Package 'QFeatures'

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Title Quantitative features for mass spectrometry data

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Description The QFeatures infrastructure enables the management and processing of quantitative features for high-throughput mass spectrometry assays. It provides a familiar Bioconductor user experience to manages quantitative data across different assay levels (such as peptide spectrum matches, peptides and proteins) in a coherent and tractable format.

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`aggregateFeatures` *Aggregate assays' quantitative features*

Description

This function aggregates the quantitative features of one or multiple assays, applying a summarisation function (`fun`) to sets of features. The `fcol` variable name points to a rowData column that defines how to group the features during aggregate. This variable can eigher be a vector (we then refer to an *aggregation by vector*) or an adjacency matrix (*aggregation by matrix*).

The rowData of the aggregated `SummarizedExperiment` assays contains a `.n` variable that provides the number of parent features that were aggregated.

When aggregating with a vector, the newly aggregated `SummarizedExperiment` assays also contains a new `aggcounts` assay containing the aggregation counts matrix, i.e. the number of features that were aggregated for each sample, which can be accessed with the `aggcounts()` accessor.

Only the rowData columns that are invariant within a group across all assays will be retained in the new assays' rowData.

Usage

```
## S4 method for signature 'QFeatures'
aggregateFeatures(
  object,
  i,
  fcol,
  name = "newAssay",
  fun = MsCoreUtils::robustSummary,
  ...
)

## S4 method for signature 'SummarizedExperiment'
aggregateFeatures(object, fcol, fun = MsCoreUtils::robustSummary, ...)

## S4 method for signature 'QFeatures'
adjacencyMatrix(object, i, adjName = "adjacencyMatrix")

adjacencyMatrix(object, i, adjName = "adjacencyMatrix") <- value

## S4 method for signature 'SummarizedExperiment'
aggcounts(object, ...)
```

Arguments

`object`	An instance of class `SummarizedExperiment` or `QFeatures`.

i	When adding an adjacency matrix to an assay of a QFeatures object, the index or name of the assay the adjacency matrix will be added to. Ignored when x is an SummarizedExperiment.
fcol	A character(1) naming a rowdata variable (of assay i in case of a QFeatures) defining how to aggregate the features of the assays. This variable is either a character or a (possibly sparse) matrix. See below for details.
name	A character() naming the new assays. name must have the same length as i. Default is newAssay. Note that the function will fail if there's already an assay with name.
fun	A function used for quantitative feature aggregation. See Details for examples.
...	Additional parameters passed the fun.
adjName	character(1) with the variable name containing the adjacency matrix. Default is "adjacencyMatrix".
value	An adjacency matrix with row and column names. The matrix will be coerced to compressed, column-oriented sparse matrix (class dgCMatrix) as defined in the Matrix package, as generaled by the Matrix::sparseMatrix() constructor.

Details

Aggregation is performed by a function that takes a matrix as input and returns a vector of length equal to ncol(x). Examples thereof are

- MsCoreUtils::medianPolish() to fits an additive model (two way decomposition) using Tukey's median polish_ procedure using stats::medpolish();
- MsCoreUtils::robustSummary() to calculate a robust aggregation using MASS::rlm() (default);
- base::colMeans() to use the mean of each column;
- colMeansMat(x, MAT) to aggregate feature by the calculating the mean of peptide intensities via an adjacency matrix. Shared peptides are re-used multiple times.
- matrixStats::colMedians() to use the median of each column.
- base::colSums() to use the sum of each column;
- colSumsMat(x, MAT) to aggregate feature by the summing the peptide intensities for each protein via an adjacency matrix. Shared peptides are re-used multiple times.

See MsCoreUtils::aggregate_by_vector() for more aggregation functions.

Value

A QFeatures object with an additional assay or a SummarizedExperiment object (or subclass thereof).

Missing quantitative values

Missing quantitative values have different effects based on the aggregation method employed:

- The aggregation functions should be able to deal with missing values by either ignoring or propagating them. This is often done with an `na.rm` argument, that can be passed with `...`. For example, `rowSums`, `rowMeans`, `rowMedians`, ... will ignore `NA` values with `na.rm = TRUE`, as illustrated below.
- Missing values will result in an error when using `medpolish`, unless `na.rm = TRUE` is used. Note that this option relies on implicit assumptions and/or performes an implicit imputation: when summing, the values are implicitly imputed by 0, assuming that the `NA` represent a trully absent features; when averaging, the assumption is that the `NA` represented a genuinely missing value.
- When using robust summarisation, individual missing values are excluded prior to fitting the linear model by robust regression. To remove all values in the feature containing the missing values, use `filterNA()`.

More generally, missing values often need dedicated handling such as filtering (see `filterNA()`) or imputation (see `impute()`).

Missing values in the row data

Missing values in the row data of an assay will also impact the resulting (aggregated) assay row data, as illustrated in the example below. Any feature variables (a column in the row data) containing `NA` values will be dropped from the aggregated row data. The reasons underlying this drop are detailed in the `reduceDataFrame()` manual page: only invariant aggregated rows, i.e. rows resulting from the aggregation from identical variables, are preserved during aggregations.

The situation illustrated below should however only happen in rare cases and should often be imputable using the value of the other aggregation rows before aggregation to preserve the invariant nature of that column. In cases where an `NA` is present in an otherwise variant column, the column would be dropped anyway.

Using an adjacency matrix

When considering non-unique peptides explicitly, i.e. peptides that map to multiple proteins rather than as a protein group, it is convenient to encode this ambiguity explicitly using a peptide-by-proteins (sparse) adjacency matrix. This matrix is typically stored in the rowdata and set/retrieved with the `ProtGenerics::adjacencyMatrix()` function. It can be created manually (as illustrated below) or using `PSMatch::makeAdjacencyMatrix()`.

See Also

The *QFeatures* vignette provides an extended example and the *Processing* vignette, for a complete quantitative proteomics data processing pipeline. The `MsCoreUtils::aggregate_by_vector()` manual page provides further details.

Examples

```
## ----------------------------------------
## An example QFeatures with PSM-level data
## ----------------------------------------
data(feat1)
feat1
```

```
## Aggregate PSMs into peptides
feat1 <- aggregateFeatures(feat1, "psms", "Sequence", name = "peptides")
feat1

## Aggregate peptides into proteins
feat1 <- aggregateFeatures(feat1, "peptides", "Protein", name = "proteins")
feat1

assay(feat1[[1]])
assay(feat1[[2]])
aggcounts(feat1[[2]])
assay(feat1[[3]])
aggcounts(feat1[[3]])

## ---------------------------------------------
## Aggregation with missing quantitative values
## ---------------------------------------------
data(ft_na)
ft_na

assay(ft_na[[1]])
rowData(ft_na[[1]])

## By default, missing values are propagated
ft2 <- aggregateFeatures(ft_na, 1, fcol = "X", fun = colSums)
assay(ft2[[2]])
aggcounts(ft2[[2]])

## The rowData .n variable tallies number of initial rows that
## were aggregated (irrespective of NAs) for all the samples.
rowData(ft2[[2]])

## Ignored when setting na.rm = TRUE
ft3 <- aggregateFeatures(ft_na, 1, fcol = "X", fun = colSums, na.rm = TRUE)
assay(ft3[[2]])
aggcounts(ft3[[2]])

## ------------------------------------------------
## Aggregation with missing values in the row data
## ------------------------------------------------
## Row data results without any NAs, which includes the
## Y variables
rowData(ft2[[2]])

## Missing value in the Y feature variable
rowData(ft_na[[1]])[1, "Y"] <- NA
rowData(ft_na[[1]])

ft3 <- aggregateFeatures(ft_na, 1, fcol = "X", fun = colSums)
## The Y feature variable has been dropped!
assay(ft3[[2]])
rowData(ft3[[2]])
```

```
## ------------------------------------------
## Using a peptide-by-proteins adjacency matrix
## ------------------------------------------

## Let's use assay peptides from object feat1 and
## define that peptide SYGFNAAR maps to proteins
## Prot A and B

se <- feat1[["peptides"]]
rowData(se)$Protein[3] <- c("ProtA;ProtB")
rowData(se)

## This can also be defined using anadjacency matrix, manual
## encoding here. See PSMatch::makeAdjacencyMatrix() for a
## function that does it automatically.
adj <- matrix(0, nrow = 3, ncol = 2,
              dimnames = list(rownames(se),
                              c("ProtA", "ProtB")))
adj[1, 1] <- adj[2, 2] <- adj[3, 1:2] <- 1
adj

adjacencyMatrix(se) <- adj
rowData(se)
adjacencyMatrix(se)

## Aggregation using the adjacency matrix
se2 <- aggregateFeatures(se, fcol = "adjacencyMatrix",
                         fun = MsCoreUtils::colMeansMat)

## Peptide SYGFNAAR was taken into account in both ProtA and ProtB
## aggregations.
assay(se2)


## Aggregation by matrix on a QFeature object works as with a
## vector
ft <- QFeatures(list(peps = se))
ft <- aggregateFeatures(ft, "peps", "adjacencyMatrix", name = "protsByMat",
                        fun = MsCoreUtils::colMeansMat)
assay(ft[[2]])
rowData(ft[[2]])
```

`AllGenerics` *Placeholder for generics functions documentation*

Description

Placeholder for generics functions documentation

AssayLinks *Links between Assays*

Description

Links between assays within a QFeatures object are handled by an AssayLinks object. It is composed by a list of AssayLink instances.

