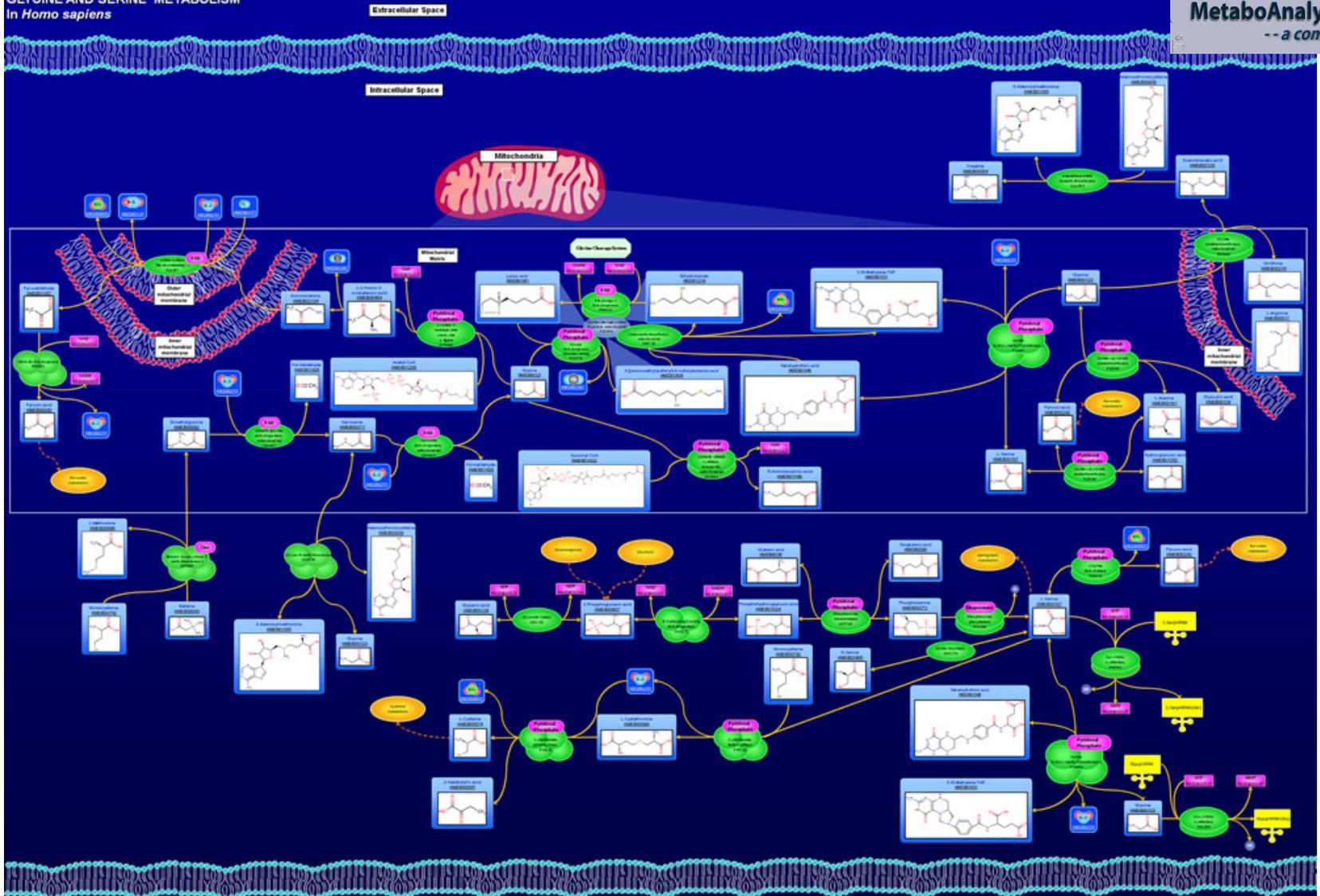
MetaboAnalyst 2.0
-- a comprehensive

- Over-representation Analysis (ORA)
- Single sample profiling (SSP)
 - Reference concentrations of human biofluid
- Quantitative enrichment Analysis (QEA)
 - Quantification data sets
- Metabolic Pathway Analysis
 - Enrichment analysis + Network topology
 - Metabolic pathways identification
 - Link to DBs



