STATISTICS & ML WITH R

(special topics)

- **MetaboAnalyst**
- **Power Analysis**

2024

M. Chiara Mimmi & Luisa M. Mimmi

WORKSHOP SCHEDULE

- Modules
  - 1. Intro to R and data analysis
  - 2. Statistical inference & hypothesis testing
  - 3. Modeling correlation and regression
  - 4 Mapping causal & predictive approaches
  - 5. Machine Learning
  - 6. Extra topics:
    - MetaboAnalyst;
    - Power Analysis

- Each day will include:
  - Frontal class (MORNING)
  - Practical training with R about the topics discussed in the morning. (AFTERNOON)

DAY 6 – *Extra* TOPICS

- MetaboAnalyst
  - Overview
  - Workflow
- Power analysis
  - Hypothesis testing
  - Decision errors
  - Statistical power
  - Effect size

DAY 4 – LECTURE OUTLINE

- MetaboAnalyst
  1. Overview
  2. Workflow
- Power analysis
  1. Hypothesis testing
  2. Decision errors
  3. Statistical power
  4. Effect size

MetaboAnalyst

An R-driven Software

Introduction to MetaboAnalyst

https://www.metaboanalyst.ca

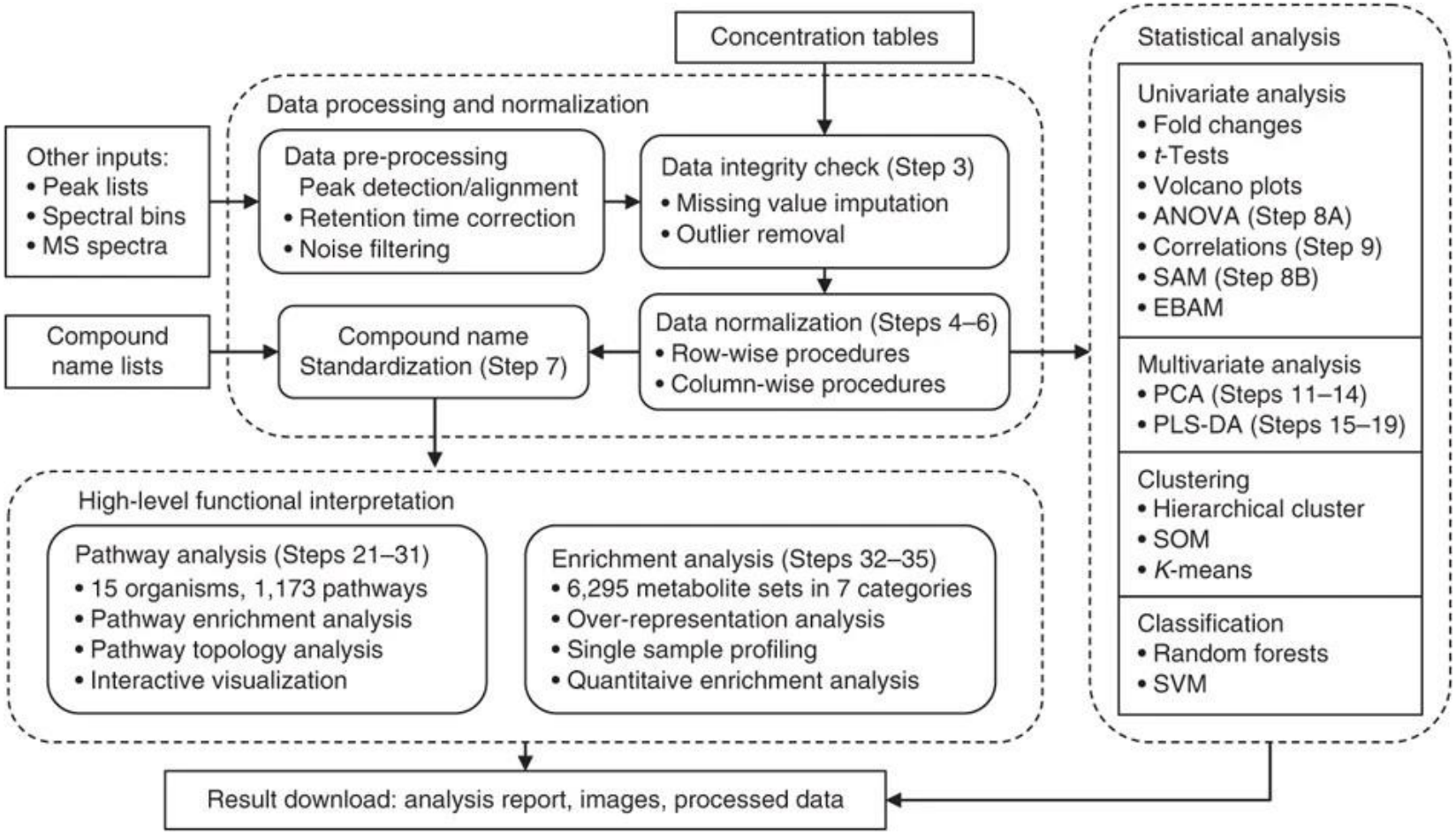
From raw spectra to biomarkers, patterns, functions and systems biology

- it is a free web-based platform
- it works with **R** but it has a *friendlier* GUI: anyone can make metabolomics data analysis, interpretation and integration with other omics data
- the whole metabolomics community uses it!!!

…but

- you need a statistical background to interpret the **MetaboAnalyst** outputs and to get the most of it!

