Package ‘scp’

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Title  Mass Spectrometry-Based Single-Cell Proteomics Data Analysis

Version  1.14.0

Description  Utility functions for manipulating, processing, and analyzing mass spectrometry-based single-cell proteomics data. The package is an extension to the 'QFeatures' package and relies on 'SingleCellExperiment' to enable single-cell proteomics analyses. The package offers the user the functionality to process quantitative table (as generated by MaxQuant, Proteome Discoverer, and more) into data tables ready for downstream analysis and data visualization.

Depends  R (>= 4.3.0), QFeatures (>= 1.13.5)

Imports  dplyr, IHW, ggplot2, ggrepel, matrixStats, metapod, methods, MsCoreUtils, MultiAssayExperiment, nipals, RColorBrewer, S4Vectors, SingleCellExperiment, SummarizedExperiment, stats, utils

Suggests  BiocStyle, MsDataHub (>= 1.3.3), impute, knitr, patchwork, preprocessCore, rmarkdown, scdata, sva, testthat, vsn, uwot

License  Artistic-2.0

Encoding  UTF-8

VignetteBuilder  knitr

biocViews  GeneExpression, Proteomics, SingleCell, MassSpectrometry, Preprocessing, CellBasedAssays

BugReports  https://github.com/UCLouvain-CBIO/scp/issues

URL  https://UCLouvain-CBIO.github.io/scp

Roxygen  list(markdown=TRUE)

RoxygenNote  7.3.1

git_url  https://git.bioconductor.org/packages/scp

git_branch  RELEASE_3_19

git_last_commit  15a429b
addReducedDims

Add scplainer Component Analysis Results

Description

The function will add the component results computed by `scpComponentAnalysis()` to a SingleCellExperiment's reducedDims slot, to all using the many scater functions, such as `scater::plotReducedDim()`, `scater::plotTSNE()`, ...
aggregateFeaturesOverAssays

Usage

addReducedDims(sce, x)

Arguments

sce  An instance of class SingleCellExperiment.
x  A List of DataFrames containing principal components, as produced by scpComponentAnalysis().

Value

A SingleCellExperiment with updated reducedDims.

Author(s)

Laurent Gatto and Christophe Vanderaa

Examples

library("scater")
data("leduc_minimal")
leduc_minimal$cell <- rownames(colData(leduc_minimal))
pcs <- scpComponentAnalysis(
    leduc_minimal, method = "ASCA",
    effects = "SampleType")$bySample

reducedDims(leduc_minimal)
leduc_minimal <- addReducedDims(leduc_minimal, pcs)
reducedDims(leduc_minimal)
plotReducedDim(leduc_minimal, dimred = "ASCA_SampleType",
              colour_by = "SampleType")

leduc_minimal <- runTSNE(leduc_minimal, dimred = "ASCA_SampleType")
plotTSNE(leduc_minimal, colour_by = "SampleType")

aggregateFeaturesOverAssays

Aggregate features over multiple assays

Description

This function is a wrapper function around QFeatures::aggregateFeatures. It allows the user to provide multiple assays for which aggregateFeatures will be applied sequentially.

Usage

aggregateFeaturesOverAssays(object, i, fcol, name, fun, ...)
computeSCR

Arguments

object A QFeatures object

i A numeric(1) or character(1) indicating which assay to transfer the colData to.

fcol The feature variables for each assays i defining how to summarise the QFeatures. If fcol has length 1, the variable name is assumed to be the same for all assays.

name A character() naming the new assay. name must have the same length as i. Note that the function will fail if of the names in name is already present.

fun A function used for quantitative feature aggregation.

Value

A QFeatures object

See Also

QFeatures::aggregateFeatures

Examples

data("scp1")
scp1 <- aggregateFeaturesOverAssays(scp1,
  i = 1:3,
  fcol = "peptide",
  name = paste0("peptides", 1:3),
  fun = colMeans,
  na.rm = TRUE)

scp1

computeSCR Compute the sample over carrier ratio (SCR)

Description

The function computes the ratio of the intensities of sample channels over the intensity of the carrier channel for each feature. The ratios are averaged within the assay.
Usage

```r
computeSCR(
  object, 
  i, 
  colvar, 
  samplePattern, 
  sampleFUN = "mean", 
  carrierPattern, 
  carrierFUN = sampleFUN, 
  rowDataName = "SCR"
)
```

Arguments

- `object`: A `QFeatures` object.
- `i`: A character() or integer() indicating for which assay(s) the SCR needs to be computed.
- `colvar`: A character(1) indicating the variable to take from `colData(object)` that gives the sample annotation.
- `samplePattern`: A character(1) pattern that matches the sample encoding in `colvar`.
- `sampleFUN`: A character(1) or function that provides the summarization function to use (e.g., mean, sum, median, max, ...). Only used when the pattern matches multiple samples. Default is mean. Note for custom function, `na.rm = TRUE` is passed to `sampleFUN` to ignore missing values, make sure to provide a function that accepts this argument.
- `carrierPattern`: A character(1) pattern that matches the carrier encoding in `colvar`. Only one match per assay is allowed, otherwise only the first match is taken.
- `carrierFUN`: A character(1) or function that provides the summarization function to use (e.g., mean, sum, median, max, ...). Only used when the pattern matches multiple carriers. Default is the same function as `sampleFUN`. Note for custom function, `na.rm = TRUE` is passed to `carrierFUN` to ignore missing values, make sure to provide a function that accepts this argument.
- `rowDataName`: A character(1) giving the name of the new variable in the `rowData` where the computed SCR will be stored. The name cannot already exist in any of the assay `rowData`.

Value

A `QFeatures` object for which the `rowData` of the given assay(s) is augmented with the mean SCR.

Examples

data("scp1")

```r
cp1 <- computeSCR(scp1, 
  i = 1, 
  colvar = "SampleType", 
  carrierPattern = "Carrier",
)```
cumulativeSensitivityCurve

Cumulative sensitivity curve

Description

The cumulative sensitivity curve is used to evaluate if the sample size is sufficient to accurately estimate the total sensitivity. If it is not the case, an asymptotic regression model may provide a prediction of the total sensitivity if more samples would have been acquired.

Usage

```r
cumulativeSensitivityCurve(
  object,
  i,
  by = NULL,
  batch = NULL,
  nsteps = 30,
  niters = 10
)
```

```r
predictSensitivity(df, nSamples)
```

Arguments

- `object` An object of class `QFeatures`.
- `i` The index of the assay in `object`. The assay must contain an identification matrix, that is a matrix where an entry is `TRUE` if the value is observed and `FALSE` if the value is missing (see examples).
- `by` A vector of length equal to the number of columns in assay `i` that defines groups for a cumulative sensitivity curve will be computed separately. If missing, the sensitivity curve is computed for the completed dataset.
- `batch` A vector of length equal to the number of columns in assay `i` that defines the cell batches. All cells in a batch will be aggregated to a single sample.
- `nsteps` The number of equally spaced sample sizes to compute the sensitivity.
- `niters` The number of iteration to compute
- `df` The output from `cumulativeSensitivityCurve()`.
- `nSamples` A numeric() of samples sizes. If Inf, the prediction provides the extrapolated total sensitivity.
cumulativeSensitivityCurve

Details

As more samples are added to a dataset, the total number of distinct features increases. When sufficient number of samples are acquired, all peptides that are identifiable by the technology and increasing the sample size no longer increases the set of identified features. The cumulative sensitivity curve depicts the relationship between sensitivity (number of distinct peptides in the data) and the sample size. More precisely, the curve is built by sampling cells in the data and count the number of distinct features found across the sampled cells. The sampling is repeated multiple times to account for the stochasticity of the approach. Datasets that have a sample size sufficiently large should have a cumulative sensitivity curve with a plateau.

The set of features present in a cell depends on the cell type. Therefore, we suggest to build the cumulative sensitivity curve for each cell type separately. This is possible when providing the by argument.

For multiplexed experiments, several cells are acquired in a run. In that case, when a features is identified in a cell, it is frequently also identified in all other cells of that run, and this will distort the cumulative sensitivity curve. Therefore, the function allows to compute the cumulative sensitivity curve at the batches level rather than at the cell level. This is possible when providing the batch argument.

Once the cumulative sensitivity curve is computed, the returned data can be visualized to explore the relationship between the sensitivity and the sample size. If enough samples are acquired, the curve should plateau at high numbers of samples. If it is not the case, the total sensitivity can be predicted using an asymptotic regression curve. To predict the total sensitivity, the model is extrapolated to infinite sample size. Therefore, the accuracy of the extrapolation will highly depend on the available data. The closer the curve is to the plateau, the more accurate the prediction.

Value

A data.frame with groups as many rows as pairs of cells and the following column(s):

- jaccard: the computed Jaccard index
- by: if by is not NULL, the group of the pair of cells for which the Jaccard index is computed.

Examples

