

Package ‘scpdata’

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Type Package

Title Single-Cell Proteomics Data Package

Version 1.2.0

Description The package disseminates mass spectrometry (MS)-based single-cell proteomics (SCP) datasets. The data were collected from published work and formatted using the `scp` data structure. The data sets contain quantitative information at spectrum, peptide and/or protein level for single cells or minute sample amounts.

Depends R (>= 4.1), QFeatures, ExperimentHub

Imports utils, AnnotationHub, SingleCellExperiment, S4Vectors

Suggests scp, magrittr, dplyr, knitr, BiocStyle, BiocCheck, rmarkdown, testthat

biocViews ExperimentData, ExpressionData, ExperimentHub, ReproducibleResearch, MassSpectrometryData, Proteome, SingleCellData

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cong2020AC

Cong et al. 2020 (Ana. Chem.): HeLa single cells

Description

Single-cell proteomics using the nanoPOTS sample processing device in combination with ultranarrow-bore (20um i.d.) packed-column LC separations and the Orbitrap Eclipse Tribrid MS. The dataset contains label-free quantitative information at PSM, peptide and protein level. The samples are single HeLa cells. Bulk samples (100 and 20 cells) were also included in the experiment to increase the identification rate thanks to between-run matching (cf MaxQuant).

Usage

cong2020AC

Format

A [QFeatures](#) object with 9 assays, each assay being a [SingleCellExperiment](#) object:

- 100/20 HeLa cells: 2 assays containing PSM data for a bulk of 100 or 20 HeLa cells, respectively.
- Blank: assay containing the PSM data for a blank sample
- Single cell X: 4 assays containing PSM data for a single cell. The X indicates the replicate number.
- peptides: quantitative data for 12590 peptides in 7 samples (all runs combined).
- proteins: quantitative data for 1801 proteins in 7 samples (all runs combined).

Sample annotation is stored in `colData(cong2020AC())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation:** The HeLa cells were diluted and aspirated using a microcapillary with a pulled tip.
- **Sample preparation** performed using the nanoPOTs device. Protein extraction using RapiGest (+ DTT) + alkylation (IAA) + Lys-C digestion + cleave RapiGest (formic acid)
- **Separation:** UltiMate 3000 RSLCnano pump with a home-packed nanoLC column (60cm x 20um i.d.; approx. 20 nL/min)
- **Ionization:** ESI (2,000V; Nanospray Flex)
- **Mass spectrometry:** Thermo Fisher Orbitrap Fusion Eclipse. MS1 settings: accumulation time = 246ms; resolution = 120,000; AGC = 1E6. MS/MS settings depend on quantity. All: AGC = 1E5. 20-100 cels: accumulation time = 246ms; resolution = 120,000. Single cells: accumulation time = 500ms; resolution = 240,000.
- **Data analysis:** MaxQuant (v1.6.3.3) + Excel

Data collection

The PSM, peptide and protein data were collected from the PRIDE repository (accession ID: PXD016921). We downloaded the evidence.txt file containing the PSM identification and quantification results. The sample annotation was inferred from the samples names. The data were then converted to a [QFeatures](#) object using the `scp::readSCP` function.

The peptide data were processed similarly from the peptides.txt file. The quantitative column names were adapted to match the PSM data. The peptide data were added to [QFeatures](#) object and link between the features were stored.

The protein data were similarly processed from the proteinGroups.txt file. The quantitative column names were adapted to match the PSM data. The peptide data were added to [QFeatures](#) object and link between the features were stored.

Source

All files can be downloaded from the PRIDE repository PXD016921. The source link is: <ftp://ftp.pride.ebi.ac.uk/pride/data/ar>

References

Cong, Yongzheng, Yiran Liang, Khatereh Motamedchaboki, Romain Huguet, Thy Truong, Rui Zhao, Yufeng Shen, Daniel Lopez-Ferrer, Ying Zhu, and Ryan T. Kelly. 2020. "Improved Single-Cell Proteome Coverage Using Narrow-Bore Packed NanoLC Columns and Ultrasensitive Mass Spectrometry." *Analytical Chemistry*, January. ([link to article](#)).

Examples

cong2020AC()

`dou2019_boosting`*Dou et al. 2019 (Anal. Chem.): testing boosting ratios*

Description

Single-cell proteomics using nanoPOTS combined with TMT isobaric labeling. It contains quantitative information at PSM and protein level. The cell types are either "Raw" (macrophage cells), "C10" (epithelial cells), or "SVEC" (endothelial cells). Each cell is replicated 2 or 3 times. Each cell type was run using 3 levels of boosting: 0 ng (no boosting), 5 ng or 50 ng. When boosting was applied, 1 reference well and 1 boosting well were added, otherwise 1 empty well was added. Each boosting setting (0ng, 5ng, 50ng) was run in duplicate.

Usage

`dou2019_boosting`

Format

A `QFeatures` object with 7 assays, each assay being a `SingleCellExperiment` object:

- `Boosting_X_run_Y`: PSM data with 10 columns corresponding to the TMT-10plex channels. The X indicates the boosting amount (0ng, 5ng or 50ng) and Y indicates the run number (1 or 2).
- `proteins`: protein data containing quantitative data for 1436 proteins and 60 samples (all runs combined).

Sample annotation is stored in `colData(dou2019_boosting())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation**: single-cells from the three murine cell lines were isolated using FACS (BD Influx II cell sorter). Boosting sample were prepared (presumably in bulk) from 1:1:1 mix of the three cell lines.
- **Sample preparation** performed using the nanoPOTs device. Protein extraction (DMM + TCEAP) + alkylation (IAA) + Lys-C digestion + trypsin digestion + TMT-10plex labeling and pooling.
- **Separation**: nanoLC (Dionex UltiMate with an in-house packed 50cm x 30um LC columns; 50nL/min)
- **Ionization**: ESI (2,000V)
- **Mass spectrometry**: Thermo Fisher Orbitrap Fusion Lumos Tribrid (MS1 accumulation time = 50ms; MS1 resolution = 120,000; MS1 AGC = 1E6; MS2 accumulation time = 246ms; MS2 resolution = 60,000; MS2 AGC = 1E5)
- **Data analysis**: MS-GF+ + MASIC (v3.0.7111) + RomicsProcessor (custom R package)

Data collection

The PSM data were collected from the MassIVE repository MSV000084110 (see Source section). The downloaded files are:

- Boosting_*ng_run*_msgfplus.mzid: the MS-GF+ identification result files.
- Boosting_*ng_run*_ReporterIons.txt: the MASIC quantification result files.

