R documentation

of 'Exp1_R25_pept.Rd'

October 6, 2016

`Exp1_R25_pept` *Exp1_R25_pept dataset*

Description

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Giai Gianetto et al. (2016) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 25 fmol and 10 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2.5. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp1_R25_pept.txt), or as a `MSnSet` structure (Exp1_R25_pept). In the latter case, the quantitative data are those of the raw intensities.

Usage

```
data(Exp1_R25_pept)
```

Format

An object of class `MSnSet` related to peptide quantification. It contains 6 samples divided into two conditions (25fmol and 10fmol) and 13918 peptides.

The data frame exprs(Exp1_R25_pept) contains six columns that are the quantitation of peptides for the six replicates.

The data frame fData(Exp1_R25_pept) contains the meta data about the peptides.

The data frame pData(Exp1_R25_pept) contains the experimental design and gives few informations about the samples.

Value

An object of class `MSnSet` related to peptides quantification.

References

Cox J., Hein M.Y., Luber C.A., Paron I., Nagaraj N., Mann M. Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. Mol Cell Proteomics. 2014 Sep, 13(9):2513-26.

Giai Gianetto, Q., Combes, F., Ramus, C., Bruley, C., Coute, Y., Burger, T. (2016). Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. Proteomics, 16(1), 29-32.

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