Usage

```
## S4 method for signature 'AssayLink'
show(object)

## S4 method for signature 'AssayLinks'
updateObject(object, ..., verbose = FALSE)

## S4 method for signature 'AssayLink'
updateObject(object, ..., verbose = FALSE)

AssayLink(name, from = NA_character_, fcol = NA_character_, hits = Hits())

AssayLinks(..., names = NULL)

assayLink(x, i)

assayLinks(x, i)

## S4 method for signature 'AssayLink,character,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'AssayLinks,list,ANY,ANY'
x[i, j, ..., drop = TRUE]

addAssayLink(object, from, to, varFrom, varTo)

addAssayLinkOneToOne(object, from, to)
```

Arguments

object	An AssayLink object to show.
...	A set of AssayLink objects or a list thereof.
verbose	logical (default FALSE) whether to print extra messages
name	A mandatory name of the assay(s).
from	A character() or integer() indicating which assay(s) to link from in object
fcol	The feature variable of the parent assay used to generate the current assay (used in aggregateFeatures). NA_character_, if not applicable.

hits	An object of class S4Vectors::Hits matching the features of two assays.
names	A character() of AssayLink names. If provided, ... are ignored, and names is used to create an AssayLinks object with AssayLink instances with names names.
x	An instance of class QFeatures.
i	The index or name of the assay whose AssayLink and parents AssayLink instances are to be returned. For [, the feature names to filter on.
j	ignored.
drop	ignored.
to	A character(1) or integer(1) indicating which assay to link to in object
varFrom	A character() indicating the feature variable(s) to use to match the from assay(s) to the to assay. varFrom must have the same length as from and is assumed to be ordered as from.
varTo	A character(1) indicating the feature variable to use to match the to assay to the from assay(s).

Value

assayLink returns an instance of class AssayLink.

assayLinks returns an instance of class AssayLinks.

Constructors

Object can be created with the AssayLink() and AssayLinks() constructors.

Methods and functions

- assayLink(x, i) accesses the AssayLink at position i or with name i in the QFeatures object x.
- parentAssayLinks(x, i, recursive = FALSE) accesses the parent(s) AssayLinks or assay with index or name i.

Creating links between assays

- addAssayLink takes a parent assay and a child assay contained in the QFeatures object and creates a link given a matching feature variable in each assay's rowData. addAssayLink also allows to link an assay from multiple parent assays (see examples below).
- addAssayLinkOneToOne links two assays contained in the QFeatures object. The parent assay and the child assay must have the same size and contain the same rownames (a different ordering is allowed). The matching is performed based on the row names of the assays, instead of a supplied variable name in rowData. Providing multiple parents is not supported.

Examples

```
##-----------------------------
## Creating an AssayLink object
##-----------------------------

al1 <- AssayLink(name = "assay1")
al1

##-----------------------------
## Creating an AssayLinks object
##-----------------------------

AssayLinks(al1)

al2 <- AssayLinks(names = c("Assay1", "Assay2"))
al2

##---------------------------------------
## Adding an AssayLink between two assays
##---------------------------------------

## create a QFeatures object with 2 (identical) assays
## see also '?QFeatures'
se <- SummarizedExperiment(matrix(runif(20), ncol = 2,
                                  dimnames = list(LETTERS[1:10],
                                                  letters[1:2])),
                           rowData = DataFrame(ID = 1:10))
ft <- QFeatures(list(assay1 = se, assay2 = se))

## assay1 and assay2 are not linked
assayLink(ft, "assay2") ## 'from' is NA
assayLink(ft, "assay1") ## 'from' is NA

## Suppose assay2 was generated from assay1 and the feature variable
## 'ID' keeps track of the relationship between the two assays
ftLinked <- addAssayLink(ft, from = "assay1", to = "assay2",
                         varFrom = "ID", varTo = "ID")
assayLink(ftLinked, "assay2")

## For one-to-one relationships, you can also use
ftLinked <- addAssayLinkOneToOne(ft, from = "assay1", to = "assay2")
assayLink(ftLinked, "assay2")

##---------------------------------------
## Adding an AssayLink between more assays
##---------------------------------------

## An assay can also be linked to multiple parent assays
## Create a QFeatures object with 2 parent assays and 1 child assay
ft <- QFeatures(list(parent1 = se[1:6, ], parent2 = se[4:10, ], child = se))
ft <- addAssayLink(ft, from = c("parent1", "parent2"), to = "child",
                   varFrom = c("ID", "ID"), varTo = "ID")
```

```
assayLink(ft, "child")
```

---

countUniqueFeatures *Count Unique Features*

Description

This function counts the number of unique features per sample. A grouping structure can be provided to count higher level features from assays, for example counting the number of unique proteins from PSM data.

Usage

```
countUniqueFeatures(object, i, groupBy = NULL, colDataName = "count")
```

Arguments

object	An object of class QFeatures.
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 count the unique number of peptides or proteins expressed in each samples (column). If groupBy is missing, the number of non zero elements per sample will be stored.
colDataName	A character(1) giving the name of the new variable in the colData where the number of unique features will be stored. The name cannot already exist in the colData.

Value

An object of class QFeatures.

Examples

```
data("ft_na")
## Count number of (non-missing) PSMs
ft_na <- countUniqueFeatures(ft_na,
                             i = "na",
                             colDataName = "counts")
ft_na$counts
## Count number of unique rowData feature
ft_na <- countUniqueFeatures(ft_na,
                             i = "na",
                             groupBy = "Y",
                             colDataName = "Y_counts")
ft_na$Y_counts
```

createPrecursorId *Create precursor identfiers*

Description

The createPrecursorId() is used to create new precursor identifier columns in a QFeatures object's assays (more precisely in their rowData). The new variable is called by default "Precursor.Id", and is generated by the concatenation of other rowData variables that, together, should create unique identifiers.

These precursor identifiers, assuming they are unique, can then be used to join assays using joinAssays(), rather than using the rownames, as illustrated below.

Usage

```
createPrecursorId(
  object,
  name = "Precursor.Id",
  fcols = c("Modified.Sequence", "Precursor.Charge"),
  i = seq_along(object)
)
```

Arguments

object	An instance of class QFeatures.
name	character(1) with the name of the new rowData variable. Default in "Precursor.Id".
fcols	character() with the rowData variables names that need to be paste0()ed together to create the new name variable. Default is c("Modified.Sequence", "Precursor.Charge"). Note that these must be present in *all* assays.
i	The assays of object whose rowData need to be updated. By default, all assays are considered.

Value

An updated QFeatures instance.

Author(s)

Laurent Gatto

Examples

```
## Let use PSM assay of feat3, that don't have any precursor identifiers
data(feat4)
feat4
rowDataNames(feat4)

## Create precursor identifiers by concatenating the charge and the
```

```
## sequencing
feat4 <- createPrecursorId(feat4,
                           name = "Precursor.Id",
                           fcols = c("charge", "Sequence"))
rowDataNames(feat4)
rowData(feat4[[1]])[, c("Sequence", "charge", "Precursor.Id")]

## As can be seen below, some precursors are duplicated, which will be
## problematic when joining the assays. Should we join `1SYGFNAAR` in the
## second assay with the first or the second `1SYGFNAAR` in the first assay?
rowData(feat4[[1]])[, "Precursor.Id", drop = FALSE]
rowData(feat4[[2]])[, "Precursor.Id", drop = FALSE]

## Here, one can either aggregate PSMs into PSMs with unique identifers (see
## ?aggregateFeatures) or remove duplicated entries.
nrows(feat4) ## before filtering
feat4 <- filterFeatures(feat4, ~ !isDuplicated(Precursor.Id))
nrows(feat4) ## after filtering

## The assays can now be joined, using the newly created identifier rather
## than the (default) rownames.
feat4 <- joinAssays(feat4, i = 1:2,
                    name = "Precursors",
                    fcol = "Precursor.Id")
feat4
```

`display` *Interactive MultiAssayExperiment Explorer*

Description

A shiny app to browser and explore the assays in an `MultiAssayExperiment` object. Each assay can be selected from the dropdown meny in the side panel, and the quantitative data and row metadata are displayed in the respective *Assay* and *Row data* tabs. The *Heatmap* tab displays a heatmap of the assay. The selection of rows in the *Row data* table is used to subset the features displayed in the *Assay* table and the heatmap to those currectly selected. See QFeatures for an example.