```r
## Simulate data
## 1000 features in 100 cells
library(SingleCellExperiment)
id <- matrix(FALSE, 1000, 100)
id[sample(1:length(id), 500)] <- TRUE
dimnames(id) <- list(paste0("feat", 1:1000), paste0("cell", 1:100))
sce <- SingleCellExperiment(assays = List(id))
sim <- QFeatures(experiments = List(id = sce))
sim$batch <- rep(1:100, each = 10)
sim$SampleType <- rep(c("A", "B"), each = 500)
sim
```

```r
## Compute the cumulative sensitivity curve, take batch and sample
```
## divideByReference

Divide assay columns by a reference column

### Description

The function divides the sample columns by a reference column. The sample and reference columns are defined based on the provided `colvar` variable and on regular expression matching.

### Usage

```r
divideByReference(object, i, colvar, samplePattern = ".", refPattern)
```

### Arguments

- `object` A `QFeatures` object
- `i` A numeric() or character() vector indicating from which assays the `rowData` should be taken.
- `colvar` A character(1) indicating the variable to take from `colData(object)` that gives the sample annotation.
- `samplePattern` A character(1) pattern that matches the sample encoding in `colvar`. By default all samples are divided (using the regex wildcard `.`).
- `refPattern` A character(1) pattern that matches the carrier encoding in `colvar`. Only one match per assay is allowed, otherwise only the first match is taken

### Details

The supplied assay(s) are replaced with the values computed after reference division.

### Value

A `QFeatures` object

```r
## type into account
csc <- cumulativeSensitivityCurve(
  sim, "id", by = sim$SampleType,
  batch = sim$batch
)
predCSC <- predictSensitivity(csc, nSample = 1:50)

library(ggplot2)
ggplot(csc) +
aes(x = SampleSize, y = Sensitivity, colour = by) +
  geom_point() +
  geom_line(data = predCSC)

## Extrapolate the total sensitivity
predictSensitivity(csc, nSamples = Inf)
## (real total sensitivity = 1000)
```
jaccardIndex

Examples

data("scp1")
scp1 <- divideByReference(scp1,
  i = 1,
  colvar = "SampleType",
  samplePattern = "Macrophage",
  refPattern = "Ref")

jaccardIndex

Compute the pairwise Jaccard index

Description

The function computes the Jaccard index between all pairs of cells.

Usage

jaccardIndex(object, i, by = NULL)

Arguments

object An object of class QFeatures.

i The index of the assay in object. The assay must contain an identification
    matrix, that is a matrix where an entry is TRUE if the value is observed and
    FALSE is the value is missing (see examples).

by A vector of length equal to the number of columns in assay i that defines groups
    for which the Jaccard index should be computed separately. If missing, the
    Jaccard indices are computed for all pairs of cells in the dataset.

Value

A data.frame with as many rows as pairs of cells and the following column(s):

- jaccard: the computed Jaccard index
- by: if by is not NULL, the group of the pair of cells for which the Jaccard index is computed.

Examples

data("scp1")

## Define the identification matrix
peps <- scp1["peptides"]
assay(peps) <- ifelse(is.na(assay(peps)), FALSE, TRUE)
scp1 <- addAssay(scp1, peps, "id")

## Compute Jaccard indices
jaccardIndex(scp1, "id")
## Compute Jaccard indices by sample type

```
jaccardIndex(scp1, "id", scp1$SampleType)
```

### Description

A `SingleCellExperiment` object that has been minimally processed. The data set is published by Leduc et al. 2022 (see references) and retrieved using `scpdata::leduc2022_pSCoPE()`. The data processing was conducted with QFeatures and scp. Quality control was performed, followed by building the peptide data and log2-transformation. To limit the size of the data, only cells associated to the 3 first and 3 last MS acquisition runs were kept. For the same reason, 200 peptides were randomly sampled. Therefore, the data set consists of 200 peptides and 73 cells. Peptide annotations can be retrieved from the `rowData` and cell annotations can be retrieved from the `colData`.

### Usage

```
data("leduc_minimal")
```

### Format

An object of class `SingleCellExperiment` with 200 rows and 73 columns.

### Quality control

Any zero value has been replaced by NA.

A peptide was removed from the data set if:

- it matched to a decoy or contaminant peptide
- it had a parental ion fraction below 60
- it had a DART-ID adjusted q-value superior to 1
- it had an average sample to carrier ratio above 0.05

A cell was removed from the data set if:

- it had a median coefficient of variation superior to 0.6
- it had a log2 median intensity outside (6, 8)
- it contained less than 750 peptides

### Building the peptide matrix

PSMs belonging to the same peptide were aggregating using the median value. Some peptides were mapped to a different protein depending on the MS acquisition run. To solve this issue, a majority vote was applied to assign a single protein to each peptide. Protein IDs were translated into gene symbols using the `ensembldb` package.
**medianCVperCell**

**Author(s)**

Christophe Vanderaa, Laurent Gatto

**References**


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**medianCVperCell**

*Compute the median coefficient of variation (CV) per cell*

**Description**

The function computes for each cell the median CV and stores them accordingly in the colData of the QFeatures object. The CVs in each cell are computed from a group of features. The grouping is defined by a variable in the rowData. The function can be applied to one or more assays, as long as the samples (column names) are not duplicated. Also, the user can supply a minimal number of observations required to compute a CV to avoid that CVs computed on too few observations influence the distribution within a cell. The quantification matrix can be optionally normalized before computing the CVs. Multiple normalizations are possible.

**Usage**