For each batch, the quantification and identification data were combined based on the scan number (common to both data sets). The combined datasets for the different runs were then concatenated feature-wise. The sample annotation table was manually created based on the available information provided in the article. The data were then converted to a [QFeatures](#) object using the `scp::readSCP` function.

The protein data were downloaded from Supporting information section from the publisher's website (see Sources). The data is supplied as an Excel file `ac9b03349_si_004.xlsx`. The file contains 7 sheets from which we took the 2nd, 4th and 6th sheets (named 01 - No Boost raw data, 03 - 5ng boost raw data, 05 - 50ng boost raw data, respectively). The sheets contain the combined protein data for the duplicate runs given the boosting amount. We joined the data for all boosting ratios based on the protein name and converted the data to a [SingleCellExperiment](#) object. We then added the object as a new assay in the [QFeatures](#) dataset (containing the PSM data). Links between the proteins and the corresponding PSM were created.

Source

The PSM data can be downloaded from the massIVE repository MSV000084110. FTP link: <ftp://massive.ucsd.edu/MSV000084110>

The protein data can be downloaded from the [ACS Publications](#) website (Supporting information section).

References

Dou, Maowei, Jeremy Clair, Chia-Feng Tsai, Kerui Xu, William B. Chrisler, Ryan L. Sontag, Rui Zhao, et al. 2019. "High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform." *Analytical Chemistry*, September ([link to article](#)).

See Also

[dou2019_lystates](#), [dou2019_mouse](#)

Examples

```
dou2019_boosting()
```

dou2019_lysates

Dou et al. 2019 (Anal. Chem.): HeLa lysates

Description

Single-cell proteomics using nanoPOTS combined with TMT multiplexing. It contains quantitative information at PSM and protein level. The samples are commercial HeLa lysates diluted to single-cell amounts (0.2 ng). The boosting wells contain the same digest but at higher amount (10 ng).

Usage

dou2019_lysates

Format

A [QFeatures](#) object with 3 assays, each assay being a [SingleCellExperiment](#) object:

- `HeLa_run_1`: PSM data with 10 columns corresponding to the TMT-10plex channels. Columns hold quantitative information for HeLa lysate samples (either 0, 0.2 or 10ng). This is the data for run 1.
- `HeLa_run_2`: PSM data with 10 columns corresponding to the TMT-10plex channels. Columns hold quantitative information for HeLa lysate samples (either 0, 0.2 or 10ng). This is the data for run 2.
- `proteins`: protein data containing quantitative data for 1641 proteins and 20 samples (run 1 and run 2 combined).

Sample annotation is stored in `colData(dou2019_lysates())`. The description of the `rowData` fields for the PSM data can be found in the [MaxQuant documentation](#).

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation**: commercially available HeLa protein digest (Thermo Scientific).
- **Sample preparation** performed using the nanoPOTs device. Protein extraction (DMM + TCEAP) + alkylation (IAA) + Lys-C digestion + trypsin digestion + TMT-10plex labeling and pooling.
- **Separation**: nanoLC (Dionex UltiMate with an in-house packed 50cm x 30um LC columns; 50nL/min)
- **Ionization**: ESI (2,000V)
- **Mass spectrometry**: Thermo Fisher Orbitrap Fusion Lumos Tribrid (MS1 accumulation time = 50ms; MS1 resolution = 120,000; MS1 AGC = 1E6; MS2 accumulation time = 246ms; MS2 resolution = 60,000; MS2 AGC = 1E5)
- **Data analysis**: MS-GF+ + MASIC (v3.0.7111) + RomicsProcessor (custom R package)

Data collection

The PSM data were collected from the MassIVE repository MSV000084110 (see Source section). The downloaded files are:

- `Hela_run_*_msgfplus.mzid`: the MS-GF+ identification result files
- `Hela_run_*_ReporterIons.txt`: the MASIC quantification result files

For each batch, the quantification and identification data were combined based on the scan number (common to both data sets). The combined datasets for the different runs were then concatenated feature-wise. The sample annotation table was manually created based on the available information provided in the article. The data were then converted to a [QFeatures](#) object using the `scp::readSCP` function.

The protein data were downloaded from Supporting information section from the publisher's website (see Sources). The data is supplied as an Excel file `ac9b03349_si_003.xlsx`. The file contains 7 sheets from which we only took the sheet 6 (named 5 - Run 1 and 2 raw data) with the combined protein data for the two runs. We converted the data to a [SingleCellExperiment](#) object and added the object as a new assay in the [QFeatures](#) dataset (containing the PSM data). Links between the proteins and the corresponding PSM were created.

Source

The PSM data can be downloaded from the massIVE repository MSV000084110. FTP link: <ftp://massive.ucsd.edu/MSV000084110>

The protein data can be downloaded from the [ACS Publications](#) website (Supporting information section).

References

Dou, Maowei, Jeremy Clair, Chia-Feng Tsai, Kerui Xu, William B. Chrisler, Ryan L. Sontag, Rui Zhao, et al. 2019. "High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform." *Analytical Chemistry*, September ([link to article](#)).

See Also

[dou2019_mouse](#), [dou2019_boosting](#)

Examples

```
dou2019_lystates()
```

dou2019_mouse

Dou et al. 2019 (Anal. Chem.): murine cell lines

Description

Single-cell proteomics using nanoPOTS combined with TMT isobaric labeling. It contains quantitative information at PSM and protein level. The cell types are either "Raw" (macrophage cells), "C10" (epithelial cells), or "SVEC" (endothelial cells). Out of the 132 wells, 72 contain single cells, corresponding to 24 C10 cells, 24 RAW cells, and 24 SVEC. The other wells are either boosting channels (12), empty channels (36) or reference channels (12). Boosting and reference channels are balanced (1:1:1) mixes of C10, SVEC, and RAW samples at 5 ng and 0.2 ng, respectively. The different cell types were evenly distributed across 4 nanoPOTS chips. Samples were 11-plexed with TMT labeling.

