

NMR Metabolomics Analysis

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NIH Common Fund Eastern Regional Comprehensive Metabolomics
Resource Core (ERCMRC)

Outline of Today's Training

- Introduction: Wimal Pathmasiri

- NMR Metabolomics: Wimal Pathmasiri
 - Study Design
 - Sample Preparation
 - Data Acquisition
 - Data Pre-processing
 - Statistical Analysis
 - Library Matching
 - Pathway Analysis

- Hands On Exercise: Delisha Stewart

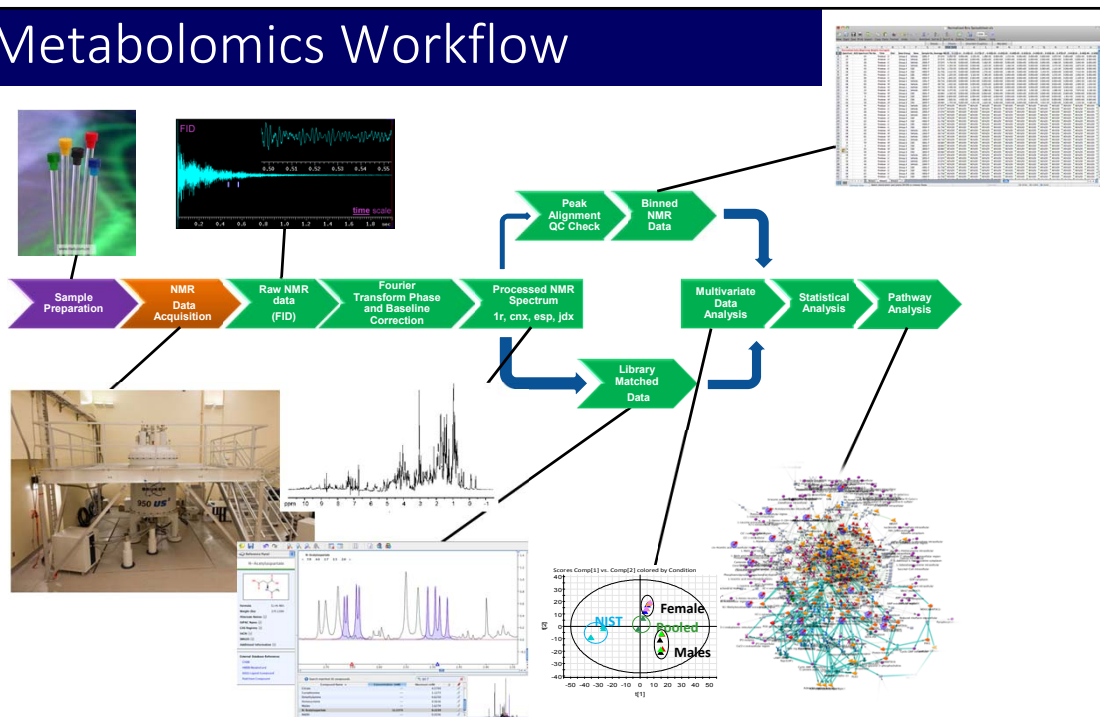
NMR Metabolomics

- Broad Spectrum
 - High throughput
 - NMR Binning
 - Multivariate analysis and other statistics
 - Identifying bins important for separating study groups
 - Library matching of bins to metabolites

- Targeted Metabolomics
 - Identifying a set of metabolites
 - Quantifying metabolites
 - Multivariate analysis and other statistics

- Pathway analysis
 - Use identified metabolites
 - Use other omics data for integrated analysis

NMR Metabolomics Workflow



Free Software available for NMR Metabolomics

- NMR Data Processing
 - ACD Software for Academics (ACD Labs, Toronto, Canada)
- Multivariate data analysis
 - MetaboAnalyst 3.0 (<http://www.metaboanalyst.ca>)
 - MetATT (<http://metatt.metabolomics.ca/MetATT/>)
 - MUMA (<http://www.biomolnmr.org/software.html>)
 - Other R-packages
- Library matching and Identification
 - BATMAN (Imperial College), Bayesil (David Wishart lab)
 - Use of databases
 - Birmingham Metabolite library, HMDB, BMRB
- Pathway analysis
 - Metaboanalyst, metaP Server, Met-PA, Cytoscape, KEGG, IMPALA

Also available through www.metabolomicsworkbench.org

Other Software available for NMR Metabolomics

COMMERCIAL

- NMR Data-preprocessing
 - ACD Software (ACD Labs, Toronto, Canada)
 - Chenomx NMR Suite 8.1 Professional
- Multivariate data analysis
 - SIMCA 14
- Other statistical analysis
 - SAS, SPSS
- Library matching and quantification
 - Chenomx NMR Suite 8.1 Professional
- Pathway analysis
 - GeneGo (MetaCore Module)
 - Ingenuity Pathway Analysis (IPA)

Sample Preparation, Data Acquisition, and Pre-processing

Important Steps in Metabolomics Analysis

- Study design
 - Match for factors such as gender, ethnicity, age, BMI (human studies)
 - Use of same strains in animal studies
- Sample collection
 - Collection vials, anticoagulant use (heparin, citrate, EDTA)
- Sample storage
 - -20 °C, -80 °C, minimize freeze-thaw cycles
- Sample preparation
 - Optimize the methods and use them consistently throughout study
 - Daily balance and pipette checks
- Use of Quality Check (QC) samples
 - Pooled QC samples (Phenotypic and combined pooled samples)
 - Use matching external pooled QC samples where pool samples cannot be prepared from study samples
- **Consistency and reproducibility are the keys for a successful metabolomics study**

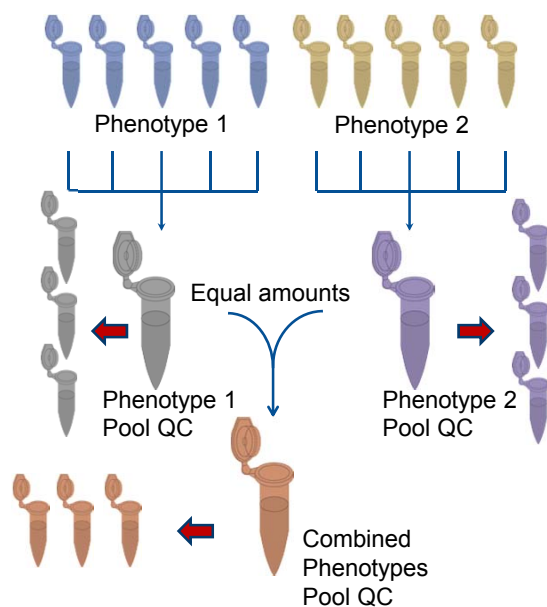
Sample Preparation for Metabolomics Analysis

Current sample preparation practices (in brief)

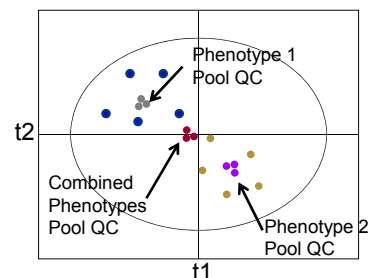
- **Biofluids**
 - Dilute with D₂O/ buffer/ 0.9% Saline
 - Add internal standard (ISTD, eg. Chenomx) solution or formate (for serum).
 - Centrifuge and transfer an aliquot into NMR tube
- **Tissue and Cells**
 - Homogenization performed in ice cold 50/50 acetonitrile/water
 - Supernatant dried down (lyophilized)
 - Reconstituted in D₂O and ISTD (eg. Chenomx) solution
- **Pooled QC Samples (Sample Unlimited)**
 - Mix equal volume of study samples to get pooled QC samples
 - 10% QC samples
- **Pooled QC Samples (Sample Limited)**
 - Use independent pool of similar samples
 - 10% QC samples
- **Daily balance and pipette check**

Samples are randomized for preparation and data acquisition

Preparing Pooled QC Samples



- Aliquots from each sample in the study phenotype are pooled (phenotypic pool)
- Equal amount of each phenotypic pools are pooled (Combined phenotypic pool)
- Replicates of pools are prepared
- Pool samples are prepared along with the study samples



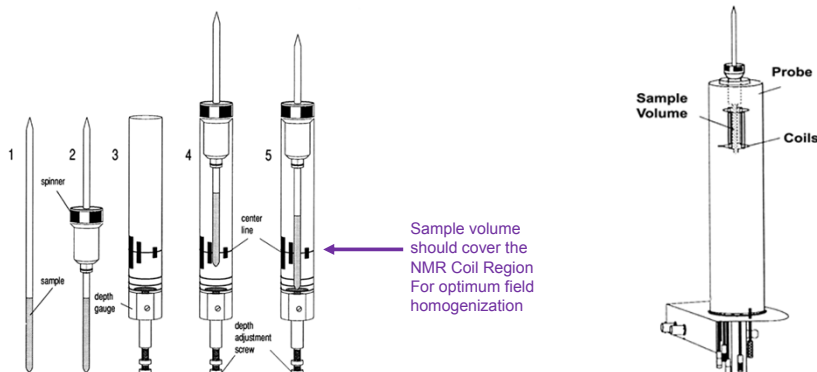
Pooled samples should cluster tightly

NMR Data Acquisition

- 1D NMR
 - 1st increment of NOESY
 - noesyprid (Bruker)
 - CPMG (serum or plasma)
 - cpmgpr1d (Bruker)
 - To remove broadening of signals due to macromolecules (eg. Proteins and lipids)
- 2D NMR (for structure elucidation)
 - 2D J-Resolved
 - COSY
 - TOCSY
 - HSQC
 - HMBC



Sample Amount in NMR tube



- At least 10% D₂O in the sample
- Optimum volume
 - 550 – 600 uL (5mm tube)
 - 200 uL (3 mm tube)
- Sample gauge is used

For very small sample amounts, a NMR with a microcoil probe is an option.

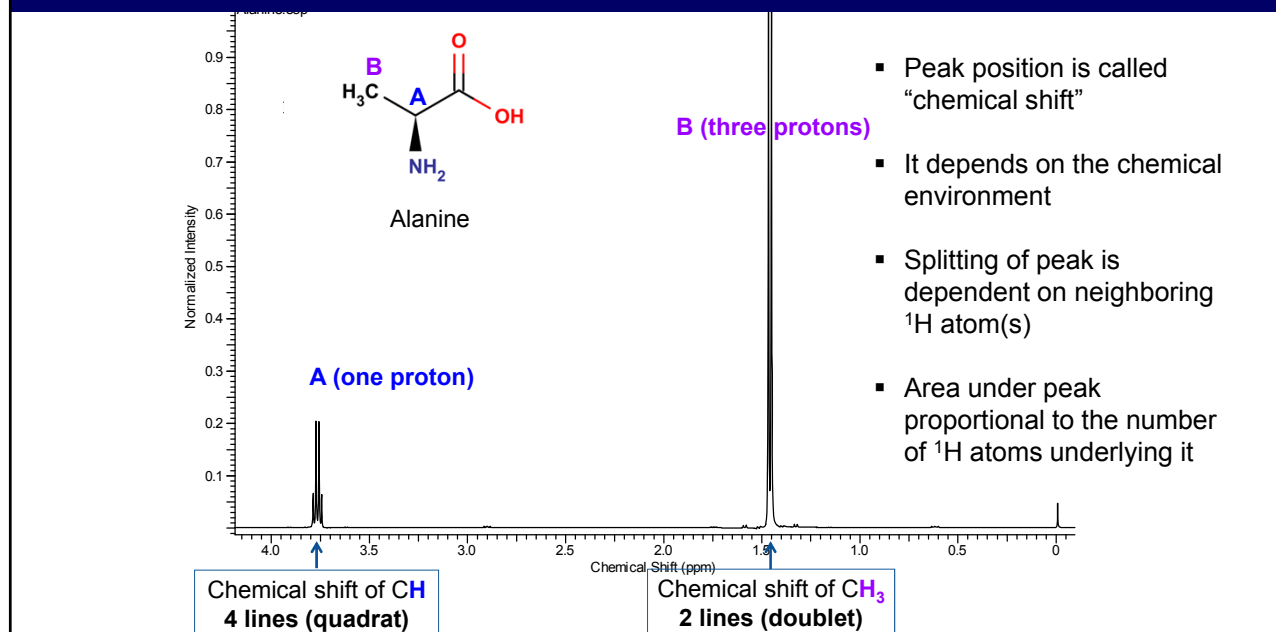
AVANCE Beginners User Guide 004 (Bruker, Germany)