Usage

```
display(object, n = 100, ...)
```

Arguments

`object`	An instance inheriting from `MultiAssayExperiment`.
`n`	A `numeric(1)` indicating the maximum number of features (rows) to consider before disabling row clustering and displaying feature names for speed purposes. Default is 100.
`...`	Additional parameters (other than `Rowv` and `labRow`, which are set internally based on the value of `n`) passed to heatmap.

Value

Used for its side effect.

Author(s)

Laurent Gatto

Examples

```
## Not run:
data(feat2)
display(feat2)

## End(Not run)
```

`feat1` *Feature example data*

Description

`feat1` is a small test `QFeatures` object for testing and demonstration. `feat2` is used to demonstrate assay joins. `ft_na` is a tiny test set that contains missing values used to demonstrate and test the impact of missing values on data processing. `se_na2` is an `SummarizedExperiment` with missing values of mixed origin.

Usage

```
feat1
```

Format

An object of class `QFeatures` of length 1.

`feat3` *Example* `QFeatures` *object after processing*

Description

`feat3` is a small `QFeatures` object that contains 7 assays: `psms1`, `psms2`, `psmsall`, `peptides`, `proteins`, `normpeptides`, `normproteins`. The dataset contains example data that could be obtained after running a simple processing pipeline. You can use it to get your hands on manipulating `AssayLinks` since all 3 general cases are present:

- One parent to one child `AssayLink`: the relationship can either be one row to one row (e.g. "peptides" to "normpeptides") or multiple rows to one row (e.g. "peptides" to "proteins").

- One parent to multiple children `AssayLink`: for instance "peptides" to "normpeptides" and "proteins".
- Multiple parents to one child `AssayLink`: links the rows between multiple assays to a single assays where some rows in different parent assays may point to the same row in the child assay. E.g. "psms1" and "psms2" to "psmsall"

Usage

```
feat3
```

Format

An object of class `QFeatures` of length 7.

Source

`feat3` was built from `feat1`. The source code is available in `inst/scripts/test_data.R`

See Also

See `?feat1` for other example/test data sets.

Examples

```
data("feat3")
plot(feat3)
```

`feat4` *Example* `QFeatures`

Description

`feat3` is a small `QFeatures` object that contains 2 PSM-level assays used to illustrate to creation of unique precursor identifiers and merging, as shown in `createPrecursorId()`.

Usage

```
feat4
```

Format

An object of class `QFeatures` of length 2.

Source

`feat4` was built from `feat3`. The source code is available in `inst/scripts/make-feat4.R`

See Also

See ?feat1 for other example/test data sets.

Examples

```
data("feat4")
feat4
```

---

hlpsms *hyperLOPIT PSM-level expression data*

Description

A data.frame with PSM-level quantitation data by Christoforou *et al.* (2016). This is the first replicate of a spatial proteomics dataset from a hyperLOPIT experimental design on Mouse E14TG2a embryonic stem cells. Normalised intensities for proteins for TMT 10-plex labelled fractions are available for 3 replicates acquired in MS3 mode using an Orbitrap Fusion mass-spectrometer.

The variable names are

- X126, X127C, X127N, X128C, X128N, X129C, X129N, X130C, X130N and X131: the 10 TMT tags used to quantify the peptides along the density gradient.
- Sequence: the peptide sequence.
- ProteinDescriptions: the description of the protein this peptide was associated to.
- NbProteins: the number of proteins in the protein group.
- ProteinGroupAccessions: the main protein accession number in the protein group.
- Modifications: post-translational modifications identified in the peptide.
- qValue: the PSM identification q-value.
- PEP: the PSM posterior error probability.
- IonScore: the Mascot ion identification score.
- NbMissedCleavages: the number of missed cleavages in the peptide.
- IsolationInterference: the calculated precursor ion isolation interference.
- IonInjectTimems: the ions injection time in milli-seconds.
- Intensity: the precursor ion intensity.
- Charge: the peptide charge.
- mzDa: the peptide mass to charge ratio, in Daltons.
- MHDa: the peptide mass, in Daltons.
- DeltaMassPPM: the difference in measure and calculated mass, in parts per millions.
- RTmin: the peptide retention time, in minutes.
- markers: localisation for well known sub-cellular markers. QFeatures of unknown location are encode as "unknown".

For further details, install the pRolocdata package and see ?hyperLOPIT2015.

Usage

```
hlpsms
```

Format

An object of class `data.frame` with 3010 rows and 28 columns.

Source

The `pRolocdata` package: http://bioconductor.org/packages/pRolocdata/

References

A draft map of the mouse pluripotent stem cell spatial proteome Christoforou A, Mulvey CM, Breckels LM, Geladaki A, Hurrell T, Hayward PC, Naake T, Gatto L, Viner R, Martinez Arias A, Lilley KS. Nat Commun. 2016 Jan 12;7:8992. doi: 10.1038/ncomms9992. PubMed PMID: 26754106; PubMed Central PMCID: PMC4729960.

See Also

See QFeatures to import this data using the `readQFeatures()` function.

`impute` *Quantitative proteomics data imputation*

Description

The `impute` method performs data imputation on `QFeatures` and `SummarizedExperiment` instance using a variety of methods.

Users should proceed with care when imputing data and take precautions to assure that the imputation produce valid results, in particular with naive imputations such as replacing missing values with 0.

See `MsCoreUtils::impute_matrix()` for details on the different imputation methods available and strategies.

Usage

```
impute

## S4 method for signature 'SummarizedExperiment'
impute(object, method, ...)

## S4 method for signature 'QFeatures'
impute(object, method, ..., i, name = "imputedAssay")
```

Arguments

object	A SummarizedExperiment or QFeatures object with missing values to be imputed.
method	character(1) defining the imputation method. See imputeMethods() for available ones. See MsCoreUtils::impute_matrix() for details.
...	Additional parameters passed to the inner imputation function. See MsCoreUtils::impute_matrix() for details.
i	A logical(1) or a character(1) that defines which element of the QFeatures instance to impute. It cannot be missing and must be of length one.
name	A character(1) naming the new assay name. Default is imputedAssay.

Format

An object of class standardGeneric of length 1.

Examples

```
MsCoreUtils::imputeMethods()

data(se_na2)
## table of missing values along the rows (proteins)
table(rowData(se_na2)$nNA)
## table of missing values along the columns (samples)
colData(se_na2)$nNA

## non-random missing values
notna <- which(!rowData(se_na2)$randna)
length(notna)
notna

impute(se_na2, method = "min")

if (require("imputeLCMD")) {
  impute(se_na2, method = "QRILC")
  impute(se_na2, method = "MinDet")
}

if (require("norm"))
  impute(se_na2, method = "MLE")

impute(se_na2, method = "mixed",
       randna = rowData(se_na2)$randna,
       mar = "knn", mnar = "QRILC")

## neighbour averaging
x <- se_na2[1:4, 1:6]
assay(x)[1, 1] <- NA ## min value
assay(x)[2, 3] <- NA ## average
assay(x)[3, 1:2] <- NA ## min value and average
## 4th row: no imputation
```

```
assay(x)

assay(impute(x, "nbavg"))
```

`joinAssays` *Join assays in a QFeatures object*

Description

This function applies a full-join type of operation on 2 or more assays in a `QFeatures` instance.

Usage

```
joinAssays(x, i, name = "joinedAssay", fcol = NULL)
```

Arguments

`x`	An instance of class QFeatures.
`i`	The indices or names of al least two assays to be joined.
`name`	A `character(1)` naming the new assay. Default is `joinedAssay`. Note that the function will fail if there's already an assay with `name`.
`fcol`	Default is `NULL`, to use assay rownames when joining. Alternatively, `fcol` can be a `character(1)` defining a rowData variable, present in all assays, that will be used to join assays. See `createPrecursorId()` for an example.

Details

The rows to be joined are chosen based on the rownames of the respective assays. It is the user's responsability to make sure these are meaningful, such as for example refering to unique precursors, peptide sequences or proteins.

The join operation acts along the rows and expects the samples (columns) of the assays to be disjoint, i.e. the assays mustn't share any samples. Rows that aren't present in an assay are set to `NA` when merged.

The `rowData` slots are also joined. However, only columns that are shared and that have the same values for matching columns/rows are retained. For example of a feature variable `A` in sample `S1` contains value `a1` and variable `A` in sample `S2` in a different assay contains `a2`, then the feature variable `A` is dropped in the merged assay.

The joined assay is linked to its parent assays through an `AssayLink` object. The link between the child assay and the parent assays is based on the assay row names, just like the procedure for joining the parent assays.

Value

A `QFeatures` object with an additional assay.