Usage

dou2019_mouse

Format

A [QFeatures](#) object with 13 assays, each assay being a [SingleCellExperiment](#) object:

- `Single_Cell_Chip_X_Y`: PSM data with 11 columns corresponding to the TMT channels (see Notes). The X indicates the chip number (from 1 to 4) and Y indicates the row name on the chip (from A to C).
- `proteins`: protein data containing quantitative data for 2331 proteins and 132 samples (all runs combined).

Sample annotation is stored in `colData(dou2019_mouse())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation**: single-cells from the three murine cell lines were isolated using FACS (BD Influx II cell sorter).
- **Sample preparation** performed using the nanoPOTs device. Protein extraction (DMM + TCEAP) + alkylation (IAA) + Lys-C digestion + trypsin digestion + TMT-10plex labeling and pooling.
- **Separation**: nanoLC (Dionex UltiMate with an in-house packed 50cm x 30um LC columns; 50nL/min)
- **Ionization**: ESI (2,000V)
- **Mass spectrometry**: Thermo Fisher Orbitrap Fusion Lumos Tribrid (MS1 accumulation time = 50ms; MS1 resolution = 120,000; MS1 AGC = 1E6; MS2 accumulation time = 246ms; MS2 resolution = 60,000; MS2 AGC = 1E5)
- **Data analysis**: MS-GF+ + MASIC (v3.0.7111) + RomicsProcessor (custom R package)

Data collection

The PSM data were collected from the MassIVE repository MSV000084110 (see Source section). The downloaded files are:

- `Single_Cell_Chip_*_*_msgfplus.mzid`: the MS-GF+ identification result files.
- `Single_Cell_Chip_*_*_ReporterIons.txt`: the MASIC quantification result files.

For each batch, the quantification and identification data were combined based on the scan number (common to both data sets). The combined datasets for the different runs were then concatenated feature-wise. The sample annotation table was manually created based on the available information provided in the article. The data were then converted to a `QFeatures` object using the `scp::readSCP` function.

The protein data were downloaded from Supporting information section from the publisher's website (see Sources). The data is supplied as an Excel file `ac9b03349_si_005.xlsx`. The file contains 7 sheets from which we only took the 2nd (named 01 - Raw sc protein data) with the combined protein data for the 12 runs. We converted the data to a `SingleCellExperiment` object and added the object as a new assay in the `QFeatures` dataset (containing the PSM data). Links between the proteins and the corresponding PSM were created.

Note

Although a TMT-10plex labeling is reported in the article, the PSM data contained 11 channels for each run. Those 11th channel contain mostly missing data and are hence assumed to be empty channels.

Source

The PSM data can be downloaded from the massIVE repository MSV000084110. FTP link: <ftp://massive.ucsd.edu/MSV000084110>

The protein data can be downloaded from the [ACS Publications](#) website (Supporting information section).

References

Dou, Maowei, Jeremy Clair, Chia-Feng Tsai, Kerui Xu, William B. Chrisler, Ryan L. Sontag, Rui Zhao, et al. 2019. "High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform." *Analytical Chemistry*, September ([link to article](#)).

See Also

[dou2019_lysat](#), [dou2019_boosting](#)

Examples

```
dou2019_mouse()
```

liang2020_hela

Liang et al. 2020 ((Anal. Chem.)): HeLa cells (MaxQuant preprocessing)

Description

Single-cell proteomics data from HeLa cells using the autoPOTS acquisition workflow. The samples contain either no cells (blanks), 1 cell, 10 cells, 150 cells or 500 cells. Samples containing between 0 and 10 cells are isolated using micro-pipetting while samples containing between 150 and 500 cells were prepared using dilution of a bulk sample.

Usage

liang2020_hela

Format

A `QFeatures` object with 17 assays, each assay being a `SingleCellExperiment` object:

- `HeLa_*`: 15 assays containing PSM data.
- `peptides`: quantitative data for 48705 peptides in 15 samples (all runs are combined).
- `proteins`: quantitative data for 3970 protein groups in 15 samples (all runs combined).

Sample annotation is stored in `colData(liang2020_hela_MQ())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation:** The HeLa cells come from a commercially available cell line. Samples containing between 0 and 10 cells were isolated using micro-manipulation and the counts were validated using a microscope. Samples containing between 150 and 500 cells were prepared by diluting a bulk sample and the exact counts were evaluated by obtaining photomicrographs.
- **Sample preparation** performed using the autoPOTS workflow that relied on the OT-2 pipetting robot. Cells are lysed using sonication. Samples are then processed by successive incubation with DTT (reduction), then IAA (alkylation), then Lys-C and trypsin (protein digestion).
- **Separation:** Samples were injected on the column using a modified Ultimate WPS-3000 TPL autosampler coupled to an UltiMate 3000 RSLCnano pump. The LC column is a home-packed nanoLC column (45cm x 30um; 40nL/min)
- **Ionization:** Nanospray Flex ion source (2,000V)
- **Mass spectrometry:** Orbitrap Exploris 480. MS1 settings: accumulation time = 250 ms (0-10 cells) or 100 ms (150-500 cells); resolution = 120,000; AGC = 100\ duration = 90 s (0-10 cells) or 60 s (150-500 cells) ; accumulation time = 500 ms (0-1 cell), 250 ms (10 cells), 100 ms (150 cells) or 50 ms (500 cells); resolution = 60,000 (0-10 cells) or 30,000 (150-500 cells); AGC = 5E3 (0-1 cells) or 1E4 (10-500 cells).
- **Data analysis:** MaxQuant (v1.6.7.0) and the search database is Swiss-Prot (July 2020).

Data collection

All data were collected from the PRIDE repository (accession ID: PXD021882).