NMR Data

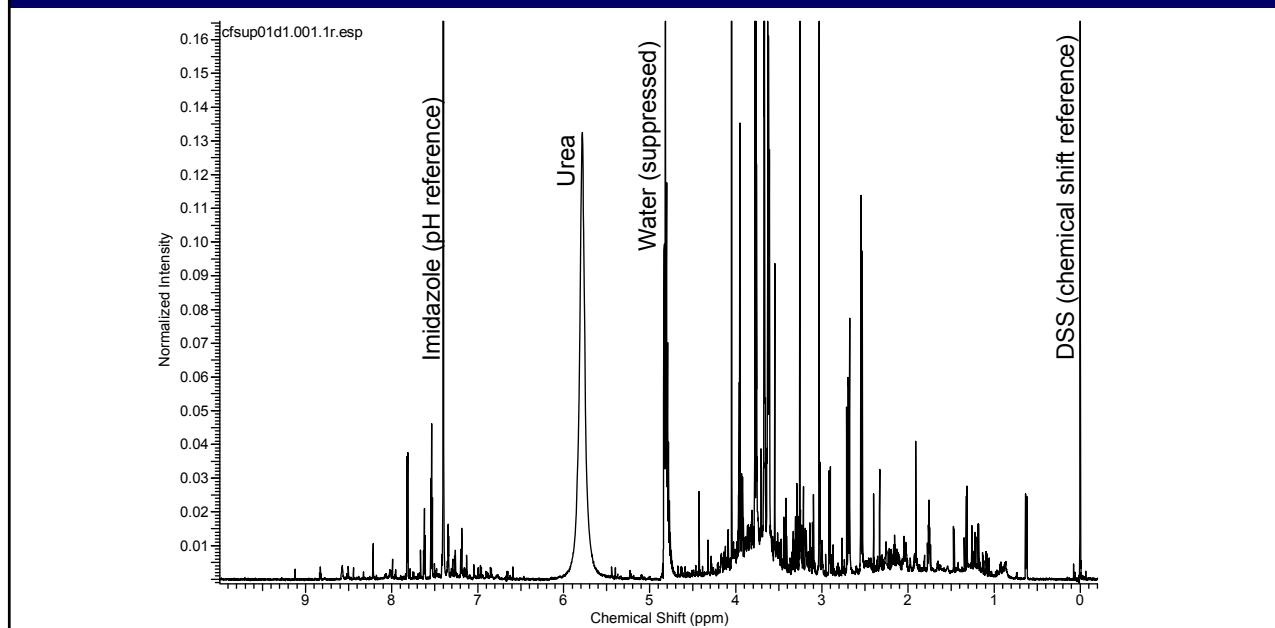
- A typical ^1H NMR Spectrum consists of thousands of sharp lines or signals.
- The intensity of the peak is directly related to the number of protons underlying the peak.
- The position of a particular peak in the X-axis of the NMR spectrum is called the “Chemical Shift” and it is measured in ppm scale
- The NMR spectrum obtained for the biological sample is referenced using a reference compound such as DSS, TSP, or Formate added to the sample in sample preparation step.
- pH indicator may also be used (for example, Imidazole)

DSS=4,4-dimethyl-4-silapentane-1-sulfonic acid, TSP=Trimethylsilyl propionate

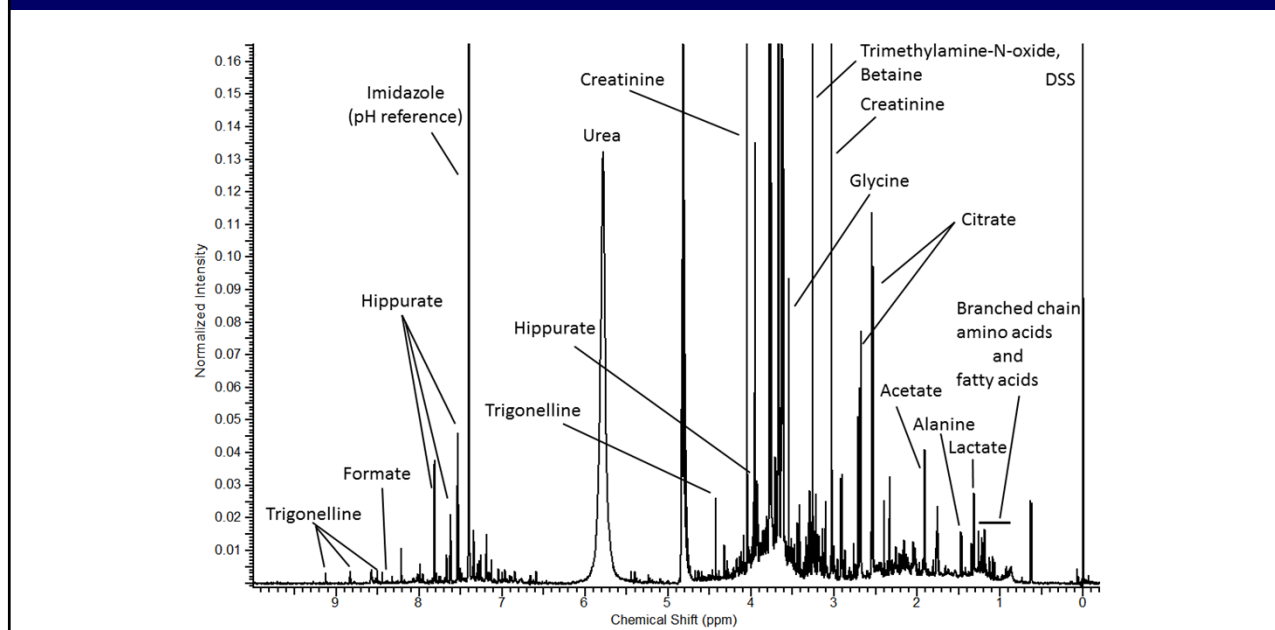
^1H NMR Spectrum for Alanine



Typical ^1H NMR Spectrum of Urine



Typical ^1H NMR Spectrum of Urine



Data Pre-processing

- After NMR data acquisition, the result is a set of spectra for all samples.
- For each spectrum, quality of the spectra should be assessed.
 - Line shape, Phase, Baseline
- Spectra should be referenced
 - Compounds commonly used: DSS, TSP, Formate
- Variations of pH, ionic strength of samples has effects on chemical shift
 - Peak alignment
 - Binning or Bucket integration
- Remove unwanted regions
- Normalize data (remove variation in concentration of samples)

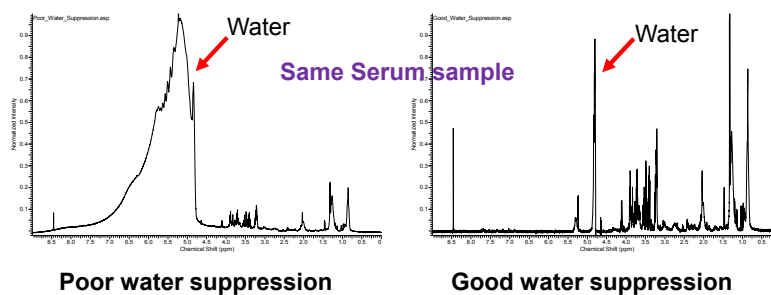
High quality data are needed

Quality Control Steps

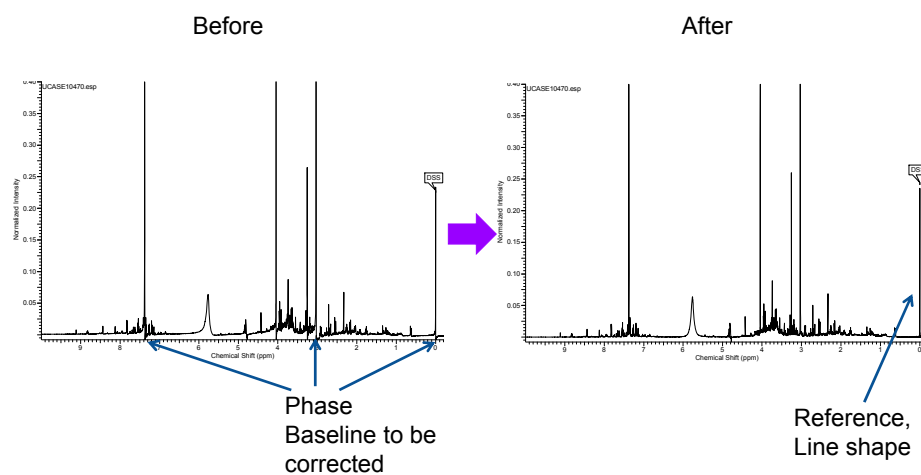
- Quality of metabolomics analysis depends on data quality
- Typical problems
 - Water peak (suppression issues)
 - Baseline (not set at zero and not a flat line)
 - Alignment of peaks (chemical shift, due to pH variation)
 - Variation in concentration (eg. Urine)
- High quality of data is needed for best results

Water Suppression Effects and Other Artifacts

- If water is not correctly suppressed or removed there will be effects on normalization
- Need to remove other artifacts
- Remove drug or drug metabolites



NMR Pre-processing



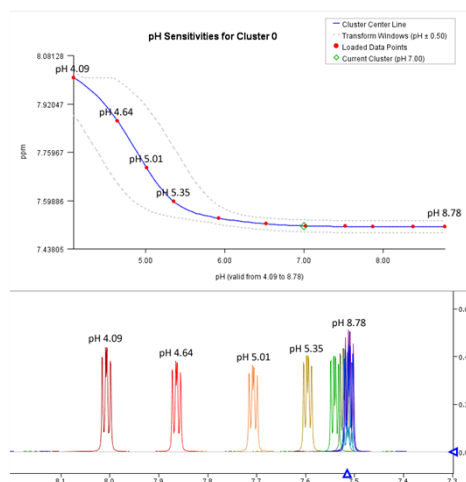
pH Dependence of Chemical Shift

Chemical shift variability

- pH
- ionic strength
- metal concentration

Methods to overcome this problem

- Use a buffer when preparing samples
- Binning (Bucketing)
 - Fixed binning
 - Intelligent binning
 - Optimized binning
- Available data alignment tools
 - Recursive Segment-wise Peak Alignment (RSPA)
 - Icoshift
 - speaq



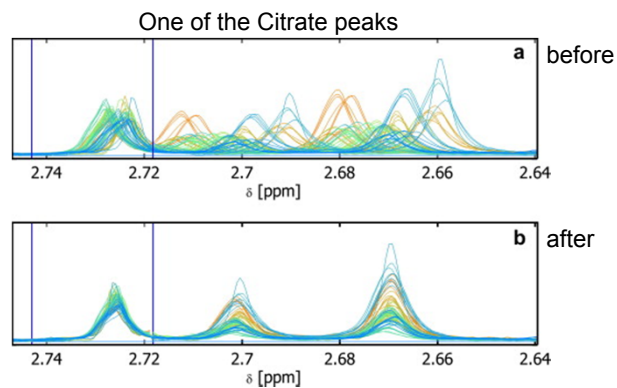
<http://www.chenomx.com/software/software.php>

Savorani, F. et al., *Journal of Magnetic Resonance*, Volume 202, Issue 2, 2010, 190 – 202
 Vu, T. N. et al., *BMC Bioinformatics* 2011, 12:405

Peak Alignment

Example

icoshift

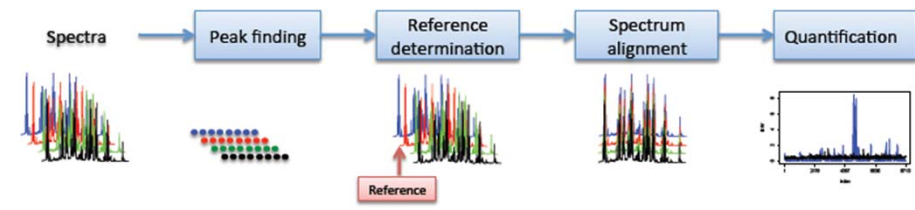


Savorani, F. et al., *Journal of Magnetic Resonance*, Volume 202, Issue 2, 2010, 190 - 202