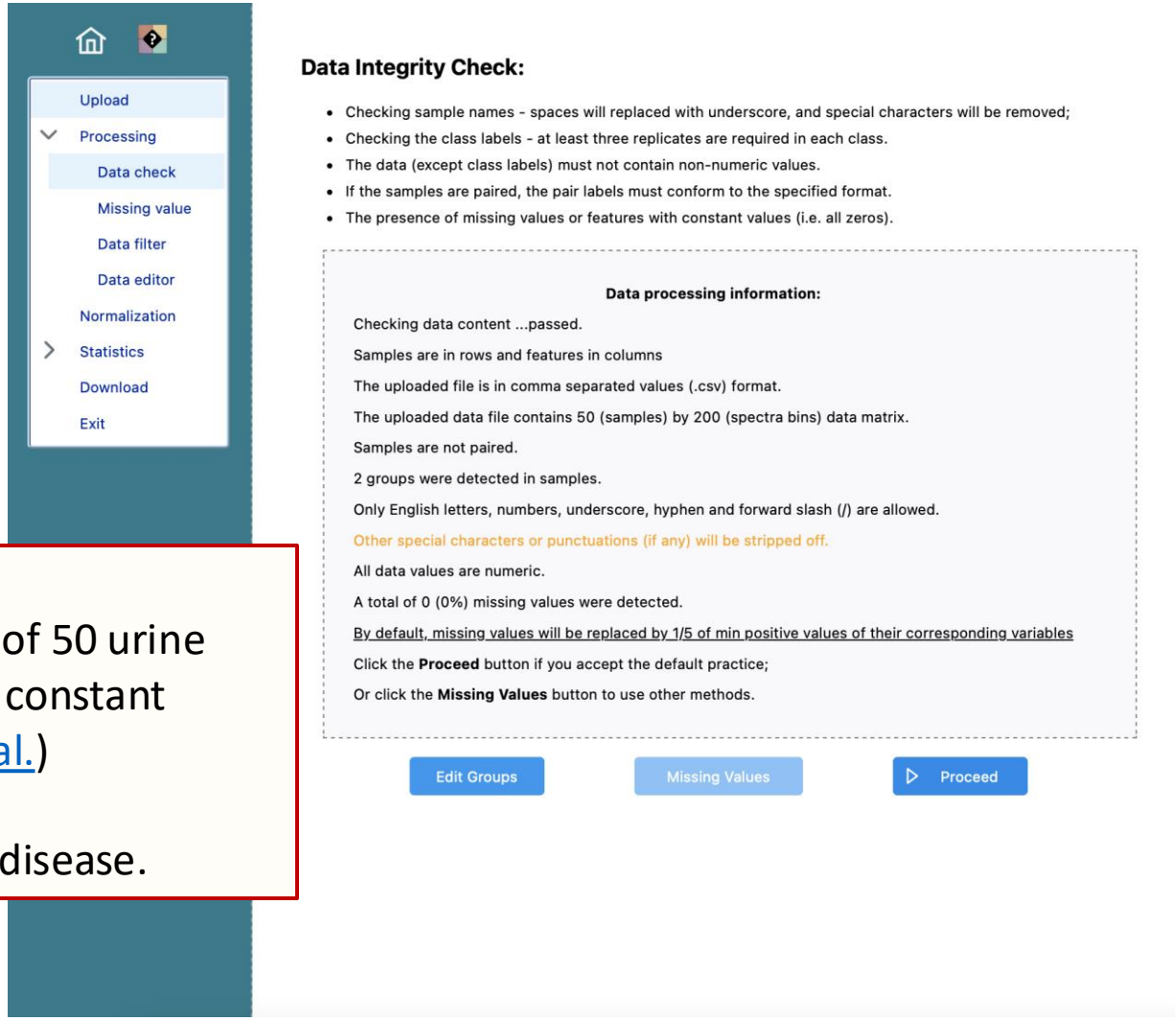
MetaboAnalyst overview



*Source: Xia, J., Wishart, D. Nat Protoc **6**, 743–760 (2011).*

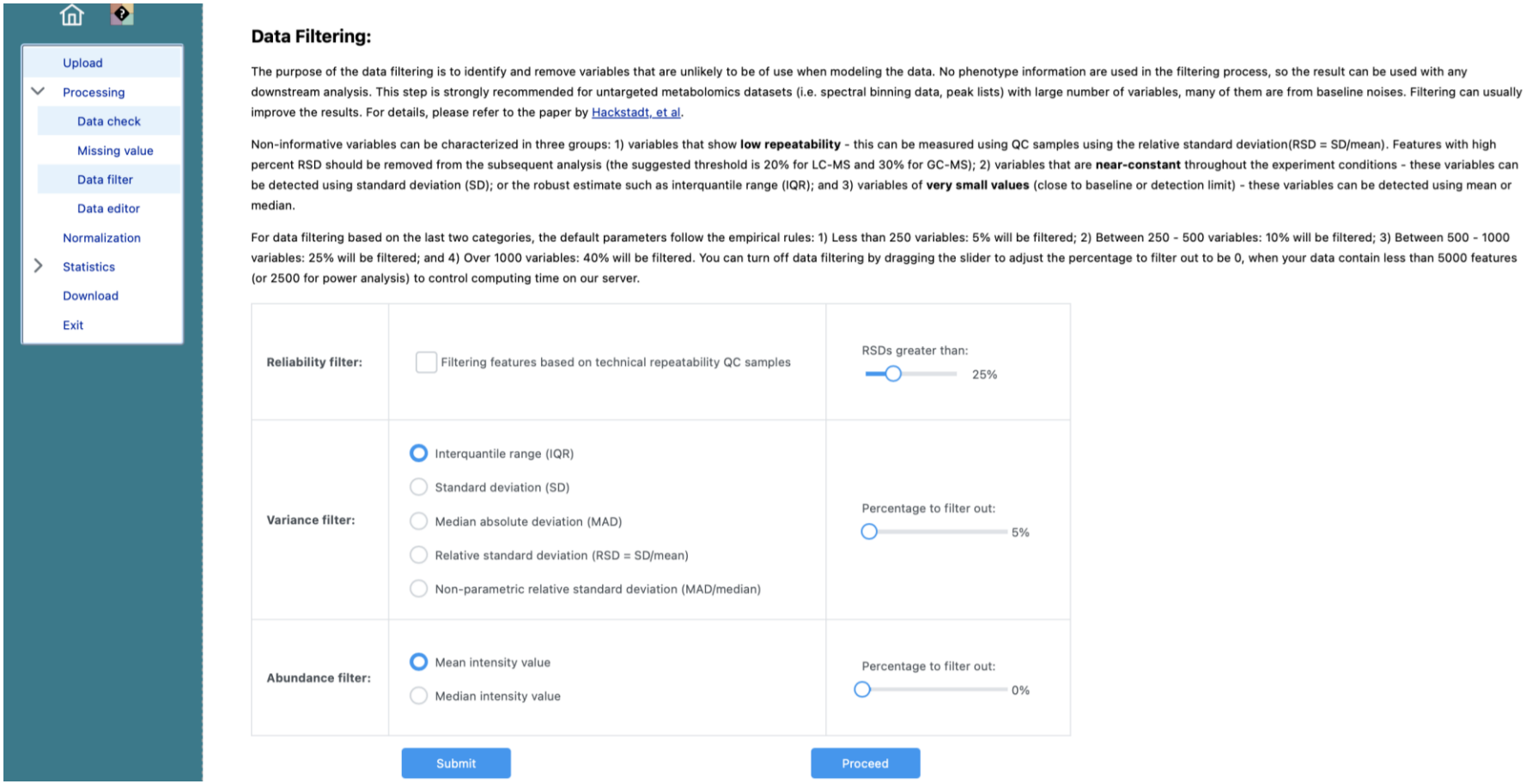
MetaboAnalyst workflow

1) data upload

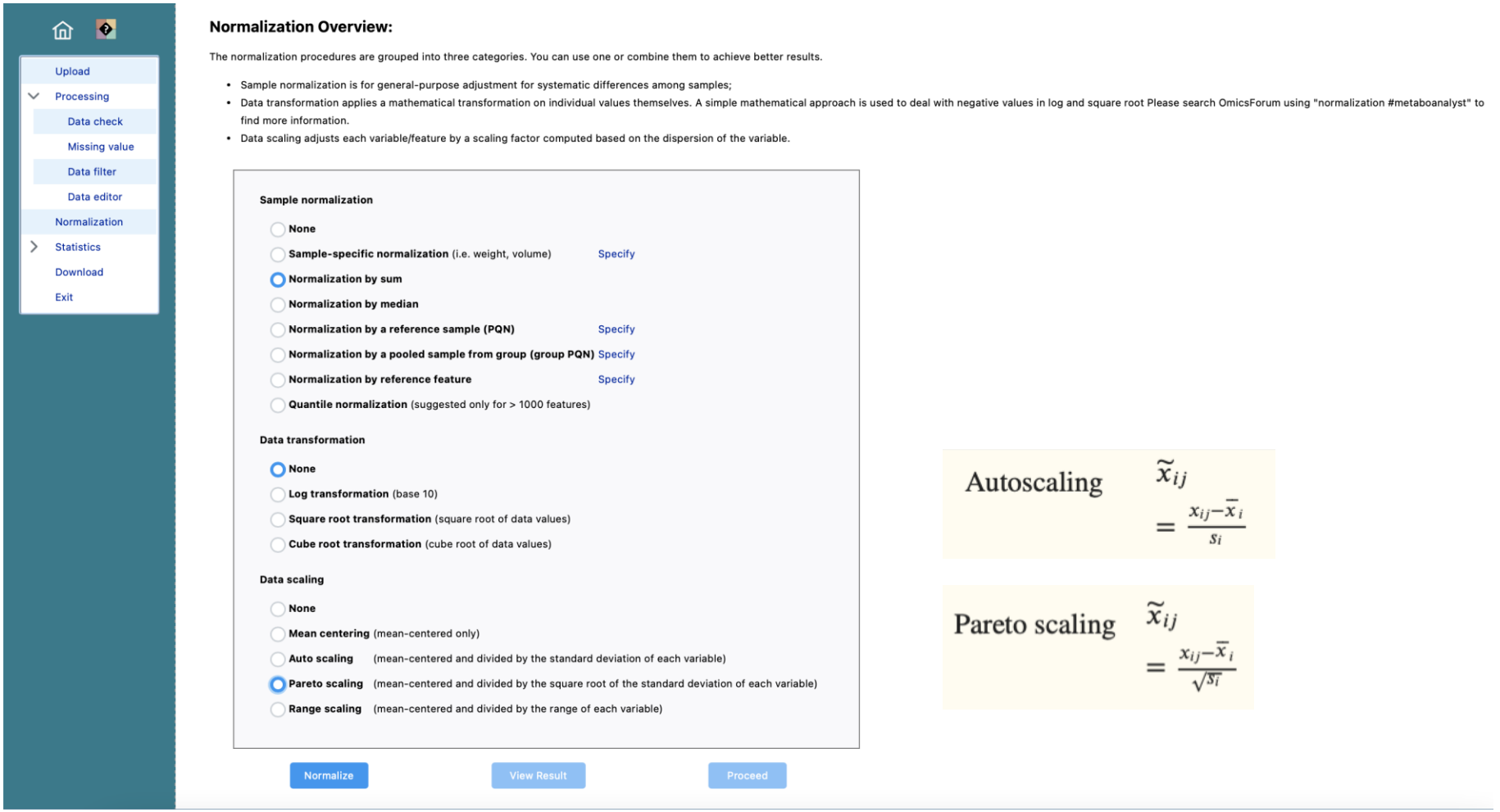


Test data 1:
Binned 1H NMR spectra of 50 urine samples using 0.04 ppm constant width (Psihogios NG, et al.)
Group 1- control;
Group 2 - severe kidney disease.

MetaboAnalyst workflow
2) data filtering



MetaboAnalyst workflow
3) data normalization

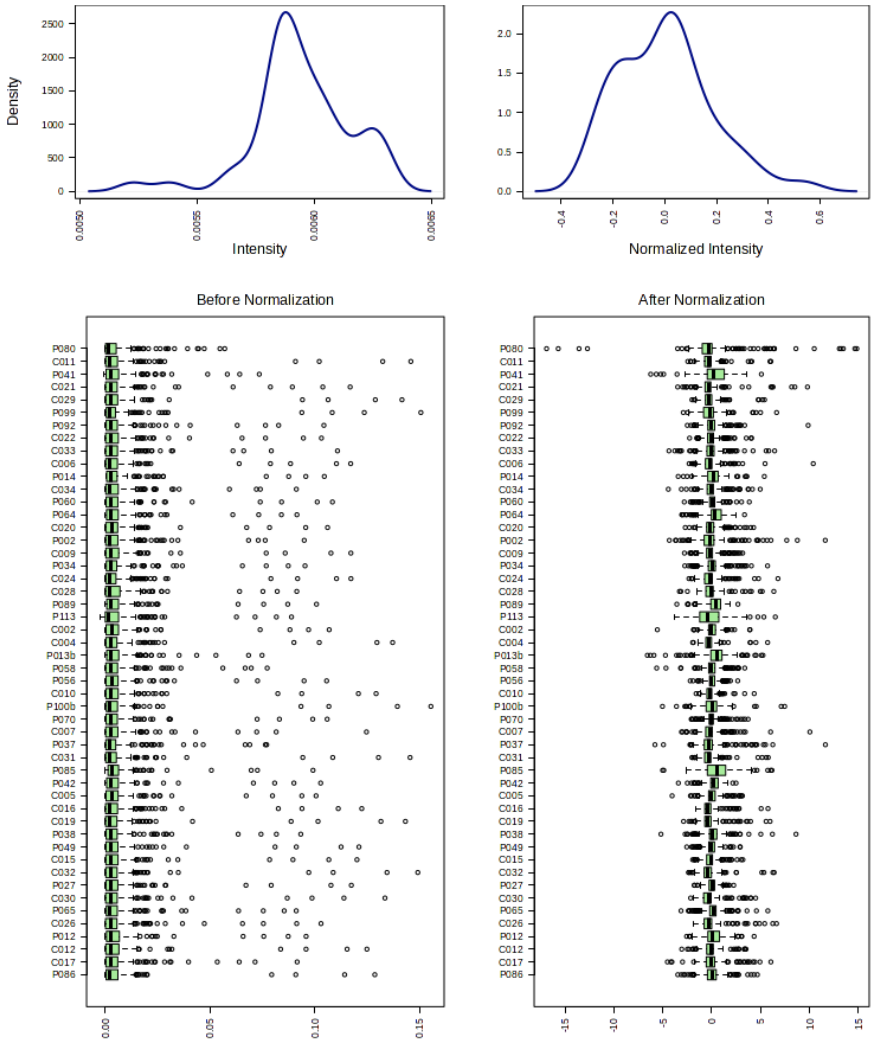


Autoscaling $\tilde{x}_{ij} = \frac{x_{ij} - \bar{x}_i}{s_i}$

Pareto scaling $\tilde{x}_{ij} = \frac{x_{ij} - \bar{x}_i}{\sqrt{s_i}}$

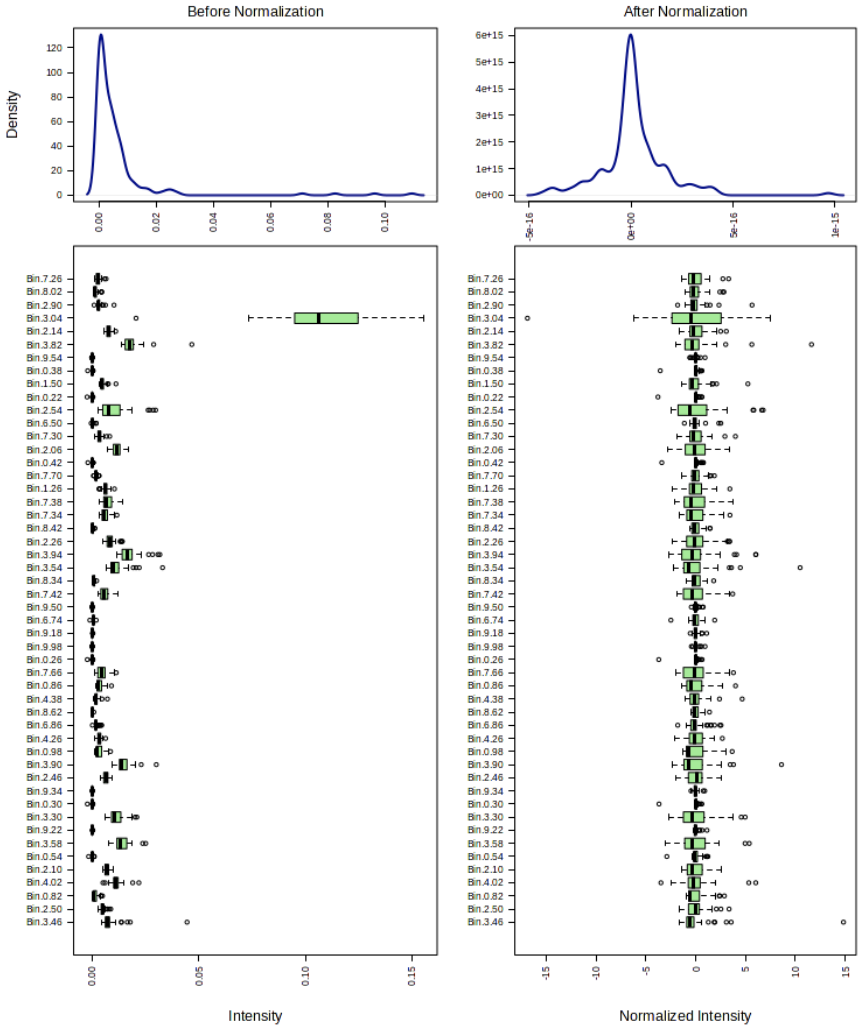
MetaboAnalyst workflow
3) data normalization

Effect of normalization over sample

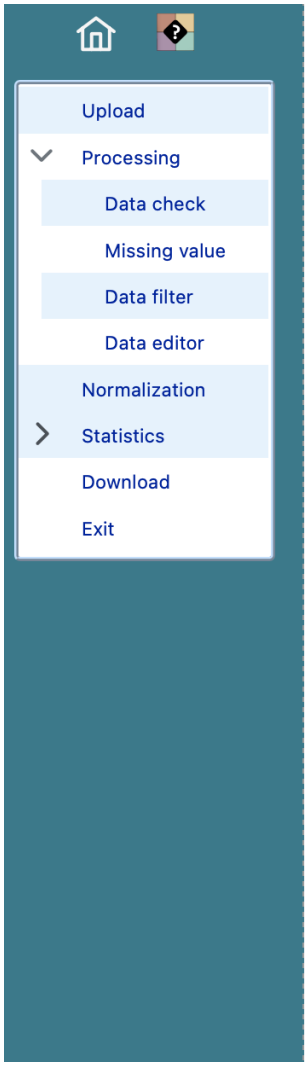


MetaboAnalyst workflow
3) data normalization

Effect of features/metabolites scaling



MetaboAnalyst workflow
4) statistical analysis



Select an analysis path to explore :

Univariate Analysis

Fold Change Analysis T-tests Volcano plot

One-way Analysis of Variance (ANOVA)

Correlation Heatmaps Pattern Search Correlation Networks (DSPC)

«Classical» analysis of variance among groups

Advanced Significance Analysis

Significance Analysis of Microarray (and Metabolites) (SAM)

Empirical Bayesian Analysis of Microarray (and Metabolites) (EBAM)

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)

Cluster Analysis

Hierarchical Clustering: Dendrogram Heatmaps

Partitional Clustering: K-means Self Organizing Map (SOM)