```r
medianCVperCell(
  object,
  i,
  groupBy,
  nobs = 5,
  na.rm = TRUE,
  colDataName = "MedianCV",
  norm = "none",
  ...
)
```

**Arguments**

- **object**
  
  A QFeatures object

- **i**
  
  A numeric() or character() vector indicating from which assays the rowData should be taken.

- **groupBy**
  
  A character(1) indicating the variable name in the rowData that contains the feature grouping.

- **nobs**
  
  An integer(1) indicating how many observations (features) should at least be considered for computing the CV. Since no CV can be computed for less than 2 observations, nobs should at least be 2.
medianCVperCell

na.rm A logical(1) indicating whether missing data should be removed before computation.

colDataName A character(1) giving the name of the new variable in the colData where the computed CVs will be stored. The name cannot already exist in the colData.

norm A character() of normalization methods that will be sequentially applied to each feature (row) in each assay. Available methods and additional information about normalization can be found in MsCoreUtils::normalizeMethods. You can also specify norm = "SCoPE2" to reproduce the normalization performed before computing the CVs as suggested by Specht et al. norm = "none" will not normalize the data (default)

... Additional arguments that are passed to the normalization method.

Details

A new column is added to the colData of the object. The samples (columns) that are not present in the selection i will get assigned an NA.

Value

A QFeatures object.

References


Examples

data("scp1")
scp1 <- filterFeatures(scp1, ~ !is.na(Proteins))
scp1 <- medianCVperCell(scp1,
  i = 1:3,
  groupBy = "Proteins",
  nobs = 5,
  na.rm = TRUE,
  colDataName = "MedianCV",
  norm = "div.median")

## Check results
hist(scp1$MedianCV)
Description

A data.frame with 1088 observations and 139 variables, as produced by reading a MaxQuant output file with `read.delim()`.

- Sequence: a character vector
- Length: a numeric vector
- Modifications: a character vector
- Modified.sequence: a character vector
- Deamidation..N..Probabilities: a character vector
- Oxidation..M..Probabilities: a character vector
- Deamidation..N..Score.Diffs: a character vector
- Oxidation..M..Score.Diffs: a character vector
- Acetyl..Protein.N.term.: a numeric vector
- Deamidation..N.: a numeric vector
- Oxidation..M.: a numeric vector
- Missed.cleavages: a numeric vector
- Proteins: a character vector
- Leading.proteins: a character vector
- protein: a character vector
- Gene.names: a character vector
- Protein.names: a character vector
- Type: a character vector
- Set: a character vector
- MS.MS.m.z: a numeric vector
- Charge: a numeric vector
- m.z: a numeric vector
- Mass: a numeric vector
- Resolution: a numeric vector
- Uncalibrated...Calibrated.m.z..ppm.: a numeric vector
- Uncalibrated...Calibrated.m.z..Da.: a numeric vector
- Mass.error..ppm.: a numeric vector
- Mass.error..Da.: a numeric vector
- Uncalibrated.mass.error..ppm.: a numeric vector
- Uncalibrated.mass.error..Da.: a numeric vector
mqScpData

- Max.intensity.m.z.0: a numeric vector
- Retention.time: a numeric vector
- Retention.length: a numeric vector
- Calibrated.retention.time: a numeric vector
- Calibrated.retention.time.start: a numeric vector
- Calibrated.retention.time.finish: a numeric vector
- Retention.time.calibration: a numeric vector
- Match.time.difference: a logical vector
- Match.m.z.difference: a logical vector
- Match.q.value: a logical vector
- Match.score: a logical vector
- Number.of.data.points: a numeric vector
- Number.of.scans: a numeric vector
- Number.of.isotopic.peaks: a numeric vector
- PIF: a numeric vector
- Fraction.of.total.spectrum: a numeric vector
- Base.peak.fraction: a numeric vector
- PEP: a numeric vector
- MS.MS.count: a numeric vector
- MS.MS.scan.number: a numeric vector
- Score: a numeric vector
- Delta.score: a numeric vector
- Combinatorics: a numeric vector
- Intensity: a numeric vector
- Reporter.intensity.corrected.0: a numeric vector
- Reporter.intensity.corrected.1: a numeric vector
- Reporter.intensity.corrected.2: a numeric vector
- Reporter.intensity.corrected.3: a numeric vector
- Reporter.intensity.corrected.4: a numeric vector
- Reporter.intensity.corrected.5: a numeric vector
- Reporter.intensity.corrected.6: a numeric vector
- Reporter.intensity.corrected.7: a numeric vector
- Reporter.intensity.corrected.8: a numeric vector
- Reporter.intensity.corrected.9: a numeric vector
- Reporter.intensity.corrected.10: a numeric vector
- RI1: a numeric vector
- RI2: a numeric vector
mqScpData

- RI3: a numeric vector
- RI4: a numeric vector
- RI5: a numeric vector
- RI6: a numeric vector
- RI7: a numeric vector
- RI8: a numeric vector
- RI9: a numeric vector
- RI10: a numeric vector
- RI11: a numeric vector
- Reporter.intensity.count.0: a numeric vector
- Reporter.intensity.count.1: a numeric vector
- Reporter.intensity.count.2: a numeric vector
- Reporter.intensity.count.3: a numeric vector
- Reporter.intensity.count.4: a numeric vector
- Reporter.intensity.count.5: a numeric vector
- Reporter.intensity.count.6: a numeric vector
- Reporter.intensity.count.7: a numeric vector
- Reporter.intensity.count.8: a numeric vector
- Reporter.intensity.count.9: a numeric vector
- Reporter.intensity.count.10: a numeric vector
- Reporter.PIF: a logical vector
- Reporter.fraction: a logical vector
- Reverse: a character vector
- Potential.contaminant: a logical vector
- id: a numeric vector
- Protein.group.IDs: a character vector
- Peptide.ID: a numeric vector
- Mod..peptide.ID: a numeric vector
- MS.MS.IDs: a character vector
- Best.MS.MS: a numeric vector
- AIF.MS.MS.IDs: a logical vector
- Deamidation..N..site.IDs: a numeric vector
- Oxidation..M..site.IDs: a logical vector
- remove: a logical vector
- dart_PEP: a numeric vector
- dart_qval: a numeric vector
- razor_protein_fdr: a numeric vector
• Deamidation..NQ..Probabilities: a logical vector
• Deamidation..NQ..Score.Diffs: a logical vector
• Deamidation..NQ.: a logical vector
• Reporter.intensity.corrected.11: a logical vector
• Reporter.intensity.corrected.12: a logical vector
• Reporter.intensity.corrected.13: a logical vector
• Reporter.intensity.corrected.14: a logical vector
• Reporter.intensity.corrected.15: a logical vector
• Reporter.intensity.corrected.16: a logical vector
• RI12: a logical vector
• RI13: a logical vector
• RI14: a logical vector
• RI15: a logical vector
• RI16: a logical vector
• Reporter.intensity.count.11: a logical vector
• Reporter.intensity.count.12: a logical vector
• Reporter.intensity.count.13: a logical vector
• Reporter.intensity.count.14: a logical vector
• Reporter.intensity.count.15: a logical vector
• Reporter.intensity.count.16: a logical vector
• Deamidation..NQ..site.IDs: a logical vector
• input_id: a logical vector
• rt_minus: a logical vector
• rt_plus: a logical vector
• mu: a logical vector
• muij: a logical vector
• sigmaij: a logical vector
• pep_new: a logical vector
• exp_id: a logical vector
• peptide_id: a logical vector
• stan_peptide_id: a logical vector
• exclude: a logical vector
• residual: a logical vector
• participated: a logical vector
• peptide: a character vector

Usage
data("mqScpData")
normalizeSCP

Format

An object of class `data.frame` with 1361 rows and 149 columns.

Details

The dataset is a subset of the SCoPE2 dataset (version 2, Specht et al. 2019, BioRXiv). The input file `evidence_unfiltered.csv` was downloaded from a Google Drive repository. The MaxQuant evidence file was loaded and the data was cleaned (renaming columns, removing duplicate fields,...). MS runs that were selected in the scp1 dataset (see `scp1`) were kept along with a blank run. The data is stored as a `data.frame`.

See Also

`readSCP()` for an example on how `mqScpData` is parsed into a `QFeatures` object.

normalizeSCP

Normalize single-cell proteomics (SCP) data

Description

This function normalises an assay in a `QFeatures` according to the supplied method (see Details). The normalized data is added as a new assay

Usage

