Package ‘QFeatures’

May 30, 2024

Title  Quantitative features for mass spectrometry data
Version  1.14.1
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.

Depends  R (>= 4.0), MultiAssayExperiment
Imports  methods, stats, utils, S4Vectors, IRanges, SummarizedExperiment, BiocGenerics, ProtGenerics (>= 1.35.1), AnnotationFilter, lazyeval, Biobase, MsCoreUtils (>= 1.7.2), igraph, grDevices, plotly, tidyselect, reshape2
Suggests  SingleCellExperiment, MsDataHub (>= 1.3.3), Matrix, HDF5Array, msdata, ggplot2, gplots, dplyr, limma, DT, shiny, shinydashboard, testthat, knitr, BiocStyle, rmarkdown, vsn, preprocessCore, matrixStats, imputeLCMD, pcaMethods, impute, norm, ComplexHeatmap
biocViews  Infrastructure, MassSpectrometry, Proteomics, Metabolomics
License  Artistic-2.0
Encoding  UTF-8
VignetteBuilder  knitr
BugReports  https://github.com/RforMassSpectrometry/QFeatures/issues
Collate  'AllGenerics.R' 'AssayLinks.R' 'QFeatures-class.R'
          'QFeatures-functions.R' 'QFeatures-processing.R'
          'QFeatures-filter.R' 'QFeatures-missing-data.R'
          'QFeatures-aggregation.R' 'QFeatures-imputation.R'
          'QFeatures-join.R' 'QFeatures-validity.R'
          'SummarizedExperiment-methods.R' 'subsetBy-methods.R'
          'readQFeatures.R' 'readQFeaturesFromDIANN.R' 'data.R'
          'reduce.R' 'utils.R' 'display.R'
aggregateFeatures

Aggregate an assay’s quantitative features
aggregateFeatures

Description

This function aggregates the quantitative features of an assay, 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 either be a vector (we then refer to an aggregation by vector) or an adjacency matrix (aggregation by matrix).

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

When aggregating with a vector, the newly aggregated SummarizedExperiment assay 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.

Usage

```r
## 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 assay. This variable is either a character or a (possibly sparse) matrix. See below for details.
- **name**: A character(1) naming the new assay. 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".

class 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 generated by the 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 fit 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 performs 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 `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

```r
## 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]])
aggrcounts(feat1[[2]])
assay(feat1[[3]])
aggrcounts(feat1[[3]])

## Aggregation with missing quantitative values
## --------------------------------------------
```
aggregateFeatures

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 an adjacency 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),

## 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 an adjacency 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),


adj[c("ProtA", "ProtB")]
adj

adjacencyMatrix(se) <- adj
rowData(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

\texttt{assayLink} returns an instance of class \texttt{AssayLink}.
\texttt{assayLinks} returns an instance of class \texttt{AssayLinks}.

Constructors

Object can be created with the \texttt{AssayLink()} and \texttt{AssayLinks()} constructors.

Methods and functions

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

Creating links between assays

- \texttt{addAssayLink} takes a parent assay and a child assay contained in the \texttt{QFeatures} object and creates a link given a matching feature variable in each assay’s \texttt{rowData}. \texttt{addAssayLink} also allows to link an assay from multiple parent assays (see examples below).
- \texttt{addAssayLinkOneToOne} links two assays contained in the \texttt{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 \texttt{rowData}. Providing multiple parents is not supported.

Examples

```r
#----------------------------------
# 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

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 currently 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

```r
## 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 a 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 assay 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)
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


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", mmar = "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"))
**Description**

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

**Usage**

```r
joinAssays(x, i, name = "joinedAssay")
```

**Arguments**

- **x**: An instance of class QFeatures.
- **i**: The indices or names of at 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.

**Details**

The rows to be joined are chosen based on the rownames of the respective assays. It is the user's responsibility to make sure these are meaningful, such as for example referring to unique 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

```r
# An example QFeatures with 3 assays to be joined
data(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 in all
# assays, the values for the shared rows are different.
rowData(feat2["joinedAssay"])
```

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 normal-
  ization.
• 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.
## filterNA

### 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 QFeatures instances.

### Examples