The sample annotations were collected from the methods section and from table S3 in the paper.

The PSM data were found in the `evidence.txt` file. The data were converted to a `QFeatures` object using the `scp::readSCP` function.

The peptide data were found in the `peptides.txt` file. The column names holding the quantitative data were adapted to match the sample names in the `QFeatures` object. The data were then converted to a `SingleCellExperiment` object and then inserted in the `QFeatures` object. Links between the PSMs and the peptides were added

A similar procedure was applied to the protein data. The data were found in the `proteinGroups.txt` file. The column names were adapted, the data were converted to a `SingleCellExperiment` object and then inserted in the `QFeatures` object. Links between the peptides and the proteins were added

Source

The PSM data can be downloaded from the PRIDE repository PXD021882 The source link is: <http://ftp.pride.ebi.ac.uk/pride/data/archive/2020/12/PXD021882/>

References

Liang, Yiran, Hayden Acor, Michaela A. McCown, Andikan J. Nwosu, Hannah Boekweg, Nathaniel B. Axtell, Thy Truong, Yongzheng Cong, Samuel H. Payne, and Ryan T. Kelly. 2020. “Fully Automated Sample Processing and Analysis Workflow for Low-Input Proteome Profiling.” *Analytical Chemistry*, December. ([link to article](#)).

Examples

```
liang2020_hela()
```

schoof2021

Schoof et al. 2021 (Nat. Comm.): acute myeloid leukemia differentiation

Description

Single-cell proteomics data from OCI-AML8227 cell culture to reconstruct the cellular hierarchy. The data were acquired using TMTpro multiplexing. The samples contain either no cells, single cells, 10 cells (reference channel) 200 cells (booster channel) or are simply empty wells. Single cells are expected to be one of progenitor cells (PROG), leukaemia stem cells (LSC), CD38- blast cells (BLAST CD38-) or CD38+ blast cells (BLAST CD38+). Booster are either a known 1:1:1 mix of cells (PROG, LSC and BLAST) or are isolated directly from the bulk sample. Samples were isolated and annotated using flow cytometry.

Usage

```
schoof2021
```

Format

A `QFeatures` object with 194 assays, each assay being a `SingleCellExperiment` object:

- `F*`: 192 assays containing PSM quantification data for 16 TMT channels. The quantification data contain signal to noise ratios as computed by Proteome Discoverer.
- `proteins`: quantitative data for 2898 protein groups in 3072 samples (all runs combined). The quantification data contain signal to noise ratios as computed by Proteome Discoverer.
- `logNormProteins`: quantitative data for 2723 protein groups in 2025 single-cell samples. This assay is the protein datasets that was processed by the authors. Dimension reduction and clustering data are also available in the `reducedDims` and `colData` slots, respectively

Sample annotation is stored in `colData(schoof2021())`. The cell type annotation is stored in the `Population` column. The flow cytometry data is also available: `FSC-A`, `FSC-H`, `FSC-W`, `SSC-A`, `SSC-H`, `SSC-W`, `APC-Cy7-A` (= `CD34`) and `PE-A` (= `CD38`).

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Sample isolation**: cultured AML 8227 cells were stained with anti-CD34 and anti-CD38. The sorting was performed by FACS Aria instrument and deposited in 384 well plates.
- **Sample preparation**: cells are lysed using freeze-boil and sonication in a lysis buffer (TFE) that also includes reduction and alkylation reagents (TCEP and CAA), followed by trypsin (protein) and benzonase (DNA) digestion, TMT-16 labeling and quenching, desalting using SOLAµ C18 plate, peptide concentration, pooling and peptide concentration again. The booster channel contains 200 cell equivalents.
- **Liquid chromatography**: peptides are separated using a C18 reverse-phase column (50cm x 75 µm i.d., Thermo EasySpray) combined to a Thermo EasyLC 1200 for 160 minute gradient with a flowrate of 100nl/min.
- **Mass spectrometry**: FAIMSPro interface is used. MS1 setup: resolution 60.000, AGC target of 300%, accumulation of 50ms. MS2 setup: resolution 45.000, AGC target of 150, 300 or 500%, accumulation of 150, 300, 500, or 1000ms.
- **Raw data processing**: Proteome Discoverer 2.4 + Sequest spectral search engine and validation with Percolator

Data collection

All data were collected from the PRIDE repository (accession ID: PXD020586). The data and metadata were extracted from the `Sceptre_FINAL.zip` file.

We performed extensive data wrangling to combine all the metadata available from different files into a single table available using `colData(schoof2021)`.

The PSM data were found in the `bulk_PSMs.txt` file. Contaminants were defined based on the protein accessions listed in `contaminant.txt`. The data were converted to a `QFeatures` object using the `scp::readSCP` function.

The protein data were found in the `bulk_Proteins.txt` file. Contaminants were defined based on the protein accessions listed in `contaminant.txt`. The column names holding the quantitative data

were adapted to match the sample names in the `QFeatures` object. Unnecessary feature annotations (such as in which assay a protein is found) were removed. Feature names were created following the procedure in `SCeptre`: features names are the protein symbol (or accession if missing) and if duplicated symbols are present (protein isoforms), they are made unique by appending the protein accession. Contaminants were defined based on the protein accessions listed in `contaminant.txt`. The data were then converted to a `SingleCellExperiment` object and inserted in the `QFeatures` object.

The log-normalized protein data were found in the `bulk.h5ad` file. This dataset was generated by the authors by running the notebook called `bulk.ipynb`. The `bulk.h5ad` was loaded as an `AnnData` object using the `scanpy` Python module. The object was then converted to a `SingleCellExperiment` object using the `zellkonverter` package. The column names holding the quantitative data were adapted to match the sample names in the `QFeatures` object. The data were then inserted in the `QFeatures` object.