```r
normalizeSCP(object, i, name = "normAssay", method, ...)
```

Arguments

- `object` An object of class `QFeatures`.
- `i` A numeric vector or a character vector giving the index or the name, respectively, of the assay(s) to be processed.
- `name` A character(1) naming the new assay name. Defaults is are `normAssay`.
- `method` character(1) defining the normalisation method to apply. See Details.
- `...` Additional parameters passed to `MsCoreUtils::normalizeMethods()`.

Details

The method parameter in `normalize` can be one of "sum", "max", "center.mean", "center.median", "div.mean", "div.median", "diff.meda", "quantiles", "quantiles.robust" or "vsn". The `MsCoreUtils::normalizeMethods()` function returns a vector of available normalisation methods.

- For "sum" and "max", each feature’s intensity is divided by the maximum or the sum of the feature respectively. These two methods are applied along the features (rows).
"center.mean" and "center.median" center the respective sample (column) intensities by subtracting the respective column means or medians. "div.mean" and "div.median" divide by the column means or medians. These are equivalent to sweeping the column means (medians) along MARGIN = 2 with FUN = "-" (for "center.*") or FUN = "/" (for "div.*").

"diff.median" centers all samples (columns) so that they all match the grand median by subtracting the respective columns medians differences to the grand median.

Using "quantiles" or "quantiles.robust" applies (robust) quantile normalisation, as implemented in preprocessCore::normalize.quantiles() and preprocessCore::normalize.quantiles.robust(). "vsn" uses the vsn::vsn2() function. Note that the latter also glog-transforms the intensities. See respective manuals for more details and function arguments.

For further details and examples about normalisation, see MsCoreUtils::normalize_matrix().

Value
A QFeatures object with an additional assay containing the normalized data.

See Also
QFeatures::normalize for more details about normalize

Examples

data("scp1")
scp1
normalizeSCP(scp1, i = "proteins", name = "normproteins",
method = "center.mean")

pep2qvalue

Description
This function computes q-values from the posterior error probabilities (PEPs). The functions takes the PEPs from the given assay’s rowData and adds a new variable to it that contains the computed q-values.

Usage
pep2qvalue(object, i, groupBy, PEP, rowDataName = "qvalue")
**Arguments**

- **object**: A QFeatures object
- **i**: A numeric() or character() vector indicating from which assays the rowData should be taken.
- **groupBy**: A character(1) indicating the variable name in the rowData that contains the grouping variable, for instance to compute protein FDR. When groupBy is not missing, the best feature approach is used to compute the PEP per group, meaning that the smallest PEP is taken as the PEP of the group.
- **PEP**: A character(1) indicating the variable names in the rowData that contains the PEPs. Since, PEPs are probabilities, the variable must be contained in (0, 1).
- **rowDataName**: A character(1) giving the name of the new variable in the rowData where the computed FDRs will be stored. The name cannot already exist in any of the assay rowData.

**Details**

The q-value of a feature (PSM, peptide, protein) is the minimum FDR at which that feature will be selected upon filtering (Savitski et al.). On the other hand, the feature PEP is the probability that the feature is wrongly matched and hence can be seen as a local FDR (Kall et al.). While filtering on PEP is guaranteed to control for FDR, it is usually too conservative. Therefore, we provide this function to convert PEP to q-values.

We compute the q-value of a feature as the average of the PEPs associated to PSMs that have equal or greater identification confidence (so smaller PEP). See Kall et al. for a visual interpretation.

We also allow inference of q-values at higher level, for instance computing the protein q-values from PSM PEP. This can be performed by supplying the groupBy argument. In this case, we adopt the best feature strategy that will take the best (smallest) PEP for each group (Savitski et al.).

**Value**

A QFeatures object.

**References**


**Examples**

data("scp1")
scp1 <- pep2qvalue(scp1,
  i = 1,
  groupBy = "protein",
  PEP = "dart_PEP")
rowDataName = "qvalue_protein")

## Check results
rowData(scp1)[[1]][, c("dart_PEP", "qvalue_protein")]

---

**readSCP**  
Read single-cell proteomics tabular data

**Description**

Function to import and convert tabular data from a spreadsheet or a data.frame into a SingleCellExperiment and QFeatures object.

**Usage**

readSCP(...)
readSCPfromDIANN(...)
readSingleCellExperiment(...)

**Arguments**

... Parameters passed to readSummarizedExperiment(), readQFeatures() or readQFeaturesFromDIANN(). See these respective manual pages for details.

**Value**

An instance of class SingleCellExperiment or a QFeatures, composed of SingleCellExperiment objects.

**Note**

The SingleCellExperiment class is built on top of the RangedSummarizedExperiment class. This means that some column names are forbidden in the rowData. Avoid using the following names: seqnames, ranges, strand, start, end, width, element

**See Also**

- The more general QFeatures::readQFeatures() function, which this function depends on.
- The more general QFeatures::readQFeaturesFromDIANN() function, for details and an example on how to read label-free and plexDIA (mTRAQ) data processed with DIA-NN.
- The QFeatures::readSummarizedExperiment() function, which readSingleCellExperiment() depends on.
- The SingleCellExperiment::SingleCellExperiment() class.
Examples

```
# Load a single acquisition as a SingleCellExperiment

## Load a data.frame with PSM-level data
data("mqScpData")

## Create the QFeatures object
sce <- readSingleCellExperiment(mqScpData,
    quantCols = grep("RI", colnames(mqScpData)))
sce

# Load multiple acquisitions as a QFeatures

## Load an example table containing MaxQuant output
data("mqScpData")

## Load the (user-generated) annotation table
data("sampleAnnotation")

## Format the tables into a QFeatures object
readSCP(assayData = mqScpData,
    colData = sampleAnnotation,
    runCol = "Raw.file")
```

---

reportMissingValues  Four metrics to report missing values

Description

The function computes four metrics to report missing values in single-cell proteomics.

Usage

```
reportMissingValues(object, i, by = NULL)
```

Arguments

- **object**: An object of class `QFeatures`.
- **i**: The index of the assay in `object`. The assay must contain an identification matrix, that is a matrix where an entry is TRUE if the value is observed and FALSE is the value is missing (see examples). `i` may be numeric, character or logical, but it must select only one assay.
- **by**: A vector of length equal to the number of columns in assay `i` that defines groups for which the metrics should be computed separately. If missing, the metrics are computed for the complete assay.
Value

A data.frame with groups as rows and 5 columns:

- LocalSensitivityMean: the average number of features per cell.
- LocalSensitivitySd: the standard deviation of the local sensitivity.
- TotalSensitivity: the total number of features found in the dataset.
- Completeness: the proportion of values that are not missing in the data.
- NumberCells: the number of cells in the dataset.

Examples

data("scp1")

## Define the identification matrix
peps <- scp1["peptides"]
assay(peps) <- !is.na(assay(peps))
scp1 <- addAssay(scp1, peps, "id")

## Report metrics
reportMissingValues(scp1, "id")
## Report metrics by sample type
reportMissingValues(scp1, "id", scp1$SampleType)

data

---

defaultAnnotation     Single cell sample annotation

Description

A data frame with 48 observations on the following 6 variables.

- Set: a character vector
- Channel: a character vector
- SampleType: a character vector
- lcbatch: a character vector
- sortday: a character vector
- digest: a character vector

Usage

data("sampleAnnotation")

Format

An object of class data.frame with 64 rows and 6 columns.
Details

### The dataset is a subset of the SCoPE2 dataset (version 2, Specht et al. 2019, BioRXiv). The input files batch.csv and annotation.csv were downloaded from a Google Drive repository. The two files were loaded and the columns names were adapted for consistency with mqScpData table (see ?mqScpData). The two tables were filtered to contain only sets present in “mqScpData. Data. The tables were then merged based on the run ID, hence merging the sample annotation and the batch annotation. Finally, annotation for the blank run was added manually. The data is stored as a data.frame'.

See Also

readSCP() to see how this file is used.

---

scp1 Single Cell QFeatures data

Description

A small QFeatures object with SCoPE2 data. The object is composed of 5 assays, including 3 PSM-level assays, 1 peptide assay and 1 protein assay.

Usage

data("scp1")

Format

An object of class QFeatures of length 5.

Details

The dataset is a subset of the SCoPE2 dataset (version 2, Specht et al. 2019, BioRXiv). This dataset was converted to a QFeatures object where each assay in stored as a SingleCellExperiment object. One assay per chromatographic batch ("LCA9", "LCA10", "LCB3") was randomly sampled. For each assay, 100 proteins were randomly sampled. PSMs were then aggregated to peptides and joined in a single assay. Then peptides were aggregated to proteins.

Examples

data("scp1")
scp1
scpAnnotateResults

Annotate single-cell proteomics analysis output

Description

The function takes as input a list of DFrame and a table with additional annotations. The annotation tables is automatically merged into all tables of the list by matching the specified columns (given by the arguments by and by2). This function is useful to add annotation to analysis results generated by scpVarianceAnalysis(), scpDifferentialAnalysis(), or scpComponentAnalysis(). The annotation table is typically the colData orrowData of the object used for modelling. In case of shared column names between the input tables and the annotation table, any annotation that is already present in the list of tables will be overwritten by the new annotations.

Usage

scpAnnotateResults(tableList, annotations, by, by2 = NULL)

Arguments

tableList A list of tables, typically the output of scpVarianceAnalysis(), scpDifferentialAnalysis(), or the the bySample or byFeature elements returned by scpComponentAnalysis().

annotations A table of class ’data.frame’ or ’DFrame’ containing the annotations to add. If no further arguments are provided, the table must have row names.

by A character(1) providing the name of the column in the tables in tableList to use to match the rows of the annotation table.

by2 A character(1) providing the name of the column in the annotation table to use to match the rows of the tables in tableList. If NULL, it will be defined by by.

Author(s)

Christophe Vanderaa, Laurent Gatto

See Also

• ScpModel-VarianceAnalysis
• ScpModel-DifferentialAnalysis
• ScpModel-ComponentAnalysis

Examples

data("leduc_minimal")
var <- scpVarianceAnalysis(leduc_minimal)
colnames(var$Residuals)
## Add peptide annotations available from the rowData
var <- scpAnnotateResults(
ScpModel

A ScpModel object must be always stored in the metadata() of an object that inherits from the SingleCellExperiment class. The ScpModel object should **never be accessed directly** by the user. Instead, we provide several setter function to retrieve information that may be useful to the user. The ScpModel class contains several slots:

- **scpModelFormula**: a formula object controlling which variables are to be modelled.
- **scpModelInputIndex**: a numeric(1), selecting the assay to use in the SingleCellExperiment object as input matrix. Note that this slot serves as a pointer, meaning that the quantitative data is not duplicated. Any change to the assay in the SingleCellExperiment will impact the estimation of the ScpModel object.
- **scpModelFilterThreshold**: A numeric(1) indicating the minimal n/p ratio required for a feature to be included in further model exploration. n/p is the number of measured values for a features divided by the number of coefficients to estimate. n/p cannot be smaller than 1 because this would lead to over-specified models.
- **scpModelFitList**: A List that contains the model results for each feature. Each element is a ScpModelFit object (see [ScpModelFit](#))

**Usage**