```r
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)
```

### 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.

---

<table>
<thead>
<tr>
<th>QFeatures</th>
<th>Quantitative MS QFeatures</th>
</tr>
</thead>
</table>

---
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 responsibility 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)

## 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

longFormat(object, colvars = NULL, rowvars = NULL, index = 1L)
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.
QFeatures

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.

colvars A character() that selects column(s) in the colData.

index The assay indicator within each SummarizedExperiment object. A vector input is supported in the case that the SummarizedExperiment object(s) has more than one assay (default 1L)

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 responsibility 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 `longFormat` accessor takes a `QFeatures` object and returns it in a long format DataFrame. Each quantitative value is reported on a separate line. `colData` and `rowData` data can also be added. This function is an extension of the `longFormat` function in the `MultiAssayExperiment::MultiAssayExperiment`.

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 `colData(y)` and `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
QFeatures

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 row-Data.
- 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

```r
## ------------------------
## 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)

e1 <- list(assay1 = se1, assay2 = se2)
fts1 <- QFeatures(e1, colData = cd)
fts1
fts1[[1]]
fts1["assay1"]

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

Filter features based on their rowData

Description
The `filterFeatures` method 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
```r
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, ...)

Arguments

- `field` character(1) referring 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 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.

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 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.

Author(s)

Laurent Gatto

See Also

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

## Creating character and numeric variable filters

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

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

e.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 forumula interface, exact match
filterFeatures(feat1, ~ location == "Mitochondrion")

## using the forumula interface, 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"))

## 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% c("Mitochondrion", NA)))[[1]])
rowData(filterFeatures(Feat1, ~ location %in% c("Mitochondrion", NA)))[[1]])

# Explicit handling
filterFeatures(Feat1, ~ !is.na(location) & location == "Mitochondrion")

# Using the pipe operator
feat1 |>
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:

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

See the \textit{Processing} vignette for examples.

Usage

\begin{verbatim}
## 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, \ldots)

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

## S4 method for signature 'SummarizedExperiment'
sweep(x, MARGIN, STATS, FUN = ",", check.margin = TRUE, \ldots)
\end{verbatim}
## 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 `scaleTransform` 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.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
An processed object of the same class as x or object.

Examples
MsCoreUtils::normalizeMethods()

---

readQFeatures QFeatures from tabular data

Description
These functions convert tabular data into dedicated data objects. The readSummarizedExperiment() function takes a file name or data.frame and converts it into a 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

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

- **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`, if 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 NAs.

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

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)
```

---

**ReadDIA-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 quantCols is "Ms1.Area".

**Usage**

```
readQFeaturesFromDIANN(
  assayData,
  colData = NULL,
)```
readQFeaturesFromDIANN

```r
quantCols = "Ms1.Area",
runcol = "File.Name",
multiplexing = c("none", "mTRAQ"),
extimatedData = 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`, if 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) or "mTRAQ" (for plexDIA experiments).

- **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 quantitative data of each acquisition run is stored in a separate set as a `SummarizedExperiment` object.

Author(s)

Laurent Gatto, Christophe Vanderaa
reduceDataFrame

Reduces and expands a DataFrame

Description

A long dataframe can be reduced by merging 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.
reduceDataFrame

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
subsetByFeature <- reduceDataFrame(df, df$k)

## 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)

## 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.
**unfoldDataFrame**

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**

```r
eexample(aggregateFeatures)

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

---

**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

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>a;b</td>
</tr>
<tr>
<td>2</td>
<td>c</td>
</tr>
</tbody>
</table>

is unfolded based on the Y variable and becomes

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>a</td>
</tr>
<tr>
<td>1</td>
<td>b</td>
</tr>
<tr>
<td>2</td>
<td>c</td>
</tr>
</tbody>
</table>

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.

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>a;b</td>
<td>x;y</td>
</tr>
<tr>
<td>2</td>
<td>c</td>
<td>z</td>
</tr>
</tbody>
</table>
becomes

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>a</td>
<td>x</td>
</tr>
<tr>
<td>1</td>
<td>b</td>
<td>y</td>
</tr>
<tr>
<td>2</td>
<td>c</td>
<td>z</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>a;b</td>
<td>x;y</td>
</tr>
<tr>
<td>2</td>
<td>c</td>
<td>x;y</td>
</tr>
</tbody>
</table>

produces

<table>
<thead>
<tr>
<th>X</th>
<th>Y</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>a</td>
<td>x;y</td>
</tr>
<tr>
<td>1</td>
<td>b</td>
<td>x;y</td>
</tr>
<tr>
<td>2</td>
<td>c</td>
<td>x;y</td>
</tr>
</tbody>
</table>

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

```r
(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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