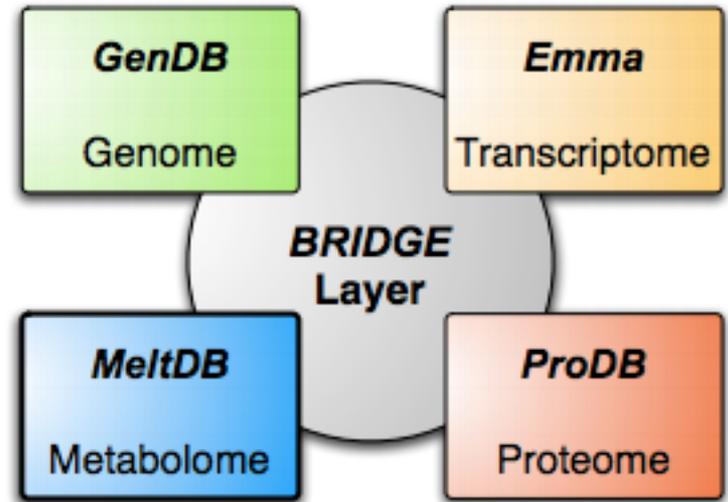
Pathway link

GLYCINE AND SERINE METABOLISM
In *Homo sapiens*



MeltDB

- Raw GC- or LC-MS data sets
- Spectra processing
- R functions integrated
 - T-test, ANOVA
 - PCA
 - Hierarchical Clustering
- Link with omics DBs
- On-line forum
 - Real-time discussion



MetaP server

- No pre-processing
- Common statistical tools
 - PCA
 - Correlation
 - Hypothesis tests
- Ready-to-use PDF reports
 - Box plots, PCA plots, etc...

*meta***P**



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R packages

- MS-specific
- CRMN: Cross-contribution compensating multiple standard normalization for quantification of MS metabolomics data sets
- Metab: GC-MS specific for spectra deconvolution and compound identification



```
## CRMN: Cross-contribution compensating multiple standard normalization for quantification of MS metabolomics data sets
##
## Author: M. J. Griffin, M. J. Griffin, M. J. Griffin
##
## This code is part of the CRMN package, which is distributed under the terms of the GNU General Public License (GPL)
##
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## <http://www.gnu.org/licenses/>.
##
## CRMN: Cross-contribution compensating multiple standard normalization for quantification of MS metabolomics data sets
##
## Author: M. J. Griffin, M. J. Griffin, M. J. Griffin
##
## This code is part of the CRMN package, which is distributed under the terms of the GNU General Public License (GPL)
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## <http://www.gnu.org/licenses/>.
```

1 R packages - Bioconductor

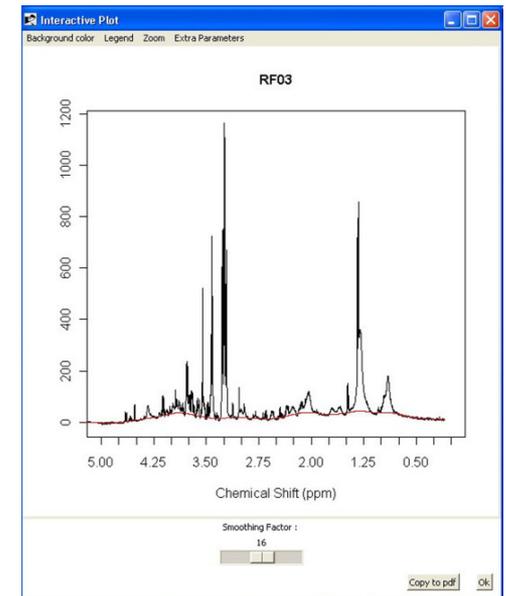
- Flagme
- Target Search



- GC-MS spectra processing
 - Peak detection, alignment, retention time shifts, plot spectra, de-noising, etc..
- No statistical analysis

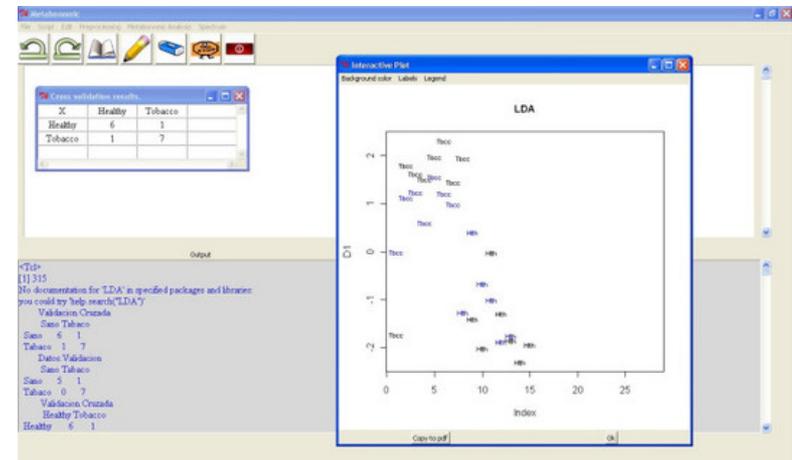
1 Metabonomic R package

- R-Tcl/Tk Graphical User Interface (GUI)
- R functions
- Windows OS
- Import NMR spectra
 - Processed (text file)
 - Raw (FID, Bruker)
- *Not excellent for spectra management*