```R
scpModelFormula(object, name)
scpModelInput(object, name, filtered = TRUE)
scpModelFilterThreshold(object, name)
scpModelFilterNPRatio(object, name, filtered = TRUE)
scpModelResiduals(object, name, join = TRUE, filtered = TRUE)
scpModelEffects(object, name, join = TRUE, filtered = TRUE)
scpModelNames(object)
scpModelFilterThreshold(object, name) <- value
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object that inherits from the <code>SingleCellExperiment</code> class.</td>
</tr>
<tr>
<td>name</td>
<td>A character(1) providing the name to use to store or retrieve the modelling results. When retrieving a model and name is missing, the name of the first model found in object is used.</td>
</tr>
<tr>
<td>filtered</td>
<td>A logical(1) indicating whether the output should return all features (FALSE) or the features that comply to the n/p ratio threshold (TRUE).</td>
</tr>
<tr>
<td>join</td>
<td>A logical(1) indicating whether the output should be combined in a single matrix (TRUE) or it should be returned as a list with one element for each feature (FALSE). When TRUE, any gaps across features will be filled with NA's.</td>
</tr>
<tr>
<td>value</td>
<td>An numeric(1), the new value for the n/p ratio threshold</td>
</tr>
</tbody>
</table>

Getters

Each slot has a getter function associated:

- `scpModelNames()`: returns a vector of names of `ScpModel` objects stored in the `SingleCellExperiment` object.
- `scpModelFormula()`: returns the formula slot of the `ScpModel` within an object that inherits from the `SummarizedExperiment` class.
- `scpModelFilterThreshold()`: returns the n/p ration threshold used for feature filtering.
- `scpModelInput()`: returns a matrix with the quantitative values used as input of the model. Hence, the matrix contains the data before modelling. If `filtered = TRUE`, the feature of the matrix are restricted to the features that satisfy the n/p ratio threshold.
- `scpModelFilterNPRatio()`: returns the computed n/p ratio for each feature. If `filtered = TRUE`, the function returns only the n/p of the features that satisfy the n/p ratio threshold.
- `scpModelResiduals()`: when `join = FALSE`, the function returns a list where each element corresponds to a feature and contains the estimated residuals. When `join = TRUE` (default), the function combines the list into a matrix with features in rows and cells in columns, and filling the gaps with NA. If `filtered = TRUE`, the feature of the matrix are restricted to the features that satisfy the n/p ratio threshold.
- `scpModelEffects()`: when `join = FALSE`, the function return a list where each element of the list corresponds to a feature. Each element contains another list with as many elements as variable in the model and each element contains the data effect vector for that vector. When `join = TRUE` (default), each element of the list is a matrix with features in rows and cells in columns where gaps are filled with NA. If `filtered = TRUE`, the feature of the matrix are restricted to the features that satisfy the n/p ratio threshold.

Setter:

- `scpModelFilterThreshold<-()`: the function changes the n/p ratio threshold used for filtering features.

Author(s)

Christophe Vanderaa, Laurent Gatto
See Also

- `ScpModelFit` for a description of the class that store modelling results
- `ScpModel-Workflow` that uses the class to store the estimated model.

Examples

data("leduc_minimal")

####---- Getters ----####
scpModelNames(leduc_minimal)
scpModelFormula(leduc_minimal)
dim(leduc_minimal)
dim(scpModelInput(leduc_minimal))
dim(scpModelInput(leduc_minimal, filtered = FALSE))
head(scpModelFilterNPRatio(leduc_minimal))
dim(scpModelResiduals(leduc_minimal))
dim(scpModelResiduals(leduc_minimal, filtered = FALSE))
scpModelResiduals(leduc_minimal, join = FALSE)
scpModelEffects(leduc_minimal)
dim(scpModelEffects(leduc_minimal)$Set)
dim(scpModelEffects(leduc_minimal, filtered = FALSE)$Set)
scpModelEffects(leduc_minimal, join = FALSE)[[1]]
scpModelFilterThreshold(leduc_minimal)

####---- Setter ----####
scpModelFilterThreshold(leduc_minimal) <- 2
scpModelFilterThreshold(leduc_minimal)

---

**ScpModel-DataCorrection**

*Correct single-cell proteomics data*

**Description**

The function uses the data modelling output to generate corrected data that can be used for downstream analysis. The input is expected to be a `SingleCellExperiment` object that contains an estimated `ScpModel`. There are two approaches:

- `scpKeepEffect()`: keep the effects of interests. The reconstructed data is the sum of the effect matrices for the variable of interest and the residuals. Note that the intercepts (baseline intensity of each feature) are not included by default, but they can be added when `intercept = TRUE`. 
- `scpRemoveBatchEffect()`: remove any undesired effect. The batch corrected data is the input data minus the effect matrices that correspond to batch effect variables. Note that the intercepts (baseline intensity of each feature) are removed by default, but they can be kept when `intercept = FALSE`.

Despite the two approaches are conceptually different, they can lead to similar results if the effects that are used to reconstruct the data are the ones that are not removed when performing batch correction (see examples).

The function returns a new `SingleCellExperiment` that contains an assay with the batch corrected data. Note that the 'ScpModel' is erased in this new object.

**Usage**

```r
scpKeepEffect(object, effects = NULL, intercept = FALSE, name)
scpRemoveBatchEffect(object, effects = NULL, intercept = TRUE, name)
```

**Arguments**

- `object` An object that inherits from the `SingleCellExperiment` class. It must contain an estimated `ScpModel` in its metadata.
- `effects` A character() vector. For `scpKeepEffect()`, which model variable should be used to reconstruct the data. For `scpRemoveBatchEffect()`, which model variable should be removed from the data.
- `intercept` A logical(1). For `scpKeepEffect()`, should the intercepts be included when reconstructing the data? Defaults to `FALSE`, hence the intercepts are not included. For `scpRemoveBatchEffect()`, should the intercepts be removed from the data? Defaults to `TRUE`, hence the intercepts are removed from the data.
- `name` A character(1) providing the name to use to retrieve the model results. When retrieving a model and `name` is missing, the name of the first model found in `object` is used.

**Author(s)**

Christophe Vanderaa, Laurent Gatto

**See Also**

- `ScpModel` for functions to extract information from the `ScpModel` object
- `ScpModel-Workflow` to run a model on SCP data required for batch correction.

**Examples**

```r
data("leduc_minimal")
scpModelFormula(leduc_minimal)
reconstructed <- scpKeepEffect(leduc_minimal, effects = "SampleType")
batchCorrected <- scpRemoveBatchEffect(
    leduc_minimal, effects = c("Channel", "Set", "MedianIntensity")
)```
The two approaches are identical

\[
\text{identical}(\text{reconstructed}, \text{batchCorrected})
\]

---

**ScpModel-DifferentialAnalysis**

*Differential abundance analysis for single-cell proteomics*

**Description**

Differential abundance analysis assess the statistical significance of the differences observed between group of samples of interest.

**Usage**