The script to reproduce the `QFeatures` object is available at `system.file("scripts", "make-data_schoof2021.R", package = "scpdata")`

Source

The PSM and protein data can be downloaded from the PRIDE repository PXD020586 The source link is: <https://www.ebi.ac.uk/pride/archive/projects/PXD020586>

References

Schoof, Erwin M., Benjamin Furtwängler, Nil Üresin, Nicolas Rapin, Simonas Savickas, Coline Gentil, Eric Lechman, Ulrich auf Dem Keller, John E. Dick, and Bo T. Porse. 2021. “Quantitative Single-Cell Proteomics as a Tool to Characterize Cellular Hierarchies.” *Nature Communications* 12 (1): 745679. ([link to article](#)).

Examples

```
schoof2021()
```

scpdata

Single-Cell Proteomics Data Package

Description

The `scpdata` package distributes mass spectrometry-based single-cell proteomics datasets. The datasets were collected from published work and formatted to a standardized data framework. The `scp` frameworks stores the expression data for different MS levels (identified spectrum, peptide, or protein) in separate assays. Each assay is an object of class `SingleCellExperiment` that allows easy integration with state-of-the-art single-cell analysis tools. All assays are contained in a single object of class `QFeatures`. An overview of the data structure is shown provided in the `scp` package.

The `scpdata()` function returns a summary table with all currently available datasets in the package. More information about the data content and the data collection can be found in the corresponding manual pages.

Usage

```
scpdata()
```

Value

A DataFrame table containing a summary of the available datasets.

Author(s)

Christophe Vanderaa

See Also

More information about the data manipulation can be found in the scp package.

Examples

```
## List available datasets and their metadata
scpdata()

## Load data using the ExperimentHub interface
hub <- ExperimentHub()

## Download the data set of interest using ExperimentHub indexing
hub[["EH3899"]]
## Download the same data set using the build-in function
specht2019v2()
```

specht2019v2

*Specht et al. 2019 - SCoPE2 (biorRxiv): macrophages vs monocytes
(version 2)*

Description

Single cell proteomics data acquired by the Slavov Lab. This is the version 2 of the data released in December 2019. It contains quantitative information of macrophages and monocytes at PSM, peptide and protein level.

Usage

```
specht2019v2
```

Format

A `QFeatures` object with 179 assays, each assay being a `SingleCellExperiment` object:

- Assay 1-63: PSM data for SCoPE2 sets acquired with a TMT-11plex protocol, hence those assays contain 11 columns. Columns hold quantitative information from single-cell channels, carrier channels, reference channels, empty (blank) channels and unused channels.
- Assay 64-177: PSM data for SCoPE2 sets acquired with a TMT-16plex protocol, hence those assays contain 16 columns. Columns hold quantitative information from single-cell channels, carrier channels, reference channels, empty (blank) channels and unused channels.
- `peptides`: peptide data containing quantitative data for 9208 peptides and 1018 single-cells.
- `proteins`: protein data containing quantitative data for 2772 proteins and 1018 single-cells.

The `colData(specht2019v2())` contains cell type annotation and batch annotation that are common to all assays. The description of the `rowData` fields for the PSM data can be found in the [MaxQuant documentation](#).

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation**: flow cytometry (BD FACSAria I).
- **Sample preparation** performed using the SCoPE2 protocol. mPOP cell lysis + trypsin digestion + TMT-11plex or 16plex labelling and pooling.
- **Separation**: online nLC (DionexUltiMate 3000 UHPLC with a 25cm x 75um IonOpticksAurora Series UHPLC column; 200nL/min).
- **Ionization**: ESI (2,200V).
- **Mass spectrometry**: Thermo Scientific Q-Exactive (MS1 resolution = 70,000; MS1 accumulation time = 300ms; MS2 resolution = 70,000).
- **Data analysis**: DART-ID + MaxQuant (1.6.2.3).

Data collection

The PSM data were collected from a shared Google Drive folder that is accessible from the SlavovLab website (see Source section). The folder contains the following files of interest:

- `ev_updated.txt`: the MaxQuant/DART-ID output file
- `annotation_fp60-97.csv`: sample annotation
- `batch_fp60-97.csv`: batch annotation

We combined the the sample annotation and the batch annotation in a single table. We also formatted the quantification table so that columns match with those of the annotation and filter only for single-cell runs. Both table are then combined in a single `QFeatures` object using the `scp::readSCP` function.

The peptide data were taken from the Slavov lab directly (`Peptides-raw.csv`). It is provided as a spreadsheet. The data were formatted to a `SingleCellExperiment` object and the sample metadata were matched to the column names (mapping is retrieved after running the SCoPE2 R script) and

stored in the colData. The object is then added to the [QFeatures](#) object (containing the PSM assays) and the rows of the peptide data are linked to the rows of the PSM data based on the peptide sequence information through an AssayLink object.

The protein data (Proteins-processed.csv) is formatted similarly to the peptide data, and the rows of the proteins were mapped onto the rows of the peptide data based on the protein sequence information.

Source

The data were downloaded from the [Slavov Lab](#) website via a shared Google Drive [folder](#). The raw data and the quantification data can also be found in the massIVE repository MSV000083945: <ftp://massive.ucsd.edu/MSV000083945>.

References

Specht, Harrison, Edward Emmott, Aleksandra A. Petelski, R. Gray Huffman, David H. Perlman, Marco Serra, Peter Kharchenko, Antonius Koller, and Nikolai Slavov. 2019. "Single-Cell Mass-Spectrometry Quantifies the Emergence of Macrophage Heterogeneity." bioRxiv. ([link to article](#)).

Examples

```
specht2019v2()
```

specht2019v3	<i>Specht et al. 2019 - SCoPE2 (biorRxiv): macrophages vs monocytes (version 3)</i>
--------------	---

Description

Single cell proteomics data acquired by the Slavov Lab. This is the version 3 of the data released in October 2020. It contains quantitative information of macrophages and monocytes at PSM, peptide and protein level.

Usage

```
specht2019v3
```

Format

A [QFeatures](#) object with 179 assays, each assay being a [SingleCellExperiment](#) object:

- Assay 1-63: PSM data for SCoPE2 sets acquired with a TMT-11plex protocol, hence those assays contain 11 columns. Columns hold quantitative information from single-cell channels, carrier channels, reference channels, empty (blank) channels and unused channels.
- Assay 64-177: PSM data for SCoPE2 sets acquired with a TMT-16plex protocol, hence those assays contain 16 columns. Columns hold quantitative information from single-cell channels, carrier channels, reference channels, empty (blank) channels and unused channels.

