Package 'DAPARdata'

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Type Package

Title Data accompanying the DAPAR and Prostar packages

Version 1.0.1

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Description Mass-spectrometry based UPS proteomics data sets.

Depends R (>= 3.3)

Suggests DAPAR, Prostar

Imports utils, knitr, MSnbase

License GPL-2

biocViews ExperimentData, MassSpectrometryData

NeedsCompilation no

RoxygenNote 5.0.1

R topics documented:

DAPARdata *Available datasets in the DAPARdata package*

Description

This function lists the datasets available in DAPARdata package

Usage

```
DAPARdata()
```

Value

A list of datasets

Examples

```
DAPARdata()
```

UPSpep2 *UPSpep2 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 25fmol and 10fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. Three technical replicates were acquired for each condition.

To identify and quantify peptides, spectra were searched using MaxQuant (version 1.5.1.2) against the Uniprot database, the UPS database and the frequently observed contaminants database. Maximum false discovery rates were set to 0.01 by employing a reverse database strategy.

The dataset is either available as a CSV file (see inst/extdata/UPSpep2.txt), or as a `MSnSet` structure (UPSpep2). In the latter case, the quantitative data are those of the raw intensities.

Usage

```
data(UPSpep2)
```

Format

An object of class MSnSet related to peptide quantification. It contains 6 samples divided into two conditions (10fmol and 5fmol) and 14048 peptides.

The data frame exprs(UPSpep2) contains six columns that are the quantitation of peptides for the six replicates.

The data frame fData(UPSpep2) contains the meta data about the peptides.

The data frame pData(UPSpep2) 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.

UPSpep25 *UPSpep25 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 25fmol and 10fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. Three technical replicates were acquired for each condition.

To identify and quantify peptides, spectra were searched using MaxQuant (version 1.5.1.2) against the Uniprot database, the UPS database and the frequently observed contaminants database. Maximum false discovery rates were set to 0.01 by employing a reverse database strategy.

The dataset is either available as a CSV file (see inst/extdata/UPSpep25.txt), or as a MSnSet structure (UPSpep25). In the latter case, the quantitative data are those of the raw intensities.

Usage

```
data(UPSpep25)
```

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(UPSpep25) contains six columns that are the quantitation of peptides for the six replicates.

The data frame fData(UPSpep25) contains the meta data about the peptides.

The data frame pData(UPSpep25) 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.

UPSprot2 *UPSprot2 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 proteins identified and quantified in these two conditions. The two conditions represent the measured abundances of proteins when respectively 25fmol and 10fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. Three technical replicates were acquired for each condition.

To identify and quantify proteins, spectra were searched using MaxQuant (version 1.5.1.2) against the Uniprot database, the UPS database and the frequently observed contaminants database. Maximum false discovery rates were set to 0.01 at peptide and protein levels by employing a reverse database strategy. The abundance values of the dataset were obtained from LFQ values calculated using MaxQuant from MS intensity of unique peptides (see Cox et al. (2014)).

From a statistical viewpoint, the goal is to find which proteins are differentially abundant between the two conditions among the 2394 quantified proteins. Ideally, the 46 quantified human proteins (out of the original 48 ones) should be concluded as differentially abundant.

The dataset is either available as a CSV file (see inst/extdata/UPSprot2.txt), or as a MSnSet structure (UPSprot2.MSnset). In the latter case, the quantitative data are those of the raw intensities.

Usage

```
data(UPSprot2)
```

Format

An object of class MSnSet related to proteins quantification. It contains 6 samples divided into two conditions (10fmol and 5fmol) and 2394 proteins.

The data frame exprs(UPSprot2) contains six columns that are the quantitation of proteins for the six replicates.

The data frame fData(UPSprot2) contains the meta data about the proteins.

The data frame pData(UPSprot2) contains the experimental design and gives few informations about the samples.

Value

An object of class MSnSet related to proteins 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.

UPSprot25 *UPSprot25 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 proteins identified and quantified in these two conditions. The two conditions represent the measured abundances of proteins when respectively 25fmol and 10fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. Three technical replicates were acquired for each condition.

To identify and quantify proteins, spectra were searched using MaxQuant (version 1.5.1.2) against the Uniprot database, the UPS database and the frequently observed contaminants database. Maximum false discovery rates were set to 0.01 at peptide and protein levels by employing a reverse database strategy. The abundance values of the dataset were obtained from LFQ values calculated using MaxQuant from MS intensity of unique peptides (see Cox et al. (2014)).

From a statistical viewpoint, the goal is to find which proteins are differentially abundant between the two conditions among the 2384 quantified proteins. Ideally, the 46 quantified human proteins (out of the original 48 ones) should be concluded as differentially abundant.

The dataset is either available as a CSV file (see inst/extdata/UPSprot25.txt), or as a `MSnSet` structure (UPSprot25.MSnset). In the latter case, the quantitative data are those of the raw intensities.

Usage

```
data(UPSprot25)
```

Format

An object of class `MSnSet` related to proteins quantification. It contains 6 samples divided into two conditions (25fmol and 10fmol) and 2384 proteins.

The data frame exprs(UPSprot25) contains six columns that are the quantitation of proteins for the six replicates.

The data frame fData(UPSprot25) contains the meta data about the proteins.

The data frame pData(UPSprot25) contains the experimental design and gives few informations about the samples.

Value

An object of class `MSnSet` related to proteins 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.

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