```r
scpDifferentialAnalysis(object, coefficients = NULL, contrasts = NULL, name)
scpDifferentialAggregate(differentialList, fcol, ...)
scpVolcanoPlot(differentialList, fdrLine = 0.05, top = 10, by = "padj", decreasing = FALSE, textBy = "feature", pointParams = list(), labelParams = list())
```

**Arguments**

- **object**
  An object that inherits from the `SingleCellExperiment` class. It must contain an estimated `ScpModel` in its metadata.

- **coefficients**
  A character() vector with coefficient names to test. `coefficients` and `contrasts` cannot be both NULL.

- **contrasts**
  A list() where each element is a contrast to test. Each element must be a vector with 3 strings: 1. The name of a categorical variable to test; 2. The name of the first category of interest; 3. The name of the second category of interest. `coefficients` and `contrasts` cannot be both NULL.

- **name**
  A character(1) providing the name to use to retrieve the model results. When retrieving a model and `name` is missing, the name of the first model found in `object` is used.

- **differentialList**
  A list of tables returned by `scpDifferentialAnalysis()`.
A character(1) indicating the column to use for grouping features. Typically, this would be protein or gene names for grouping proteins.

Further arguments passed to `metapod::combineGroupedPValues()`.

A numeric(1) indicating the FDR threshold bar to show on the plot.

A numeric(1) indicating how many features should be labelled on the plot.

A character(1) used to order the features. It indicates which variable should be considered when sorting the results. Can be one of: "Estimate", "SE", "Df", "tstatistic", "pvalue", "padj" or any other annotation added by the user.

A logical(1) indicating whether the features should be ordered decreasingly (TRUE, default) or increasingly (FALSE) depending on the value provided by `by`.

A character(1) indicating the name of the column to use to label points.

pointParams A list where each element is an argument that is provided to `ggplot2::geom_point()`. This is useful to change point size, transparency, or assign colour based on an annotation (see `ggplot2::aes()`).

labelParams A list where each element is an argument that is provided to `ggrepel::geom_label_repel()`. This is useful to change label size, transparency, or assign colour based on an annotation (see `ggplot2::aes()`).

Running the differential abundance analysis

`scpDifferentialAnalysis()` performs a t-test on a coefficient of interest or on coefficients that distinguish two groups of cells of interests (provided as a contrast). Contrasts must be provided as a list where each element is a three-element character vector. The first element of the vector provides the name of the categorical variable to test, the second element provides the name of the first category (that is one of the factor levels), the third element provides the name of the other category to compare. Numerical variables can be tested by providing the coefficient argument, that is the name of the coefficient associated to that numerical variable. The statistical tests are conducted for each feature independently. The p-values are adjusted using `IHW::ihw()`, where each test is weighted using the feature intercept (that is the average baseline intensity). The function returns a list of DataFrames with one table for each test contrast and/or coefficient. It provides the adjusted p-values and the estimates. For contrast, the estimates represent the estimated log fold changes between the groups. For coefficients, the estimates are the estimated slopes.

`scpDifferentialAggregate()` combines the differential abundance analysis results for groups of features. This is useful, for example, to return protein-level results when data is modelled at the peptide level. The function heavily relies on the approaches implemented in `metapod::combineGroupedPValues()`. The p-values are combined into a single value using one of the following methods: Simes’ method (default), Fisher’s method, Berger’s method, Pearson’s method, minimum Holm’s approach, Stouffer’s Z-score method, and Wilkinson’s method. We refer to the `metapod` documentation for more details on the assumptions underlying each approach. The estimates are combined using the representative estimate, as defined by `metapod`. Which estimate is representative depends on the selected combination method. The function takes the list of tables generated by `scpDifferentialAnalysis()` and returns a new list of DataFrames with aggregated results.

Volcano plots

`scpAnnotateResults()` adds annotations to the differential abundance analysis results. The annotations are added to all elements of the list returned by `()`. See the associated man page for more...
scpVolcanoPlot() takes the list of tables generated by scpDifferentialAnalysis() and returns a ggplot2 scatter plot. The plots show the adjusted p-values with respect to the estimate. A horizontal bar also highlights the significance threshold (defaults to 5%, fdrLine). The top (default 10) features with lowest p-values are labeled on the plot. You can control which features are labelled using the top, by and decreasing arguments. Finally, you can change the point and label aesthetics thanks to the pointParams and the labelParams arguments, respectively.

Author(s)

Christophe Vanderaa, Laurent Gatto

See Also

• ScpModel-Workflow to run a model on SCP data upstream of differential abundance analysis.
• scpAnnotateResults() to annotate analysis of variance results.

Examples

library("patchwork")
library("ggplot2")
data("leduc_minimal")
## Add n/p ratio information in rowData
rowData(leduc_minimal)$npRatio <-
    scpModelFilterNPRatio(leduc_minimal, filtered = FALSE)
####---- Run differential abundance analysis ----####
(res <- scpDifferentialAnalysis(,
    leduc_minimal, coefficients = "MedianIntensity",
    contrasts = list(c("SampleType", "Melanoma", "Monocyte"))
))
## IHW return a message because of the example data set has only few
## peptides, real dataset should not have that problem.
####---- Annotate results ----####
## Add peptide annotations available from the rowData
res <- scpAnnotateResults(
    res, rowData(leduc_minimal),
    by = "feature", by2 = "Sequence"
)
####---- Plot results ----####
scpVolcanoPlot(res, textBy = "gene") |> 
    wrap_plots(guides = "collect")
## Modify point and label aesthetics
scpVolcanoPlot(
    res, textBy = "gene", top = 20,
### ScpModel-VarianceAnalysis

*Analysis of variance for single-cell proteomics*

---

**Description**

Analysis of variance investigates the contribution of each effects in capturing the variance in the data.

**Usage**