Author(s)

Laurent Gatto

Examples

```
## ------------------------------------------------
## An example QFeatures with 3 assays to be joined
## ------------------------------------------------
data(feat2)
feat2

feat2 <- joinAssays(feat2, 1:3)

## Individual assays to be joined, each with 4 samples and a
## variable number of rows.
assay(feat2[[1]])
assay(feat2[[2]])
assay(feat2[[3]])

## The joined assay contains 14 rows (corresponding to the union
## of those in the initial assays) and 12 samples
assay(feat2[["joinedAssay"]])

## The individual rowData to be joined.
rowData(feat2[[1]])
rowData(feat2[[2]])
rowData(feat2[[3]])

## Only the 'Prot' variable is retained because it is shared among
## all assays and the values and coherent across samples (the
## value of 'Prot' for row 'j' is always 'Pj'). The variable 'y' is
## missing in 'assay1' and while variable 'x' is present is all
## assays, the values for the shared rows are different.
rowData(feat2[["joinedAssay"]])
```

`longForm,QFeatures-method`

Reshape into a long data format

Description

The `longForm()` method transform a QFeatures or SummarizedExperiment::SummarizedExperiment instance into a long *tidy* S4Vectors::DataFrame that contains the assay data, where each quantitative value is reported on a separate line. `colData` and `rowData` varibales can also be added. This function is an extension of the `longForm()` method in the MultiAssayExperiment::MultiAssayExperiment.

Note that the previous `longFormat` implementation is not defunct.

Usage

```
## S4 method for signature 'QFeatures'
longForm(object, colvars = NULL, rowvars = NULL, i = 1L)

## S4 method for signature 'SummarizedExperiment'
longForm(object, colvars = NULL, rowvars = NULL, i = seq_along(assays(object)))
```

Arguments

object	An instance of class QFeatures or SummarizedExperiment::SummarizedExperiment.
colvars	A character() that selects column(s) in the colData.
rowvars	A character() with the names of the rowData variables (columns) to retain in any assay.
i	When object is an instance of class QFeatures, a numeric(1) indicating what assay within each SummarizedExperiment object to return. Default is 1L. If object is a SummarizedExperiment, a numeric() indicating what assays to pull and convert. Default is to use all assays.

Value

A DataFrame instance.

Examples

```
data(feat2)

longForm(feat2)

## add a colData variable and use it in longFrom
colData(feat2)$colvar <- paste0("Var", 1:12)
colData(feat2)
longForm(feat2, colvars = "colvar")

## use a rowData variable in longFrom
rowDataNames(feat2)
longForm(feat2, rowvar = "Prot")

## use both col/rowData
longForm(feat2, colvar = "colvar", rowvar = "Prot")

## also works on a single SE
se <- getWithColData(feat2, 1)
longForm(se)
longForm(se, colvar = "colvar")
longForm(se, rowvar = "Prot")
longForm(se, colvar = "colvar", rowvar = "Prot")
```

missing-data *Managing missing data*

Description

This manual page describes the handling of missing values in QFeatures objects. In the following functions, if `object` is of class `QFeatures`, an optional assay index or name `i` can be specified to define the assay (by name of index) on which to operate.

The following functions are currently available:

- `zeroIsNA(object, i)` replaces all 0 in `object` by `NA`. This is often necessary when third-party software assume that features that weren't quantified should be assigned an intensity of 0.
- `infIsNA(object, i)` replaces all infinite values in `object` by `NA`. This is necessary when third-party software divide expression data by zero values, for instance during custom normalization.
- `nNA(object, i)` returns a list of missing value summaries. The first element `nNA` gives a `DataFrame` with the number and the proportion of missing values for the whole assay; the second element `nNArows` provides a `DataFrame` with the number and the proportion of missing values for the features (rows) of the assay(s); the third element `nNAcols` provides the number and the proportions of missing values in each sample of the assay(s). When `object` has class `QFeatures` and additional column with the assays is provided in each element's `DataFrame`.
- `filterNA(object, pNA, i)` removes features (rows) that contain a proportion of more missing values of `pNA` or higher.

See the *Processing* vignette for examples.

Usage

```
## S4 method for signature 'SummarizedExperiment,missing'
zeroIsNA(object, i)

## S4 method for signature 'QFeatures,integer'
zeroIsNA(object, i)

## S4 method for signature 'QFeatures,numeric'
zeroIsNA(object, i)

## S4 method for signature 'QFeatures,character'
zeroIsNA(object, i)

## S4 method for signature 'SummarizedExperiment,missing'
infIsNA(object, i)

## S4 method for signature 'QFeatures,integer'
infIsNA(object, i)
```

```
## S4 method for signature 'QFeatures,numeric'
infIsNA(object, i)

## S4 method for signature 'QFeatures,character'
infIsNA(object, i)

## S4 method for signature 'SummarizedExperiment,missing'
nNA(object, i)

## S4 method for signature 'QFeatures,integer'
nNA(object, i)

## S4 method for signature 'QFeatures,numeric'
nNA(object, i)

## S4 method for signature 'QFeatures,character'
nNA(object, i)

## S4 method for signature 'SummarizedExperiment'
filterNA(object, pNA = 0)

## S4 method for signature 'QFeatures'
filterNA(object, pNA = 0, i)
```

Arguments

object	An object of class QFeatures or SummarizedExperiment.
i	One or more indices or names of the assay(s) to be processed.
pNA	numeric(1) providing the maximum proportion of missing values per feature (row) that is acceptable. Feature with higher proportions are removed. If 0 (default), features that contain any number of NA values are dropped.

Value

An instance of the same class as object.

See Also

The impute() for QFeautres instances.

Examples

```
data(ft_na)

## Summary if missing values
nNA(ft_na, 1)

## Remove rows with missing values
```

```
assay(filterNA(ft_na, i = 1))

## Replace NAs by zero and back
ft_na <- impute(ft_na, i = 1, method = "zero")
assay(ft_na)
ft_na <- zeroIsNA(ft_na, 1)
assay(ft_na)
```

QFeatures *Quantitative MS QFeatures*

Description

Conceptually, a QFeatures object holds a set of *assays*, each composed of a matrix (or array) containing quantitative data and row annotations (meta-data). The number and the names of the columns (samples) must always be the same across the assays, but the number and the names of the rows (features) can vary. The assays are typically defined as SummarizedExperiment objects. In addition, a QFeatures object also uses a single DataFrame to annotate the samples (columns) represented in all the matrices.

The QFeatures class extends the MultiAssayExperiment::MultiAssayExperiment and inherits all the functionality of the MultiAssayExperiment::MultiAssayExperiment class.

A typical use case for such QFeatures object is to represent quantitative proteomics (or metabolomics) data, where different assays represent quantitation data at the PSM (the main assay), peptide and protein level, and where peptide values are computed from the PSM data, and the protein-level data is calculated based on the peptide-level values. The largest assay (the one with the highest number of features, PSMs in the example above) is considered the main assay.

The recommended way to create QFeatures objects is the use the readQFeatures() function, that creates an instance from tabular data. The QFeatures constructor can be used to create objects from their bare parts. It is the user's responsability to make sure that these match the class validity requirements.

Usage

```
QFeatures(..., assayLinks = NULL)

## S4 method for signature 'QFeatures'
show(object)

## S3 method for class 'QFeatures'
plot(x, interactive = FALSE, ...)

## S4 method for signature 'QFeatures,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'QFeatures,character,ANY,ANY'
x[i, j, k, ..., drop = TRUE]
```

```
## S4 method for signature 'QFeatures'
c(x, ...)

## S4 method for signature 'QFeatures'
dims(x, use.names = TRUE)

## S4 method for signature 'QFeatures'
nrows(x, use.names = TRUE)

## S4 method for signature 'QFeatures'
ncols(x, use.names = TRUE)

replaceColnames(object, scol)

## S4 method for signature 'QFeatures'
rowData(x, use.names = TRUE, ...)

## S4 replacement method for signature 'QFeatures,DataFrameList'
rowData(x) <- value

## S4 replacement method for signature 'QFeatures,ANY'
rowData(x) <- value

rbindRowData(object, i)

selectRowData(x, rowvars)

rowDataNames(x)

## S4 replacement method for signature 'QFeatures,character'
names(x) <- value

addAssay(x, y, name, assayLinks)

removeAssay(x, i)

replaceAssay(x, y, i)

## S4 replacement method for signature 'QFeatures,ANY,ANY'
x[[i, j, ...]] <- value

## S4 method for signature 'QFeatures'
updateObject(object, ..., verbose = FALSE)

dropEmptyAssays(object, dims = 1:2)
```

Arguments

...	See MultiAssayExperiment for details. For plot, further arguments passed to igraph::plot.igraph.
assayLinks	An optional AssayLinks.
object	An instance of class QFeatures.
x	An instance of class QFeatures.
interactive	A logical(1). If TRUE, an interactive graph is generated using plotly. Else, a static plot using igraph is generated. We recommend interactive exploration when the QFeatures object contains more than 50 assays.
i	An indexing vector. See the corresponding section in the documentation for more details.
j	character(), logical(), or numeric() vector for subsetting by colData rows.
drop	logical (default TRUE) whether to drop empty assay elements in the ExperimentList.
k	character(), logical(), or numeric() vector for subsetting by assays
use.names	A logical(1) indicating whether the rownames of each assay should be propagated to the corresponding rowData.
scol	character(1) naming the column in colData(object) to use as replacement sample names across all assays. Values in that column must be unique.
value	The values to use as a replacement. See the corresponding section in the documentation for more details.
rowvars	A character() with the names of the rowData variables (columns) to retain in any assay.
y	An object that inherits from SummarizedExperiment or a *named* list of assays. When y is a list, each element must inherit from a SummarizedExperiment and the names of the list are used as the names of the assays to add. Hence, the list names must be unique and cannot overlap with the names of the assays already present in x.
name	A character(1) naming the single assay. Ignored if y is a list of assays.
verbose	logical (default FALSE) whether to print extra messages
dims	numeric() that defines the dimensions to consider to drop empty assays. 1 for rows (i.e. assays without any features) and 2 for columns (i.e. assays without any samples). Default is 1:2. Any value other that 1 and/or 2 will trigger an error.