Classification & Feature Selection

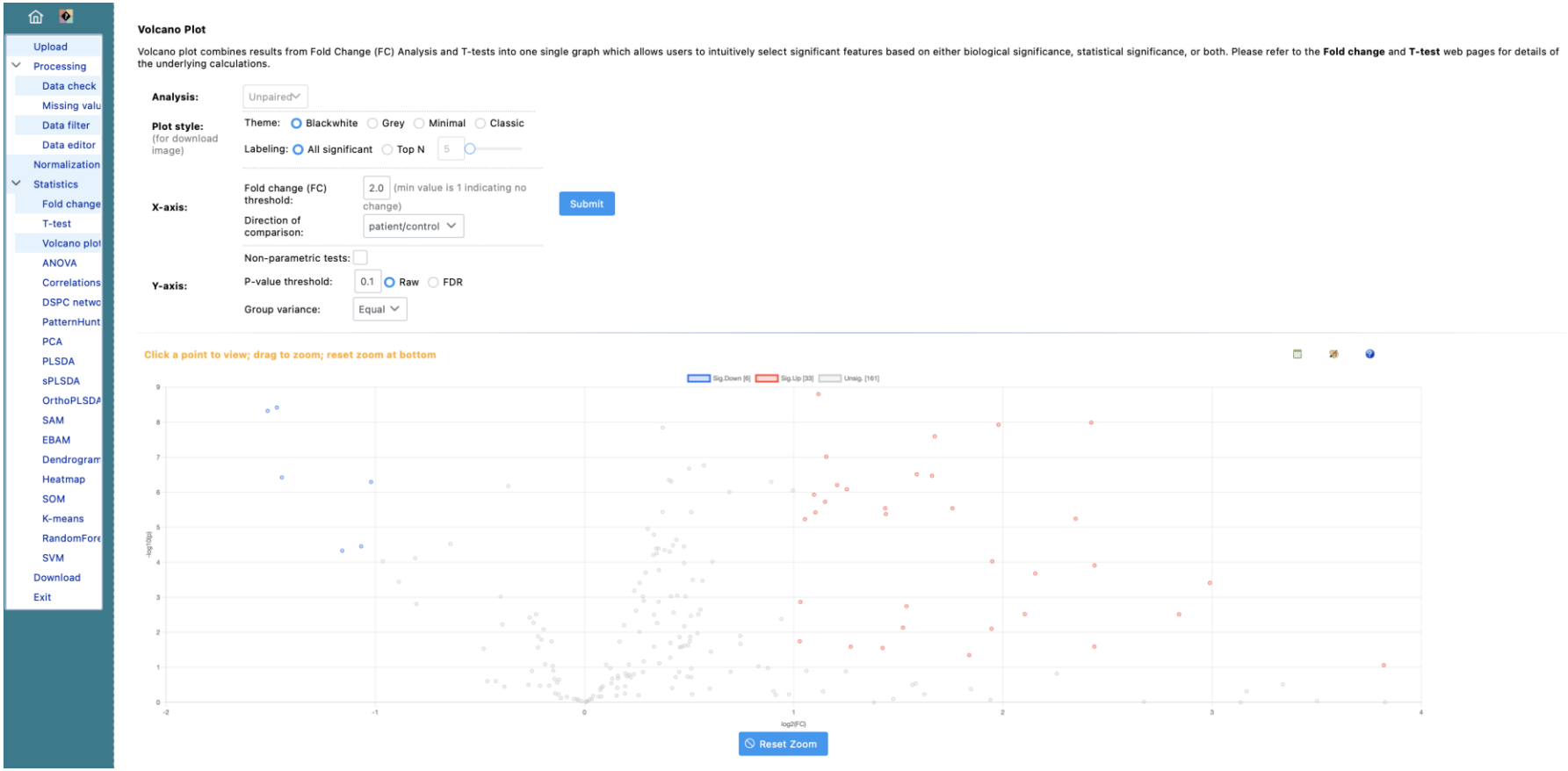
Random Forest

Support Vector Machine (SVM)

Machine learning algorithms

MetaboAnalyst workflow
4) univariate analysis

MetaboAnalyst workflow
4) univariate analysis



MetaboAnalyst workflow
5) chemometric analysis

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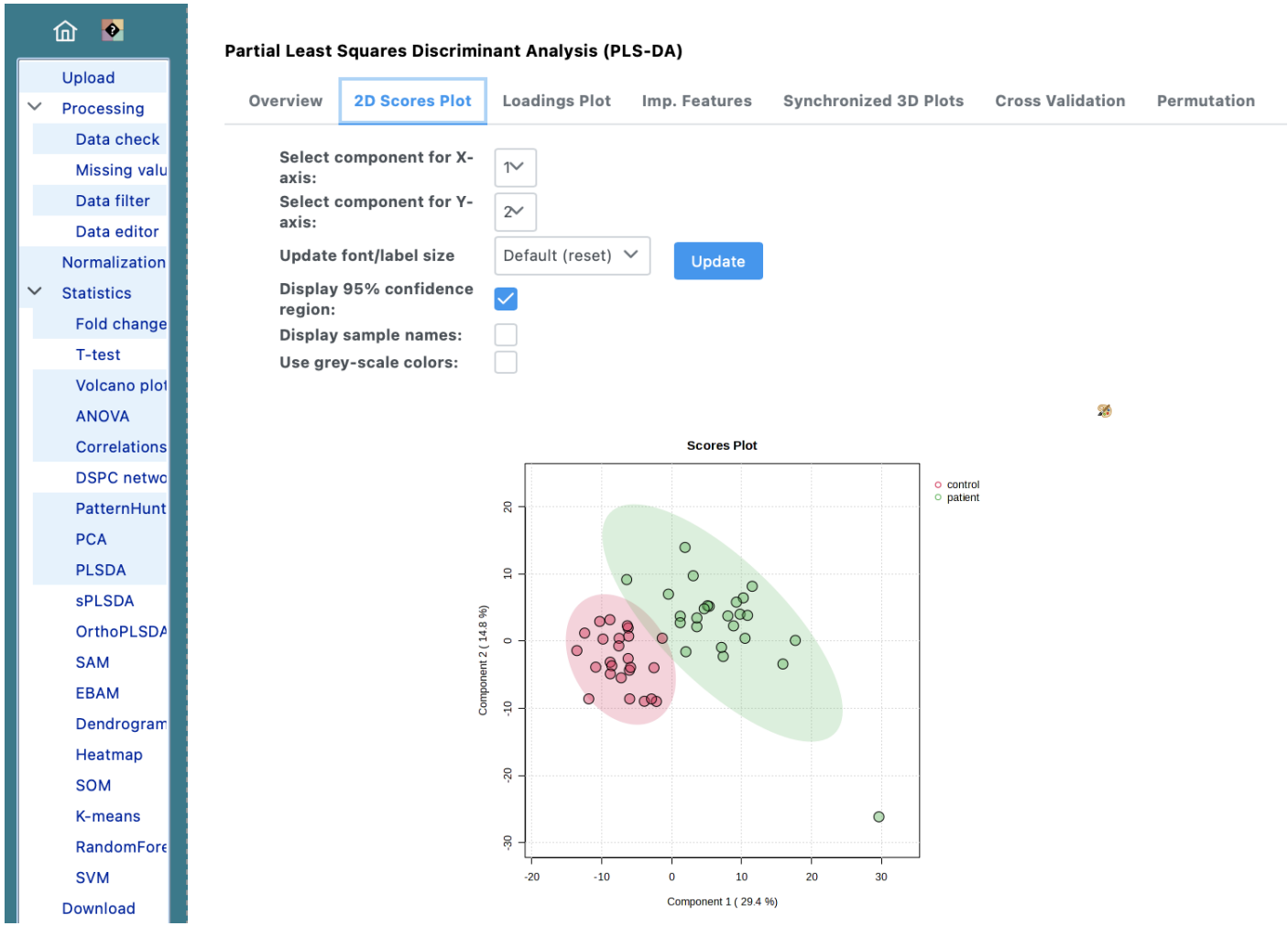
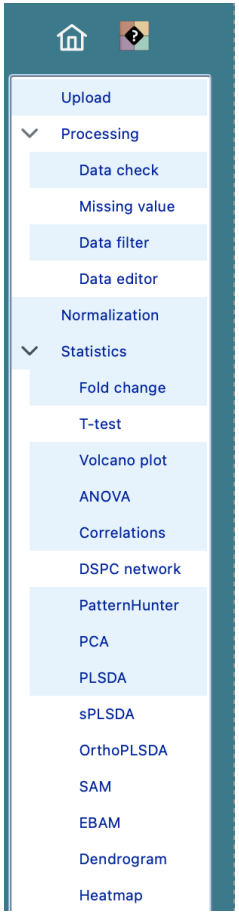


MetaboAnalyst workflow
5) chemometric analysis



Partial Least Squares Discriminant Analysis (PLS-DA)

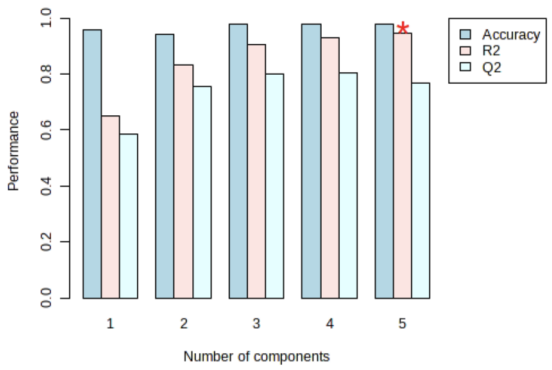
Overview | 2D Scores Plot | Loadings Plot | Imp. Features | Synchronized 3D Plots | Cross Validation | Permutation

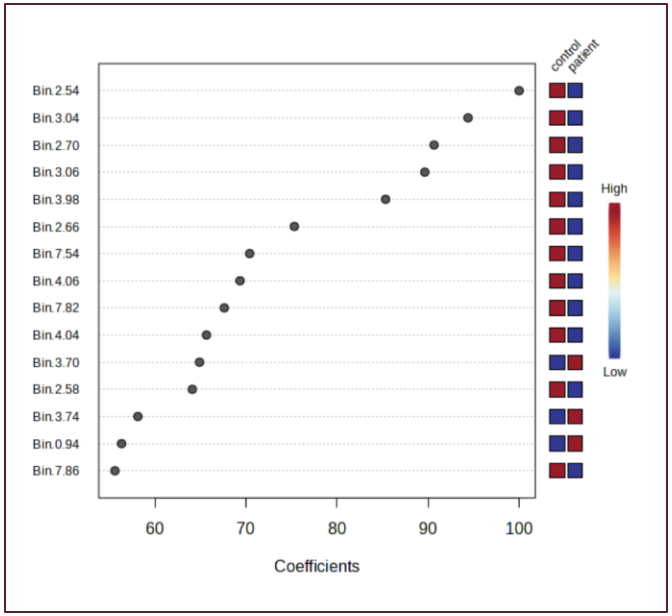
Select optimal number of components for classification