Peak Alignment

Example

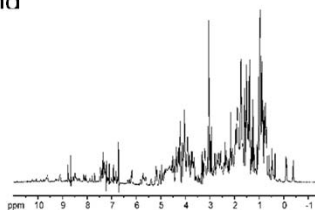
speaq



Vu, T. N. et al., *BMC Bioinformatics* 2011, 12:405

NMR Binning

- A form of quantification that consists of segmenting a spectrum into small areas (bins/buckets) and attaining an integral value for that segment
- Binning attempts to minimize effects from variations in peak positions caused by pH, ionic strength, and other factors.
- Two main types of binning
 - Fixed binning
 - Flexible binning

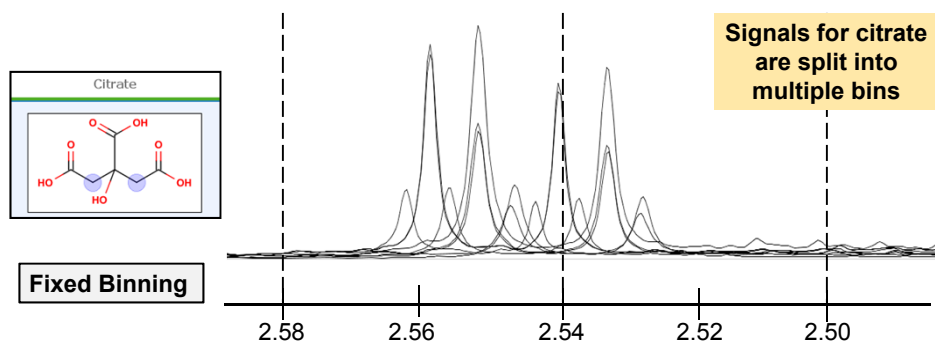


A screenshot of a software interface displaying a table of NMR data. The table has multiple columns, including chemical shift (ppm), integration, and other parameters. The data is organized into rows, likely representing different peaks or bins.

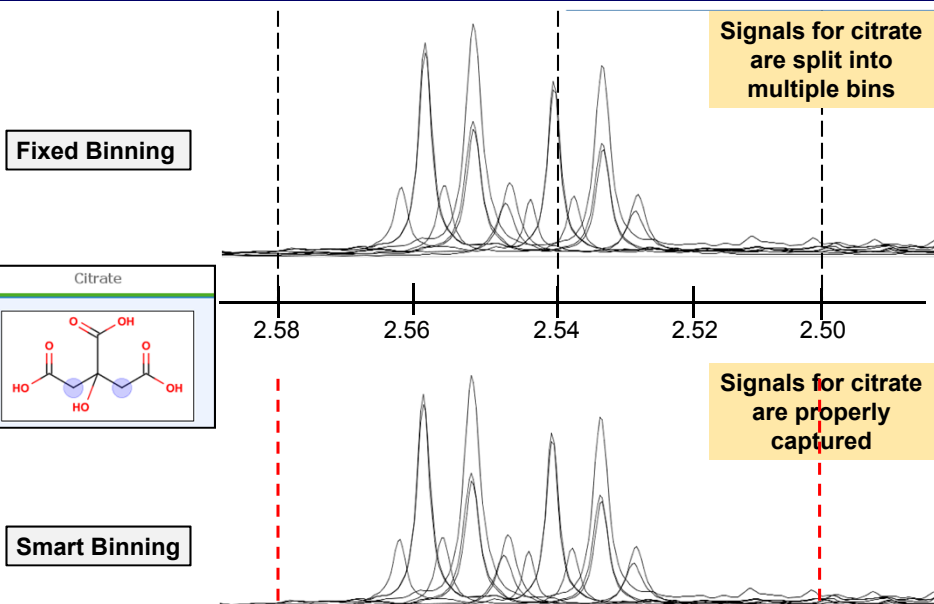
NMR Binning

Peak shift can cause the same peak across multiple samples to fall into different bins

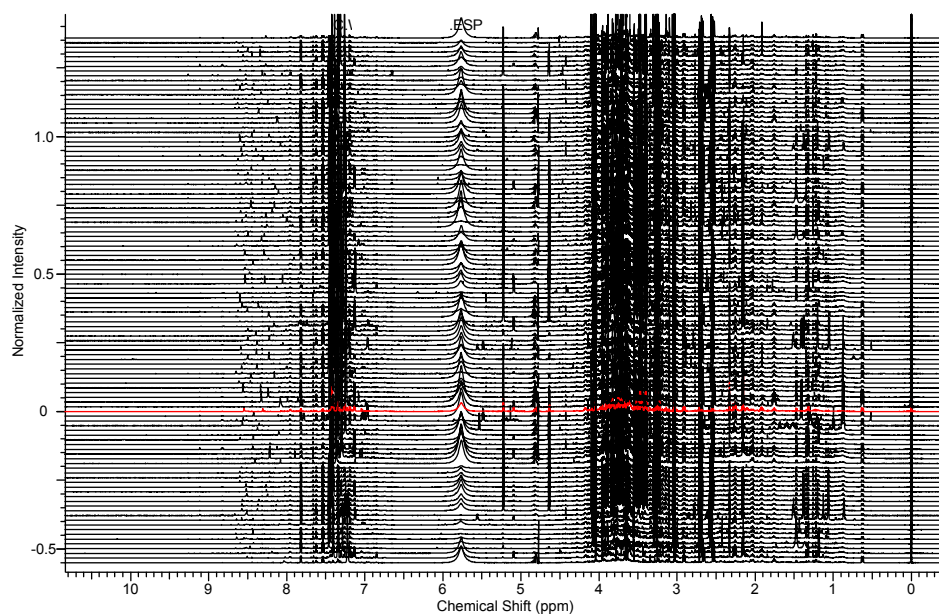
- The entire NMR spectrum is split into evenly spaced integral regions with a spectral window of typically 0.04 ppm.
- The major drawback of fixed binning is the non-flexibility of the boundaries.
- If a peak crosses the border between two bins it can significantly influence your data analysis



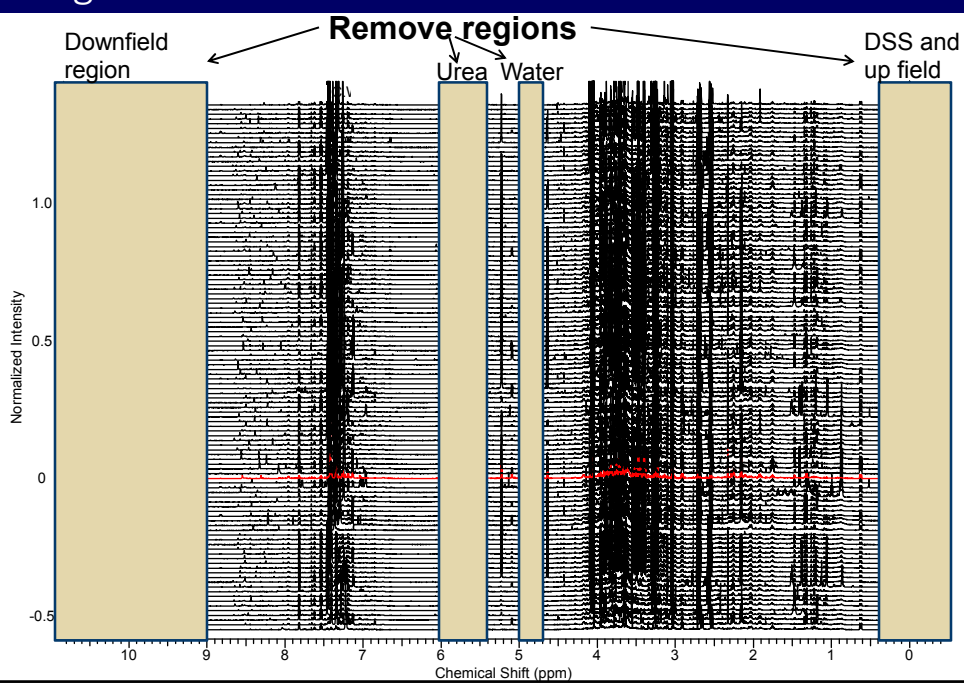
NMR Binning



NMR Binning



NMR Binning



NMR Binning

- Integrate bins (0.04 ppm bin size)
- Normalize integral of each bin to the total integral of each spectrum
- Merge metadata
- Result is a spreadsheet ready for further multivariate data analysis and other statistical analysis

Sample ID	Disease Group	[0.40 .. 0.46]	[0.46 .. 0.52]	[0.52 .. 0.54]	[0.54 .. 0.57]	[0.57 .. 0.60]	[0.60 .. 0.66]	[0.66 .. 0.68]	[0.68 .. 0.71]	[0.71 .. 0.75]
C0559	Cases	7.60E-05	0.00E+00	7.32E-02	8.48E-02	3.20E-02	1.84E+00	1.31E-01	3.60E-01	3.67E-01
C0629	Cases	0.00E+00	1.78E-02	0.00E+00	2.18E-02	0.00E+00	1.08E+01	0.00E+00	0.00E+00	3.02E-02
C0640	Cases	3.44E-04	0.00E+00	1.83E-03	1.86E-04	0.00E+00	4.51E+00	0.00E+00	0.00E+00	0.00E+00
C0835	Cases	6.41E-04	0.00E+00	6.44E-03	0.00E+00	3.96E-03	3.28E+00	0.00E+00	5.12E-03	1.75E-02
D0613	Cases	6.63E-03	0.00E+00	0.00E+00	1.06E-02	0.00E+00	5.79E+00	0.00E+00	6.36E-02	3.02E-01
D0762	Cases	0.00E+00	0.00E+00	1.79E-02	1.98E-02	0.00E+00	9.37E+00	0.00E+00	0.00E+00	1.74E-02
D1113	Cases	3.14E-03	2.42E-03	8.02E-02	1.04E-01	5.32E-03	3.74E+00	0.00E+00	2.02E-02	1.84E-01
D1158	Cases	0.00E+00	3.71E-03	2.35E-02	4.83E-02	0.00E+00	5.02E+00	0.00E+00	1.91E-02	0.00E+00
D2090	Cases	0.00E+00	0.00E+00	2.45E-03	9.98E-04	0.00E+00	5.76E+00	0.00E+00	1.24E-02	1.04E-02
E0004	Cases	1.72E-03	0.00E+00	6.85E-02	3.05E-02	0.00E+00	1.47E+00	6.90E-02	3.61E-01	4.08E-01
E0195	Cases	0.00E+00	1.69E-03	5.57E-02	6.29E-02	0.00E+00	2.77E+00	1.34E-01	2.04E-01	4.56E-01
E0225	Cases	1.25E-03	0.00E+00	1.00E-03	1.99E-02	0.00E+00	9.17E+00	0.00E+00	1.08E-02	2.30E-02
E0339	Cases	4.11E-03	0.00E+00	2.62E-02	1.82E-03	3.08E-03	3.92E+00	0.00E+00	3.28E-02	9.09E-01
E0487	Cases	1.72E-03	0.00E+00	0.00E+00	1.00E-02	0.00E+00	4.00E+00	0.00E+00	1.36E-02	0.00E+00
F0036	Cases	1.66E-02	0.00E+00	0.00E+00	2.06E-02	0.00E+00	1.22E+01	1.04E-02	0.00E+00	5.97E-01
F0108	Cases	0.00E+00	2.31E-03	6.30E-03	1.11E-02	0.00E+00	7.17E+00	0.00E+00	1.65E-02	2.21E-01
A0233	Control	0.00E+00	1.86E-02	0.00E+00	1.82E-02	0.00E+00	1.61E+01	0.00E+00	2.91E-03	0.00E+00
A0490	Control	0.00E+00	0.00E+00	2.99E-03	3.60E-02	0.00E+00	2.97E+00	0.00E+00	4.00E-02	5.46E-01
A2003	Control	0.00E+00	0.00E+00	3.45E-02	2.20E-02	0.00E+00	1.80E+00	0.00E+00	0.00E+00	0.00E+00
C0586	Control	0.00E+00	1.69E-02	0.00E+00	6.64E-03	0.00E+00	1.92E+01	0.00E+00	6.51E-02	0.00E+00
C2177	Control	0.00E+00	0.00E+00	3.02E-02	3.59E-02	0.00E+00	2.35E+00	0.00E+00	3.19E-02	1.49E-01
D0177	Control	9.21E-03	0.00E+00	1.69E-02	1.47E-02	0.00E+00	2.43E+00	0.00E+00	4.46E-02	0.00E+00
D0729	Control	0.00E+00	1.88E-03	5.58E-02	7.87E-02	2.92E-02	3.16E+00	6.59E-02	2.80E-01	4.30E-01
D0909	Control	0.00E+00	1.08E-03	0.00E+00	5.69E-03	0.00E+00	2.49E+00	0.00E+00	1.01E-02	1.87E-01
D0945	Control	0.00E+00	4.79E-04	7.00E-03	0.00E+00	4.19E-03	3.99E+00	0.00E+00	1.11E-03	3.96E-02
D1174	Control	0.00E+00	9.33E-04	0.00E+00	3.43E-03	1.30E-02	7.21E+00	6.53E-03	0.00E+00	1.66E-02
D2054	Control	1.55E-03	0.00E+00	0.00E+00	1.22E-02	0.00E+00	2.07E+00	0.00E+00	1.28E-02	3.90E-01
D2062	Control	2.39E-05	0.00E+00	6.04E-02	2.99E-02	0.00E+00	4.94E+00	0.00E+00	9.95E-03	0.00E+00
D2079	Control	2.73E-02	0.00E+00	1.81E-03	1.17E-02	0.00E+00	3.38E+01	7.87E-02	0.00E+00	5.91E+00