Constructors

- QFeatures(..., assayLinks) allows the manual construction of objects. It is the user's responsability to make sure these comply. The arguments in ... are those documented in MultiAssayExperiment::MultiAssayExperiment(). For details about assayLinks, see AssayLinks. An example is shown below.
- The readQFeatures() function constructs a QFeatures object from text-based spreadsheet or a data.frame used to generate an assay. See the function manual page for details and an example.

Accessors

- The QFeatures class extends the MultiAssayExperiment::MultiAssayExperiment class and inherits all its accessors and replacement methods.
- The rowData method returns a DataFrameList containing the rowData for each assay of the QFeatures object. On the other hand, rowData can be modified using rowData(x) <- value, where value is a list of tables that can be coerced to DFrame tables. The names of value point to the assays for which the rowData must be replaced. The column names of each table are used to replace the data in the existing rowData. If the column name does not exist, a new column is added to the rowData.
- The rbindRowData functions returns a DFrame table that contains the row binded rowData tables from the selected assays. In this context, i is a character(), integer() or logical() object for subsetting assays. Only rowData variables that are common to all assays are kept.
- The rowDataNames accessor returns a list with the rowData variable names.
- The longForm() accessor takes a QFeatures instance and returns it in a long *tidy* DataFrame, where each quantitative value is reported on a separate line.
- The replaceColnames function replaces assay sample names (column names) across all assays using values from a colData column.

Adding, removing and replacing assays

- The aggregateFeatures() function creates a new assay by aggregating features of an existing assay.
- addAssay(x, y, name, assayLinks): Adds one or more new assay(s) y to the QFeatures instance x. name is a character(1) naming the assay if only one assay is provided, and is ignored if y is a list of assays. assayLinks is an optional AssayLinks. The colData(y) is automatically added to colData(x) by matching sample names, that is colnames(y). If the samples are not present in x, the rows of colData(x) are extended to account for the new samples. Be aware that conflicting information between the colData(y) and the colData(x) will result in an error.
- removeAssay(x, i): Removes one or more assay(s) from the QFeatures instance x. In this context, i is a character(), integer() or logical() that indicates which assay(s) to remove.
- replaceAssay(x, y, i): Replaces one or more assay(s) from the QFeatures instance x. In this context, i is a character(), integer() or logical() that indicates which assay(s) to replace. The AssayLinks from or to any replaced assays are automatically removed, unless the replacement has the same dimension names (columns and row, order agnostic). Be aware that conflicting information between colData(y) and colData(x) will result in an error.
- x[[i]] <- value: a generic method for adding (when i is not in names(x)), removing (when value is null) or replacing (when i is in names(x)). Note that the arguments j and ... from the S4 replacement method signature are not allowed.

Subsetting

- QFeatures object can be subset using the x[i, j, k, drop = TRUE] paradigm. In this context, i is a character(), integer(), logical() or GRanges() object for subsetting by rows. See the argument descriptions for details on the remaining arguments.

- The subsetByFeature() function can be used to subset a QFeatures object using one or multiple feature names that will be matched across different assays, taking the aggregation relation between assays.
- The selectRowData(x, rowvars) function can be used to select a limited number of rowData columns of interest named in rowvars in the x instance of class QFeatures. All other variables than rowvars will be dropped. In case an element in rowvars isn't found in any rowData variable, a message is printed.
- The dropEmptyAssays(object, dims) function removes empty assays from a QFeatures. Empty assays are defined as having 0 rows and/or 0 columns, as defined by the dims argument.

Author(s)

Laurent Gatto

See Also

- The readQFeatures() constructor and the aggregateFeatures() function. The *QFeatures* vignette provides an extended example.
- The QFeatures-filtering manual page demonstrates how to filter features based on their rowData.
- The missing-data manual page to manage missing values in QFeatures objects.
- The QFeatures-processing and aggregateFeatures() manual pages and *Processing* vignette describe common quantitative data processing methods using in quantitative proteomics.

Examples

```
## ------------------------
## An empty QFeatures object
## ------------------------

QFeatures()

## -----------------------------------
## Creating a QFeatures object manually
## -----------------------------------

## two assays (matrices) with matching column names
m1 <- matrix(1:40, ncol = 4)
m2 <- matrix(1:16, ncol = 4)
sample_names <- paste0("S", 1:4)
colnames(m1) <- colnames(m2) <- sample_names
rownames(m1) <- letters[1:10]
rownames(m2) <- letters[1:4]

## two corresponding feature metadata with appropriate row names
df1 <- DataFrame(Fa = 1:10, Fb = letters[1:10],
                 row.names = rownames(m1))
df2 <- DataFrame(row.names = rownames(m2))

(se1 <- SummarizedExperiment(m1, df1))
```

```
(se2 <- SummarizedExperiment(m2, df2))

## Sample annotation (colData)
cd <- DataFrame(Var1 = rnorm(4),
                Var2 = LETTERS[1:4],
                row.names = sample_names)

el <- list(assay1 = se1, assay2 = se2)
fts1 <- QFeatures(el, colData = cd)
fts1
fts1[[1]]
fts1[["assay1"]]

## Rename assay
names(fts1) <- c("se1", "se2")

## Add an assay
fts1 <- addAssay(fts1, se1[1:2, ], name = "se3")

## Get the assays feature metadata
rowData(fts1)

## Rename samples using colData column
replaceColnames(fts1, "Var2")

## Keep only the Fa variable
selectRowData(fts1, rowvars = "Fa")

## ------------------------------------
## See ?readQFeatures to create a
## QFeatures object from a data.frame
## or spreadsheet.
## ------------------------------------
```

QFeatures-filtering *Filter features based on their rowData*

Description

The `filterFeatures` methods enables users to filter features based on a variable in their `rowData`. The features matching the filter will be returned as a new object of class `QFeatures`. The filters can be provided as instances of class `AnnotationFilter` (see below) or as formulas.

Usage

```
VariableFilter(field, value, condition = "==", not = FALSE)

## S4 method for signature 'QFeatures,AnnotationFilter'
filterFeatures(object, filter, i, na.rm = FALSE, keep = FALSE, ...)
```

```
## S4 method for signature 'QFeatures,formula'
filterFeatures(object, filter, i, na.rm = FALSE, keep = FALSE, ...)

isDuplicated(x)
```

Arguments

field	character(1) refering to the name of the variable to apply the filter on.
value	character() or integer() value for the CharacterVariableFilter and NumericVariableFilter filters respectively.
condition	character(1) defining the condition to be used in the filter. For NumericVariableFilter, one of "==", "!=", ">", "<", ">=" or "<=". For CharacterVariableFilter, one of "==", "!=", "startsWith", "endsWith" or "contains". Default condition is "==".
not	logical(1) indicating whether the filtering should be negated or not. TRUE indicates is negated (!). FALSE indicates not negated. Default not is FALSE, so no negation.
object	An instance of class QFeatures.
filter	Either an instance of class AnnotationFilter::AnnotationFilter or a formula.
i	A numeric, logical or character vector pointing to the assay(s) to be filtered.
na.rm	logical(1) indicating whether missing values should be removed. Default is FALSE.
keep	logical(1) indicating whether to keep the features of assays for which at least one of the filtering variables are missing in the rowData. When FALSE (default), all such assay will contain 0 features; when TRUE, the assays are untouched.
...	Additional parameters. Currently ignored.
x	A vector() that will be checked for duplications.

Value

An filtered QFeature object.

The filtering procedure

filterFeatures() will go through each assay of the QFeatures object and apply the filtering on the corresponding rowData. Features that do not pass the filter condition are removed from the assay. In some cases, one may want to filter for a variable present in some assay, but not in other. There are two options: either provide keep = FALSE to remove all features for those assays (and thus leaving an empty assay), or provide keep = TRUE to ignore filtering for those assays.

Because features in a QFeatures object are linked between different assays with AssayLinks, the links are automatically updated. However, note that the function doesn't propagate the filter to parent assays. For example, suppose a peptide assay with 4 peptides is linked to a protein assay with 2 proteins (2 peptides mapped per protein) and you apply filterFeatures(). All features pass the filter except for one protein. The peptides mapped to that protein will remain in the QFeatures object. If propagation of the filtering rules to parent assay is desired, you may want to use x[i, ,] instead (see the *Subsetting* section in ?QFeature).