Maximum components to search: 5

Cross validation (CV) method: LOOCV Update

Performance measure: R2

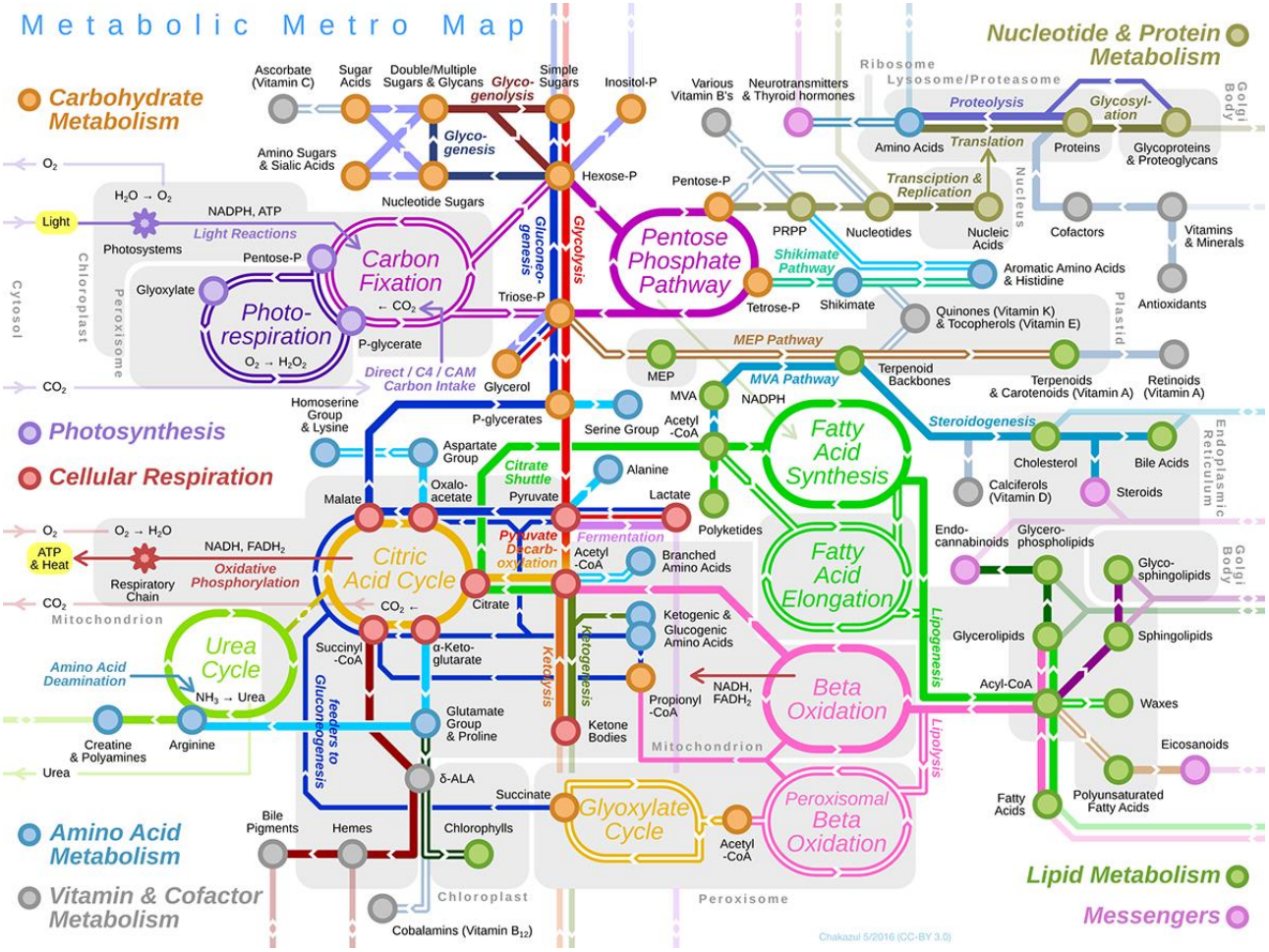




MetaboAnalyst workflow
5) chemometric analysis

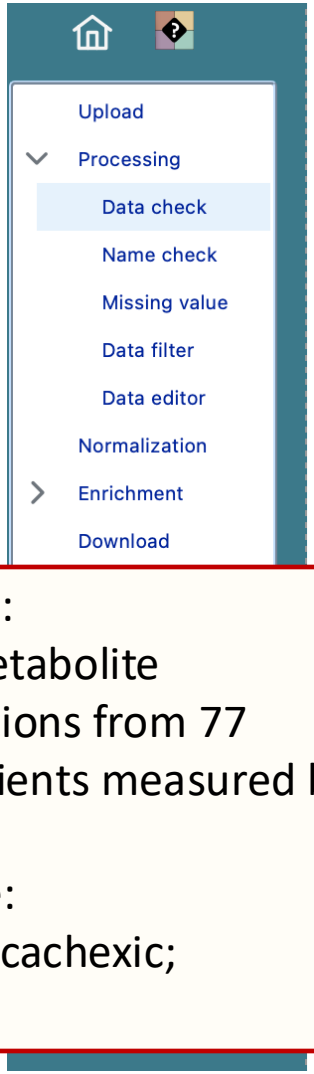
Heatmap of the top 25 T-test features

Identifying the metabolic pathways deregulated by a pathology is finding a target for pharmacological therapy!



Source: https://www.behance.net/gallery/38270165/Metro-Map-of-Metabolism-The-Overview

MetaboAnalyst workflow
6) enrichment analysis



Data Integrity Check:

- Checking sample names - spaces will replaced with underscore, and special characters will be removed;
- Checking the class labels - at least three replicates are required in each class.
- The data (except class labels) must not contain non-numeric values.
- If the samples are paired, the pair labels must conform to the specified format.
- 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 77 (samples) by 63 (compounds) data matrix.

Samples are not paired.

2 groups were detected in samples.

Only English letters, numbers, underscore, hyphen and forward slash (/) are allowed.

Other special characters or punctuations (if any) will be stripped off.

All data values are numeric.

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

By default, missing values will be replaced by 1/5 of min positive values of their corresponding variables

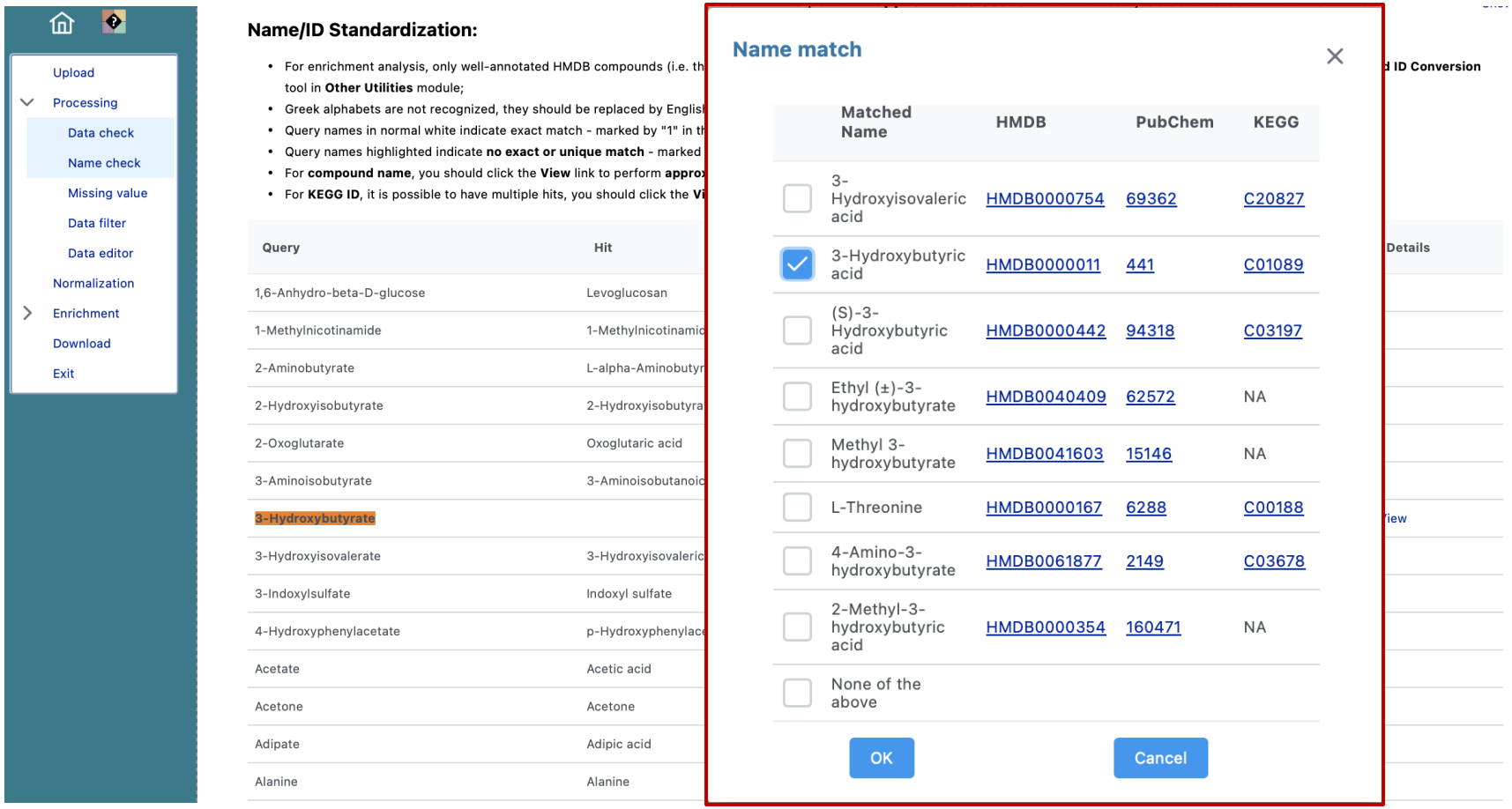
Click the **Proceed** button if you accept the default practice;

Or click the **Missing Values** button to use other methods.

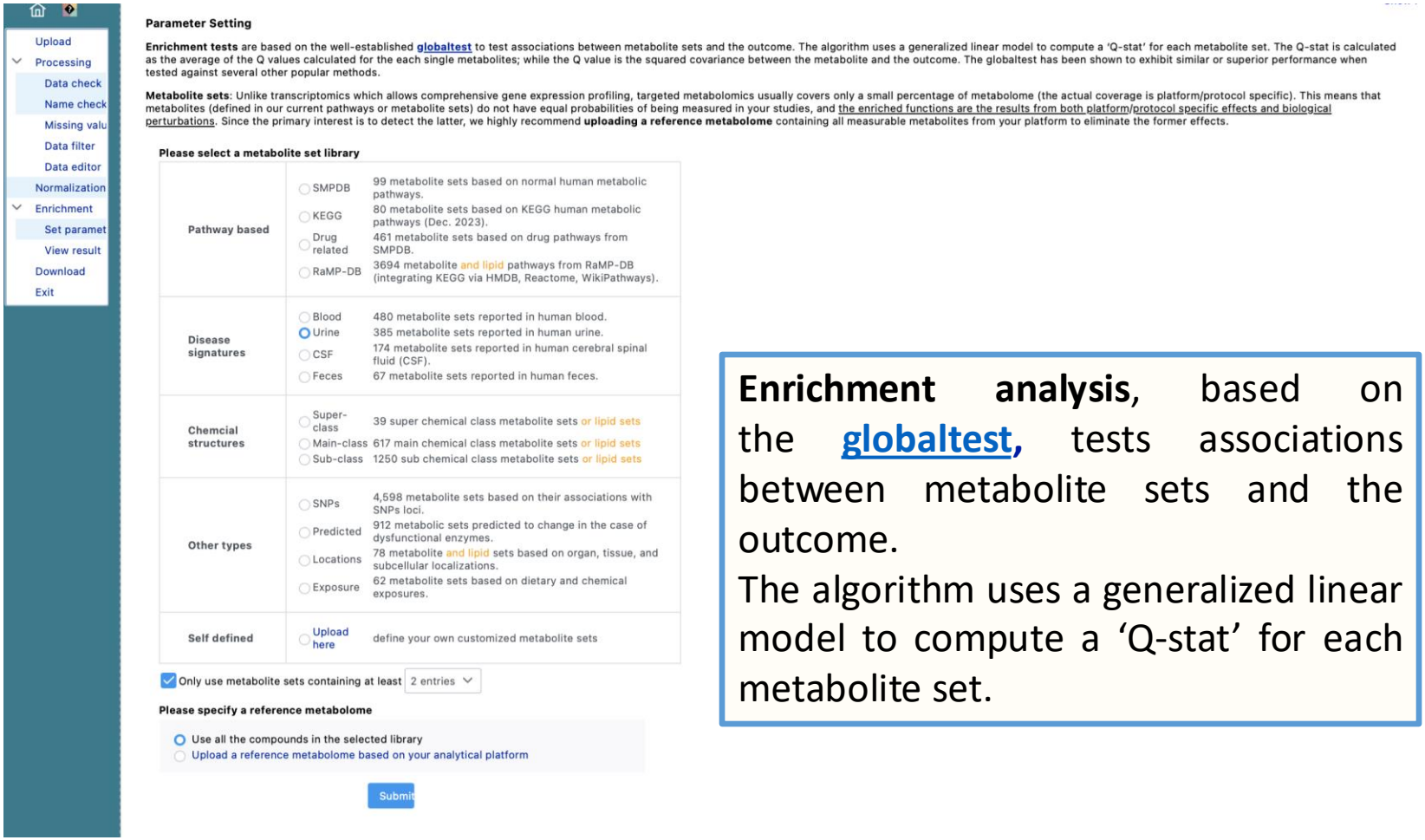
Edit Groups | Missing Values | Proceed

Test data 2:
Urinary metabolite concentrations from 77 cancer patients measured by 1H NMR.
Phenotype:
N - cancer cachexic;
Y - control

MetaboAnalyst workflow
6) enrichment analysis



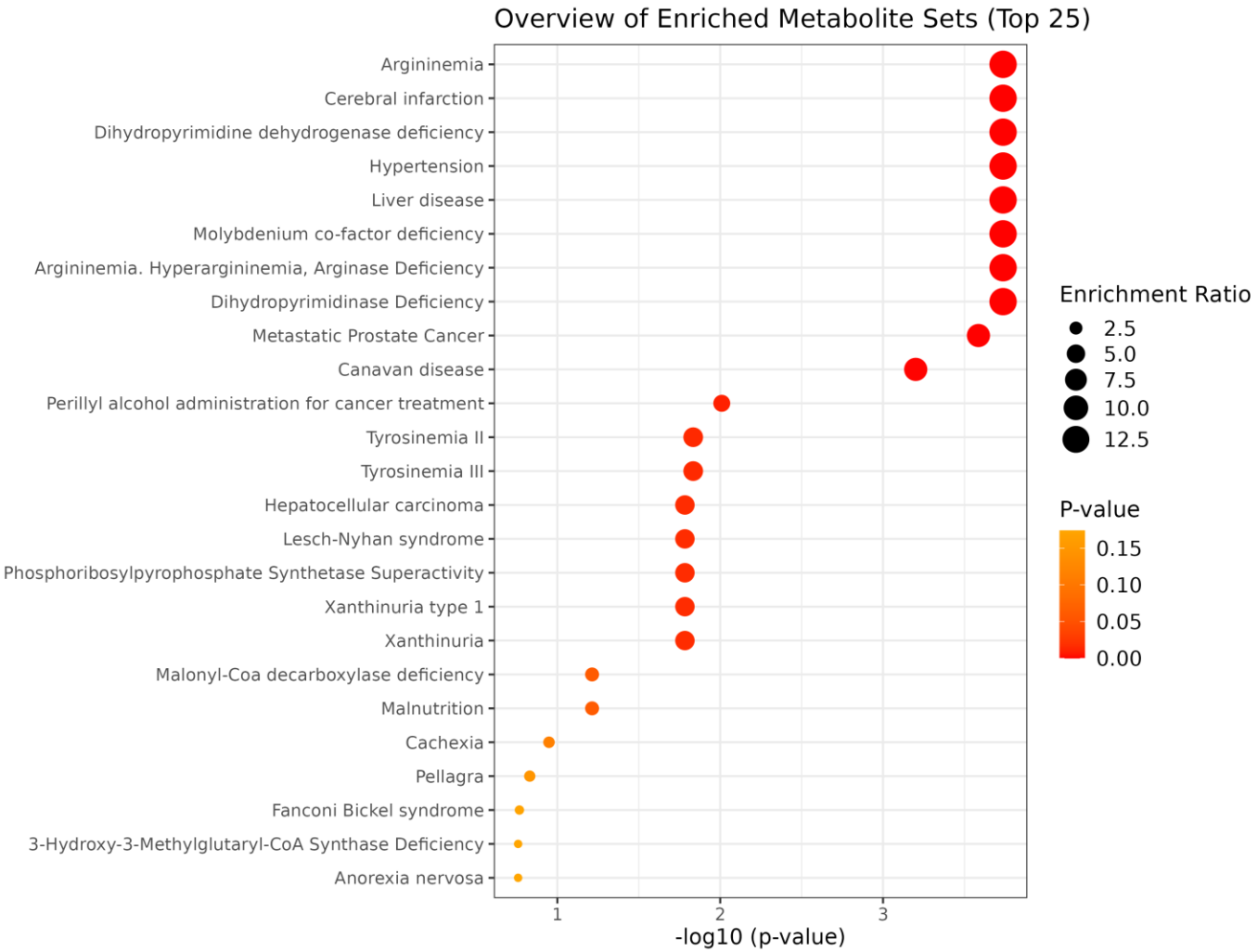
MetaboAnalyst workflow
6) enrichment analysis



Enrichment analysis, based on the **globaltest**, tests associations between metabolite sets and the outcome.