Data Normalization,
Transformation, and Scaling

Normalization

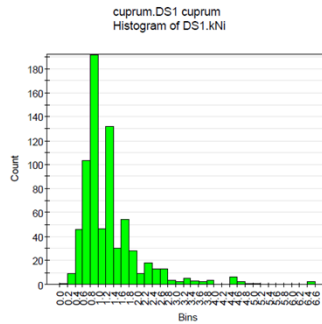
- Normalization reduces the sample to sample variability due to differences in sample concentrations—particularly important when the matrix is urine
 - Normalization to total intensity is the most common method
 - For each sample, divide the individual bin integral by the total integrated intensity
 - Other Methods
 - Normalize to a peak that is always present in the same concentration, for example normalizing to creatinine
 - Probabilistic quotient normalization
 - Quantile and cubic spline normalization

Centering, Scaling, and Transformations

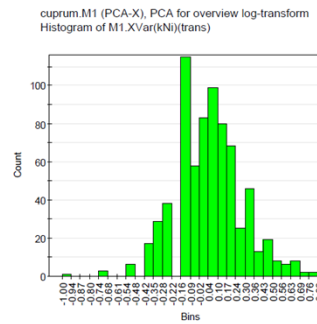
I	Centering	$\tilde{x}_{ij} = x_{ij} - \bar{x}_i$	III	Log transformation	$\tilde{x}_{ij} = \log(x_{ij})$ $\tilde{x}_{ij} = \tilde{x}_{ij} - \bar{\tilde{x}}_i$
<hr/>					
II	Autoscaling	$\tilde{x}_{ij} = \frac{x_{ij} - \bar{x}_i}{s_i}$		Power transformation	$\tilde{x}_{ij} = \sqrt{x_{ij}}$ $\tilde{x}_{ij} = \tilde{x}_{ij} - \bar{\tilde{x}}_i$
	Range scaling	$\tilde{x}_{ij} = \frac{x_{ij} - \bar{x}_i}{(x_{i_{\max}} - x_{i_{\min}})}$		Analysis results vary depending on the scaling/ transformation methods used.	
	Pareto scaling	$\tilde{x}_{ij} = \frac{x_{ij} - \bar{x}_i}{\sqrt{s_i}}$			
	Vast scaling	$\tilde{x}_{ij} = \frac{(x_{ij} - \bar{x}_i)}{s_i} \cdot \frac{\bar{x}_i}{s_i}$		Van den Berg et al 1006, BMC Genomics, 7, 142	
	Level scaling	$\tilde{x}_{ij} = \frac{x_{ij} - \bar{x}_i}{\bar{x}_i}$			

Data Transformation

- Before transformation
 - skew distribution



- After log-transformation
 - More close to normal distribution



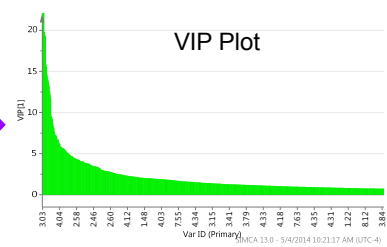
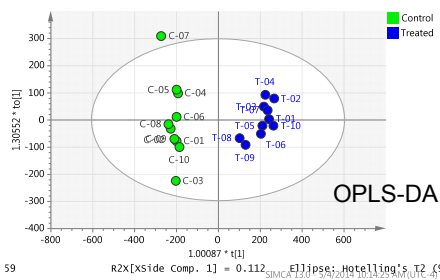
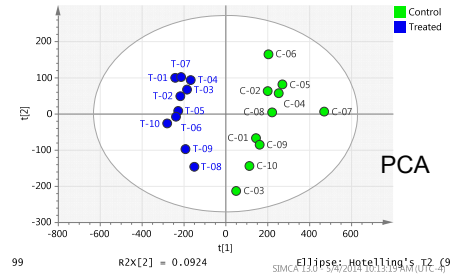
Susan Wicklund, Multivariate data analysis for omics, Sept 2-3 2008, Umetrics training

Scaling

- Unit variance (autoscaling) divides the bin intensity by the standard deviation
 - May increase your baseline noise
 - Dimensionless value after scaling
- Pareto scaling divides the bin intensity by the square root of the standard deviation
 - Not dimensionless after scaling
- For NMR data, centering with pareto scaling is commonly used

Multivariate Data Analysis and Other Statistical Analyses

- Mean centered and scaled data
- Non-supervised analysis
 - Principal component analysis (PCA)
- Supervised analysis
 - PLS-DA and OPLS-DA
- Loadings plots and VIP Plots to identify discriminatory bins
- p-Value, fold change



Library Matching Pathway Analysis

Chenomx Library

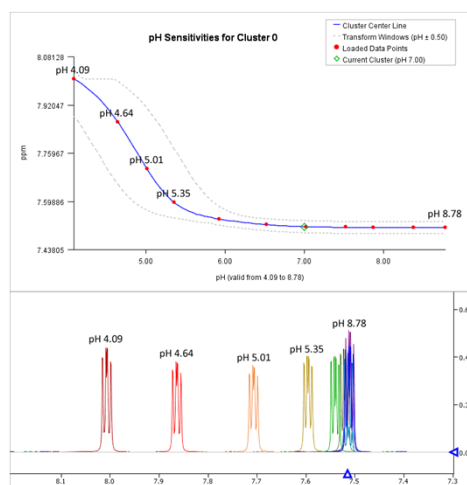
1,3-Dihydroxyacetone, 1,3-Dimethylurate, 1,6-Anhydro- β -D-glucose, 1,7-Dimethylxanthine, 1-Methylnicotinamide, 2'-Deoxyadenosine, 2'-Deoxyguanosine, 2'-Deoxyinosine, 2-Amino adipate, 2-Aminobutyrate, 2-Ethylacrylate, 2-Furoate, 2-Hydroxy-3-methylvalerate, 2-Hydroxybutyrate, 2-Hydroxyglutarate, 2-Hydroxyisobutyrate, 2-Hydroxyisocaproate, 2-Hydroxyisovalerate, 2-Hydroxyphenylacetate, 2-Hydroxyvalerate, 2-Methylglutarate, 2-Octenoate, 2-Oxobutyrate, 2-Oxocaproate, 2-Oxoglutarate, 2-Oxopropionate, 2-Phosphoglycerate, 3,4-Dihydroxymandelate, 3,5-Dibromotyrosine, 3-Aminoisobutyrate, 3-aminobutyrate, 3-Hydroxy-3-methylglutarate, 3-Hydroxybutyrate, 3-Hydroxyisovalerate, 3-Hydroxymandelate, 3-Hydroxyphenylacetate, 3-Indoxylsulfate, 3-Methyl-2-oxovalerate, 3-Methyladipate, 3-Methylxanthine, 3-Phenyllactate, 3-Phenylpropionate, 4-Aminobutyrate, 4-Aminohippurate, 4-Hydroxy-3-methoxymandelate, 4-Hydroxybutyrate, 4-Hydroxybutyrate, 4-Hydroxyphenylacetate, 4-Hydroxyphenyllactate, 4-Pyridoxate, 5,6-Dihydroxytryptamine, 5,6-Dihydrotryptamin, 5-Amino levulinic acid, 5-Hydroxyindole-3-acetate, 5-Hydroxylysine, 5-Methoxysalicylate, Acetaldehyde, Acetamide, Acetaminophen, Acetate, Acetoacetate, Acetone, Acetylsalicylate, Adenine, Adenosine, Adipate, Alanine, Allantoin, Alloisoleucine, Anserine, Arginine, Argininosuccinate, Asparagine, Aspartate, Benzoate, Betaine, Biotin, Butyrate, Butyrolactone, Caffeine, Caprate, Caprylate, Carnitine, Carnosine, Choline, Cinnamate, Citrate, Citrulline, Creatine, Creatinine, Cysteine, Cystine, Cytidine, Cytosine, DSS (Chemical Shift Indicator), Dimethylamine, Epicatechin, Ethanol, Ethanolamine, Ethylene glycol, Ethylmalonate, Ferulate, Formate, Fructose, Fucose, Fumarate, Galactarate, Galactitol, Galactonate, Galactose, Gentisate, Glucarate, Glucose, Glutamate, Glutamine, Glutarate, Glutaric acid monomethyl ester, Glutathione, Glycerate, Glycerol, Glycine, Glycolate, Glycylproline, Guanoacetate, Guanine, Hippurate, Histidine, Homocitrulline, Homocystine, Homogentisate, Homoserine, Homovanillate, Hypoxanthine, Ibuprofen, Imidazole, Indole-3-acetate, Inosine, Isobutyrate, Isocaproate, Isocitrate, Isoleucine, Isopropanol, Isovalerate, Kynurenate, Kynurenine, Lactate, Lactose, Leucine, Levulinic acid, Lysine, Malate, Maleate, Malonate, Mannitol, Mannose, Methanol, Methionine, Methylamine, Methylguanidine, Methylmalonate, Methylsuccinate, N,N-Dimethylformamide, N,N-Dimethylglycine, N-Acetylaspartate, N-Acetylglutamate, N-Acetylglycine, N-Carbamoyl- β -alanine, N-Carbamoylaspartate, N-Isovaleroylglycine, NAD⁺, Niacinamide, Nicotinate, O-Acetylcarnitine, O-Phosphocholine, O-Phosphoethanolamine, O-Phosphoserine, Ornithine, Oxalacetate, Oxypurinol, Pantothenate, Phenol, Phenylacetate, Phenylacetylglucine, Phenylalanine, Pimelate, Proline, Propionate, Propylene glycol, Protocatechuic acid, Pyridoxine, Pyroglutamate, Pyruvate, Quinolinate, Riboflavin, Ribose, S-Adenosylhomocysteine, S-Sulfocysteine, Salicylate, Salicylurate, Sarcosine, Serine, Suberate, Succinate, Succinylacetone, Sucrose, Tartrate, Taurine, Theophylline, Threonate, Threonine, Thymine, Thymol, Tiglylglycine, Trigonelline, Trimethylamine, Trimethylamine N-oxide, Tryptophan, Tyramine, Tyrosine, Uracil, Urea, Uridine, Urocanate, Valerate, Valine, Valproate, Vanillate, Xanthine, Xanthosine, Xylose, cis-Aconitate, myo-Inositol, o-Cresol, p-Cresol, trans-4-Hydroxy-L-proline, trans-Aconitate, β -Alanine, n-Methylhistidine, τ -Methylhistidine