- `peptides`: peptide data containing quantitative data for 9208 peptides and 1018 single-cells.
- `proteins`: protein data containing quantitative data for 2772 proteins and 1018 single-cells.

The `colData(specht2019v2())` contains cell type annotation and batch annotation that are common to all assays. The description of the `rowData` fields for the PSM data can be found in the [MaxQuant documentation](#).

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation**: flow cytometry (BD FACSAria I).
- **Sample preparation** performed using the SCoPE2 protocol. mPOP cell lysis + trypsin digestion + TMT-11plex or 16plex labeling and pooling.
- **Separation**: online nLC (DionexUltiMate 3000 UHPLC with a 25cm x 75um IonOpticksAurora Series UHPLC column; 200nL/min).
- **Ionization**: ESI (2,200V).
- **Mass spectrometry**: Thermo Scientific Q-Exactive (MS1 resolution = 70,000; MS2 accumulation time = 300ms; MS2 resolution = 70,000).
- **Data analysis**: DART-ID + MaxQuant (1.6.2.3).

Data collection

The PSM data were collected from a shared Google Drive folder that is accessible from the SlavovLab website (see Source section). The folder contains the following files of interest:

- `ev_updated_v2.txt`: the MaxQuant/DART-ID output file
- `annotation_fp60-97.csv`: sample annotation
- `batch_fp60-97.csv`: batch annotation

We combined the the sample annotation and the batch annotation in a single table. We also formatted the quantification table so that columns match with those of the annotation and filter only for single-cell runs. Both table are then combined in a single `QFeatures` object using the `scp::readSCP` function.

The peptide data were taken from the Slavov lab directly (`Peptides-raw.csv`). It is provided as a spreadsheet. The data were formatted to a `SingleCellExperiment` object and the sample metadata were matched to the column names (mapping is retrieved after running the SCoPE2 R script) and stored in the `colData`. The object is then added to the `QFeatures` object (containing the PSM assays) and the rows of the peptide data are linked to the rows of the PSM data based on the peptide sequence information through an `AssayLink` object.

The protein data (`Proteins-processed.csv`) is formatted similarly to the peptide data, and the rows of the proteins were mapped onto the rows of the peptide data based on the protein sequence information.

Note

Since version 2, a serious bug in the data were corrected for TMT channels 12 to 16. Many more cells are therefore contained in the data. Version 2 is maintained for backward compatibility. Although the final version of the article was published in 2021, we have kept specht2019v3 as the data set name for consistency with the previous data version specht2019v2.

Source

The data were downloaded from the [Slavov Lab](#) website via a shared Google Drive [folder](#). The raw data and the quantification data can also be found in the massIVE repository MSV000083945: <ftp://massive.ucsd.edu/MSV000083945>.

References

Specht, Harrison, Edward Emmott, Aleksandra A. Petelski, R. Gray Huffman, David H. Perlman, Marco Serra, Peter Kharchenko, Antonius Koller, and Nikolai Slavov. 2021. "Single-Cell Proteomic and Transcriptomic Analysis of Macrophage Heterogeneity Using SCoPE2." *Genome Biology* 22 (1): 50. ([link to article](#)).

Examples

```
specht2019v3()
```

zhu2018MCP

Zhu et al. 2018 (Mol. Cel. Prot.): rat brain laser dissections

Description

Near single-cell proteomics data of laser captured micro-dissection samples. The samples are 24 brain sections from rat pups (day 17). The slices are 12 um thick squares of either 50, 100, or 200 um width. 5 samples were dissected from the corpus callum (CC), 4 samples were dissected from the corpus colosum (CP), 13 samples were extracted from the cerebral cortex (CTX), and 2 samples are labeled as (Mix).

Usage

```
zhu2018MCP
```

Format

A [QFeatures](#) object with 1 assay called peptides. It is a [SingleCellExperiment](#) object containing the quantitative data for 13055 peptides in 24 samples.

Sample annotation is stored in `colData(zhu2018MCP())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the original article (see References).

- **Cell isolation:** brain patches were collected using laser-capture microdissection (PALM MicroBeam) on flash frozen rat (*Rattus norvegicus*) brain tissues. Note that the samples were stained with H&E before dissection for histological analysis. DMSO is used as sample collection solution
- **Sample preparation** performed using the nanoPOTs device: DMSO evaporation + protein extraction (DMM + DTT) + alkylation (IAA)
 - Lys-C digestion + trypsin digestion.
- **Separation:** nanoLC (Dionex UltiMate with an in-house packed 60cm x 30um LC columns; 50nL/min)
- **Ionization:** ESI (2,000V)
- **Mass spectrometry:** Thermo Fisher Orbitrap Fusion Lumos Tribrid (MS1 accumulation time = 246ms; MS1 resolution = 120,000; MS1 AGC = 3E6). The MS/MS settings depend on the sample size, excepted for the AGC = 1E5. 50um (time = 502ms; resolution = 240,000), 100um (time = 246ms; resolution = 120,000), 200um (time = 118ms; resolution = 60,000).
- **Data analysis:** MaxQuant (v1.5.3.30) + Perseus (v1.5.6.0) + Origin Pro 2017

Data collection

The PSM data were collected from the PRIDE repository (accession ID: PXD008844). We downloaded the MaxQuant_Peptides.txt file containing the combined identification and quantification results. The sample annotation was inferred from the names of columns holding the quantification data. The data were then converted to a [QFeatures](#) object using the [scp::readSCP](#) function.

Source

The PSM data can be downloaded from the PRIDE repository PXD008844. FTP link <ftp://ftp.pride.ebi.ac.uk/pride/data/archives/1/100/PXD008844>

References

Zhu, Ying, Maowei Dou, Paul D. Piehowski, Yiran Liang, Fangjun Wang, Rosalie K. Chu, William B. Chrisler, et al. 2018. “Spatially Resolved Proteome Mapping of Laser Capture Microdissected Tissue with Automated Sample Transfer to Nanodroplets.” *Molecular & Cellular Proteomics: MCP* 17 (9): 1864–74 ([link to article](#)).