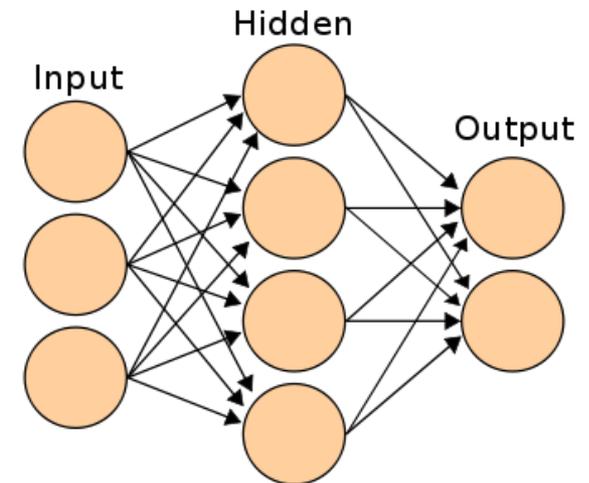
1 Metabonomic R package

- Spectra pre-processing
 - Region exclusions
 - Baseline correction (LOESS, FTICRMS)
 - Binning
 - Peak detection
 - Alignment
- Statistics
 - PCA
 - LDA
 - PLS-DA
 - KNN classification



1 Metabonomic R package

- Artificial Neural Networks (ANN)
 - Custom/Random training set
 - Single/Multiple layers networks
- Group-specific spectral differences
 - Plot means of specific ppms



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muma

<http://www.biomolnmr.org/software.html>

- Metabolomic Univariate & Multivariate Analysis
- R package
- Pipeline for statistical analysis
- Literature-based/well-established methods
- Contents
 - Data pre-processing
 - Dataset exploration
 - Univariate analysis
 - Supervised multivariate analysis
 - NMR molecular assignment
 - Biochemical interpretation
 - Data reporting
 - Graphics for publications



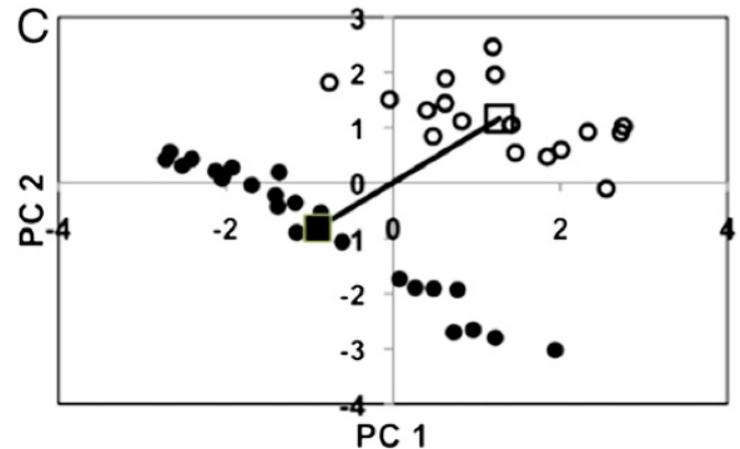
1 muma - data pre-processing

- Missing values imputation
 - Mean
 - Minimum
 - Half minimum
 - Zero
- Normalization on total spectral area
- Scaling
 - Pareto
 - Auto (Unit Variance)
 - Vast
 - Range