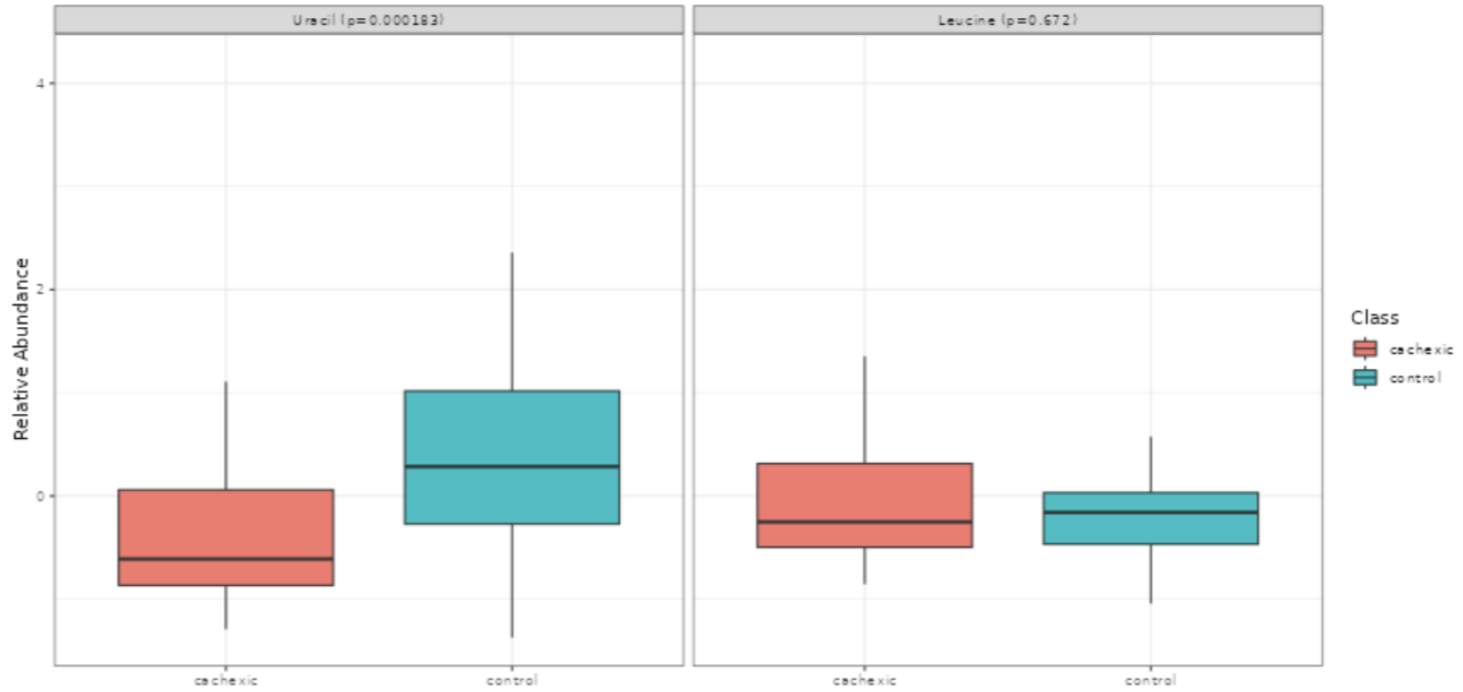
The algorithm uses a generalized linear model to compute a 'Q-stat' for each metabolite set.

MetaboAnalyst workflow
6) enrichment analysis



MetaboAnalyst workflow
6) functional interpretation

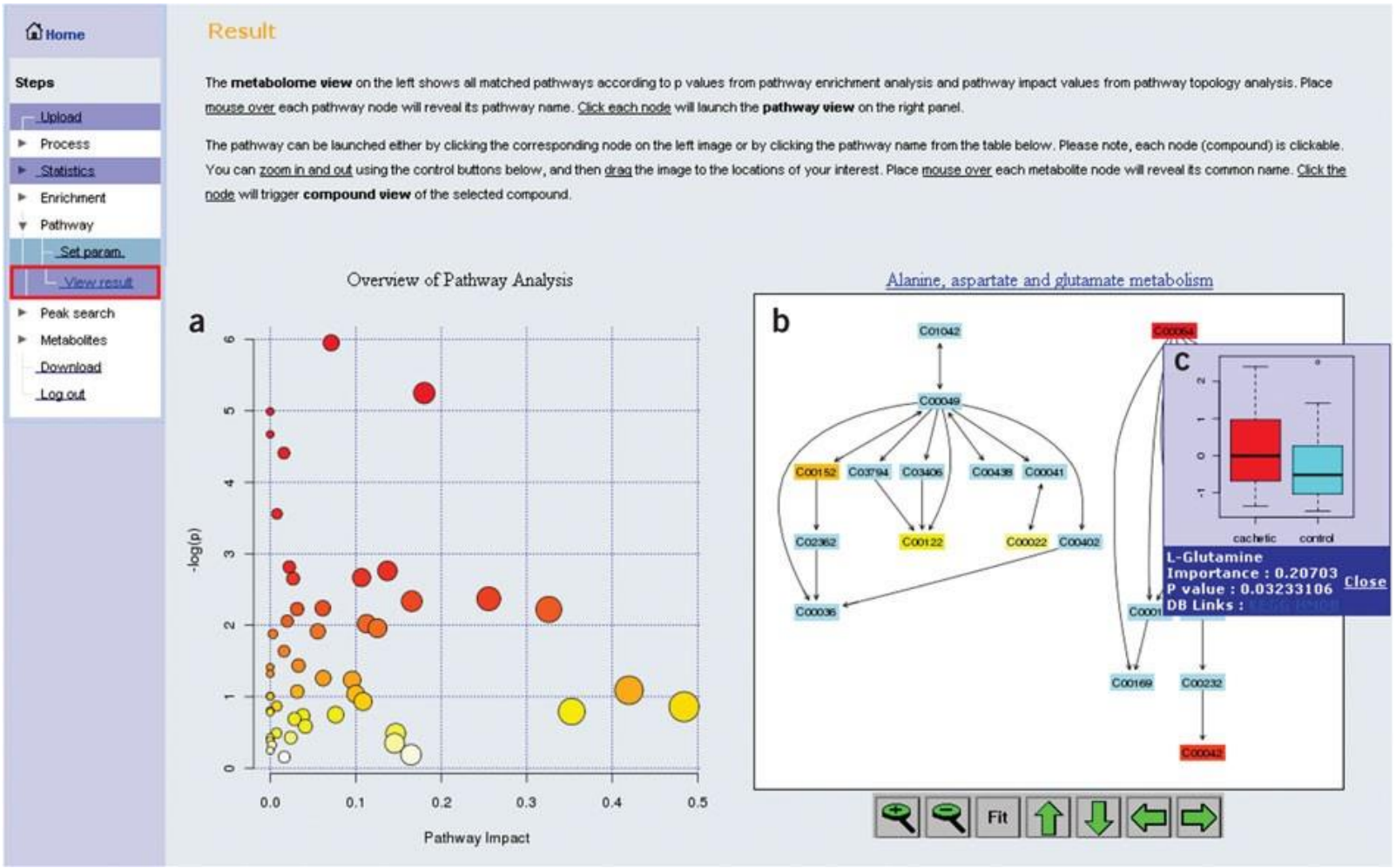
Current metabolite set:



Set Name	Metabolites	References
Metastatic Prostate Cancer	Sarcosine; **Uracil**; Kynurenine; Glycerol 3-phosphate; **Leucine**; DL-Proline	PubMed

MetaboAnalyst workflow

Metabolic pathway analysis and visualization



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DAY 4 – LECTURE OUTLINE

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  1. Overview
  2. Workflow
- Power analysis
  1. Hypothesis testing
  2. Decision errors
  3. Statistical power
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Hypothesis testing steps

1. State the hypotheses (the null hypothesis and an alternative hypothesis)
2. Design the analysis (*e.g*. the significance level is 0.05, the test method one-sample z-test)
3. Analyze sample data
4. Interpret result and make decision

What are the Null and Alternative hypotheses?

Null Hypothesis H_0	Alternative Hypothesis H_1 or H_a

• H_0 is the hypothesis that a sample data statistic occurs purely from chance
  • e.g. there is no difference between the mean pulse rate for people doing physical exercise and the normal pulse rate
• Must contain condition of equality $=, \leq$,or $\geq$
• Test the Null Hypothesis directly: reject H_0 or fail to reject H_0
	• H_1 is the hypothesis that a sample data statistic is influenced by some non-random cause
	  • e.g. the mean pulse rate for persons doing the physical exercise is higher than the normal
	• Must be true if H_0 is false (corresponding to $=, \leq$,or $\geq$ conditions)
	• `opposite' of Null Hypothesis

Decision Errors

Two types of errors can result from a hypothesis test.

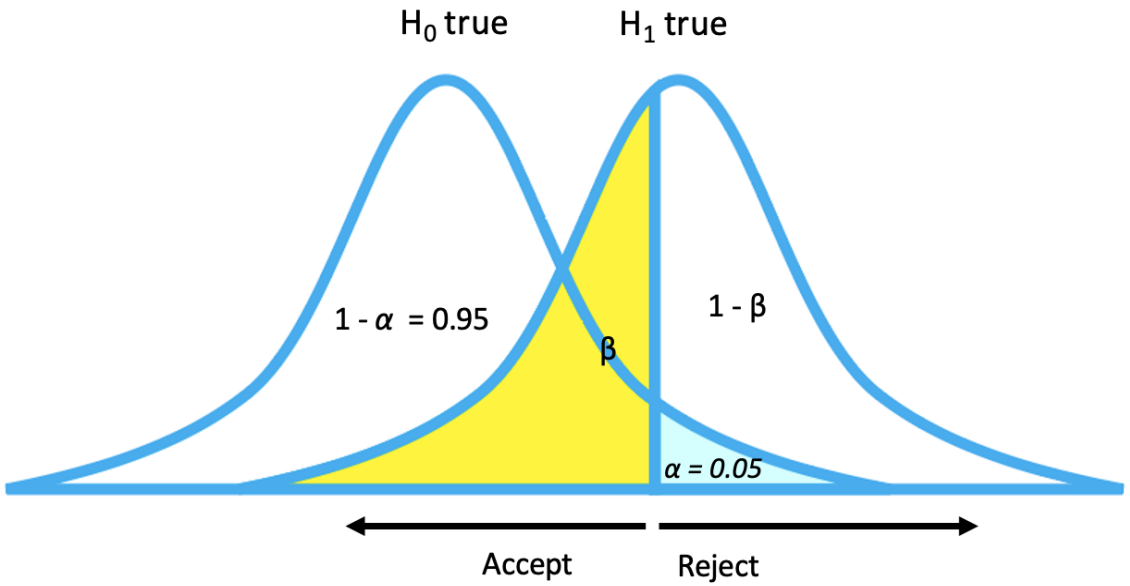
- Type I error occurs when the researcher rejects a null hypothesis when it is true. The probability of committing a Type I error is called the significance level. This probability is also called alpha, and is often denoted by α.
- Type II error occurs when the researcher fails to reject a null hypothesis that is false. The probability of committing a Type II error is called Beta, and is often denoted by β. The probability of not committing a Type II error is called the Power of the test.

Summarizing Type I and Type II Errors

	Fail to reject H0	Reject H0
H0 is true	**Correct action**	**Type I error** **FALSE POSITIVE**
probability	$1-\alpha$	α
H1 is true	**Type II error** **FALSE NEGATIVE**	**Correct action**
probability	β	*power* $= 1-\beta$

$\alpha = P(H1|H0)$

$\beta = P(H0|H1)$



Which is worse: false-positive or false-negative?