Examples

zhu2018MCP()

zhu2018NC_hela

Zhu et al. 2018 (Nat. Comm.): HeLa titration

Description

Near single-cell proteomics data of HeLa samples containing different number of cells. There are three groups of cell concentrations: low (10-14 cells), medium (35-45 cells) and high (137-141 cells). The data also contain measures for blanks, HeLa lysates (50 cell equivalent) and 2 cancer cell line lysates (MCF7 and THP1, 50 cell equivalent).

Usage

zhu2018NC_hela

Format

A [QFeatures](#) object with 2 assays:

- peptides: a [SingleCellExperiment](#) object containing the quantitative data for 37795 peptides in 21 samples.
- proteins: a [SingleCellExperiment](#) object containing the quantitative (summed intensities) data for 3984 proteins in 21 samples. Note that the iBAQ and LFQ intensities computed by MaxQuant are available from the `rowData`.

Sample annotation is stored in `colData(zhu2018NC_hela())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the original article (see References).

- **Cell isolation:** HeLa cell concentration was adjusted by serial dilution and cell counting was performed manually using an inverted microscope.
- **Sample preparation** performed using the nanoPOTs device. Protein extraction using RapiGest (+ DTT) + alkylation (IAA) + Lys-C digestion + cleave RapiGest (formic acid).
- **Separation:** nanoACQUITY UPLC pump (60nL/min) with an Self-Pack PicoFrit 70cm x 30um LC columns.
- **Ionization:** ESI (1,900V).
- **Mass spectrometry:** Thermo Fisher Orbitrap Fusion Lumos Tribrid. MS1 settings: accumulation time = 246ms; resolution = 120,000; AGC = 1E6. MS/MS settings, depend on the sample size, excepted for the AGC = 1E5. Blank and approx. 10 cells (time = 502ms; resolution = 240,000), approx. 40 cells (time = 246ms; resolution = 120,000), approx. 140 cells (time = 118ms; resolution = 60,000).
- **Data analysis:** MaxQuant (v1.5.3.30) + Perseus + OriginLab 2017

Data collection

The PSM data were collected from the PRIDE repository (accession ID: PXD006847). We downloaded the `CulturedCells_peptides.txt` file containing the combined identification and quantification results. The sample annotation was inferred from the names of columns holding the quantification data and the information in the article. The data were then converted to a `QFeatures` object using the `scp::readSCP` function.

Source

The PSM data can be downloaded from the PRIDE repository PXD006847. FTP link: <ftp://ftp.pride.ebi.ac.uk/pride/data/arch>

References

Zhu, Ying, Paul D. Piehowski, Rui Zhao, Jing Chen, Yufeng Shen, Ronald J. Moore, Anil K. Shukla, et al. 2018. "Nanodroplet Processing Platform for Deep and Quantitative Proteome Profiling of 10-100 Mammalian Cells." *Nature Communications* 9 (1): 882 ([link to article](#)).

See Also

The same experiment was conducted on HeLa lysates and the data is available in [zhu2018NC_lysates](#).

Examples

```
zhu2018NC_hela()
```

zhu2018NC_islets

Zhu et al. 2018 (Nat. Comm.): human pancreatic islets

Description

Near single-cell proteomics data human pancreas samples. The samples were collected from pancreatic tissue slices using laser dissection. The pancreata were obtained from organ donors through the JDRFNetwork for Pancreatic Organ Donors with Diabetes (nPOD) program. The sample come either from control patients (n=9) or from type 1 diabetes (T1D) patients (n=9).

Usage

```
zhu2018NC_islets
```

Format

A `QFeatures` object with 1 assay called `peptides`. It is a `SingleCellExperiment` object containing the quantitative data for 24321 peptides in 18 samples.

Sample annotation is stored in `colData(zhu2018NC_islets())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation:** The islets were extracted from the pancreatic tissues using laser-capture microdissection.
- **Sample preparation** performed using the nanoPOTs device. Protein extraction using RapiGest (+ DTT) + alkylation (IAA) + Lys-C digestion + cleave RapiGest (formic acid)
- **Separation:** nanoACQUITY UPLC pump with an Self-Pack PicoFrit 70cm x 30um LC columns; 60nL/min)
- **Ionization:** ESI (1,900V)
- **Mass spectrometry:** Thermo Fisher Orbitrap Fusion Lumos Tribrid. MS1 settings: accumulation time = 246ms; resolution = 120,000; AGC = 1E6. MS/MS settings: accumulation time = 118ms; resolution = 60,000; AGC = 1E5.
- **Data analysis:** MaxQuant (v1.5.3.30) + Perseus + OriginLab 2017

Data collection

The PSM data were collected from the PRIDE repository (accession ID: PXD006847). We downloaded the `Islet_t1d_ct_peptides.txt` file containing the combined identification and quantification results. The sample annotation was inferred from the column names holding the quantification data and from the information in the article. The data were then converted to a `QFeatures` object using the `scp::readSCP` function.

Source

The PSM data can be downloaded from the PRIDE repository PXD006847. The source link is: <ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2018/01/PXD006847>

References

Zhu, Ying, Paul D. Piehowski, Rui Zhao, Jing Chen, Yufeng Shen, Ronald J. Moore, Anil K. Shukla, et al. 2018. "Nanodroplet Processing Platform for Deep and Quantitative Proteome Profiling of 10-100 Mammalian Cells." *Nature Communications* 9 (1): 882 ([link to article](#)).

Examples

```
zhu2018NC_islets()
```

zhu2018NC_lysates *Zhu et al. 2018 (Nat. Comm.): HeLa lysates*

Description

Near single-cell proteomics data of HeLa lysates at different concentrations (10, 40 and 140 cell equivalent). Each concentration is acquired in triplicate.

Usage

zhu2018NC_lysates

Format

A [QFeatures](#) object with 1 assay called peptides. It is a [SingleCellExperiment](#) object containing the quantitative data for 14921 peptides in 9 samples.