Variable filters

The variable filters are filters as defined in the AnnotationFilter::AnnotationFilter package. In addition to the pre-defined filter, users can arbitrarily set a field on which to operate. These arbitrary filters operate either on a character variables (as `CharacterVariableFilter` objects) or numerics (as `NumericVariableFilters` objects), which can be created with the `VariableFilter` constructor.

Helper functions

- The `isDuplicated()` function takes a vector (or rowData variable when used to filter features) as input, and return a logical of the same length, with elements set to `TRUE` for unique occurence, and `FALSE` otherwise. This function is different from `BiocGenerics::duplicated()`, as here even the first occurence is set to `FALSE`. See `createPrecursorId()` for an application.

Author(s)

Laurent Gatto

See Also

The QFeatures man page for subsetting and the `QFeatures` vignette provides an extended example.

Examples

```
## ----------------------------------------
## Creating character and numberic
## variable filters
## ----------------------------------------

VariableFilter(field = "my_var",
               value = "value_to_keep",
               condition = "==")

VariableFilter(field = "my_num_var",
               value = 0.05,
               condition = "<=")

example(aggregateFeatures)

## ------------------------------------------------------------------
## Filter all features that are associated to the Mitochondrion in
## the location feature variable. This variable is present in all
## assays.
## ------------------------------------------------------------------

## using the forumla interface, exact mathc
filterFeatures(feat1, ~  location == "Mitochondrion")

## using the forumula intefrace, martial match
filterFeatures(feat1, ~startsWith(location, "Mito"))
```

```
## using a user-defined character filter
filterFeatures(feat1, VariableFilter("location", "Mitochondrion"))

## using a user-defined character filter with partial match
filterFeatures(feat1, VariableFilter("location", "Mito", "startsWith"))
filterFeatures(feat1, VariableFilter("location", "itochon", "contains"))

## ------------------------------------------------------------------
## Filter all features that aren't marked as unknown (sub-cellular
## location) in the feature variable
## ------------------------------------------------------------------

## using a user-defined character filter
filterFeatures(feat1, VariableFilter("location", "unknown", condition = "!="))

## using the forumula interface
filterFeatures(feat1, ~ location != "unknown")

## ------------------------------------------------------------------
## Filter features that have a p-values lower or equal to 0.03
## ------------------------------------------------------------------

## using a user-defined numeric filter
filterFeatures(feat1, VariableFilter("pval", 0.03, "<="))

## using the formula interface
filterFeatures(feat1, ~ pval <= 0.03)

## you can also remove all p-values that are NA (if any)
filterFeatures(feat1, ~ !is.na(pval))

## ------------------------------------------------------------------
## Negative control - filtering for an non-existing markers value,
## returning empty results.
## ------------------------------------------------------------------

filterFeatures(feat1, VariableFilter("location", "not"))

filterFeatures(feat1, ~ location == "not")

## ------------------------------------------------------------------
## Filtering for a  missing feature variable. The outcome is controled
## by keep
## ------------------------------------------------------------------
data(feat2)

filterFeatures(feat2, ~ y < 0)

filterFeatures(feat2, ~ y < 0, keep = TRUE)

## ------------------------------------------------------------------
## Example with missing values
## ------------------------------------------------------------------
```

```
data(feat1)
rowData(feat1[[1]])[1, "location"] <- NA
rowData(feat1[[1]])

## The row with the NA is not removed
rowData(filterFeatures(feat1, ~ location == "Mitochondrion")[[1]])
rowData(filterFeatures(feat1, ~ location == "Mitochondrion", na.rm = FALSE)[[1]])

## The row with the NA is removed
rowData(filterFeatures(feat1, ~ location == "Mitochondrion", na.rm = TRUE)[[1]])

## Note that in situations with missing values, it is possible to
## use the `%in%` operator or filter missing values out
## explicitly.

rowData(filterFeatures(feat1, ~ location %in% "Mitochondrion")[[1]])
rowData(filterFeatures(feat1, ~ location %in% c(NA, "Mitochondrion"))[[1]])

## Explicit handling
filterFeatures(feat1, ~ !is.na(location) & location == "Mitochondrion")

## Using the pipe operator
feat1 |>
   filterFeatures( ~ !is.na(location)) |>
   filterFeatures( ~ location == "Mitochondrion")
```

`QFeatures-processing` *QFeatures processing*

Description

This manual page describes common quantitative proteomics data processing methods using QFeatures objects. In the following functions, if `object` is of class `QFeatures`, and optional assay index or name `i` can be specified to define the assay (by name of index) on which to operate.

The following functions are currently available:

- `logTransform(object, base = 2, i, pc = 0)` log-transforms (with an optional pseudocount offset) the assay(s).
- `normalize(object, method, i)` normalises the assay(s) according to `method` (see Details).
- `scaleTransform(object, center = TRUE, scale = TRUE, i)` applies `base::scale()` to `SummarizedExperiment` and `QFeatures` objects.
- `sweep(x, MARGIN, STATS, FUN = "-", check.margin = TRUE, ...)` sweeps out array summaries from `SummarizedExperiment` and `QFeatures` objects. See `base::sweep()` for details.

See the *Processing* vignette for examples.

Usage

```
## S4 method for signature 'SummarizedExperiment'
logTransform(object, base = 2, pc = 0)

## S4 method for signature 'QFeatures'
logTransform(object, i, name = "logAssay", base = 2, pc = 0)

## S4 method for signature 'SummarizedExperiment'
scaleTransform(object, center = TRUE, scale = TRUE)

## S4 method for signature 'QFeatures'
scaleTransform(object, i, name = "scaledAssay", center = TRUE, scale = TRUE)

## S4 method for signature 'SummarizedExperiment'
normalize(object, method, ...)

## S4 method for signature 'QFeatures'
normalize(object, i, name = "normAssay", method, ...)

## S4 method for signature 'SummarizedExperiment'
sweep(x, MARGIN, STATS, FUN = "-", check.margin = TRUE, ...)

## S4 method for signature 'QFeatures'
sweep(
  x,
  MARGIN,
  STATS,
  FUN = "-",
  check.margin = TRUE,
  ...,
  i,
  name = "sweptAssay"
)
```

Arguments

object	An object of class QFeatures or SummarizedExperiment.
base	numeric(1) providing the base with respect to which logarithms are computed. Defaults is 2.
pc	numeric(1) with a pseudocount to add to the quantitative data. Useful when (true) 0 are present in the data. Default is 0 (no effect).
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 are logAssay for logTransform, scaledAssay for scaleTranform and normAssay for normalize.
center	logical(1) (default is TRUE) value or numeric-alike vector of length equal to the number of columns of object. See base::scale() for details.

scale	logical(1) (default is TRUE) or a numeric-alike vector of length equal to the number of columns of object. See base::scale() for details.
method	character(1) defining the normalisation method to apply. See Details.
...	Additional parameters passed to inner functions.
x	An object of class QFeatures or SummarizedExperiment in sweep.
MARGIN	As in base::sweep(), a vector of indices giving the extent(s) of x which correspond to STATS.
STATS	As in base::sweep(), the summary statistic which is to be swept out.
FUN	As in base::sweep(), the function to be used to carry out the sweep.
check.margin	As in base::sweep(), a logical. If TRUE (the default), warn if the length or dimensions of STATS do not match the specified dimensions of x. Set to FALSE for a small speed gain when you know that dimensions match.

Details

The method parameter in normalize can be one of "sum", "max", "center.mean", "center.median", "div.mean", "div.median", "diff.median", "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

An processed object of the same class as x or object.

Examples

```
MsCoreUtils::normalizeMethods()
```

`QFeatures-type` *Set and Get QFeatures Type*

Description

Developer-level functions to set and retrieve the type of a `QFeatures` object. This type can help internal methods adapt their behaviour to the structure of the data.

Usage

```
setQFeaturesType(object, type)

getQFeaturesType(object)

validQFeaturesTypes()
```

Arguments

`object`	An instance of class QFeatures.
`type`	`character(1)` defining the type of the QFeatures. Must be one of the values returned by `validQFeaturesTypes()`.

Details

These functions control an internal metadata slot (`._type`) used to distinguish between different structural uses of `QFeatures` objects. This slot is directly accessible with `metadata(object)[["._type"]]`.

Value

- `setQFeaturesType()`: returns the updated `QFeatures` object with the type stored in its metadata.
- `getQFeaturesType()`: returns a character string indicating the type of the `QFeatures` object. If no type is explicitly set, it is inferred from the class of the experiments. If the QFeatures contains any `SingleCellExperiment` objects, the type is set to "scp". Otherwise, it is set to "bulk".
- `validQFeaturesTypes()`: character vector of valid QFeatures types.

Warning

These functions are intended for package developers and internal use. End users should typically not call them directly.

Note

The QFeatures type slot was introduced because, in the context of the scp package, we found that SingleCellExperiment objects were slower than SummarizedExperiment objects (GH issue: scp#83). As a result, we started using SummarizedExperiment objects within scp. However, to retain information about the type of data being handled, we introduced the QFeatures type slot. This slot is, for example, used in the show method of QFeatures.