	Fail to reject H0	Reject H0
H0 is true	TRUE NEGATIVE	FALSE POSITIVE
probability	$1-\alpha$	α
H1 is true	FALSE NEGATIVE	TRUE POSITIVE
probability	β	*power* = $1-\beta$

Example 1. Covid-19 test:

- *False*
  you
  your
- *False*
  the
  You

Example 2. Quality control in a pharma production company

- *False-POSITIVE: The test declared a product faulty. We*
  thro
- *False*
  fault
  phar
  patie

Example 3. Disease diagnosis

- *False*
  disea
  wron
- *False*
  prov

Example 3. Criminal court

- *False-POSITIVE: an innocent citizen is found guilty and is sent to prison or receives the death penalty*
- *False-NEGATIVE: a criminal is declared innocent and escapes punishment*

Controlling Type I and Type II Errors

- α, β, and n are related
- when two of the three are chosen, the third is determined
- usually the researcher fix the type I error (α) he can tolerate before experiment and then compare the p-value and takes a decision

Controlling Type I and Type II error

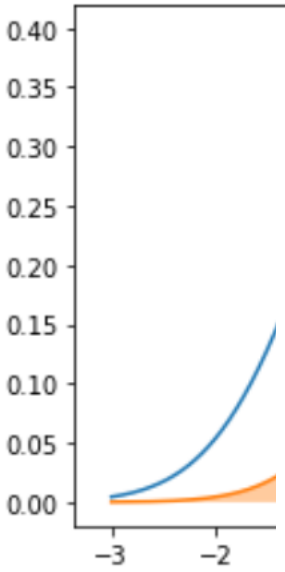


Figure 1: Equal
false negatives.

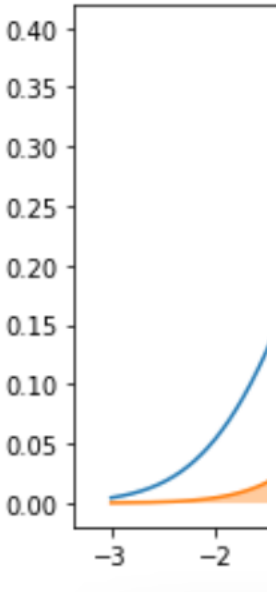


Figure 2: Greate
false negatives

Criminal court example

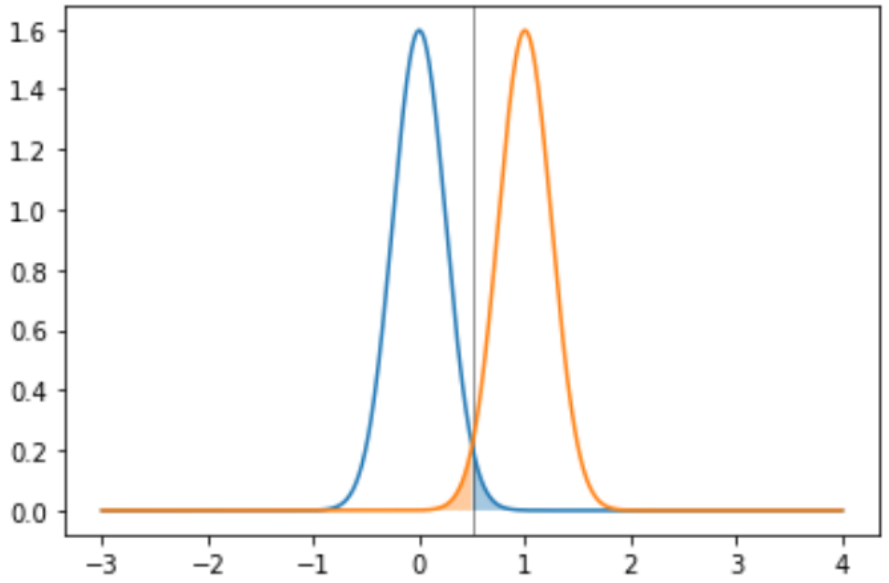
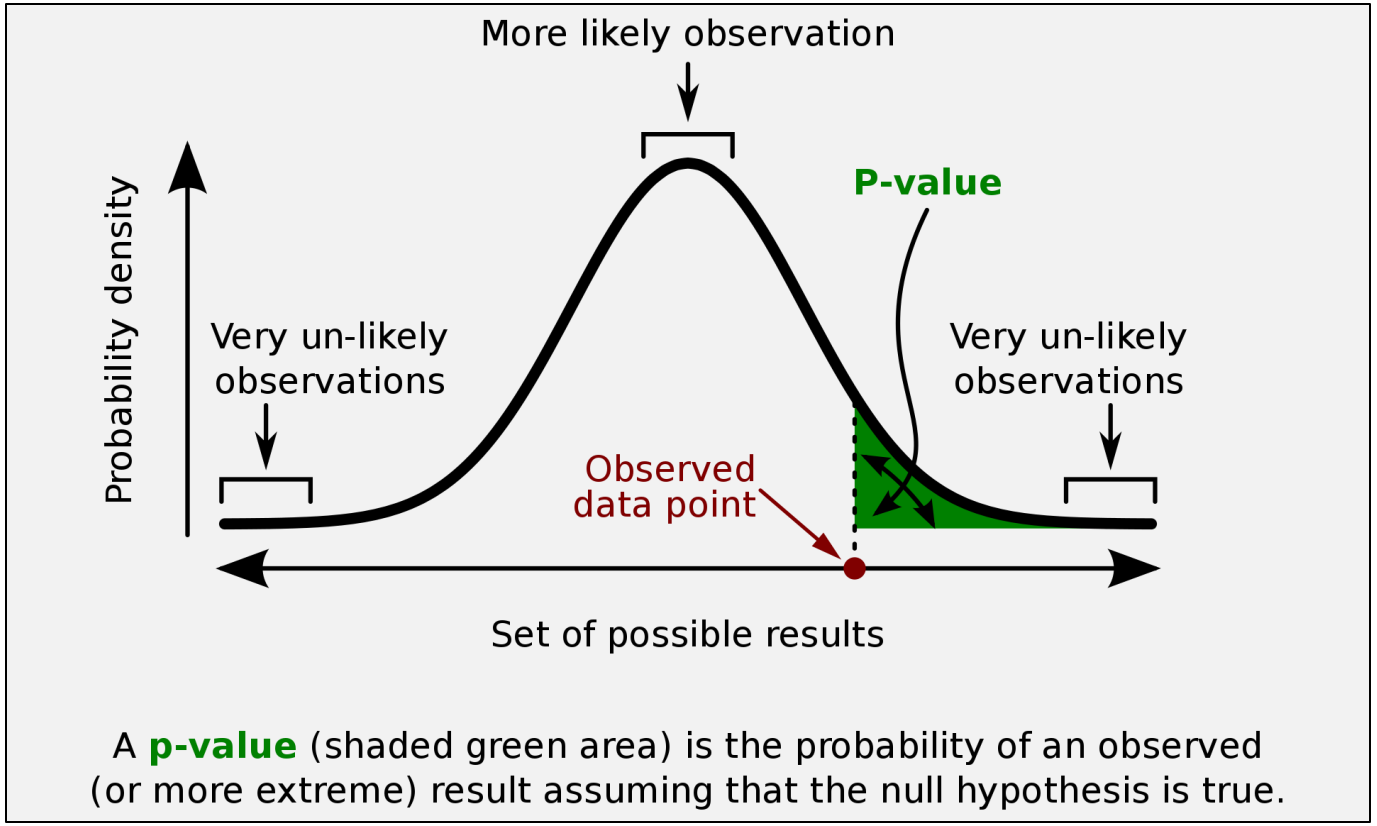


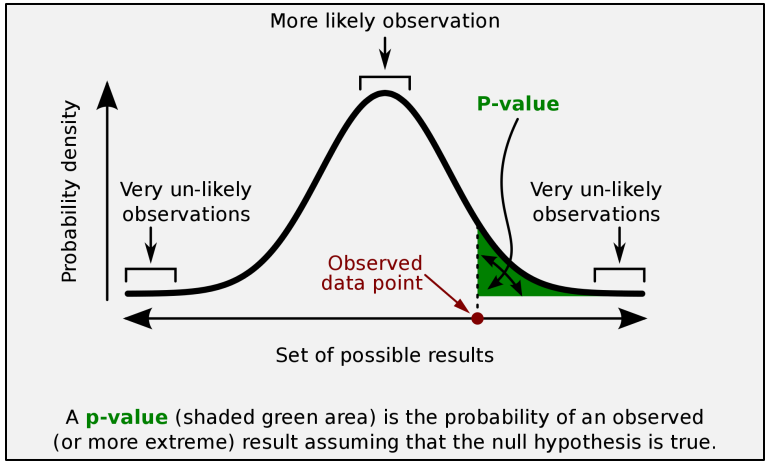
Figure 3: Lowered uncertainty through more informative features.

p-value

The p-value corresponds to the answer the question: what is the probability of the observed test statistic or one more extreme when H0 is true?



p-value interpretation



- A very small p-value means that such an extreme observed **outcome** would be very unlikely under the null hypothesis.
- Usually the researcher fix α before experiment and then compare the p-value and takes a decision.

Conventions

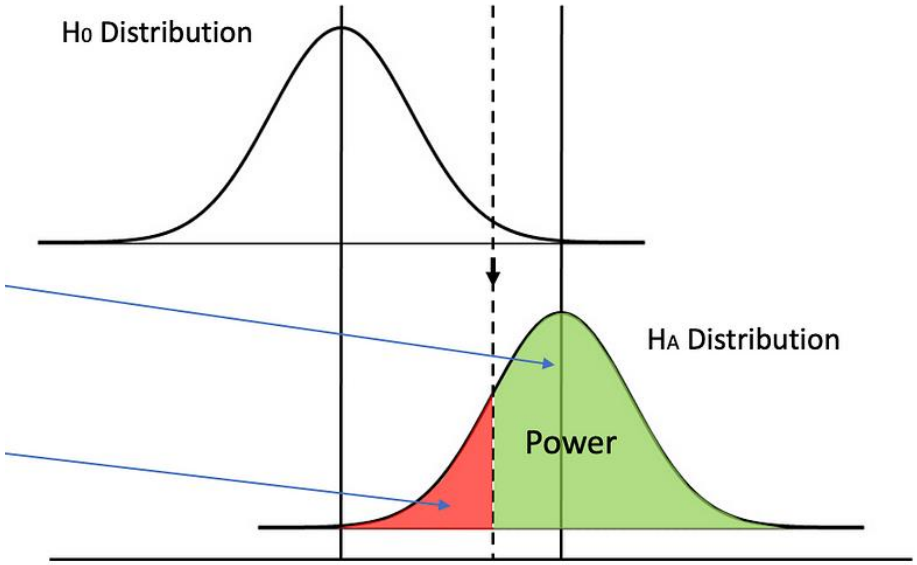
P > 0.10	⇒	*non-significant evidence against H0*
0.05 < P ≤ 0.10	⇒	*marginally significant evidence against H0*
0.01 < P ≤ 0.05	⇒	*significant evidence against H0*
P ≤ 0.01	⇒	*highly significant evidence against H0*

How to increase statistical power

	Fail to reject H0	Reject H0
H0 is true	**Correct action**	**Type I error FALSE POSITIVE**
probability	$1-\alpha$	α
H1 is true	**Type II error FALSE NEGATIVE**	**Correct action**
probability	β	*power* = $1-\beta$