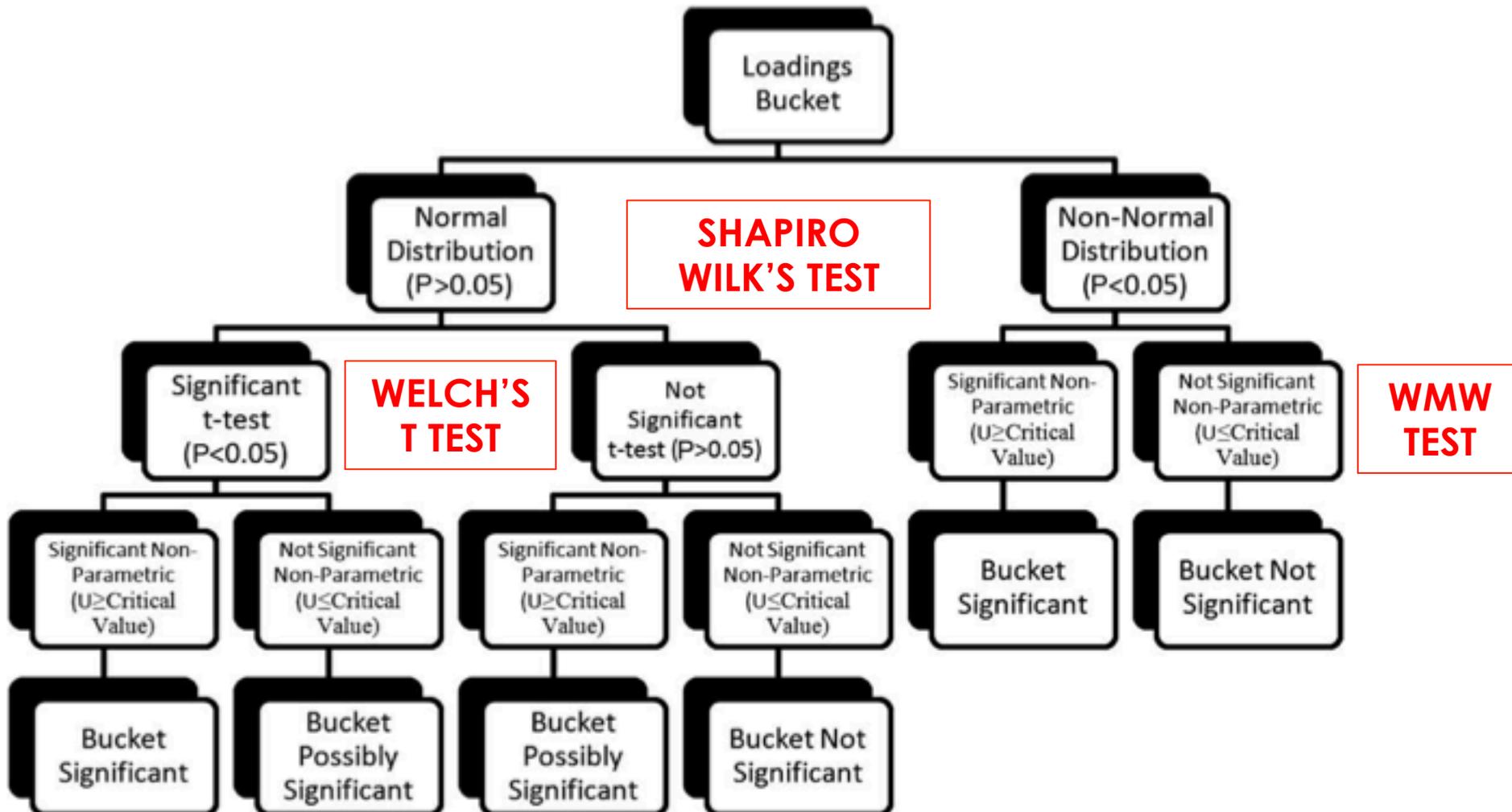
muma - exploration

- PCA
 - Graphical overview of first 10 PCs
 - Automatic ranking of best-separating pairs of PCs
 - Hotelling's T^2 test
 - F statistics
 - Identify PCs maximizing group separation
- Geometric outlier test
- Score and Loading plots