---

readQFeatures *QFeatures from tabular data*

Description

These functions convert tabular data into dedicated data objets. The readSummarizedExperiment() function takes a file name or data.frame and converts it into a SummarizedExperiment::SummarizedExperiment() object. The readQFeatures() function takes a data.frame and converts it into a QFeatures object (see QFeatures() for details). For the latter, two use-cases exist:

- The single-set case will generate a QFeatures object with a single SummarizedExperiment containing all features of the input table.
- The multi-set case will generate a QFeatures object containing multiple SummarizedExperiments, resulting from splitting the input table. This multi-set case is generally used when the input table contains data from multiple runs/batches.

Usage

```
readSummarizedExperiment(
  assayData,
  quantCols = NULL,
  fnames = NULL,
  ecol = NULL,
  ...
)

readQFeatures(
  assayData,
  colData = NULL,
  quantCols = NULL,
  runCol = NULL,
  name = "quants",
  removeEmptyCols = FALSE,
  verbose = TRUE,
  ecol = NULL,
  fnames = NULL,
  ...
)
```

Arguments

assayData	A data.frame, or any object that can be coerced into a data.frame, holding the quantitative assay. For readSummarizedExperiment(), this can also be a character(1) pointing to a filename. This data.frame is typically generated by an identification and quantification software, such as Sage, Proteome Discoverer, MaxQuant, ...
quantCols	A numeric(), logical() or character() defining the columns of the assayData that contain the quantitative data. This information can also be defined in colData (see details).
fnames	For the single- and multi-set cases, an optional character(1) or numeric(1) indicating the column to be used as feature names. Note that rownames must be unique within QFeatures sets. Default is NULL. See also section 'Feature names'.
ecol	Same as quantCols. Available for backwards compatibility. Default is NULL. If both ecol and colData are set, an error is thrown.
...	Further arguments that can be passed on to read.csv() except stringsAsFactors, which is always FALSE. Only applicable to readSummarizedExperiment().
colData	A data.frame (or any object that can be coerced to a data.frame) containing sample/column annotations, including quantCols and runCol (see details).
runCol	For the multi-set case, a numeric(1) or character(1) pointing to the column of assayData (and colData, is set) that contains the runs/batches. Make sure that the column name in both tables are identical and syntactically valid (if you supply a character) or have the same index (if you supply a numeric). Note that characters are converted to syntactically valid names using make.names
name	For the single-set case, an optional character(1) to name the set in the QFeatures object. Default is quants.
removeEmptyCols	A logical(1). If TRUE, quantitative columns that contain only missing values are removed.
verbose	A logical(1) indicating whether the progress of the data reading and formatting should be printed to the console. Default is TRUE.

Details

The single- and multi-set cases are defined by the quantCols and runCol parameters, whether passed by the quantCols and runCol vectors and/or the colData data.frame (see below).

Single-set case:

The quantitative data variables are defined by the quantCols. The single-set case can be represented schematically as shown below.

```
|------+---------------+-----------|
| cols | quantCols 1..N | more cols |
| .    | ...            | ...       |
| .    | ...            | ...       |
| .    | ...            | ...       |
|------+---------------+-----------|
```

Note that every `quantCols` column contains data for a single sample. The single-set case is defined by the absence of any `runCol` input (see next section). We here provide a (non-exhaustive) list of typical data sets that fall under the single-set case:

- Peptide- or protein-level label-free data (bulk or single-cell).
- Peptide- or protein-level multiplexed (e.g. TMT) data (bulk or single-cell).
- PSM-level multiplexed data acquired in a single MS run (bulk or single-cell).
- PSM-level data from fractionation experiments, where each fraction of the same sample was acquired with the same multiplexing label.

Multi-set case:

A run/batch variable, `runCol`, is required to import multi-set data. The multi-set case can be represented schematically as shown below.

```
|--------+------+----------------+-----------|
| runCol | cols | quantCols 1..N | more cols |
|   1    | .    | ...            | ...       |
|   1    | .    | ...            | ...       |
|--------+------+----------------+-----------|
|   2    | .    | ...            | ...       |
|--------+------+----------------+-----------|
|   .    | .    | ...            | ...       |
|--------+------+----------------+-----------|
```

Every `quantCols` column contains data for multiple samples acquired in different runs. The multi-set case applies when `runCol` is provided, which will determine how the table is split into multiple sets.

We here provide a (non-exhaustive) list of typical data sets that fall under the multi-set case:

- PSM- or precursor-level multiplexed data acquired in multiple runs (bulk or single-cell)
- PSM- or precursor-level label-free data acquired in multiple runs (bulk or single-cell)
- DIA-NN data (see also `readQFeaturesFromDIANN()`).

Adding sample annotations with `colData`:

We recommend providing sample annotations when creating a `QFeatures` object. The `colData` is a table in which each row corresponds to a sample and each column provides information about the samples. There is no restriction on the number of columns and on the type of data they should contain. However, we impose one or two columns (depending on the use case) that allow to link the annotations of each sample to its quantitative data:

- Single-set case: the `colData` must contain a column named `quantCols` that provides the names of the columns in `assayData` containing quantitative values for each sample (see single-set cases in the examples).
- Multi-set case: the `colData` must contain a column named `quantCols` that provides the names of the columns in `assayData` with the quantitative values for each sample, and a column named `runCol` that provides the MS runs/batches in which each sample has been acquired. The entries in `colData[["runCol"]]` are matched against the entries provided by `assayData[[runCol]]`.

When the `quantCols` argument is not provided to `readQFeatures()`, the function will automatically determine the `quantCols` from `colData[["quantCols"]]`. Therefore, `quantCols` and `colData` cannot be both missing.

Samples that are present in `assayData` but absent `colData` will lead to a warning, and the missing entries will be automatically added to the `colData` and filled with `NA`s.

When using the `quantCols` and `runCol` arguments only (without `colData`), the `colData` contains zero columns/variables.

Feature names:

Assay feature (i.e. rownames) are important as they are used when assays are joined with `joinAssays()`. They can be set upon creation of the `QFeatures()` object by setting the `fnames` argument. See also `createPrecursorId()` in case a precursor identifier is note readily available and should be created from other, existing rowData variables.

Value

An instance of class `QFeatures` or `SummarizedExperiment::SummarizedExperiment()`. For the former, the quantitative sets of each run are stored in `SummarizedExperiment::SummarizedExperiment()` object.

Author(s)

Laurent Gatto, Christophe Vanderaa

See Also

- The `QFeatures` (see `QFeatures()`) class to read about how to manipulate the resulting `QFeatures` object.
- The `readQFeaturesFromDIANN()` function to import DIA-NN quantitative data.

Examples

```
#####################################
## Single-set case.

## Load a data.frame with PSM-level data
data(hlpsms)
hlpsms[1:10, c(1, 2, 10:11, 14, 17)]

## Create a QFeatures object with a single psms set
qf1 <- readQFeatures(hlpsms, quantCols = 1:10, name = "psms")
qf1
colData(qf1)

#####################################
## Single-set case with colData.

(coldat <- data.frame(var = rnorm(10),
                      quantCols = names(hlpsms)[1:10]))
qf2 <- readQFeatures(hlpsms, colData = coldat)
qf2
colData(qf2)

#####################################
```

```
## Multi-set case.

## Let's simulate 3 different files/batches for that same input
## data.frame, and define a colData data.frame.

hlpsms$file <- paste0("File", sample(1:3, nrow(hlpsms), replace = TRUE))
hlpsms[1:10, c(1, 2, 10:11, 14, 17, 29)]

qf3 <- readQFeatures(hlpsms, quantCols = 1:10, runCol = "file")
qf3
colData(qf3)


#####################################
## Multi-set case with colData.

(coldat <- data.frame(runCol = rep(paste0("File", 1:3), each = 10),
                      var = rnorm(10),
                      quantCols = names(hlpsms)[1:10]))
qf4 <- readQFeatures(hlpsms, colData = coldat, runCol = "file")
qf4
colData(qf4)
```

`readQFeaturesFromDIANN` *Read DIA-NN output as a QFeatures objects*

Description

This function takes the `Report.tsv` output files from DIA-NN and converts them into a multi-set `QFeatures` object. It is a wrapper around `readQFeatures()` with default parameters set to match DIA-NN label-free and plexDIA report files: default `runCol` is `"File.Name"` and default quantColsis"Ms1.Area"‘.