Over 320 metabolites

pH sensitive library of ¹H NMR Spectra

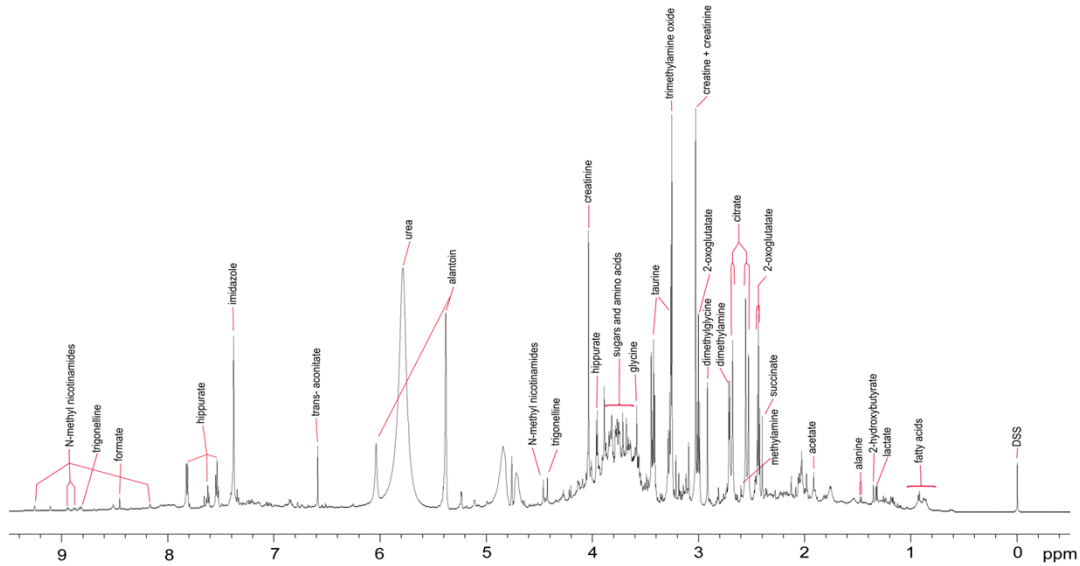
Customizable

Chemical Shift and pH Dependence

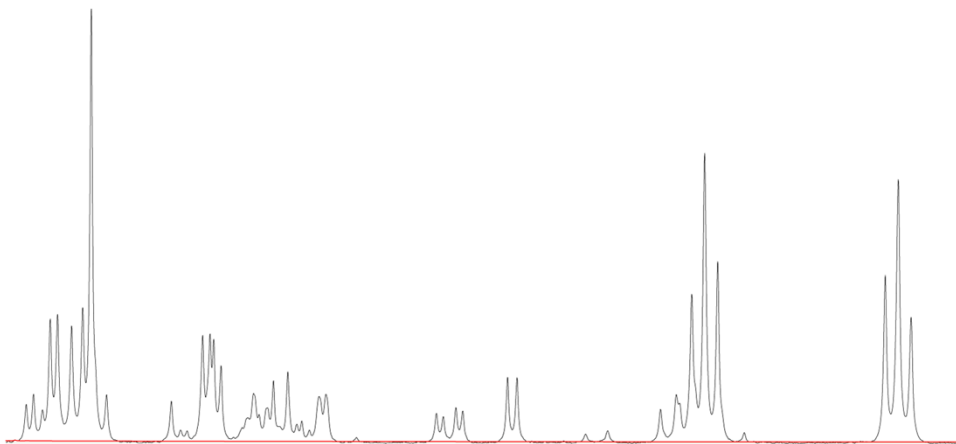


Source: <http://www.chenomx.com/software/>

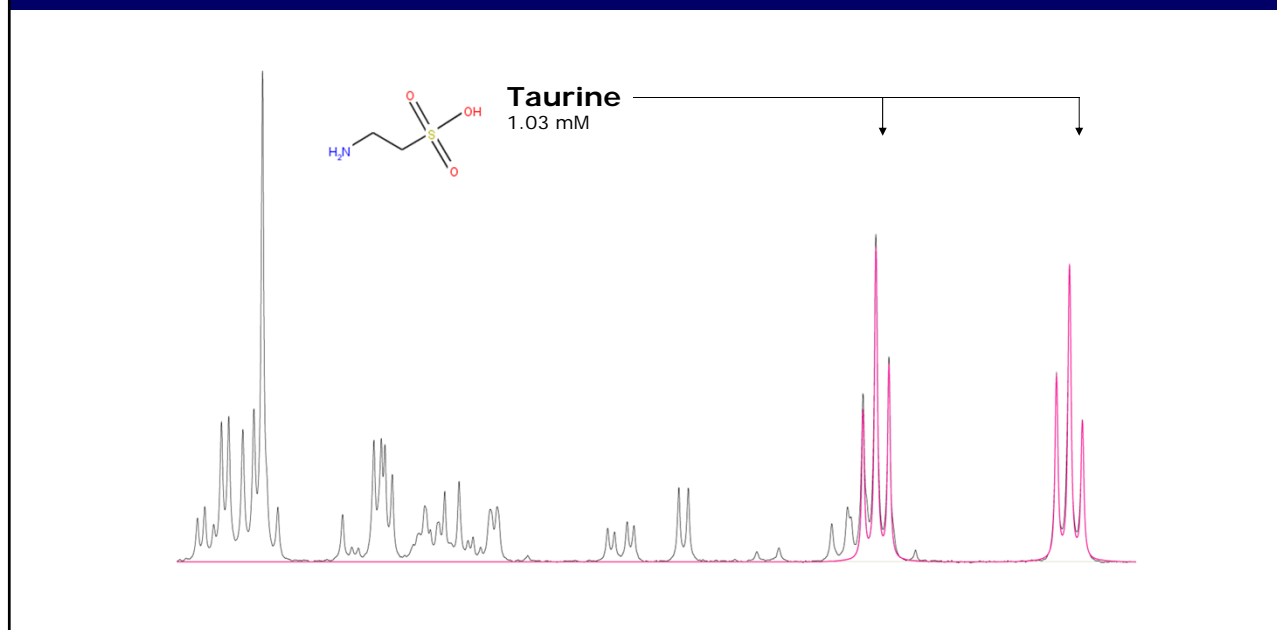
NMR Spectrum of Urine with Chenomx Library Fit of Metabolites