Sample annotation is stored in `colData(zhu2018NC_lysates())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the original article (see References).

- **Cell isolation:** HeLas were collected from cell cultures.
- **Sample preparation** performed in bulk (5E5 cells/mL). Protein extraction using RapiGest (+ DTT) + dilution to target concentration + alkylation (IAA) + Lys-C digestion + trypsin digestion + cleave RapiGest (formic acid).
- **Separation:** nanoACQUITY UPLC pump (60nL/min) with an Self-Pack PicoFrit 70cm x 30um LC columns.
- **Ionization:** ESI (1,900V).
- **Mass spectrometry:** Thermo Fisher Orbitrap Fusion Lumos Tribrid. MS1 settings: accumulation time = 246ms; resolution = 120,000; AGC = 1E6. MS/MS settings, depend on the sample size, excepted for the AGC = 1E5. Blank and approx. 10 cells (time = 502ms; resolution = 240,000), approx. 40 cells (time = 246ms; resolution = 120,000), approx. 140 cells (time = 118ms; resolution = 60,000).
- **Data analysis:** MaxQuant (v1.5.3.30) + Perseus + OriginLab 2017.

Data collection

The PSM data were collected from the PRIDE repository (accession ID: PXD006847). We downloaded the `CulturedCells_peptides.txt` file containing the combined identification and quantification results. The sample annotation was inferred from the names of columns holding the quantification data and the information in the article. The data were then converted to a [QFeatures](#) object using the `scp::readSCP` function.

Source

The PSM data can be downloaded from the PRIDE repository PXD006847. The source link is: <ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2018/01/PXD006847>

References

Zhu, Ying, Paul D. Piehowski, Rui Zhao, Jing Chen, Yufeng Shen, Ronald J. Moore, Anil K. Shukla, et al. 2018. "Nanodroplet Processing Platform for Deep and Quantitative Proteome Profiling of 10-100 Mammalian Cells." *Nature Communications* 9 (1): 882 ([link to article](#)).

See Also

The same experiment was conducted directly on HeLa cells samples rather than lysates. The data is available in [zhu2018NC_hela](#).

Examples

```
zhu2018NC_lysates()
```

zhu2019EL

Zhu et al. 2019 (eLife): chicken utricle cells

Description

Single-cell proteomics data from chicken utricle acquired to study the hair-cell development. The cells are isolated from peeled utricular epithelium and separated into hair cells (FM1-43 high) and supporting cells (FM1-43 low). The sample contain either 1 cell (n = 28), 3 cells (n = 7), 5 cells (n = 8) or 20 cells (n = 14).

Usage

```
zhu2019EL
```

Format

A [QFeatures](#) object with 62 assays, each assay being a [SingleCellExperiment](#) object:

- XYZw: 60 assays containing PSM data. The sample are annotated as follows. X indicates the experiment, either 1 or 2. Y indicated the FM1-43 signal, either high (H) or low (L). Z indicates the number of cells (0, 1, 3, 5 or 20). w indicates the replicate, starting from a, it can go up to j.
- peptides: quantitative data for 3444 peptides in 60 samples (all runs are combined).
- proteins: quantitative data for 840 proteins in 60 samples (all runs combined).

Sample annotation is stored in `colData(zhu2019EL())`.

Acquisition protocol

The data were acquired using the following setup. More information can be found in the source article (see References).

- **Cell isolation:** The cells were taken from the utricles of E15 chick embryos. Samples were stained with FM1-43FX and the cells were dissociated using enzymatic digestion. Cells were FACS sorted (BD Influx) and split based on their FM1-43 signal, while ensuring no debris, doublets or dead cells are retained.
- **Sample preparation** performed using the nanoPOTs device. Cell lysis and protein extraction and reduction are performed using dodecyl beta-D-maltoside + DTT + ammonium bicarbonate. Protein were then alkylated using IAA. Protein digestion is performed using Lys-C and trypsin. Finally samples acidification is performed using formic acid.
- **Separation:** Dionex UltiMate pump with an C18-Packed column (50cm x 30um; 60nL/min)
- **Ionization:** ESI (2,000V)
- **Mass spectrometry:** Orbitrap Fusion Lumos Tribrid. MS1 settings: accumulation time = 246ms; resolution = 120,000; AGC = 3E6. MS/MS settings: accumulation time = 502ms; resolution = 120,000; AGC = 2E5.
- **Data analysis:** Andromeda & MaxQuant (v1.5.3.30) and the search database is NCBI GRCg6a.

Data collection

All data were collected from the PRIDE repository (accession ID: PXD014256).

The sample annotation information is provided in the `Zhu_2019_chick_single_cell_samples_CORRECTED.xlsx` file. This file was given during a personal discussion and is a corrected version of the annotation table available on the PRIDE repository.

The PSM data were found in the `evidence.txt` (in the Experiment 1+ 2) folder. The PSM data were filtered so that it contains only samples that are annotated. The data were then converted to a `QFeatures` object using the `scp::readSCP` function.

The peptide data were found in the `peptides.txt` file. The column names holding the quantitative data were adapted to match the sample names in the `QFeatures` object. The data were then converted to a `SingleCellExperiment` object and then inserted in the `QFeatures` object. Links between the PSMs and the peptides were added

A similar procedure was applied to the protein data. The data were found in the `proteinGroups.txt` file. The column names were adapted, the data were converted to a `SingleCellExperiment` object and then inserted in the `QFeatures` object. Links between the peptides and the proteins were added

Source

The PSM data can be downloaded from the PRIDE repository PXD014256. The source link is: <ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2019/11/PXD014256>

References

Zhu, Ying, Mirko Scheibinger, Daniel Christian Ellwanger, Jocelyn F. Krey, Dongseok Choi, Ryan T. Kelly, Stefan Heller, and Peter G. Barr-Gillespie. 2019. "Single-Cell Proteomics Reveals Changes in Expression during Hair-Cell Development." *eLife* 8 (November). ([link to article](#)).

Examples

zhu2019EL()

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