Usage

```
readQFeaturesFromDIANN(
  assayData,
  colData = NULL,
  quantCols = "Ms1.Area",
  runCol = "File.Name",
  multiplexing = c("none", "mTRAQ", "dimethyl"),
  extractedData = NULL,
  ecol = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

assayData	A data.frame, or any object that can be coerced into a data.frame, holding the quantitative assay. For readSummarizedExperiment(), this can also be a character(1) pointing to a filename. This data.frame is typically generated by an identification and quantification software, such as Sage, Proteome Discoverer, MaxQuant, ...
colData	A data.frame (or any object that can be coerced to a data.frame) containing sample/column annotations, including quantCols and runCol (see details).
quantCols	A numeric(), logical() or character() defining the columns of the assayData that contain the quantitative data. This information can also be defined in colData (see details).
runCol	For the multi-set case, a numeric(1) or character(1) pointing to the column of assayData (and colData, is set) that contains the runs/batches. Make sure that the column name in both tables are identical and syntactically valid (if you supply a character) or have the same index (if you supply a numeric). Note that characters are converted to syntactically valid names using make.names
multiplexing	A character(1) indicating the type of multiplexing used in the experiment. One of "none" (default, for label-free experiments), "mTRAQ" (for multiplex experiments with mTRAQ labeling) or "dimethyl" (for multiplex experiments with dimethyl labeling).
extractedData	A data.frame or any object that can be coerced to a data.frame that contains the data from the *_ms1_extracted.tsv file generated by DIA-NN. This argument is optional and is currently only applicable for mTRAQ multiplexed experiments where DIA-NN was run using the plexdia module (see references).
ecol	Same as quantCols. Available for backwards compatibility. Default is NULL. If both ecol and colData are set, an error is thrown.
verbose	A logical(1) indicating whether the progress of the data reading and formatting should be printed to the console. Default is TRUE.
...	Further arguments passed to readQFeatures().

Value

An instance of class QFeatures. The quantiative data of each acquisition run is stored in a separate set as a SummarizedExperiment object.

Author(s)

Laurent Gatto, Christophe Vanderaa

References

Derks, Jason, Andrew Leduc, Georg Wallmann, R. Gray Huffman, Matthew Willetts, Saad Khan, Harrison Specht, Markus Ralser, Vadim Demichev, and Nikolai Slavov. 2022. "Increasing the Throughput of Sensitive Proteomics by plexDIA." Nature Biotechnology, July. Link to article

See Also

- The QFeatures (see QFeatures()) class to read about how to manipulate the resulting QFeatures object.
- The readQFeatures() function which this one depends on.

Examples

```
x <- read.delim(MsDataHub::benchmarkingDIA.tsv())
x[["File.Name"]] <- x[["Run"]]

################################
## Label-free multi-set case

## using default arguments
readQFeaturesFromDIANN(x)

## use the precursor identifier as assay rownames
readQFeaturesFromDIANN(x, fnames = "Precursor.Id") |>
    rownames()

## with a colData (and default arguments)
cd <- data.frame(sampleInfo = LETTERS[1:24],
                 quantCols = "Ms1.Area",
                 runCol = unique(x[["File.Name"]]))
readQFeaturesFromDIANN(x, colData = cd)

################################
## mTRAQ multi-set case

x2 <- read.delim(MsDataHub::Report.Derks2022.plexDIA.tsv())
x2[["File.Name"]] <- x2[["Run"]]
readQFeaturesFromDIANN(x2, multiplexing = "mTRAQ")
```

---

reduceDataFrame *Reduces and expands a* DataFrame

Description

A long dataframe can be *reduced* by mergeing certain rows into a single one. These new variables are constructed as a SimpleList containing all the original values. Invariant columns, i.e columns that have the same value along all the rows that need to be merged, can be shrunk into a new variables containing that invariant value (rather than in list columns). The grouping of rows, i.e. the rows that need to be shrunk together as one, is defined by a vector.

The opposite operation is *expand*. But note that for a DataFrame to be expanded back, it must not to be simplified.

Usage

```
reduceDataFrame(x, k, count = FALSE, simplify = TRUE, drop = FALSE)

expandDataFrame(x, k = NULL)
```

Arguments

x	The DataFrame to be reduced or expanded.
k	A 'vector' of length nrow(x) defining the grouping based on which the DataFrame will be shrunk.
count	logical(1) specifying of an additional column (called by default .n) with the tally of rows shrunk into on new row should be added. Note that if already existing, .n will be silently overwritten.
simplify	A logical(1) defining if invariant columns should be converted to simple lists. Default is TRUE.
drop	A logical(1) specifying whether the non-invariant columns should be dropped altogether. Default is FALSE.

Value

An expanded (reduced) DataFrame.

Missing values

Missing values do have an important effect on reduce. Unless all values to be reduces are missing, they will result in an non-invariant column, and will be dropped with drop = TRUE. See the example below.

The presence of missing values can have side effects in higher level functions that rely on reduction of DataFrame objects.

Author(s)

Laurent Gatto

Examples

```
library("IRanges")

k <- sample(100, 1e3, replace = TRUE)
df <- DataFrame(k = k,
                x = round(rnorm(length(k)), 2),
                y = seq_len(length(k)),
                z = sample(LETTERS, length(k), replace = TRUE),
                ir = IRanges(seq_along(k), width = 10),
                r = Rle(sample(5, length(k), replace = TRUE)),
                invar = k + 1)
df

## Shinks the DataFrame
```

```
df2 <- reduceDataFrame(df, df$k)
df2

## With a tally of the number of members in each group
reduceDataFrame(df, df$k, count = TRUE)

## Much faster, but more crowded result
df3 <- reduceDataFrame(df, df$k, simplify = FALSE)
df3

## Drop all non-invariant columns
reduceDataFrame(df, df$k, drop = TRUE)

## Missing values
d <- DataFrame(k = rep(1:3, each = 3),
               x = letters[1:9],
               y = rep(letters[1:3], each = 3),
               y2 = rep(letters[1:3], each = 3))
d

## y is invariant and can be simplified
reduceDataFrame(d, d$k)
## y isn't not dropped
reduceDataFrame(d, d$k, drop = TRUE)

## BUT with a missing value
d[1, "y"] <- NA
d

## y isn't invariant/simplified anymore
reduceDataFrame(d, d$k)
## y now gets dropped
reduceDataFrame(d, d$k, drop = TRUE)
```

`subsetByFeature` *Subset by feature name*

Description

This function will find the assays and features that match directly (by name) or indirectly (through aggregation) the feature name.

The `subsetByFeature` function will first identify the assay that contains the feature(s) `i` and filter the rows matching these feature names exactly. It will then find, in the other assays, the features that produces `i` through aggregation with the `aggregateQFeatures` function.

See QFeatures for an example.

Arguments

`x`	An instance of class QFeatures.

y	A character of feature names present in an assay in x.
...	Additional parameters. Ignored.

Value

An new instance of class QFeatures containing relevant assays and features.

Examples

```
example(aggregateFeatures)

## Retrieve protein 'ProtA' and its 2 peptides and 6 PSMs
feat1["ProtA", , ]
```

---

unfoldDataFrame *Unfold a data frame*

Description

A data frame is said to be *folded* when some cells contain multiple elements. These are often encode as a semi-colon separated character , such as `"a;b"`. This function will transform the data frame to that `"a"` and `"b"` are split and recorded across two lines.

The simple example below illustrates a trivial case, where the table below

X	Y
1	a;b
2	c

is unfolded based on the Y variable and becomes

X	Y
1	a
1	b
2	c

where the value 1 of variable X is now duplicated.

If there is a second variable that follows the same pattern as the one used to unfold the table, it also gets unfolded.

X	Y	Z
1	a;b	x;y
2	c	z

becomes

X	Y	Z
1	a	x
1	b	y
2	c	z

because it is implied that the element in "a;b" are match to "x;y" by their respective indices. Note in the above example, unfolding by Y or Z produces the same result.

However, the following table unfolded by Y

X	Y	Z
1	a;b	x;y
2	c	x;y

produces

X	Y	Z
1	a	x;y
1	b	x;y
2	c	x;y

because "c" and "x;y" along the second row don't match. In this case, unfolding by Z would produce a different result. These examples are also illustrated below.

Note that there is no `foldDataFrame()` function. See `reduceDataFrame()` and `expandDataFrame()` to flexibly encode and handle vectors of length > 1 within cells.

Usage

```
unfoldDataFrame(x, k, split = ";")
```

Arguments

`x`	A `DataFrame` or `data.frame` to be unfolded.
`k`	`character(1)` referring to a character variable in `x`, that will be used to unfold `x`.
`split`	`character(1)` passed to `strsplit()` to split `x[[k]]`.

Value

A new object unfolded object of class `class(x)` with numbers of rows >= `nrow(x)` and columns identical to `x`.

Author(s)

Laurent Gatto

Examples

```
(x0 <- DataFrame(X = 1:2, Y = c("a;b", "c")))
unfoldDataFrame(x0, "Y")

(x1 <- DataFrame(X = 1:2, Y = c("a;b", "c"), Z = c("x;y", "z")))
unfoldDataFrame(x1, "Y")
unfoldDataFrame(x1, "Z") ## same

(x2 <- DataFrame(X = 1:2, Y = c("a;b", "c"), Z = c("x;y", "x;y")))
unfoldDataFrame(x2, "Y")
unfoldDataFrame(x2, "Z") ## different
```

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