```r
scpVarianceAnalysis(object, name)
scpVarianceAggregate(varianceList, fcol)
scpVariancePlot(v
```  

**Arguments**

- **object**: An object that inherits from the `SingleCellExperiment` class. It must contain an estimated `ScpModel` in its metadata.
- **name**: A character(1) providing the name to use to retrieve the model results. When retrieving a model and name is missing, the name of the first model found in object is used.
- **varianceList**: A list of tables returned by `scpVarianceAnalysis()`.
fcol A character(1) indicating the column to use for grouping features. Typically, this would be protein or gene names for grouping proteins.

effect A character(1) used to filter theb results. It indicates which effect should be considered when sorting the results.

by A character(1) used to filter the results. It indicates which variable should be considered when sorting the results. Can be one of: "SS", "df", or "percentExplainedVar".

top A numeric(1) used to filter the results. It indicates how many features should be plotted. When top = Inf (default), all feature are considered.

decreasing A logical(1) indicating whether the effects should be ordered decreasingly (TRUE, default) or increasingly (FALSE) depending on the value provided by by.

combined A logical(1) indicating whether the results should be combined across all features. When TRUE, the barplot shows the explained variance for the complete dataset.

colourSeed A integer(1) providing a seed that is used when randomly sampling colours for the effects. Change the number to generate another colour scheme.

Running the variance analysis

scpVarianceAnalysis() computes the amount of data (measured as the sums of squares) that is captured by each model variable, but also that is not modelled and hence captured in the residuals. The proportion of variance explained by each effect is the sums of squares for that effect divided by the sum of all sums of squares for each effect and residuals. This is computed for each feature separately. The function returns a list of DataFrames with one table for each effect.

scpVarianceAggregate() combines the analysis of variance results for groups of features. This is useful, for example, to return protein-level results when data is modelled at the peptide level. The function takes the list of tables generated by scpVarianceAnalysis() and returns a new list of DataFrames with aggregated results.

Exploring variance analysis results

scpAnnotateResults() adds annotations to the component analysis results. The annotations are added to all elements of the list returned by scpComponentAnalysis(). See the associated man page for more information.

scpVariancePlot() takes the list of tables generated by scpVarianceAnalysis() and returns a ggplot2 bar plot. The bar plot shows the proportion of explained variance by each effect and the residual variance. By default, the function will combine the results over all features, showing the effect's contributions on the complete data set. When combine = FALSE, the results are shown for individual features, with additional arguments to control how many and which features are shown. Bars can also be grouped by fcol. This is particularly useful when exploring peptide level results, but grouping peptides that belong to the same protein (note that you should not use scpVarianceAggregate() in that case).

Author(s)

Christophe Vanderaa, Laurent Gatto
See Also

- **ScpModel-Workflow** to run a model on SCP data upstream of analysis of variance.
- **scpAnnotateResults()** to annotate analysis of variance results.

Examples

data("leduc_minimal")

####---- Run analysis of variance ----####
(var <- scpVarianceAnalysis(leduc_minimal))

####---- Annotate results ----####

## Add peptide annotations available from the rowData
var <- scpAnnotateResults(
    var, rowData(leduc_minimal), by = "feature", by2 = "Sequence"
)

####---- Plot results ----####

## Plot the analysis of variance through the whole data
scpVariancePlot(var)

## Plot the analysis of variance for the top 20 peptides with highest
## percentage of variance explained by the cell type
scpVariancePlot(
    var, effect = "SampleType", top = 20, combined = FALSE
)

## Same but grouped by protein
scpVariancePlot(
    var, effect = "SampleType", top = 20, combined = FALSE, fcol = "gene"
)

####---- Aggregate results ----####

## Aggregate to protein-level results
varProtein <- scpVarianceAggregate(var, fcol = "gene")
scpVariancePlot(
    varProtein, effect = "SampleType", top = 20, combined = FALSE
)

---

**ScpModel-Workflow**  
*Modelling single-cell proteomics data*

**Description**

Function to estimate a linear model for each feature (peptide or protein) of a single-cell proteomics data set.
Usage

scpModelWorkflow(object, formula, i = 1, name = "model", verbose = TRUE)
scpModelFilterPlot(object, name)

Arguments

object  An object that inherits from the SingleCellExperiment class.
formula  A formula object controlling which variables are to be modelled.
i  A logical, numeric or character indicating which assay of object to use as input for modelling. Only a single assay can be provided. Defaults to the first assays.
name  A character(1) providing the name to use to store or retrieve the modelling results. When retrieving a model and name is missing, the name of the first model found in object is used.
verbose  A logical(1) indicating whether to print progress to the console.

Input data

The main input is object that inherits from the SingleCellExperiment class. The quantitative data will be retrieve using assay(object). If object contains multiple assays, you can specify which assay to take as input thanks to the argument i, the function will then assume assay(object, i) as quantification input.

The objective of modelling single-cell proteomics data is to estimate, for each feature (peptide or protein), the effect of known cell annotations on the measured intensities. These annotations may contain biological information such as the cell line, FACS-derived cell type, treatment, etc. We also highly recommend including technical information, such as the MS acquisition run information or the chemical label (in case of multiplexed experiments). These annotation must be available from colData(object). formula specifies which annotations to use during modelling.

Data modelling workflow

The modelling workflow starts with generating a model matrix for each feature given the colData(object) and formula. The model matrix for peptide i, denoted $X_i$, is adapted to the pattern of missing values (see section below). Then, the functions fits the model matrix against the quantitative data. In other words, the function determines for each feature $i$ (row in the input data) the contribution of each variable in the model. More formally, the general model definition is:

$$Y_i = \beta_i X^T_{(i)} + \epsilon_i$$

where $Y$ is the feature by cell quantification matrix, $\beta_i$ contains the estimated coefficients for feature $i$ with as many coefficients as variables to estimate, $X^T_{(i)}$ is the model matrix generated for feature $i$, and $\epsilon$ is the feature by cell matrix with residuals.

The coefficients are estimated using penalized least squares regression. Next, the function computes the residual matrix and the effect matrices. An effect matrix contains the data that is captured by a given cell annotation. Formally, for each feature $i$: 
\[ \hat{M}_i^f = \hat{\beta}_i^f X_{(i)}^{fT} \]

where \( \hat{M}_i^f \) is a cell by feature matrix containing the variables associated to annotation \( f \), \( \hat{\beta}_i^f \) are the estimated coefficients associated to annotation \( f \) and estimated for feature \( i \), and \( X_{(i)}^{fT} \) is the model matrix for peptide \( i \) containing only the variables to annotation \( f \).

All the results are stored in an \texttt{ScpModel} object which is stored in the object’s metadata. Note that multiple models can be estimated for the same object. In that case, provide the \texttt{name} argument to store the results in a separate \texttt{ScpModel}.

**Feature filtering**

The proportion of missing values for each features is high in single-cell proteomics data. Many features can typically contain more coefficients to estimate than observed values. These features cannot be estimated and will be ignored during further steps. These features are identified by computing the ratio between the number of observed values and the number of coefficients to estimate. We call it the \texttt{n/p ratio}. Once the model is estimated, use \texttt{scpModelFilterPlot(object)} to explore the distribution of \( n/p \) ratios across the features. You can also extract the \( n/p \) ratio for each feature using \texttt{scpModelFilterNPRatio(object)}. By default, any feature that has an \( n/p \) ratio lower than 1 is ignored. However, feature with an \( n/p \) ratio close to 1 may lead to unreliable outcome because there are not enough observed data. You could consider the \( n/p \) ratio as the average number of replicate per coefficient to estimate. Therefore, you may want to increase the \( n/p \) threshold. You can do so using \texttt{scpModelFilter(object) <- npThreshold}.

**About missing values**

The data modelling workflow is designed to take the presence of missing values into account. We highly recommend to \texttt{not impute} the data before modelling. Instead, the modelling approach will ignore missing values and will generate a model matrix using only the observed values for each feature. However, the model matrices for some features may contain highly correlated variables, leading to near singular designs. We include a small ridge penalty to reduce numerical instability associated to correlated variables.

**Author(s)**

Christophe Vanderaa, Laurent Gatto

**See Also**

- \texttt{ScpModel} for functions to extract information from the \texttt{ScpModel} object
- \texttt{ScpModel-VarianceAnalysis, ScpModel-DifferentialAnalysis, ScpModel-ComponentAnalysis} to explore the model results
- \texttt{scpKeepEffect} and \texttt{scpRemoveBatchEffect} to perform batch correction for downstream analyses.
Examples

data("leduc_minimal")
leduc_minimal
## Overview of available cell annotations
colData(leduc_minimal)

####---- Model data ----####

f <- ~ 1 + ## intercept
  Channel + Set + ## batch variables
  MedianIntensity +## normalization
  SampleType ## biological variable

leduc_minimal <- scpModelWorkflow(leduc_minimal, formula = f)

####---- n/p feature filtering ----####

## Get n/p ratios
head(scpModelFilterNPRatio(leduc_minimal))

## Plot n/p ratios
scpModelFilterPlot(leduc_minimal)

## Change n/p ratio threshold
scpModelFilterThreshold(leduc_minimal) <- 2
scpModelFilterPlot(leduc_minimal)

Description

Component analysis is a powerful tool for exploring data. The package implements the ANOVA-
principal component analysis extended to linear models (APCA+) and derivatives (suggested by
Thiel at al. 2017). This framework is based on principal component analysis (PCA) and allows
exploring the data captured by each model variable individually.

Usage

scpModelComponentMethods

scpComponentAnalysis(
  object,
  method = "ASCA",
  effects = NULL,
  pcaFUN = "auto",
  residuals = TRUE,
  unmodelled = TRUE,
name,
...)

scpComponentAggregate(componentList, fcol, fun = colMedians, ...)

scpComponentPlot(
  componentList,
  comp = 1:2,
  pointParams = list(),
  maxLevels = NULL
)

scpComponentBiplot(
  scoreList,
  eigenvectorList,
  comp = 1:2,
  pointParams = list(),
  arrowParams = list(arrow = arrow(length = unit(0.2, "cm"))),
  labelParams = list(size = 2, max.overlaps = 10),
  textBy = "feature",
  top = 10,
  maxLevels = NULL
)

Arguments

object An object that inherits from the SingleCellExperiment class. It must contain an estimated ScpModel in its metadata.

method A character() indicating which approach(es) to use for principal component analysis (PCA). Are allowed: "ASCA", "APCA" and/or "ASCA.E" (multiple values are allowed). "ASCA", "APCA", "ASCA.E" are iterated through all effects found in the model.

effects A character() indicating on which model variables the component analysis should be performed. Default to all modelled variables.

pcaFUN A character indicating which function to use to perform PCA. "nipals" will use nipals::nipals() while "svd" will use base::svd(). If "auto", the function uses "nipals" if the data contain missing values and "svd" otherwise.

residuals A logical(1), if TRUE, PCA is performed on the residual matrix as well.

unmodelled A logical(1), if TRUE, PCA is performed on the input matrix as well.

name A character(1) providing the name to use to retrieve the model results. When retrieving a model and name is missing, the name of the first model found in object is used.

... For scpComponentAnalysis(), further arguments passed to the PCA function. For scpComponentAggregate(), further arguments passed to QFeatures::aggregateFeatures().

cOMPONENTLIST A list of components analysis results. This is typically the bySample or byFeature element of the list returned by scpComponentAnalysis().
fcoll A character(1) providing the name of the column to use to group features.
fun A function that summarizes the values for each group. See QFeatures::aggregateFeatures() for a list of available functions.
comp An integer(2) pointing to which components to fit. The values of comp are not allowed to exceed the number of computed components in componentList.
pointParams A list where each element is an argument that is provided to ggplot2::geom_point(). This is useful to change point size, transparency, or assign colour based on an annotation (see ggplot2::aes()).
maxLevels An integer(1) indicating how many colour levels should be shown on the legend when colours are derived from a discrete factor. If maxLevels = NULL, all levels are shown. This parameters is useful to colour points based on a factor with many levels that would otherwise overcrowd the legend.
scoreList A list of components analysis results. This is typically the bySample element in the list returned by scpComponentAnalysis().
eigenvectorList A list of components analysis results. This is typically the byFeature element in the list returned by scpComponentAnalysis().
arroParams A list where each element is an argument that is provided to ggplot2::geom_segment(). This is useful to change arrow head style, line width, transparency, or assign colour based on an annotation (see ggplot2::aes()).
labelParams A list where each element is an argument that is provided to ggrepel::geom_label_repel(). This is useful to change label size, transparency, or assign colour based on an annotation (see ggplot2::aes()).
textBy A character(1) indicating the name of the column to use to label arrow heads.
top An integer(1) indicating how many arrows should be drawn. The arrows are sorted based on their size as determined by the euclidean distance in the principal component space.

Format

An object of class character of length 3.

PCA - notation and algorithms

Given \( A \) a \( m \times n \) matrix, PCA can be summarized as the following decomposition:

\[
AA^T/(n-1) = VLV^T
\]

Where \( V \) is a \( m \times k \) orthogonal matrix, that is \( VV^T = I \), with \( k \) the number of components. \( V \) is called the matrix of eigenvectors. \( L \) is the \( k \times k \) diagonal matrix of eigenvalues that contains the variance associated to each component, ordered from highest to lowest variance. The unscaled PC scores are given by \( S = A^TV \).

There are 2 available algorithm to perform PCA:

- nipals: The non-linear iterative partial least squares (NIPALS) algorithm can handle missing values and approximates classical PCA, although it does not explicitly maximize the variance. This is implemented in nipals::nipals().
• svd: The singular value decomposition (SVD) is used to perform an exact PCA, but it cannot handle missing values. This is implemented in `base::svd()`.

Which algorithm to use is controlled by the `pcaFUN` argument, by default (“auto”), the function automatically uses `svd` when there is no missing values and `nipals` when there is at least one missing value.

**Component analysis methods**

`scpComponentAnalysis()` performs a PCA on the modelling output. What modelling output the function will use depends on the method. The are 3 PCA approaches:

• **ASCA** performs a PCA on the effect matrix, that is \( A = \hat{M}_f \) where \( f \) is one of the effects in the model. This PCA is useful to explore the modelled effects and the relationship between different levels of a factor.

• **ASCA.E**: perform PCA on the effect matrix, just like ASCA. The scores are then updated by projecting the effect matrix added to the residuals using the eigenvectors, that is \( \text{scores} = (\hat{M}_f + \epsilon)T V \). This PCA is useful to explore the modelled effects while blurring these effects with the unmodelled variability. Note however that for this approach, the scores are no longer guaranteed to be orthogonal and the eigenvalues are no longer meaningful. The percentage of variation should not be interpreted.

• **APCA** (default) performs PCA on the effect matrix plus the residuals, that is \( A = \hat{M}_f + \epsilon \). This PCA is useful to explore the modelled effects in relation with the unmodelled variability that is remaining in the residuals.

Available methods are listed in `scpModelComponentMethods`. Note that for all three methods, a PCA on the residual matrix is also performed when `residuals = TRUE`, that is \( A = \epsilon = Y - \hat{\beta}X^T \). A PCA on the residuals is useful to explore residual effects that are not captured by any effect in the model. Similarly, a PCA on the input data matrix, that is on the data before modelling is also performed when `unmodelled = TRUE`, that is \( A = Y \).

`scpComponentAnalysis()` always returns a list with 2 elements. The first element, `bySample` is a list where each element contains the PC scores for the desired model variable(s). The second element, `byFeature` is a list where each element contains the eigenvectors for the desired model variable(s).

**Exploring component analysis results**

`scpAnnotateResults()` adds annotations to the component analysis results. The annotations are added to all elements of the list returned by `scpComponentAnalysis()`. See the associated man page for more information.

`scpComponentPlot()` takes one of the two elements of the list generated by `scpComponentAnalysis()` and returns a list of ggplot2 scatter plots. Commonly, the first two components, that bear most of the variance, are explored for visualization, but other components can be explored as well thanks to the `comp` argument. Each point represents either a sample or a feature, depending on the provided component analysis results (see examples). Change the point aesthetics by providing geplot arguments in a list (see examples).

`scpComponentBiplot()` simultaneously explores the PC scores (sample-space) and the eigenvectors (feature-space). Scores are shown as points while eigenvectors are shown as arrows. Point
aesthetics and arrow aesthetics can be controlled with the `pointParams` and the `arrowParams` arguments, respectively. Moreover, arrows are also labelled and label aesthetics can be controlled using `labelParams` and `textBy`. Plotting all eigenvectors as arrows leads to overcrowded plots. You can limit the plotting to the top longest arrows (default to the top 10) as defined by the distance on the two selected PCs.

`scpComponentAggregate()` offers functionality to aggregate the results from multiple features. This can be used to obtain, for example, component analysis results for proteins when modelling at the peptide level. The approach is inspired from `scuttle::aggregateAcrossCells()` and combines, for each group, multiple values for each component using `QFeatures::aggregateFeatures()`. By default, values are aggregated using the median, but `QFeatures` offers other methods as well. The annotation of the component results are automatically aggregated as well. See the `aggregateFeatures()` man page for more information on available methods and expected behavior.

**Author(s)**

Christophe Vanderaa, Laurent Gatto

**References**


**See Also**

- `ScpModel-Workflow` to run a model on SCP data upstream of component analysis.
- The `nipals::nipals()` function and package for detailed information about the algorithm and associated parameters.
- The `ggplot2::ggplot()` functions and associated tutorials to manipulate and save the visualization output
- `scpAnnotateResults()` to annotate component analysis results.

**Examples**