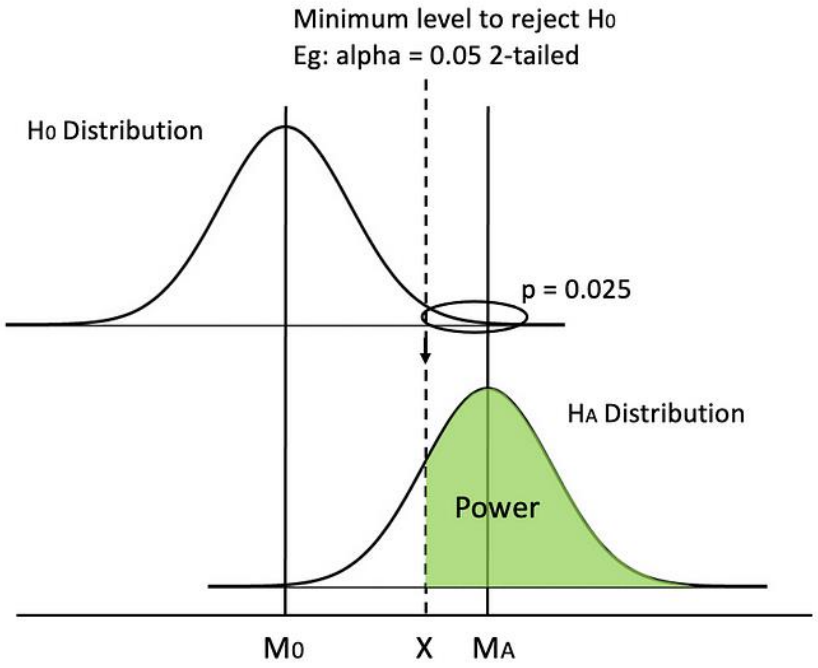
Power
1-β

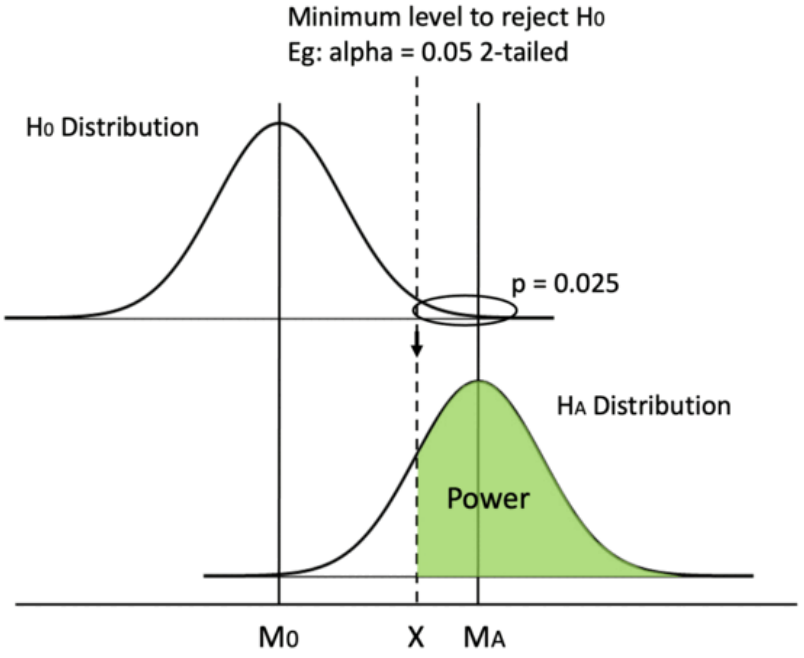
Type II error
β



How to increase statistical power

1) Raise significance level alpha (the WRONG way)

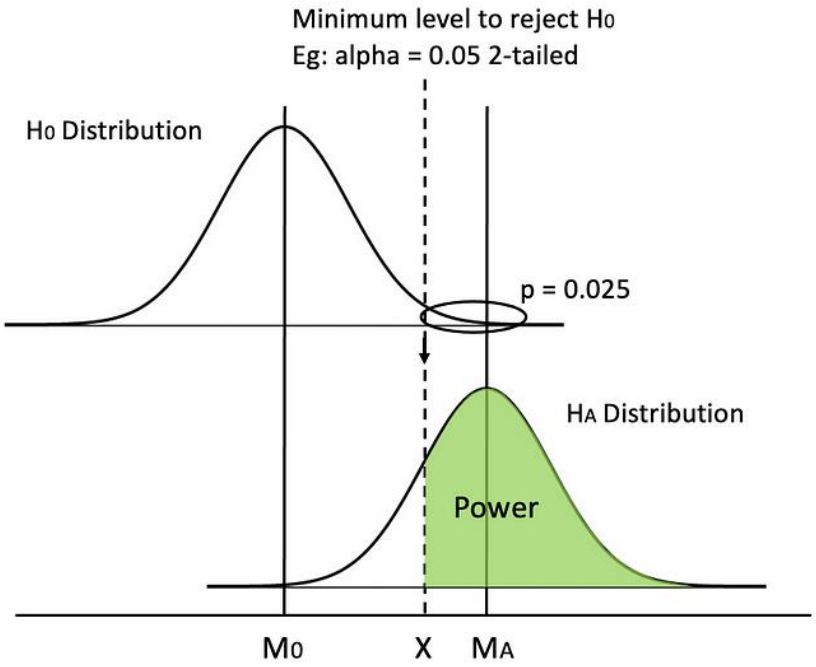


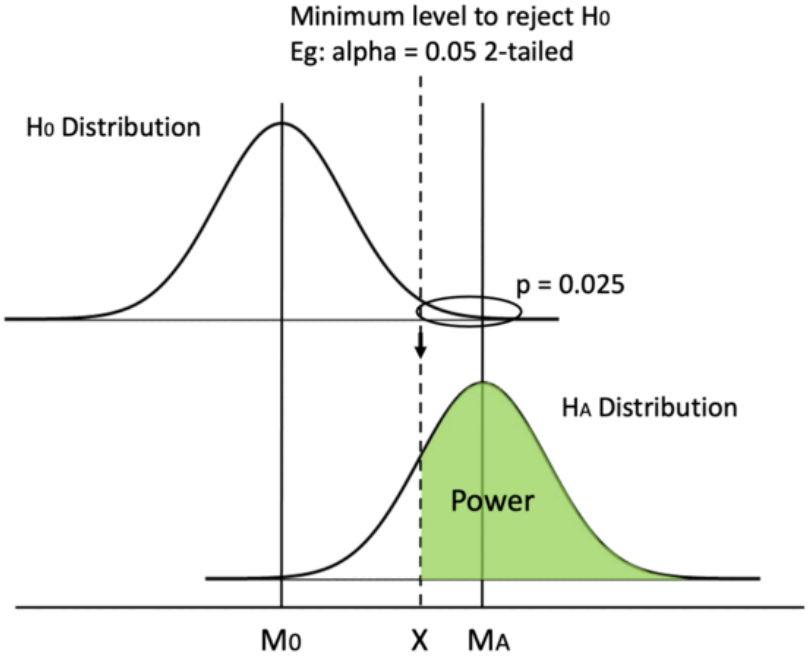


Source: https://towardsdatascience.com/5-ways-to-increase-statistical-power-377c00dd0214

How to increase statistical power

2) Switch from a 2-tailed test to a 1-tailed test (CORRECT if possible)





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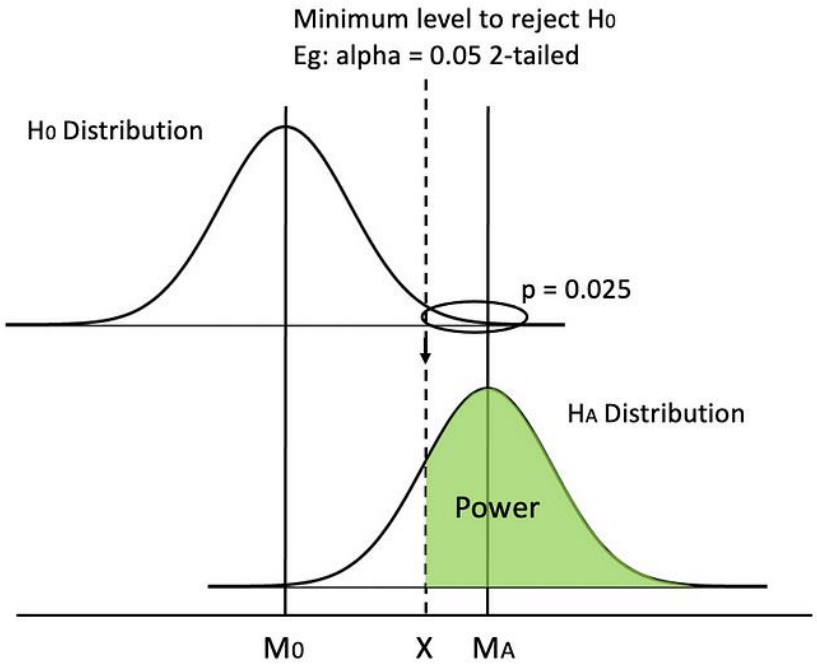
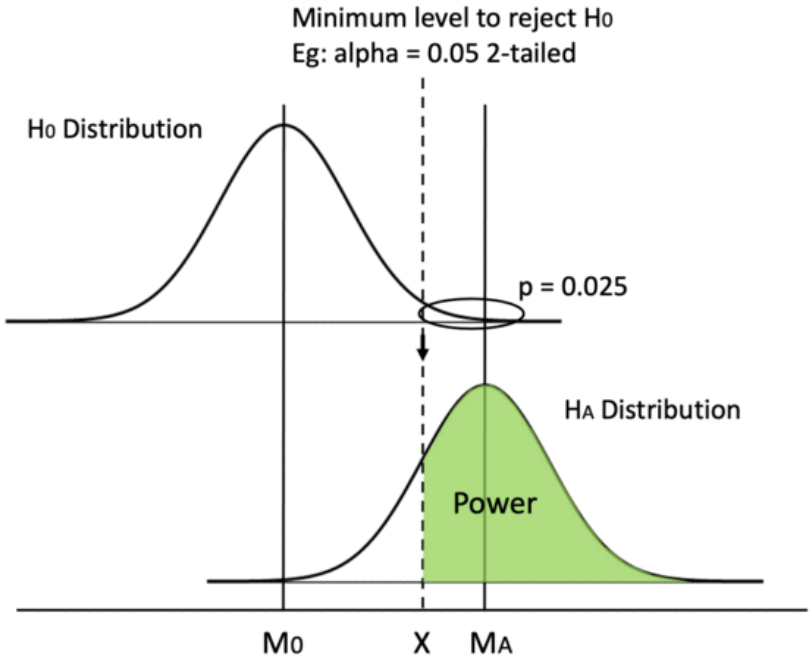
How to increase statistical power

3) Increase mean difference (or increase the effect size)





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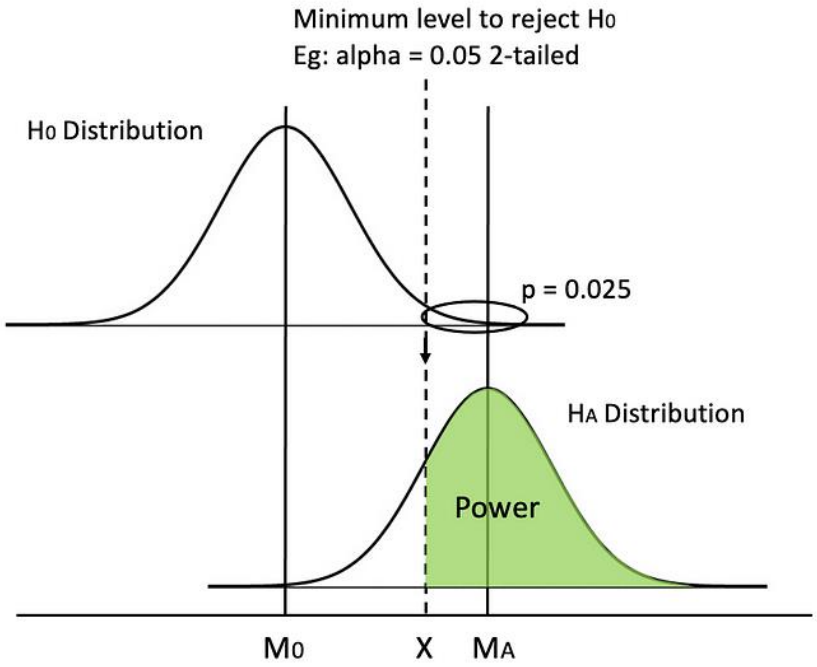
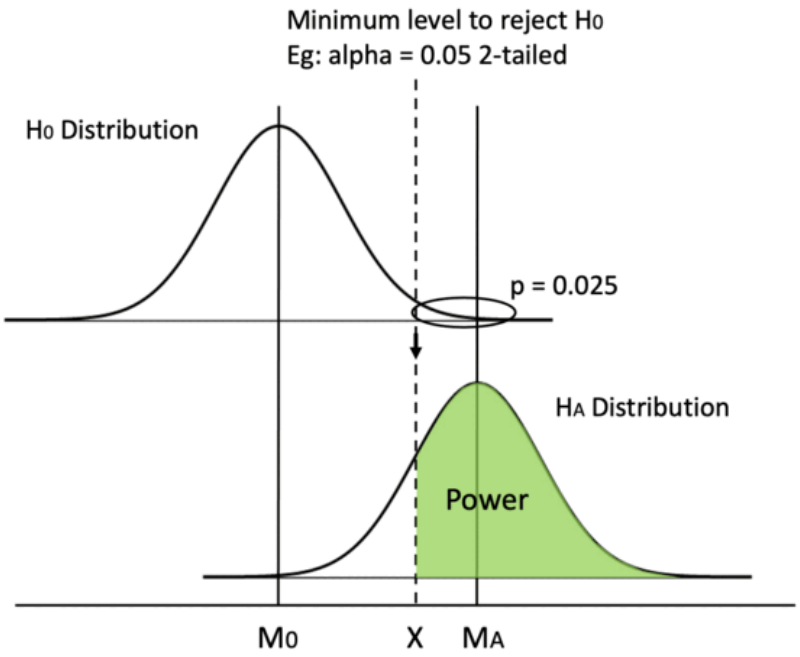
How to increase statistical power

4) Use z distribution instead of t distribution (appropriate when we know the population mean)