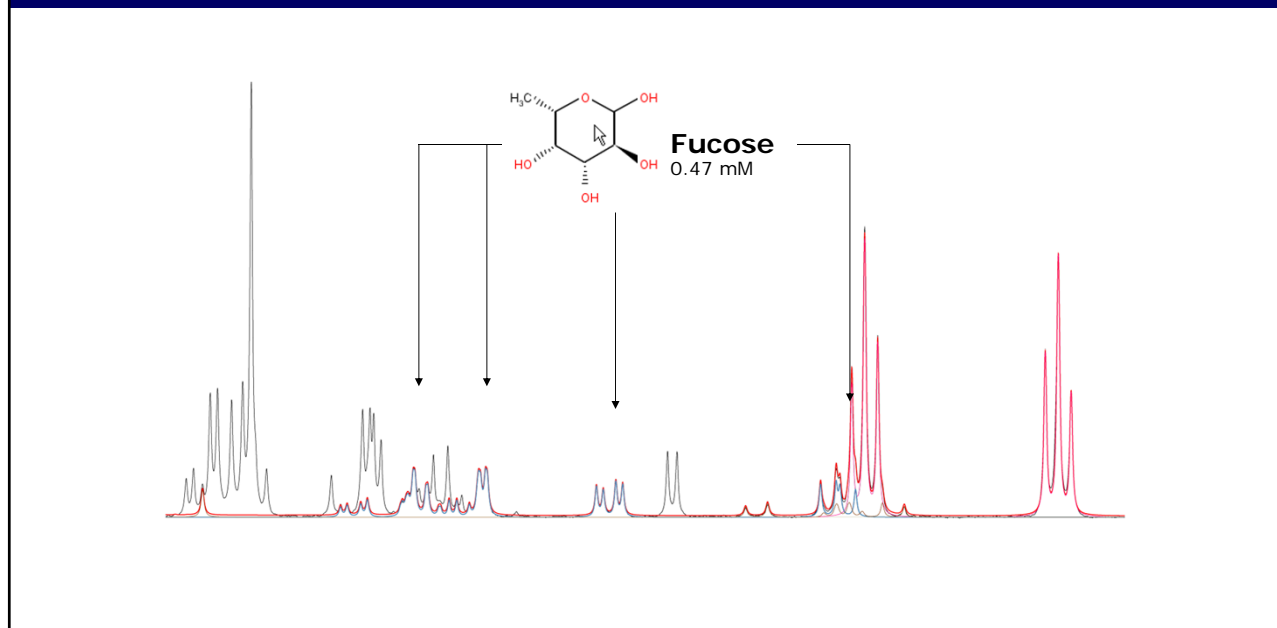
Fitting of Metabolites



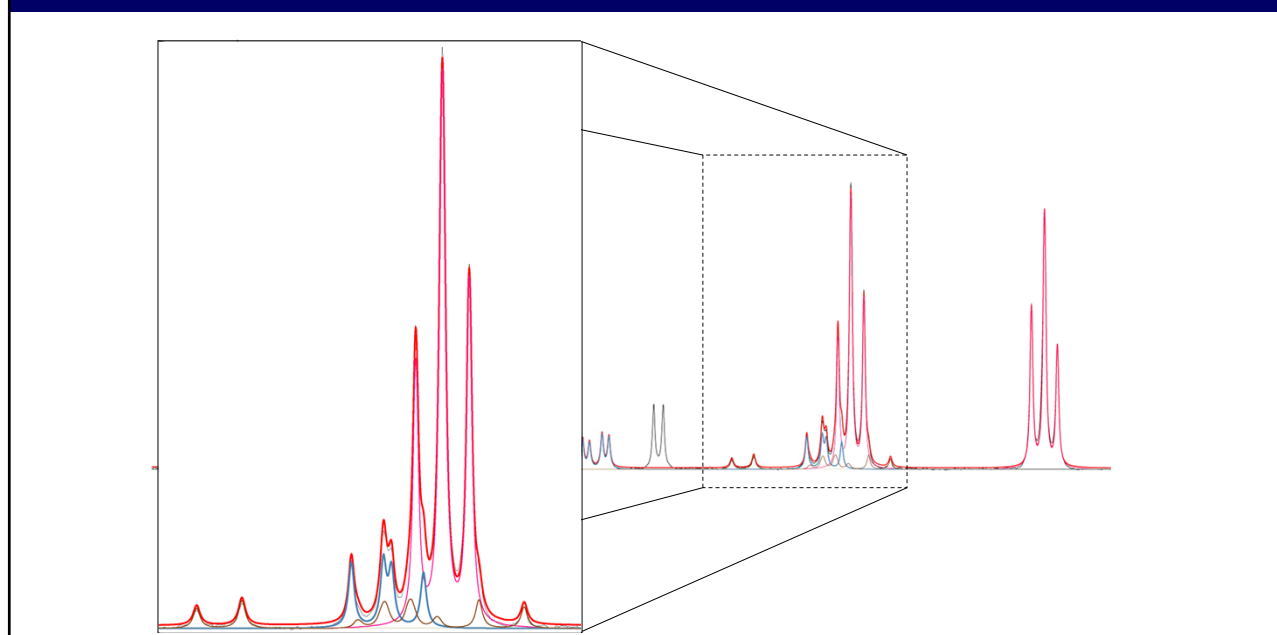
Fitting Taurine



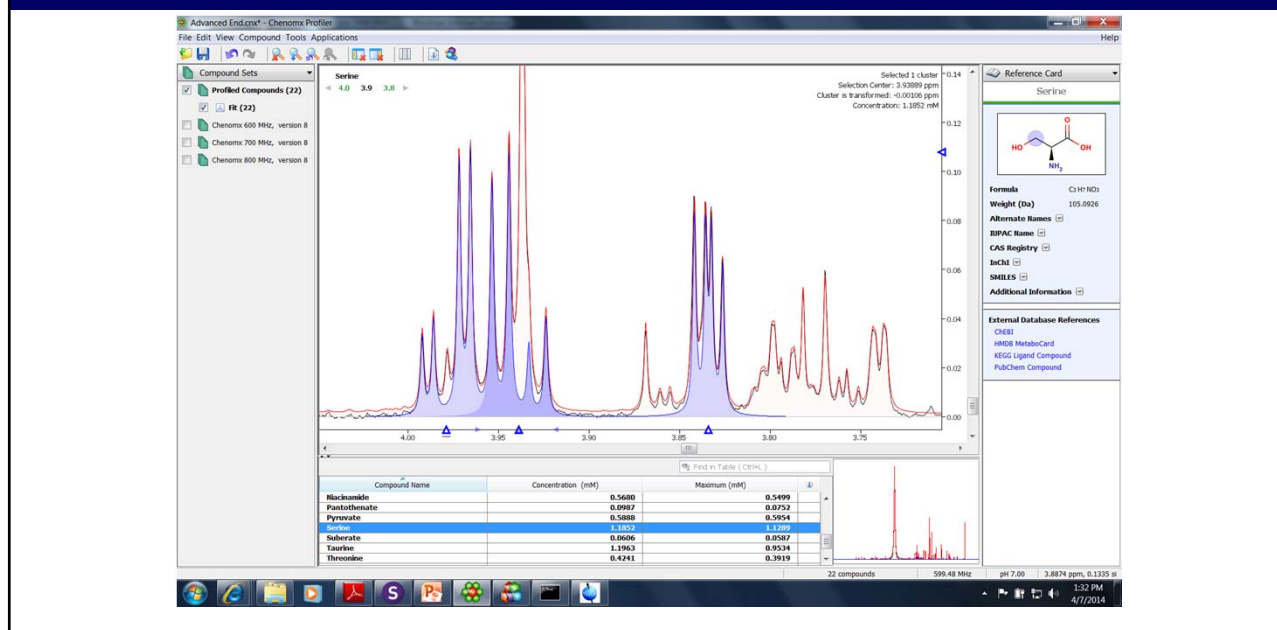
Fitting Fucose



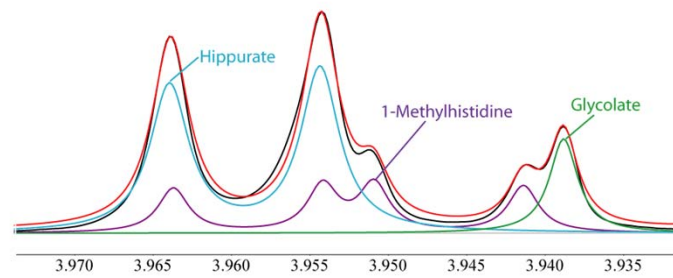
Additive Fit



Additive Fit



Chenomx Helps Resolving Ambiguity in Highly Overlapped Regions



Interpreting Results and Pathway Analysis

Once we have performed a metabolomics analysis:

- We find some important metabolites that are responsible for the separation of study groups.
- The next questions are
 - What does it means?
 - How do you correlate these finding to your study questions?
 - Does it explain any findings that are meaningful for your study hypotheses?
 - Does it generate a new hypothesis?
- How do you answer these questions?
 - Next step is to interpret results and perform metabolic pathway analysis

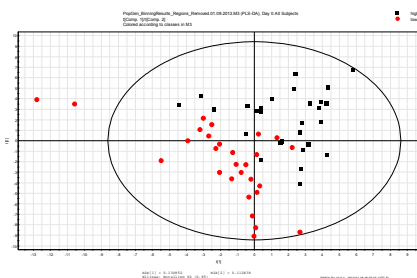
Interpreting Results and Pathway Analysis

- There are a number of freely available software
 - meta-P Server, Metaboanalyst, Met-PA, web based KEGG Pathways, Cytoscape.
 - GeneGo, Ingenuity Pathway Analysis (Commercial)
- Another way of interpreting metabolomics results is to use traditional biochemistry text books.
- The input for pathway analysis is typically a list of metabolites (with any fold change or p-value information)
- Genomics, transcriptomics, and/or proteomics data can be integrated
- Once these pathways are identified, you may perform a targeted metabolomics analysis to validate the findings from global analysis.

Study Example

Day 0 serum- Predicting Day 28 Response to Vaccine

PLS-DA
Day 0 – High Responders (Black) vs
Low Responders (Red)



Preliminary results

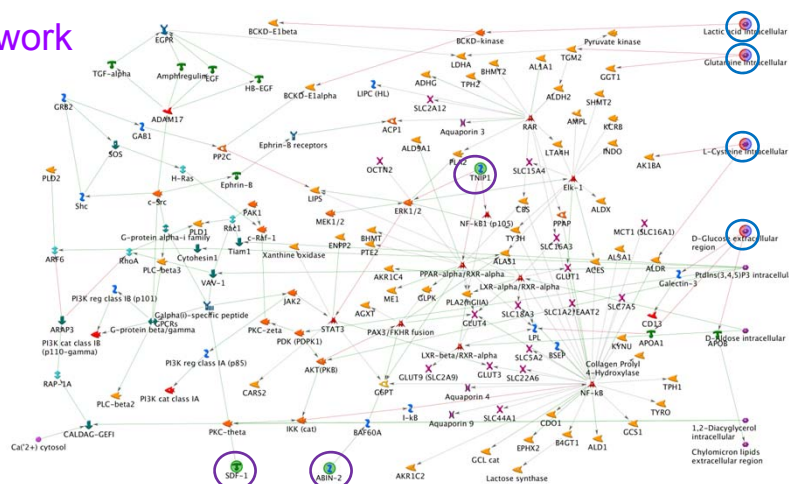
Subset of Metabolites that Influence the Separation of Subjects at Day 0 (VIP ≥ 1 or p-value ≤ 0.1)

Isoleucine**	Creatinine**
Leucine**	Cysteine**
Valine	Histidine
3-Methyl-2-oxo-isovalerate	Choline
3-Hydroxybutyrate	Glucose
Lactate	Betaine
Alanine	TMAO
Acetate**	Glycine
Proline*	Glycerol
Glutamate**	Serine
Glutamine**	Creatine
Pyruvate	Tyrosine*
2-Oxoisocaproate	Histidine
Methylguanidine**	Tryptophan
Formate	Phenylalanine

*p-value < 0.05, **p-value ≤ 0.1

Day 0 High vs Low Responders

GeneGo Network Analysis



○ Receptor ligands/binding proteins related to gene markers from genetics analysis. Majumder et al. 2012, Eur. J. Human Genetics, 1-7

○ Metabolites that linked in the pathways

Preliminary results

Literature

NMR data acquisition is performed by using methods cited in Beckonert et al. (2007), Nature Protocols, 2 (11), 2692-2703.

Xia, J. et al (2011) Web-based inference of biological patterns, functions and pathways from metabolomic data using MetaboAnalyst, Nature Protocols 6, 743–760 (2011)
doi:10.1038/nprot.2011.319

Hao, J. et al. (2014) Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN, Nature Protocols 9, 1416–1427 (2014) doi:10.1038/nprot.2014.090

Savorani , F. et al, Journal of Magnetic Resonance, Volume 202, Issue 2, 2010, 190 – 202

Vu, T. N. et al., BMC Bioinformatics 2011, 12:405

NMR Metabolomics Hands On Exercise

NMR Hands On Exercise: Study Design

- Drug Induced Liver Injury (DILI) Study using Rat Model
- 3 Study groups and 2 time points
 - Vehicle Control (time matched)
 - Low Dose ("no effect" level, Day 01 and Day 14)
 - High Dose (Day 01 and Day 14)
- 24h Urine collected
- Samples prepared by mixing an aliquot of urine with Phosphate buffer + Chenomx ISTD (DSS, D₂O, and Imidazole)
 - DSS (Chemical shift and line shape reference)
 - Imidazole (pH reference)

NMR Binned Data

- Three (3) Spreadsheets provided
 1. UAB_RFA_Metaboanalyst.csv
 2. UAB_RFA_Metaboanalyst_D14_NoPools.csv
 3. UAB_RFA_Metaboanalyst_D14_Vehicle_vs_HighDose.csv
- Spreadsheets 2-3 were derived from the initial spreadsheet no. 1 (for easy upload into Metaboanalyst in the subsequent analyses)

Metaboanalyst

Please go to the webpage: <http://www.Mw.metaboanalyst.ca/MetaboAnalyst/>

MetaboAnalyst 3.0
— a comprehensive tool suite for metabolomic data analysis

Welcome [click here to start](#) [>> access old version](#)

News & Updates

- Updated the **confidence interval** graphics for both chemometrics and ROC curves, (01/06/2015) **NEW**
- Updated the **Heatmaps** function for better visualization of large data, (12/22/2014)
- Added a new module for **Integrated Pathway Analysis** on genes and metabolites that have both changed significantly under the same experimental conditions, (12/17/2014)
- Added a new module for **Biomarker Analysis**, (12/12/2014)
- Added sorting and filtering support in the feature details table, (11/12/2014)
- Added new functions to support **interactive 3D PCA and PLS-DA** visualization, (10/31/2014)
- Added a new module on **Power Analysis** to support sample size and power analysis for pilot metabolomic studies, (10/30/2014)

[Read more >>>](#)

Please Cite:

Xia, J., Mandal, R., Siničnik, I., Broadhurst, D., and Wishart, D.S. (2012) *MetaboAnalyst 2.0 - a comprehensive server for metabolomic data analysis*. Nucl. Acids Res. 40, W127-W133.

Xia, J., Psychogios, N., Young, N. and Wishart, D.S. (2009) *MetaboAnalyst: a web server for metabolomic data analysis and interpretation*. Nucl. Acids Res. 37, W652-660.

Project objective: To provide a user-friendly, web-based analytical pipeline for high-throughput metabolomics studies. In particular, MetaboAnalyst aims to offer a variety of commonly used procedures for metabolomic data processing, normalization, multivariate statistical analysis, as well as data annotation. The current implementation focuses on exploratory statistical analysis, functional interpretation, and advanced statistics for translational metabolomics studies.

Data formats: Diverse data types from current metabolomic studies are supported ([details](#)) including compound concentrations, NMR/MS spectral bins, NMR/MS peak intensity table, NMR/MS peak lists, and LC-MS spectra.

Data processing: Depending on the type of the uploaded data, different data processing options are available ([details](#)). This is followed by data normalization steps including normalization by constant sum, normalization by a reference sample/feature, sample specific normalization, autoPathway scaling, etc.

Statistical analysis: A wide array of commonly used statistical and machine learning methods are available ([details](#)) - fold change analysis, Heat volcano plot, and one-way ANOVA, correlation analysis, [multivariate](#) - principal component analysis (PCA) and partial least squares - discriminant analysis (PLS-DA), [high-dimensional feature selection](#) - significance analysis of microarrays (and metabolites) (SAM), [new approach for gene analysis of metabolites and metabolites](#) (DEG), [rankings](#) - [relevance](#), [heatmap](#), [PCA](#), [PLS-DA](#), [MSEA](#), [ASCA](#), [ROC](#), [SVM](#), [K-means](#), [Dendrogram](#), [Heatmap](#), [K-means](#), [SVM](#).

MetaboAnalyst: Functional Modules

Please choose a functional module to proceed:

Statistical Analysis

This module offers various commonly used statistical and machine learning methods from t-tests, ANOVA to PCA and PLS-DA. It also provides clustering and visualization such as dendrogram, heatmap, K-means, as well as classification based on random forests and SVM.

Enrichment Analysis

This module performs metabolite set enrichment analysis (MSEA) for human and mammalian species based on several libraries containing ~6300 groups of biologically meaningful metabolite sets. Users can upload a list of compounds, a list of compounds with concentrations, or a concentration table.

Pathway Analysis

This module supports pathway analysis (integrating enrichment analysis and pathway topology analysis) and visualization for 21 model organisms, including Human, Mouse, Rat, Cow, Chicken, Zebrafish, Arabidopsis thaliana, Rice, Drosophila, Maliana, Budding yeast, E. coli, etc., with a total of ~1600 metabolic pathways.

Time Series Analysis

This module supports data overview (PCA and heatmaps), two-way ANOVA, multivariate empirical Bayes time-series analysis for detecting distinctive temporal profiles across different experimental conditions, and ANOVA-simultaneous component analysis (ASCA) for identification of major patterns associated with each experimental factor.

Power Analysis

This module allows you to upload a pilot data set to calculate the minimum number of samples required to detect the existence of a difference between two populations with a given degree of confidence.

Biomarker Analysis

To perform various ROC curve based biomarker analysis. It supports classical single biomarker analysis, multivariate biomarker analysis, and manual biomarker selection and evaluation.

