Package: DaparToolshedData (via r-universe)

November 25, 2026

Type Package

Title Data accompanying the DaparToolshed and Prostar 2 packages

Version 1.0.0

Date 2026-07-17

Description Mass-spectrometry based UPS proteomics data sets from Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94 and 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.

Suggests rmarkdown, BiocStyle, testthat, knitr

Depends R (>= 4.5.0)

Imports S4Vectors, utils, QFeatures, ExperimentHub, AnnotationHub

Collate doc-data.R get-data.R zzz.R DaparToolshedData.R

License GPL-2

biocViews ExperimentData, ExperimentHub, MassSpectrometryData

NeedsCompilation no

Encoding UTF-8

URL https://github.com/edyp-lab/DaparToolshedData, https://edyp-lab.github.io/DaparToolshedData/

BugReports https://github.com/edyp-lab/DaparToolshedData/issues

VignetteBuilder knitr

StagedInstall no

Config/roxygen2/version 8.0.0

Config/pak/sysreqs
cmake libglpk-dev make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:33:22 UTC

RemoteUrl https://github.com/bioc/DaparToolshedData

RemoteRef RELEASE_3_24

RemoteSha f5768150ca8636a3245d4216b073aa85f2acb407

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`access-functions` *Functions to get datasets*

Description

Functions to get datasets

Usage

```
GetData(name)
```

Arguments

`name`	The name of the dataset to load.

Value

A dataset loaded

Examples

```
GetData('Exp1_R25_prot')
```

DaparToolshedData *All DaparToolshedData datasets*

Description

The DaparToolshedData package provides example mass spectrometry data from proteomics experiments.

The [DaparToolshedData()] function returns a 'data.frame' with all the annotated datasets provided in the package.

Usage

```
DaparToolshedData()
```

Value

A 'data.frame' describing the data available in 'DaparToolshedData'.

Author(s)

Samuel Wieczorek

Examples

```
DaparToolshedData()
```

Exp1_R2_pept *Exp1_R2_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 proteins identified and quantified in these two conditions. The two conditions represent the measured abundances of proteins when respectively 5 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. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp1_R2_prot.txt)

Format

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

Value

An object of class 'QFeatures' 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.

Examples

```
GetData("Exp1_R2_pept")
```

Exp1_R2_prot *Exp1_R2_prot 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 5 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. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp1_R2_prot.txt), or as a 'QFeatures' structure (Exp1_R2_prot.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

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

Value

An object of class 'QFeatures' 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.

Examples

```
GetData("Exp1_R2_prot")
```

`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 proteins identified and quantified in these two conditions. The two conditions represent the measured abundances of proteins 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). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class ‘QFeatures‘ related to proteins quantification. It contains 6 samples divided into two conditions (25 fmol and 10 fmol) and 13919 peptides

Value

An object of class ‘QFeatures‘ 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.

Examples

```
GetData("Exp1_R25_pept")
```

`Exp1_R25_prot` *Exp1_R25_prot 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 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_prot.txt), or as a 'QFeatures' structure (Exp1_R25_prot.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

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

Value

An object of class 'QFeatures' 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.

Examples

```
GetData("Exp1_R25_prot")
```

Exp2_R10_pept *Exp2_R10_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 Ramus et al. (2015) 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 10 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 10. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp2_R10_pept.txt), or as a 'QFeatures' structure (Exp2_R10_pept.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class 'QFeatures' related to peptides quantification. It contains 6 samples divided into two conditions (10 fmol and 100 fmol) and 5633 peptides.

Value

An object of class 'QFeatures' related to peptides quantification.

References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94.PMID: 26862574.

Examples

```
GetData("Exp2_R10_pept")
```

`Exp2_R10_prot` *Exp2_R10_prot 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 Ramus et al. (2015) 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 10 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 10. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp2_R10_prot.txt), or as a 'QFeatures' structure (Exp2_R10_prot.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class 'QFeatures' related to proteins quantification. It contains 6 samples divided into two conditions (10 fmol and 100 fmol) and 948 proteins.

Value

An object of class 'QFeatures' related to proteins quantification.

References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94.PMID: 26862574.

Examples

```
GetData("Exp2_R10_prot")
```

`Exp2_R100_pept` *Exp2_R100_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 Ramus et al. (2015) 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 1 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 100. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp2_R100_pept.txt), or as a 'QFeatures' structure (Exp2_R100_peptt.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class 'QFeatures' related to peptides quantification. It contains 6 samples divided into two conditions (1 fmol and 100 fmol) and 5684 peptides.

Value

An object of class 'QFeatures' related to peptides quantification.

References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94.PMID: 26862574.

Examples

```
GetData("Exp2_R100_pept")
```

`Exp2_R100_prot` *Exp2_R100_prot 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 Ramus et al. (2015) 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 1 fmol and 100 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 100. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp2_R100_prot.txt), or as a 'QFeatures' structure (Exp2_R100_prot.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class 'QFeatures' related to proteins quantification. It contains 6 samples divided into two conditions (1 fmol and 100 fmol) and 923 proteins.

Value

An object of class 'QFeatures' related to proteins quantification.

References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94.PMID: 26862574.

Examples

```
GetData("Exp2_R100_prot")
```

Exp2_R2_pept *Exp2_R2_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 Ramus et al. (2015) 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 50 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp2_R2_pept.txt), or as a 'QFeatures' structure (Exp2_R2_pept.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class 'QFeatures' related to peptides quantification. It contains 6 samples divided into two conditions (25fmol and 50fmol) and 5390 peptides.

Value

An object of class 'QFeatures' related to peptides quantification.

References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94.PMID: 26862574.

Examples

```
GetData("Exp2_R2_pept")
```

Exp2_R2_prot *Exp2_R2_prot 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 Ramus et al. (2015) 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 50 fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. This results in a concentration ratio of 2. Three technical replicates were acquired for each condition.

The dataset is either available as a CSV file (see inst/extdata/Exp2_R2_prot.txt), or as a 'QFeatures' structure (Exp2_R2_prot.ft). In the latter case, the quantitative data are those of the raw intensities.

Format

An object of class 'QFeatures' related to proteins quantification. It contains 6 samples divided into two conditions (25 fmol and 50 fmol) and 948 proteins.

Value

An object of class 'QFeatures' related to proteins quantification.

References

Ramus C, Hovasse A, Marcellin M, Hesse AM, Mouton-Barbosa E, Bouyssie D, Vaca S, Carapito C, Chaoui K, Bruley C, Garin J, Cianferani S, Ferro M, Dorssaeler AV, Burlet-Schiltz O, Schaeffer C, Coute Y, Gonzalez de Peredo A. Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data Brief. 2015 Dec 17;6:286-94.PMID: 26862574.

Examples

```
GetData("Exp2_R2_prot")
```

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