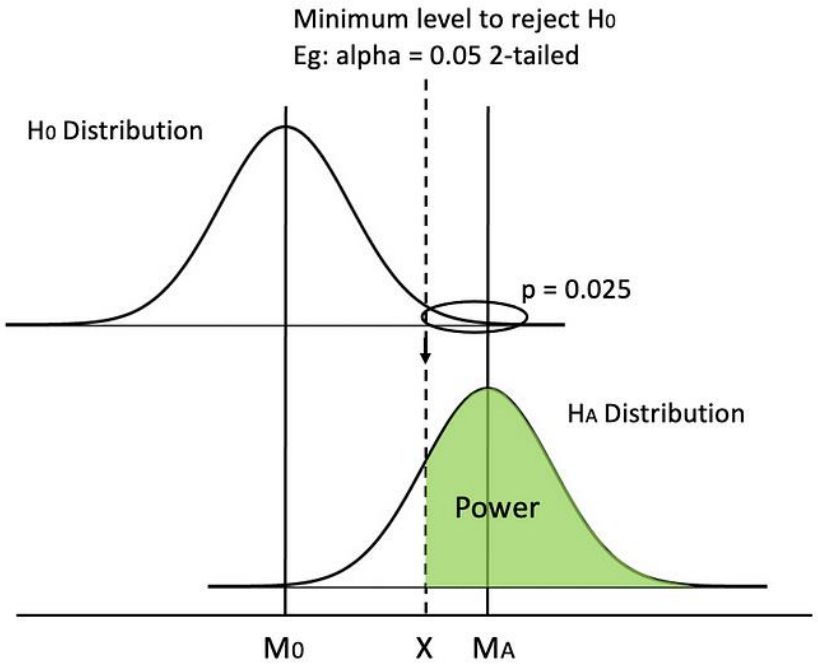


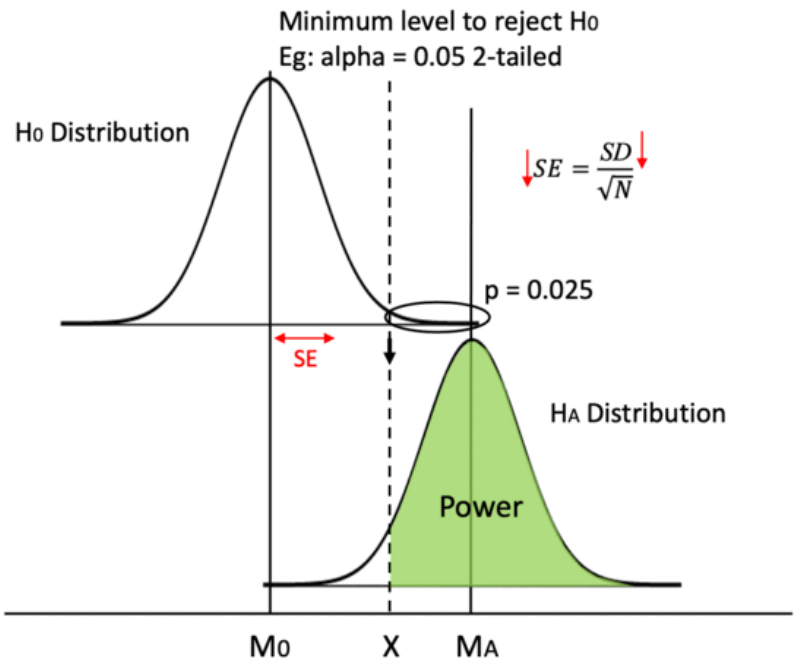


Source: https://towardsdatascience.com/5-ways-to-increase-statistical-power-377c00dd0214

How to increase statistical power

5) Decrease standard deviation (using more precise measurements to have less error and less noise)

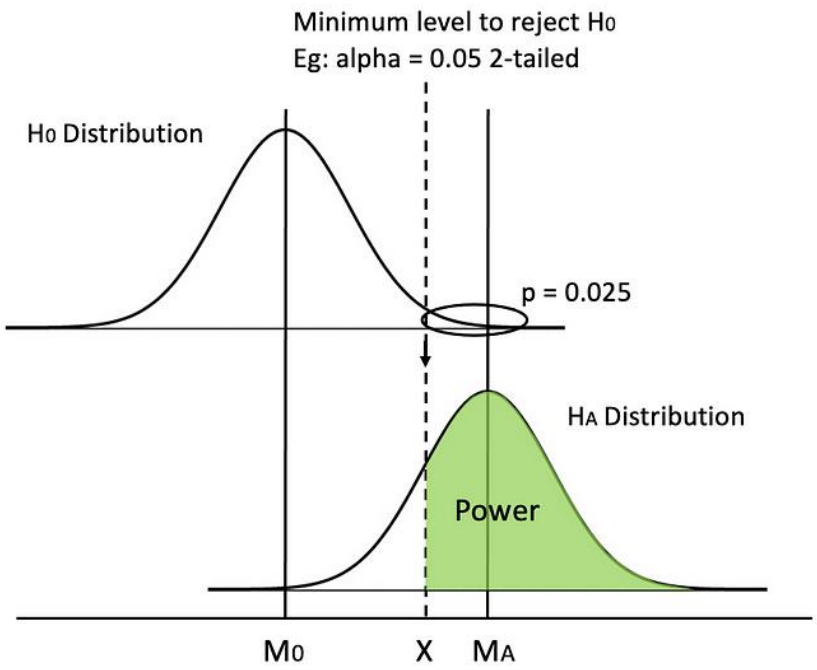


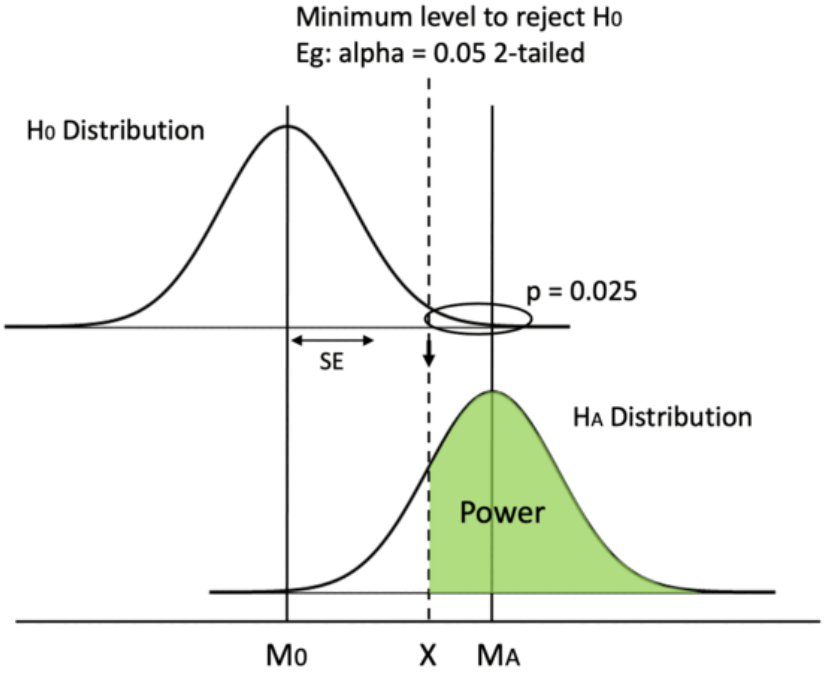


Source: https://towardsdatascience.com/5-ways-to-increase-statistical-power-377c00dd0214

How to increase statistical power

6) Increase sample size (the most practical way)





Source: https://towardsdatascience.com/5-ways-to-increase-statistical-power-377c00dd0214

Effect size

The effect size is an estimate of the difference between two or more groups.

The measurement of the effect size depends on the type of analysis your are doing:

1. Studying the mean difference between two groups

In this case you use a standardized mean difference (Cohen's *d*)

Effect size

Mean value of the population 1

Mean value of the population 2

$$Cohen's\ d = \frac{\mu_1 - \mu_2}{\sigma}$$

Standard deviation of the population

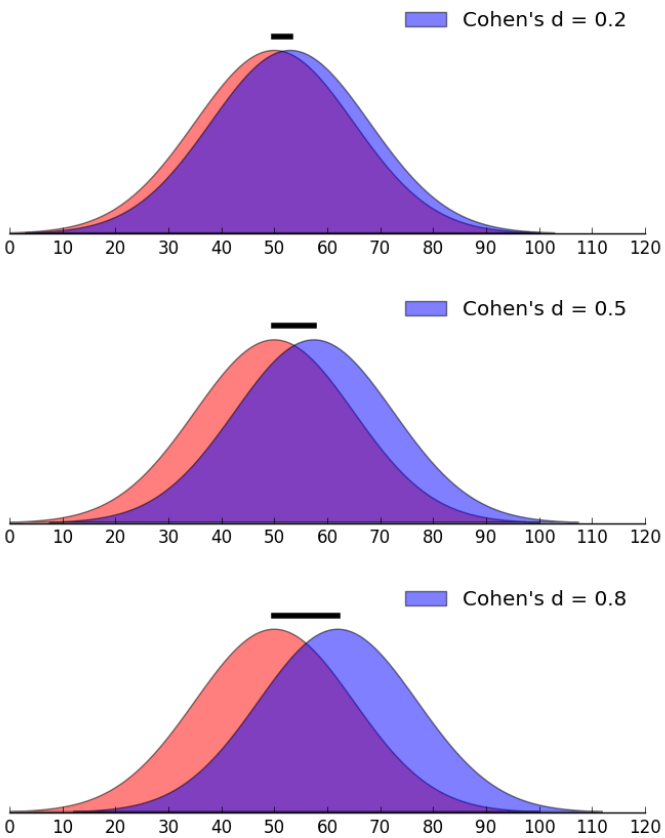
Mean value of sample 1

Mean value of sample 2

$$d = \frac{\bar{x}_1 - \bar{x}_2}{\hat{\sigma}}$$

Estimated standard deviation of the population from the sample

Cohen's d	Effect size
0.20	Small
0.5	Medium
0.8	Strong



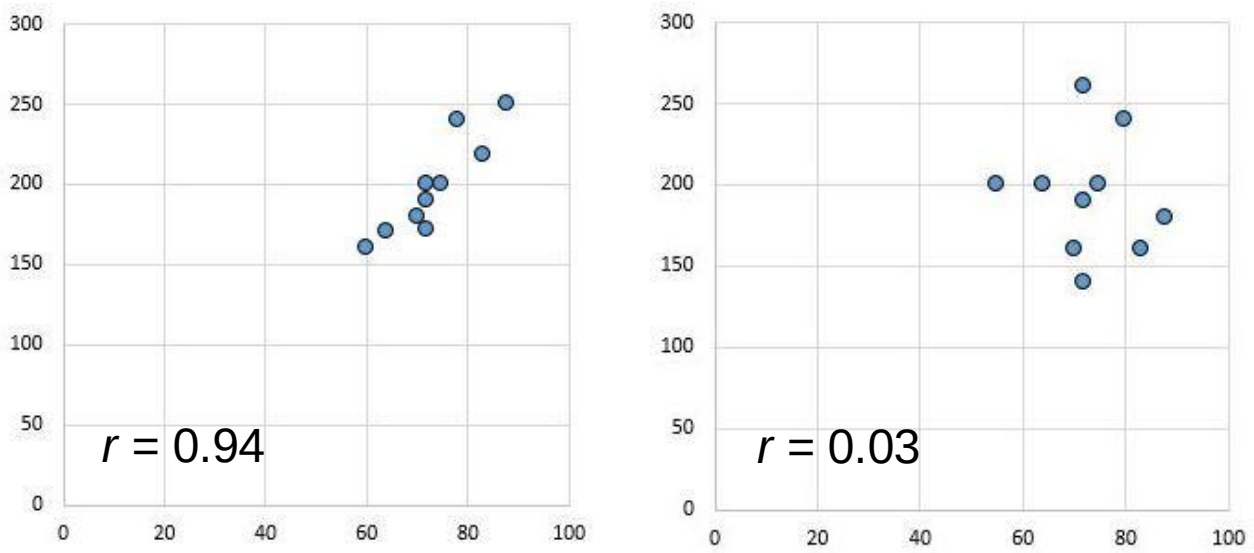
Effect size

2) Pearson Correlation Coefficient: measuring the linear association between two variables X and Y.

-1 = perfectly negative linear correlation between two variables

0 = no linear correlation between two variables

1 = perfectly positive linear correlation between two variables



Source: https://www.statology.org/effect-size/

Effect size

Pearson Correlation Coefficient

r	Effect size
0.1	small
0.3	medium
>0.5	large

Effect size in different scenarios

Test	Effect Size	Small	Medium	Large
All t-tests: • one-sample t-test • independent samples t-test • paired samples t-test	Cohen's d $d = \frac{\overline{x1} - \overline{x2}}{s}$	0.20	0.50	0.80
Difference between many means (ANOVA)	Cohen's f $f = \sqrt{\frac{\eta^2}{1-\eta^2}}$	0.10	0.25	0.40
Chi-squared test	Cohen's ω $\omega = \sqrt{\sum_{i=1}^{m} \frac{(p1i-p0i)^2}{p0i}}$	0.10	0.30	0.50
Pearson's correlation coefficient	Pearson's r	0.10	0.30	0.50
Linear Regression (entire model)	Cohen's f^2 $f^2 = \frac{R^2}{1 - R^2}$	0.02	0.15	0.35

Source: https://en.wikipedia.org/wiki/Effect_size#Overview