Integrated Pathway Analysis

To perform joint metabolic pathway analysis on results obtained from metabolomics and gene expression studies under the same experimental or biological

Other Utilities

This module contains some utility functions commonly used for metabolomics data manipulation and analysis. At this moment, compound ID conversion is

MetaboAnalyst: Data Upload

MetaboAnalyst 3.0
– a comprehensive tool suite for metabolomic data analysis

1) Upload your data

Comma Separated Values (.csv):

Data Type: Concentration Spectral bins Peak intensity table

Format:

Data File: No file chosen

Zipped Files (.zip):

Data Type: NMR peak list MS peak list MS spectra

Data File: No file chosen

Pair File: No file chosen

MetaboAnalyst: Data Integrity Check

MetaboAnalyst 3.0
– a comprehensive tool suite for metabolomic data analysis

Data Integrity Check:

1. Checking the class labels - at least three replicates are required in each class.
2. If the samples are paired, the pair labels must conform to the specified format.
3. The data (except class labels) must not contain non-numeric values.
4. The presence of missing values or features with constant values (i.e. all zeros)

Data processing information:

Checking data content...passed

Samples are in rows and features in columns

The uploaded file is in comma separated values (.csv) format.

The uploaded data file contains 38 (samples) by 231 (spectra bins) data matrix.

7 groups were detected in samples.

Samples are not paired.

All data values are numeric.

A total of 0 (0%) missing values were detected.

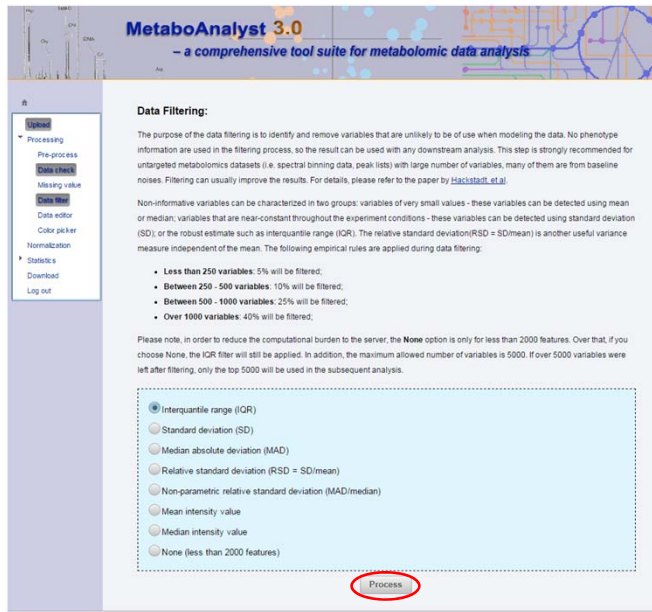
By default, these values will be replaced by a small value.

Click Skip button if you accept the default practice

Or click Missing value imputation to use other methods

Last modified 2015-02-06

MetaboAnalyst: Data Filtering



MetaboAnalyst 3.0
— a comprehensive tool suite for metabolomic data analysis

Data Filtering:

The purpose of the data filtering is to identify and remove variables that are unlikely to be of use when modeling the data. No phenotype information are used in the filtering process, so the result can be used with any downstream analysis. This step is strongly recommended for untargeted metabolomics datasets (i.e. spectral binning data, peak lists) with large number of variables, many of them are from baseline noises. Filtering can usually improve the results. For details, please refer to the paper by [Jackson et al.](#)

Non-informative variables can be characterized in two groups: variables of very small values - these variables can be detected using mean or median, variables that are near-constant throughout the experiment conditions - these variables can be detected using standard deviation (SD), or the robust estimate such as interquartile range (IQR). The relative standard deviation (RSD = SD/mean) is another useful variance measure independent of the mean. The following empirical rules are applied during data filtering:

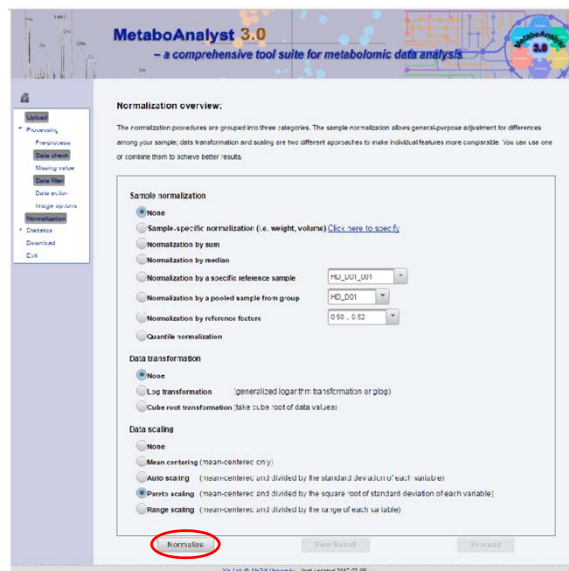
- Less than 250 variables: 5% will be filtered;
- Between 250 - 500 variables: 10% will be filtered;
- Between 500 - 1000 variables: 25% will be filtered;
- Over 1000 variables: 40% will be filtered.

Please note, in order to reduce the computational burden to the server, the **None** option is only for less than 2000 features. Over that, if you choose **None**, the IQR filter will still be applied. In addition, the maximum allowed number of variables is 5000. If over 5000 variables were left after filtering, only the top 5000 will be used in the subsequent analysis.

Interquartile range (IQR)
 Standard deviation (SD)
 Median absolute deviation (MAD)
 Relative standard deviation (RSD = SD/mean)
 Non-parametric relative standard deviation (MAD/median)
 Mean intensity value
 Median intensity value
 None (less than 2000 features)

Process

MetaboAnalyst: Data Normalization



MetaboAnalyst 3.0
— a comprehensive tool suite for metabolomic data analysis

Normalization overview:

The normalization procedures are grouped into three categories. The sample normalization allows purpose adjustment for differences among your sample; data transformation and scaling are two different approaches to make individual features more comparable. You can use one or combine them to achieve better results.

Sample normalization

None
 Sample-specific normalization (i.e. weight, volume) [Click here to specify](#)
 Normalization by sum
 Normalization by median
 Normalization by a specific reference sample:
 Normalization by a pooled sample from group:
 Normalization by reference feature:
 Quartile normalization

Data transformation

None
 Log transformation (generalized logarithm transformation or log)
 Cube root transformation (take cube root of data values)

Data scaling

None
 Mean centering (mean-centering only)
 Auto scaling (mean-centering and divided by the standard deviation of each variable)
 Parvo scaling (mean-centering and divided by the square root of standard deviation of each variable)
 Range scaling (mean-centering and divided by the range of each variable)

Normalize

MetaboAnalyst: Data Normalization Summary

MetaboAnalyst 3.0
— a comprehensive tool suite for metabolomic data analysis

Normalization overview:

The normalization procedures are grouped into three categories. The sample normalization allows general-purpose adjustment for differences among your sample; data transformation and scaling are two different approaches to make individual features more comparable. You can use one or combine them to achieve better results.

Sample normalization

- None
- Sample-specific normalization (i.e. weight, volume) [Click here to specify](#)
- Normalization by sum
- Normalization by median
- Normalization by a specific reference sample:
- Normalization by a pooled sample from group:
- Normalization by reference feature:
- Quantile normalization

Data transformation

- None
- Log transformation (generalized logarithm transformation or logp)
- Cube root transformation (take cube root of data values)

Data scaling

- None
- Mean centering (mean-centered only)
- Auto scaling (mean-centered and divided by the standard deviation of each variable)
- Pareto scaling (mean-centered and divided by the square root of standard deviation of each variable)
- Range scaling (mean-centered and divided by the range of each variable)

Buttons: **Normalize**, **View Result** (1), **Proceed** (2)

Yield: Xie Lei © Fudan University (last updated 2017-02-09)

MetaboAnalyst: Statistical Analysis

MetaboAnalyst 3.0
— a comprehensive tool suite for metabolomic data analysis

Select an analysis path to explore:

Univariate Analysis

- Fold Change Analysis
- T-tests
- Volcano plot
- One-way Analysis of Variance (ANOVA)
- Correlation Analysis
- Pattern Searching

Chemometrics Analysis

- Principal Component Analysis (PCA)
- Partial Least Squares - Discriminant Analysis (PLS-DA)
- Sparse Partial Least Squares - Discriminant Analysis (sPLS-DA)
- Orthogonal Partial Least Squares - Discriminant Analysis (orthoPLS-DA)

Feature Identification

- Significance Analysis of Microarray (and Metabolites) (SAM)
- Empirical Bayesian Analysis of Microarray (and Metabolites) (EBAM)

Cluster Analysis

- Hierarchical Clustering: [Dendrogram](#) [Heatmaps](#)
- Partitional Clustering: [K-means](#) [Self-Organizing Map \(SOM\)](#)

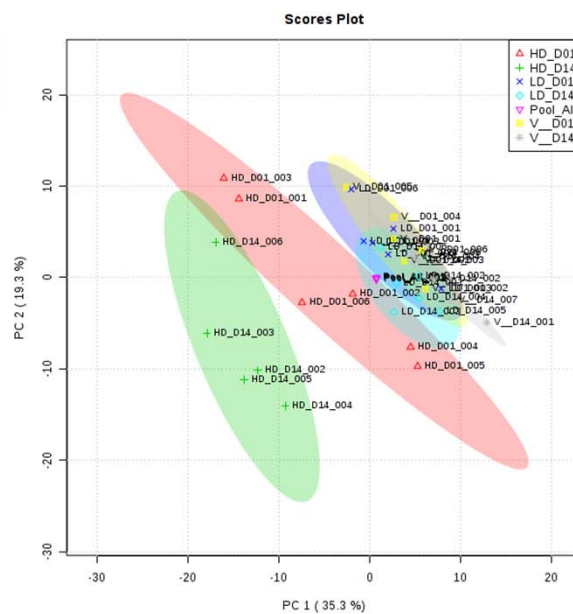
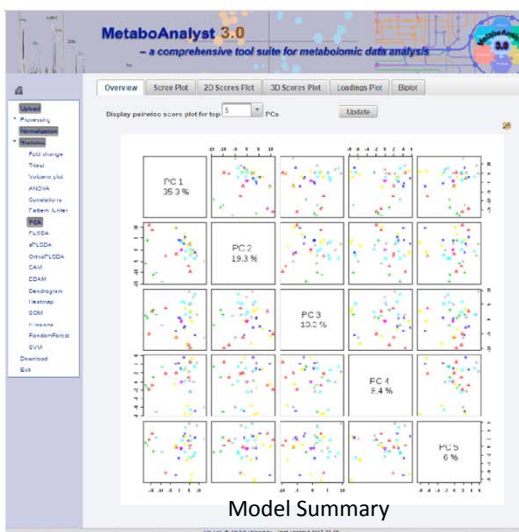
Classification & Feature Selection

- [Random Forest](#)
- [Support Vector Machine \(SVM\)](#)

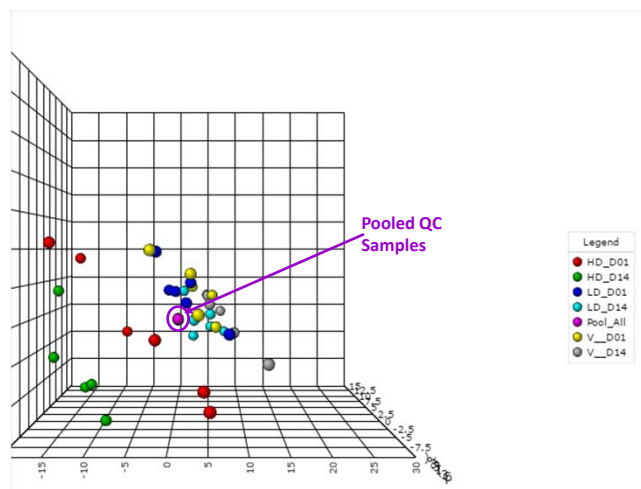
Buttons: **Update**, **Pre-process**, **Data view**, **Data editor**, **Image options**, **Download**, **Exit**

Yield: Xie Lei © Fudan University (last updated 2017-02-09)