Goodpaster et al. *Chemometr Intel Lab Sys.* 109 (2011) 162-170

muma - univariate



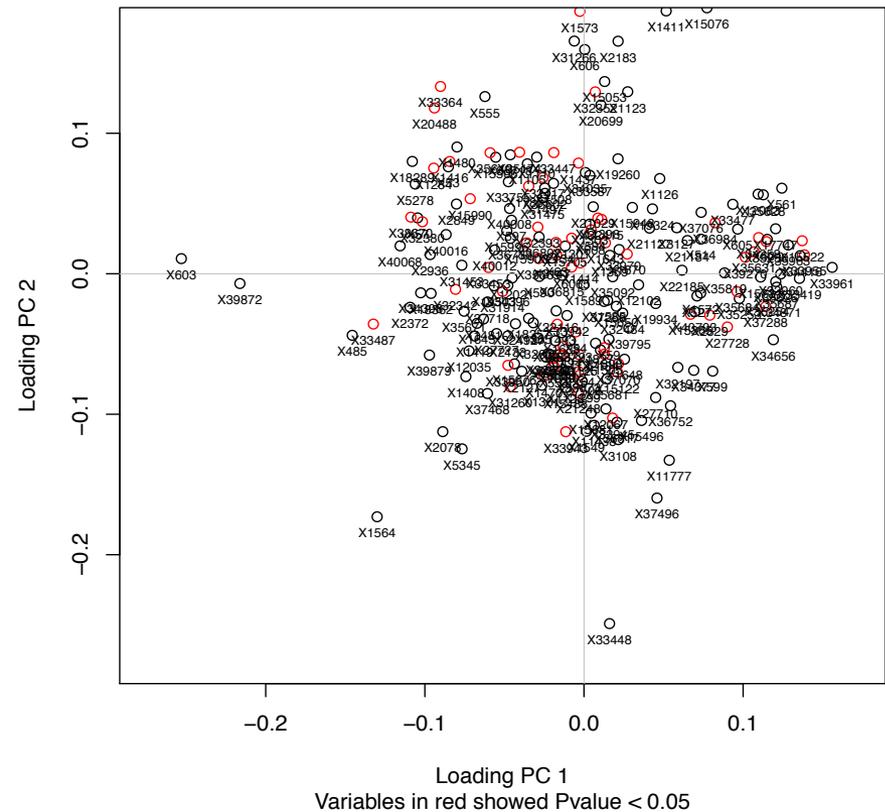
muma - multivariate

- Integration of PCA and univariate information

- PLS-DA

- OPLS-DA (2 classes)

PCA - Loading Plot (Significance-colored variables)



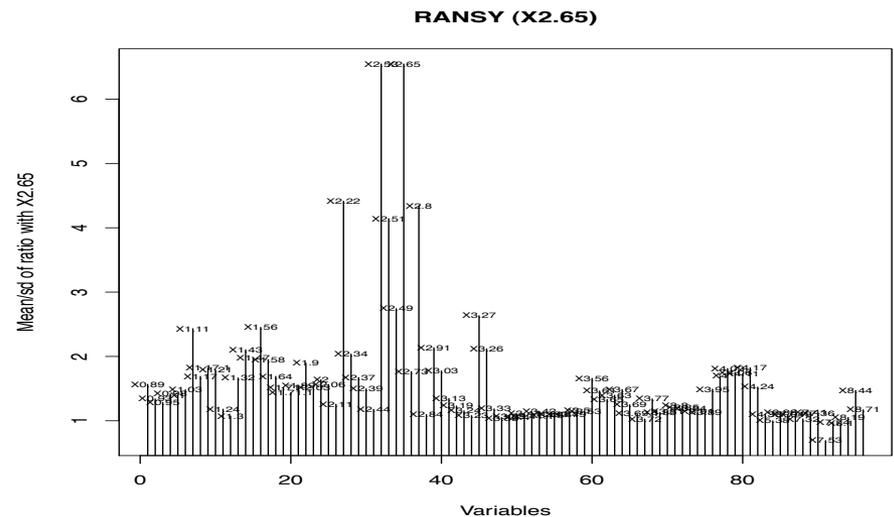
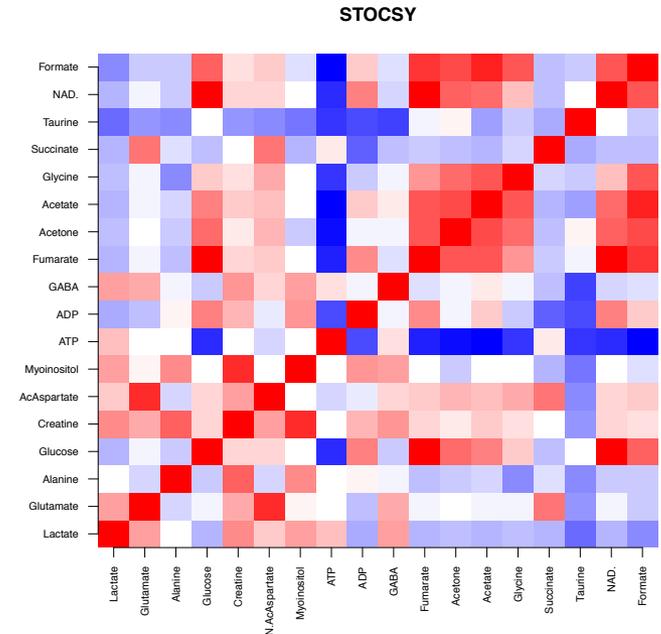
muma - interpretation

- STOCSY

- Structural correlations (> 0.95)
- Biochemical correlations (> 0.85 or < -0.85)

- RANSY

- Ratio between peaks from the same molecule is conserved
- Molecular assignment



muma - reports

- Automatic report of:
 - Graphics
 - Test results
 - Data set transformations
 - P-values