```r
library("patchwork")
library("ggplot2")
data("leduc_minimal")
leduc_minimal$cell <- rownames(colData(leduc_minimal))

####---- Run component analysis ----####
(pcs <- scpComponentAnalysis(
  leduc_minimal, method = "ASCA", effects = "SampleType",
  pcaFUN = "auto", residuals = FALSE, unmodelled = FALSE
))

####---- Annotate results ----####

## Add cell annotation available from the colData
```
bySamplePCs <- scpAnnotateResults(
  pcs$bySample, colData(leduc_minimal), by = "cell"
)

## Add peptide annotations available from the rowData
byFeaturePCs <- scpAnnotateResults(
  pcs$byFeature, rowData(leduc_minimal),
  by = "feature", by2 = "Sequence"
)

###---- Plot results ----###

## Plot result in cell-space, ie each dot is a cell
scpComponentPlot(
  bySamplePCs,
  pointParams = list(  # ggplot arguments
    aes(colour = SampleType, shape = lcbatch),
    alpha = 0.6
  )
) |> wrap_plots(guides = "collect")

## Plot result in peptide-space, ie each dot is a peptide
scpComponentPlot(
  byFeaturePCs,
  pointParams = list(colour = "dodgerblue", alpha = 0.6)
) |> wrap_plots(guides = "collect")

## Plot both
scpComponentBiplot(
  bySamplePCs, byFeaturePCs,
  pointParams = list(aes(colour = SampleType), alpha = 0.6),
  labelParams = list(max.overlaps = 20),
  textBy = "gene"
) |> wrap_plots(guides = "collect")

###---- Aggregate results ----###

## Aggregate to protein-level results
byProteinPCs <- scpComponentAggregate(
  byFeaturePCs, fcol = "Leading.razor.protein.id"
)

## Plot result in protein-space, ie each dot is a protein
scpComponentPlot(
  byProteinPCs,
  pointParams = list(colour = "firebrick", alpha = 0.6)
) |> wrap_plots(guides = "collect")
ScpModelFit

Class to store the components of an estimated model for a feature

Description

An ScpModelFit object is expected to be stored as a list element in the scpModelFitList of an ScpModel object. The ScpModelFit object should never be accessed directly by the user. Refer to the ScpModel for a list of function to access the information in an ScpModelFit. The ScpModelFit class contains several slots that contain the model output for a feature:

- n: an integer, the number of observations for the feature
- p: an integer, the number of coefficient to estimate
- coefficients: a numeric vector with the estimated coefficients
- residuals: a numeric vector with the estimated residuals
- effects: a List with the
  - df: an integer providing the number of degrees of freedom of the model estimation
  - var: a numeric vector with the residual variance of the model estimation
  - uvcov: the unscaled variance covariance matrix
  - levels: a named List where each elements corresponds to a categorical model variable and contains a vector with the possible categories.

Author(s)

Christophe Vanderaa, Laurent Gatto

See Also

ScpModel for a description of the class that relies on ScpModelFit

Examples

new("ScpModelFit") ## this should never be used by the user
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