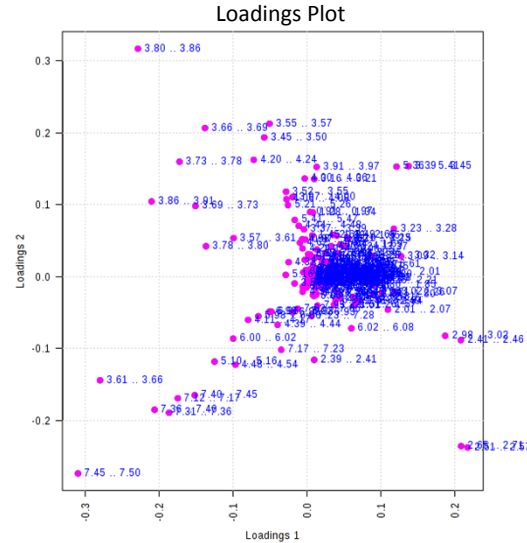
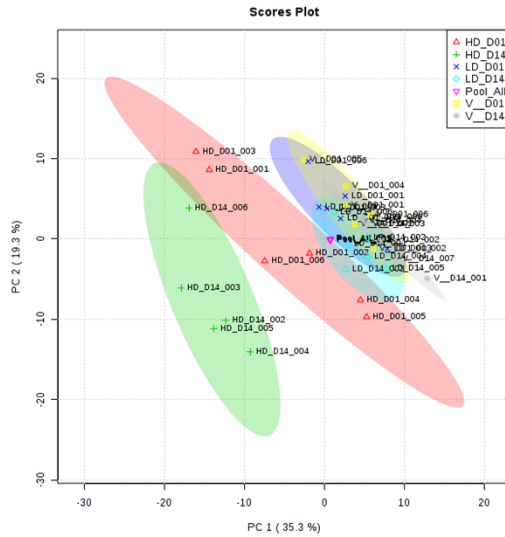
Principal Component Analysis (PCA): All Samples



Clustering of Pooled QC Samples



PCA Scores and Loadings Plots: Day 01 and Day 14



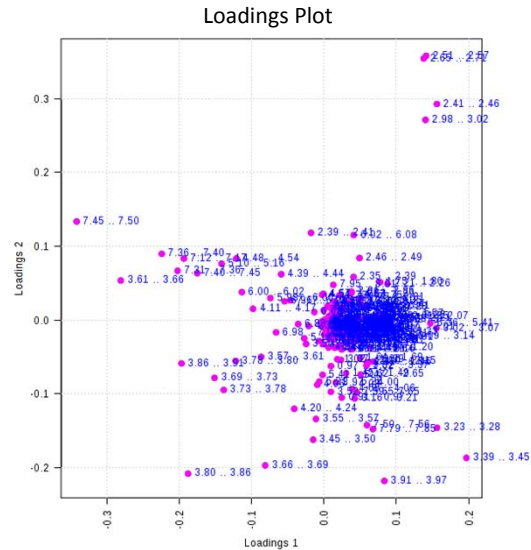
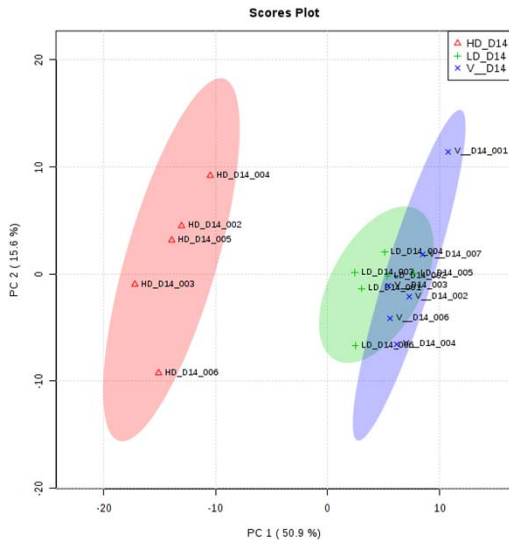
Day 14: Vehicle, Low Dose, and High Dose Groups

Please go back to the start page and upload the data

- We will compare high dose vs vehicle
 - 2. UAB_RFA_Metaboanalyst_D14_NoPools.csv
- Perform PCA
- Perform PLS-DA
- Heat map

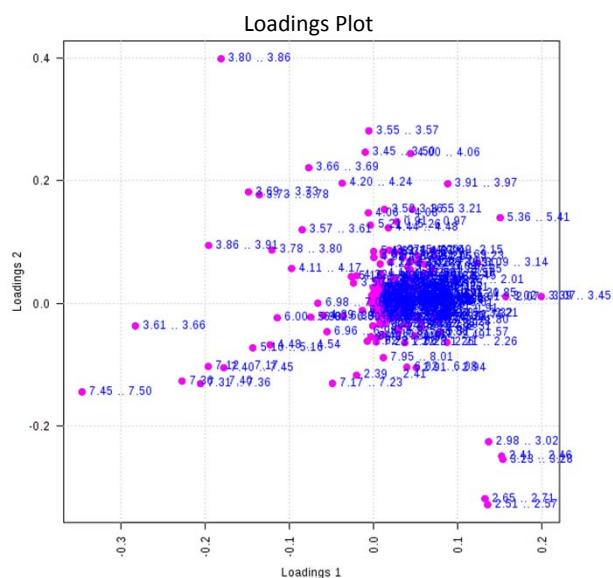
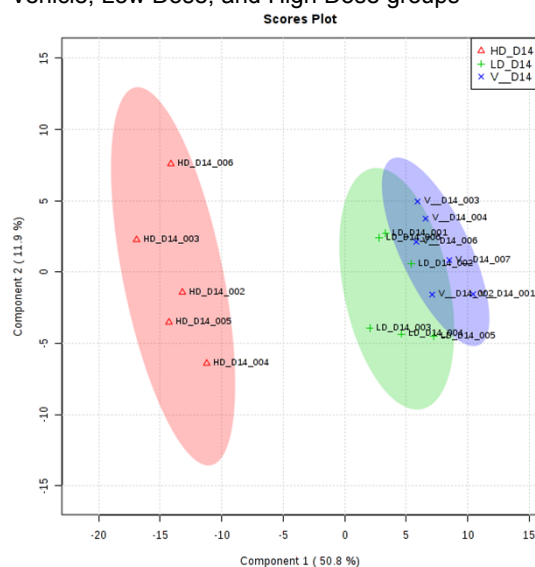
PCA Scores and Loadings Plots: Day 14

Vehicle, Low Dose, and High Dose groups

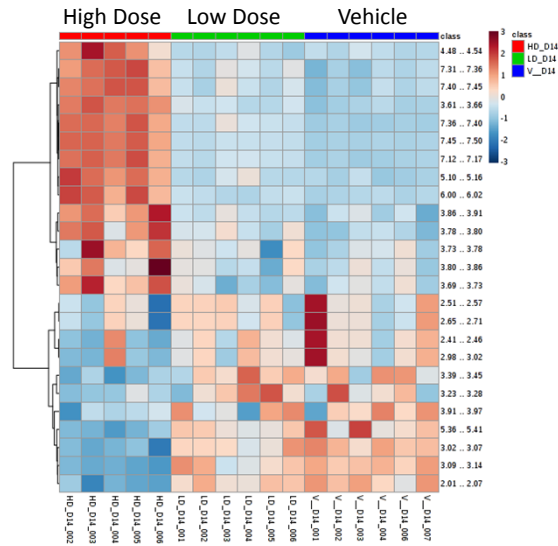


PLS-DA Scores and Loadings Plots: Day 14

Vehicle, Low Dose, and High Dose groups



Heat Map: Day 14 Samples



Top 25 NMR bins
identified by PLS-DA

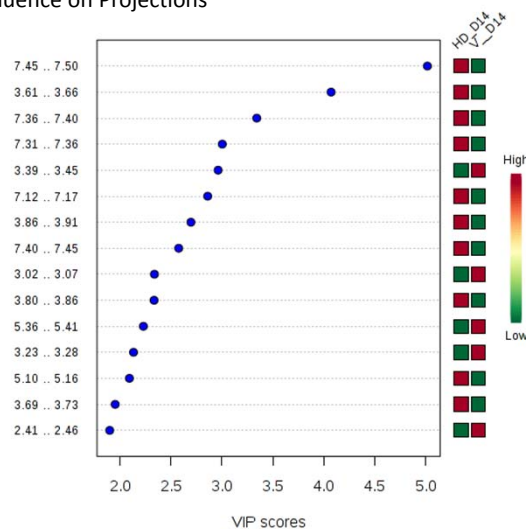
Comparison of Day 14 High Dose and Vehicle

Please start from the start page and upload the data

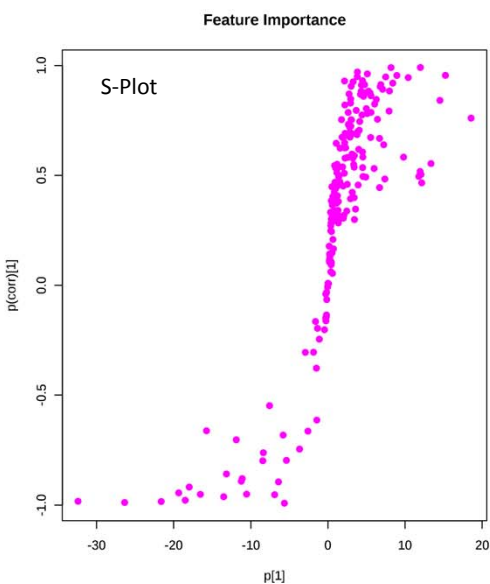
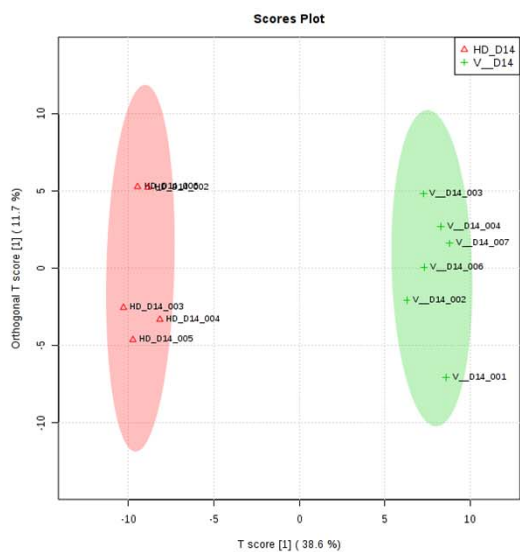
- We will compare high dose vs vehicle
 - 3. UAB_RFA_Metaboanalyst_D14_Vehicle_vs_HighDose.csv
- Perform PCA
- Perform PLS-DA
- VIP Plot
- Heat map

VIP Plot of PLS-DA: Day 14 High Dose vs Vehicle

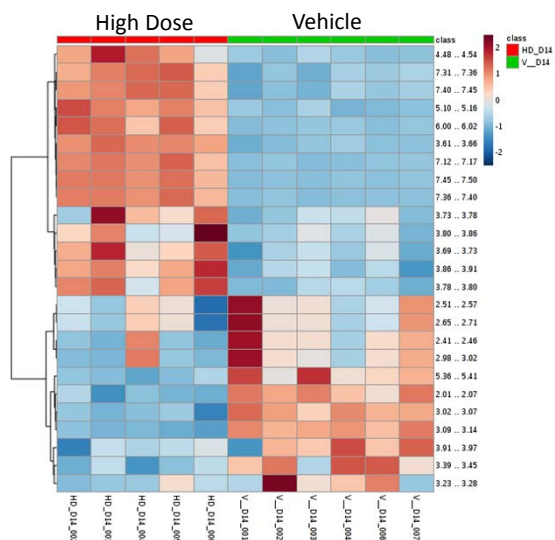
VIP = Variable Influence on Projections



OPLS-DA Scores Plot and S-Plot: Day 14 High Dose vs Vehicle



Heat Map: Day 14 High Dose vs Vehicle



Top 25 NMR bins identified by PLS-DA

Contributors through the Years

Jim Carlson
 LC- and GC-MS
Jessica Gooding
 LC-MS
Kelly Mercier
 NMR
Ninell Mortensen
 Microbiology
Wimal Pathmasiri
 NMR & GC-MS
Susan McRitchie
 Data Analysis
Zach Acuff
 Biostatistics
Bob Clark
 Genetics
Delisha Stewart
 Cell Biology
Suraj Dhungana
 LC-MS
Jason Burgess
 Program
 Coordinator
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Thank You!

If you have any questions, please e-mail me

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Useful link:

Metabolomics Workbench

<http://www.metabolomicsworkbench.org/>