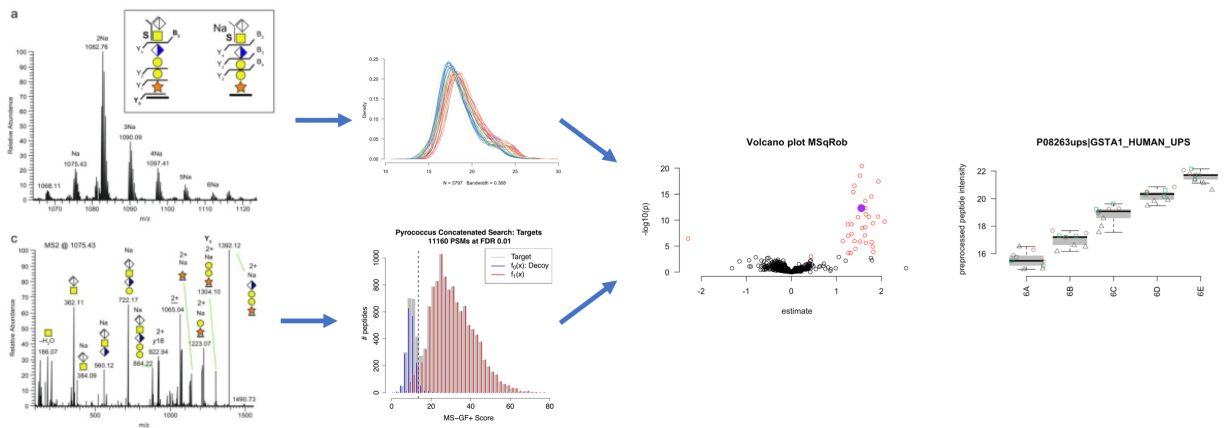


Proteomics Data Analysis 2021 (PDA21)

Contents



0.0.1 Course Description

Mass spectrometry based proteomic experiments generate ever larger datasets and, as a consequence, complex data interpretation challenges. This course focuses on the statistical concepts for peptide identification, quantification, and differential analysis. Moreover, more advanced experimental designs and blocking will also be introduced. The core focus will be on shotgun proteomics data, and quantification using label-free precursor peptide (MS1) ion intensities. The course will rely exclusively on free and userfriendly opensource tools in R/Bioconductor. The course will provide a solid basis for beginners, but will also bring new perspectives to those already familiar with standard data interpretation procedures in proteomics.

Students can sharpen their background knowledge on Mass Spectrometry, Proteomics & Bioinformatics for Proteomics here: [Mass Spectrometry and Bioinformatics for Proteomics](#)

0.0.2 Target Audience

This course is oriented towards biologists and bioinformaticians with a particular interest in differential analysis for quantitative proteomics.

According to the target audience of the course we either work with a graphical user interface (GUI) in a R/shiny App msqrob2gui (e.g. Proteomics Bioinformatics course of the EBI and the Proteomics Data Analysis course at the Gulbenkian institute) or with R/markdowns scripts (e.g. Bioinformatics Summer School at UCLouvain or the Statistical Genomics Course at Ghent University).

0.0.3 Issues

If you encounter any problems related to the course material (e.g. package installation problems, bugs in the code, typos, ...), please consider posting an issue on GitHub.

0.0.4 Statistical Data Analysis for Proteomics

0.0.4.1 Software and Data

- Install [R version 4.1 or higher] (<https://cran.r-project.org/>)
- Install Rstudio
- To install the current version of *msqrob2*, start R and run the following command.

```
if(!requireNamespace("BiocManager", quietly = TRUE)) {  
  install.packages("BiocManager")  
}  
BiocManager::install("msqrob2")
```

- To install the *msqrob2* GUI, start R and run the following commands

```
if(!requireNamespace("BiocManager", quietly = TRUE)) {  
  install.packages("BiocManager")  
}  
BiocManager::install("msqrob2gui")
```

0.0.4.2 Detailed Program

1. Identification
 2. Preprocessing & Analysis of Label Free Quantitative Proteomics Experiments with Simple Designs
 - Lecture: Preprocessing, [PDF]
 - Tutorial:
 3. Statistical Inference & Analysis of Experiments with Factorial Designs
 - Lecture: Differential Abundance Analysis, [PDF]
 - Tutorial:
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